# Sequencing Technologies

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# This is bioinformatics

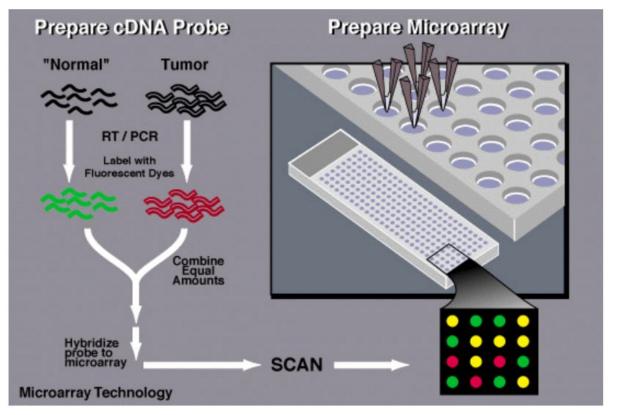




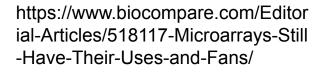
https://www.smithsonianmag.com/g ames/spot-difference-180968040/



Expression profiling with sequencing vs microarrays What are the advantages and disadvantages? What applications are best for each platform?



New Mexico INBRE IDEA Networks of Biomedical Research Excellence







10,000.000 1,000.000 Moore's Law 100.000 10.000 1.000 0.100 National Human Genome NIF Research Institute 0.010

genome.gov/sequencingcosts

2003

2004

2005

2006

2007

2008

2009

2010

2011

2012

2013

2014

2015

2016

2017

2018

2019 2020

0.001

2001

2002

#### Cost per Raw Megabase of DNA Sequence







# Barriers

Over 99% of physicians, 20.5% of whom worked in an academic setting, reported using NGS in the past 12 months, and 73.0% used NGS always or most of the time. Despite this high utilization, 80.1% of physicians experienced at least one barrier to testing.

Survey study of barriers to evidence-based decision-making in oncology care using next-generation sequencing.

( Check for updates

<u>Elizabeth A. Szamreta, Allysen Kaminski, Ruchit Shah, Ning Ning, Jyoti Aggarwal, Arif</u> <u>Hussain</u>, ...



Percentage of Physicians Reporting Each Barrier to Optimizing Clinical Impact and Utility of NGS in Routine Clinical Practice by Physician Specialty, %.

	Total	Oncology/Hematology	Pathology	Surgery
Barrier				
	(N= 201)	(N=100)	(N=51)	(N=50)
Reimbursement Challenges	87.5	85.0	90.2	90.0
Knowledge/Awareness	81.0	75.0	82.4	92.0
Evidence of clinical utility	80.1	79.0	78.4	84.0
Availability of Supportive Resources	79.6	73.0	82.4	90.0
Logistical Barriers	77.2	73.0	72.6	90.0
© 2021 by American Socie	ty of Clir	nical Oncology		

National Center for Genome Resources

R

What barriers to utilizing next generation sequencing and analysis have you experienced or seen others experience?











# NGS applications

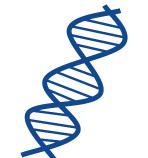




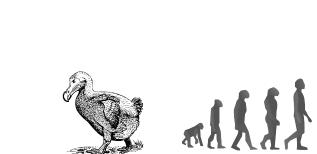
- → Genetic and genomic medicine
- → Microbiology and the environment (microbiomes and microbiota)
- → Pharmacogenetics (genetic variation and drug responses)
- → Forensics
- → Agriculture (improvement, protection)
- → Physical performance
- → Evolution
- → Extinction
- → Ecology
- → Geneology and phylogeny



E E E













Sequencing related to expression

RNA is usually converted first to cDNA then sequenced



mRNA Full-length mRNA Isoforms Nascent transcription miRNA or small RNAs Single cell **Spatial transcriptomics** Methylation and other DNA modifications Histones and histone modifications Open chromatin **Transcription Factor Binding Sites** Stranded RNA

. . .



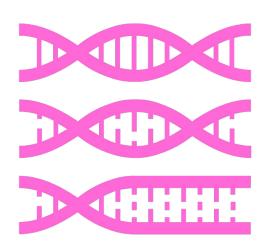
# Next Generation (NGS) Sequencing Technologies

Short Read Sanger Illumina

Long Read

PacBio

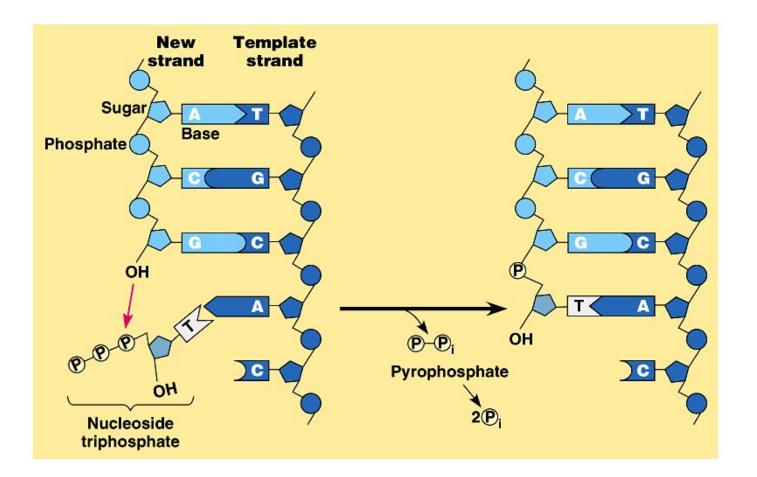
**Oxford Nanopore Technologies** 







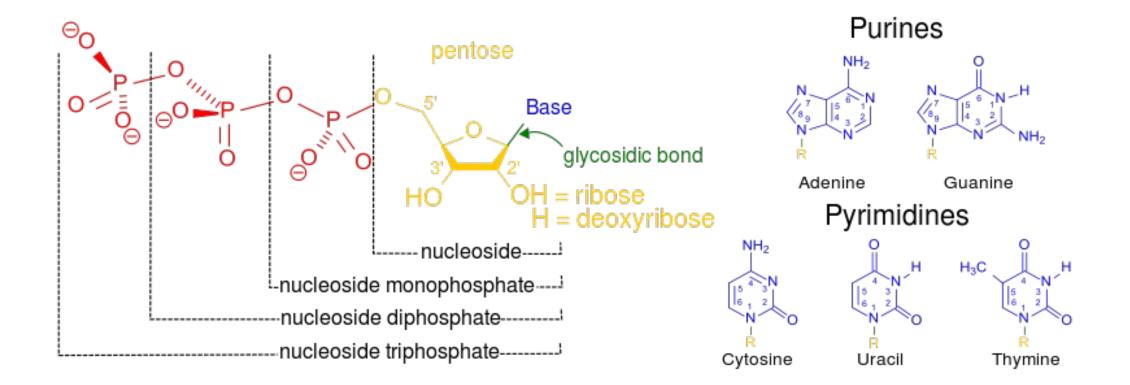
# Most sequencing technologies are based on DNA replication







# **DNA chemistry**

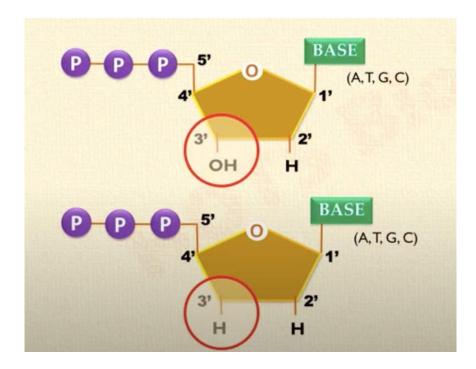


http://en.wikipedia.org/wiki/File:Nucleotides 1.svg





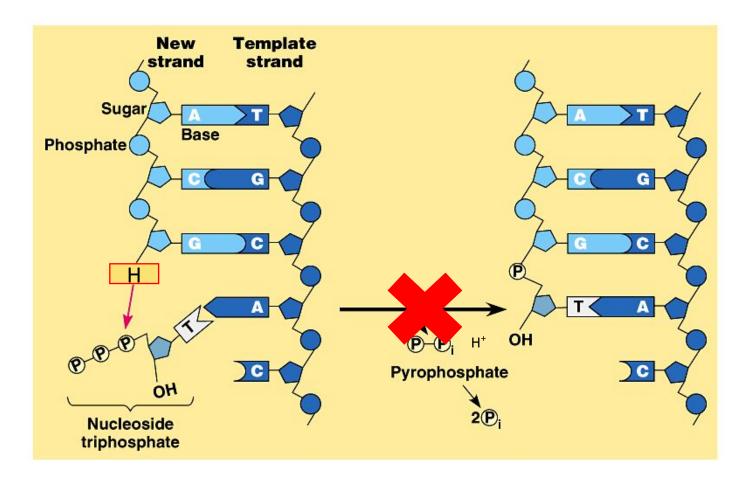
# Sanger sequencing uses dideoxy nucleotides







# ddNTPs prevent polymerization

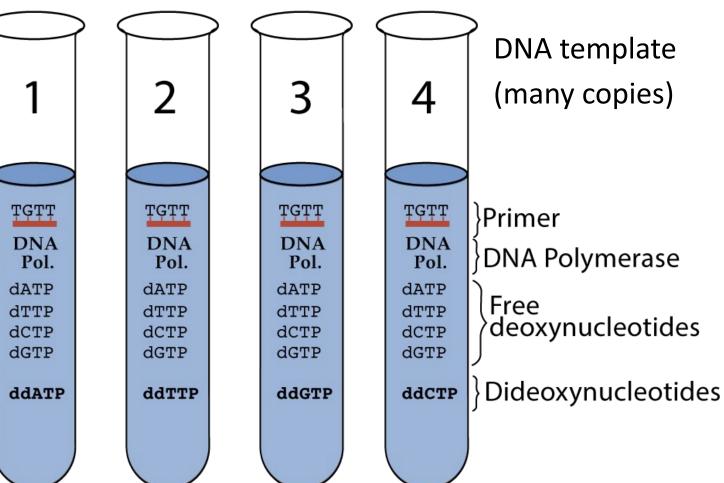






# The basis of Sanger sequencing

Different type of ddNTP's in each reaction (small amounts)





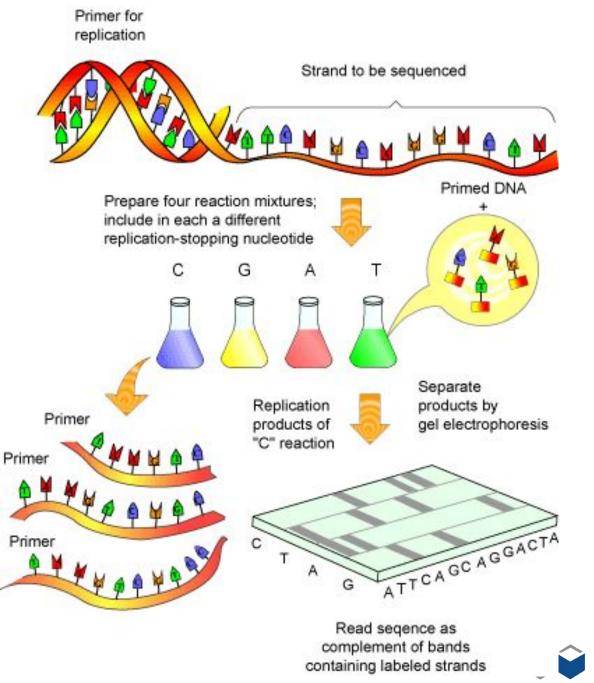


## Sanger sequencing



**New Mexico** 

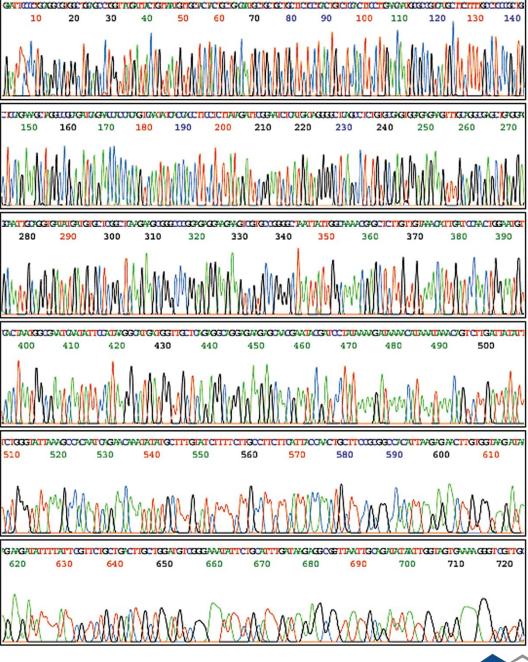
DeA Networks of Biomedical Research Excellence





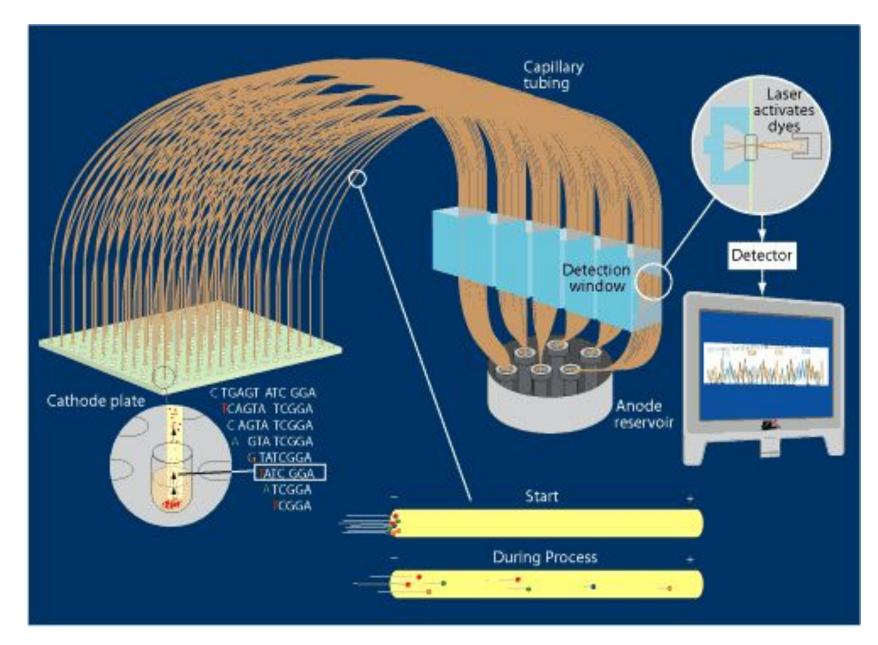


# Sanger output













# Human Genome Sequence

- •13 years (1990-2003)
- •\$2.7 B







# Illumina Sequencing Machines

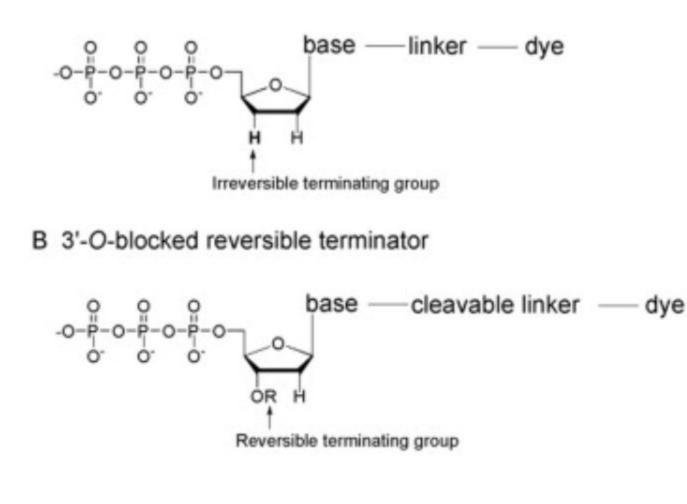






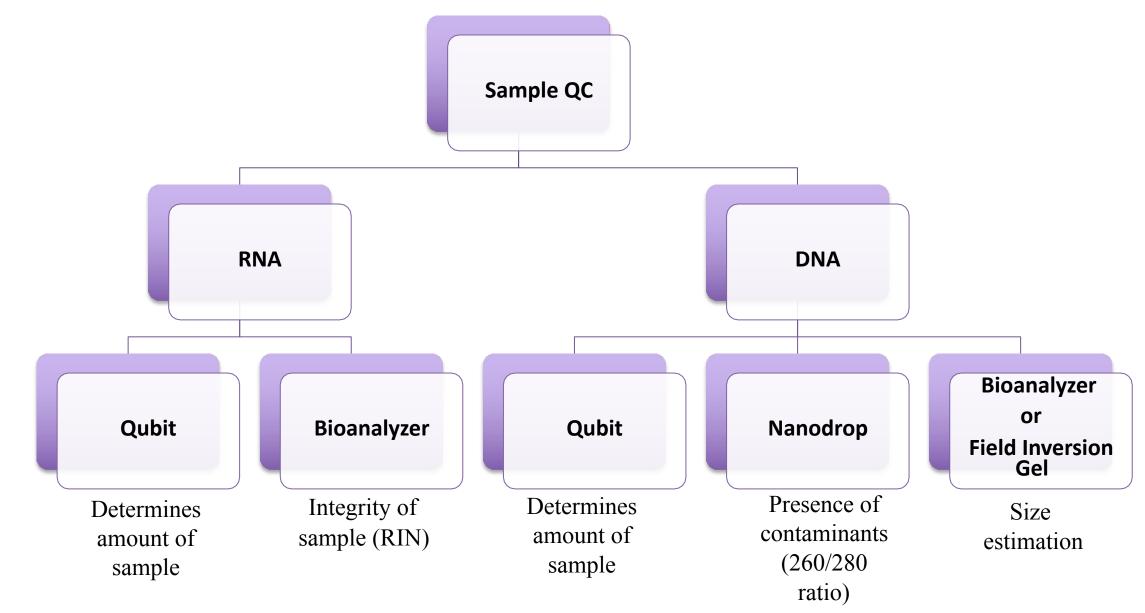
# **Reversible terminator**

A Sanger cleavable fluorescent dideoxynucleotide













#### Qubit



Fluorometer: Uses intercalating dye and is more accurate than UV absorbance based measurements such as with nanodrop

#### Nanodrop

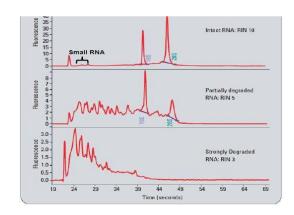


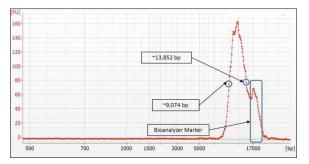
#### Bioanalyzer



Measure	Re-blank Blank	Print Screen Recording Print Report Show Report	Measurement complete	User	11/09/2009 15:44 Default	Ex
1.59 - 1.50 - 1.40 - 1.30 - 1.20 - 1.10 -	Ove	erlay control <u>Clear graph eac</u>	n Sample 🔻		Sample DNA-	50
1.00 0.90 0.80 0.80 0.80 0.80 0.80 0.80 0					A-260 10 mm path	0.775 1.425 0.769

#### 260/230 and 260/280 ratios.

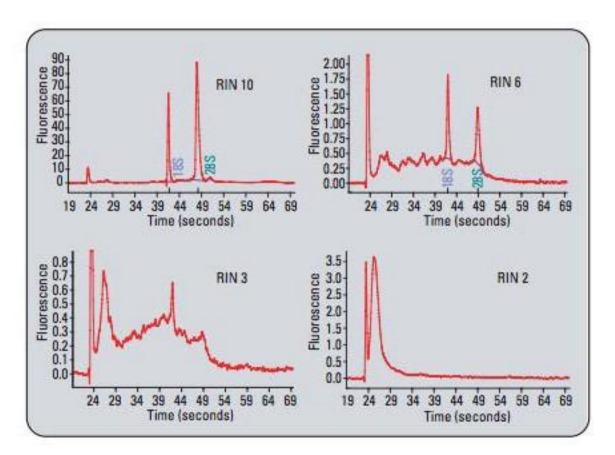








# Agilent Bioanalyzer examples



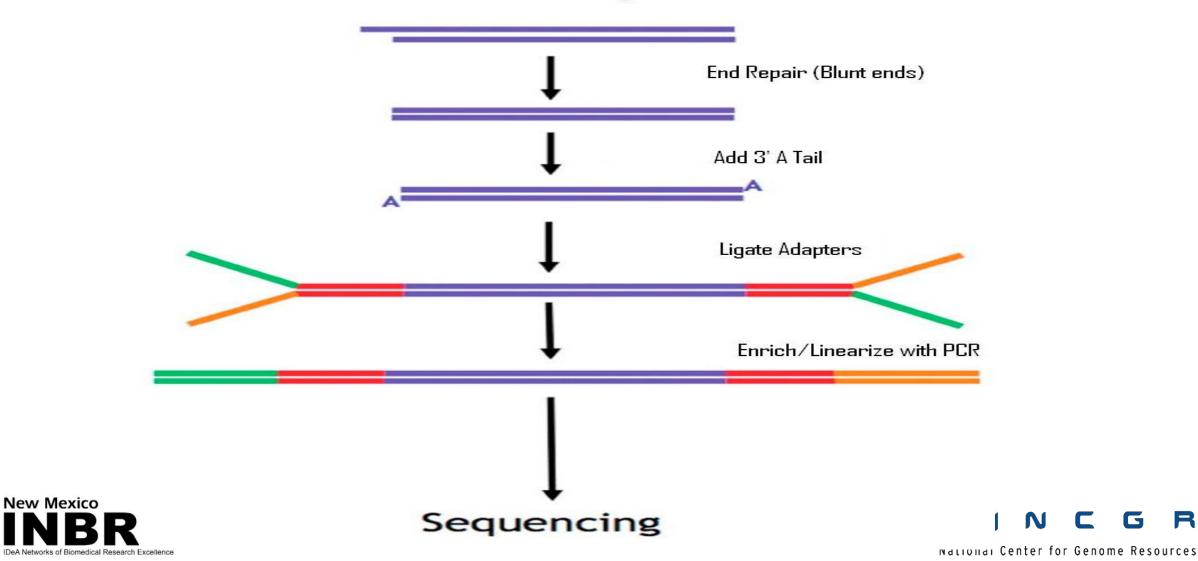
http://www.agilent.com/cs/library/applications/5989-1165EN.pdf





# Illumina library architecture

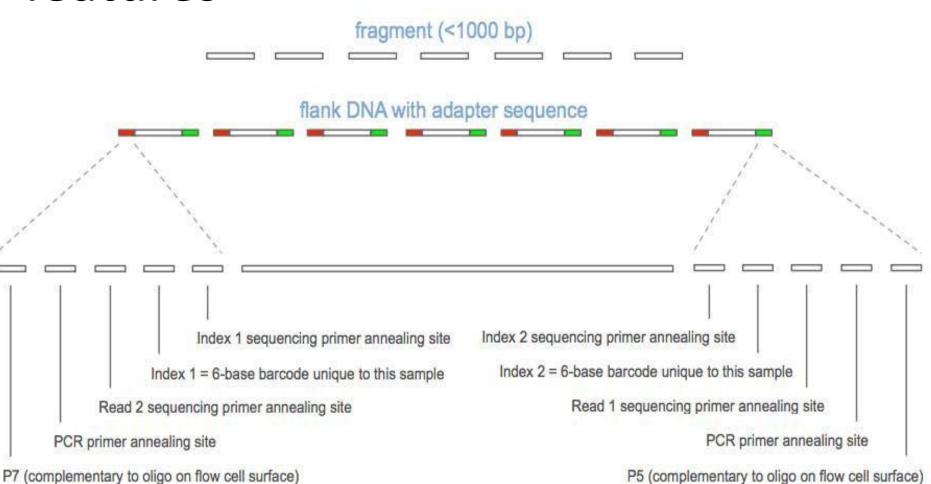
Shear Genomic DNA or begin with cDNA



R



# Adapter features



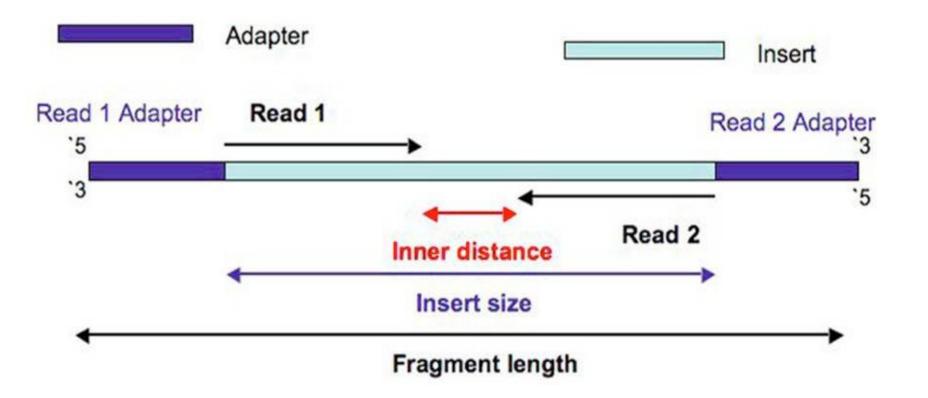
isolate DNA (or RNA)



https://www.youtube.com/watch?v=fCd6B5HRaZ8



# Commonly used terms







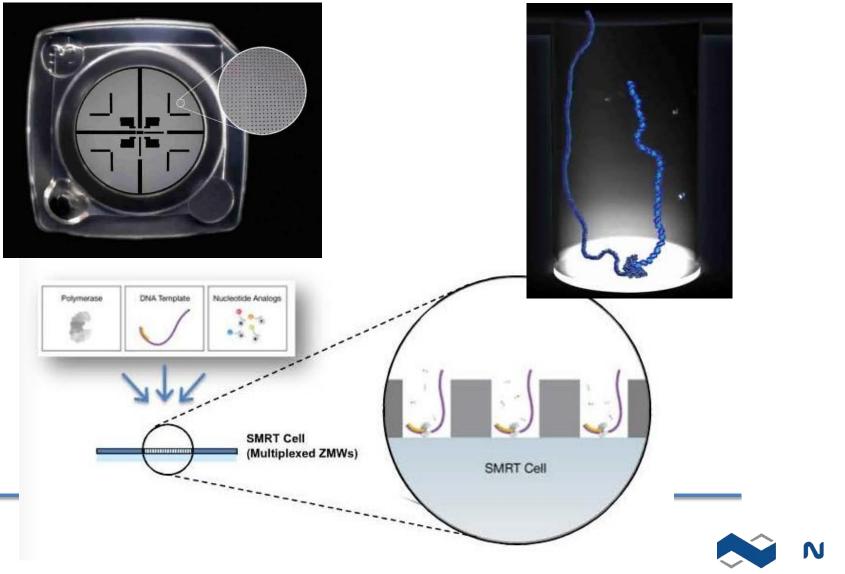
# **Pacific Biosciences**







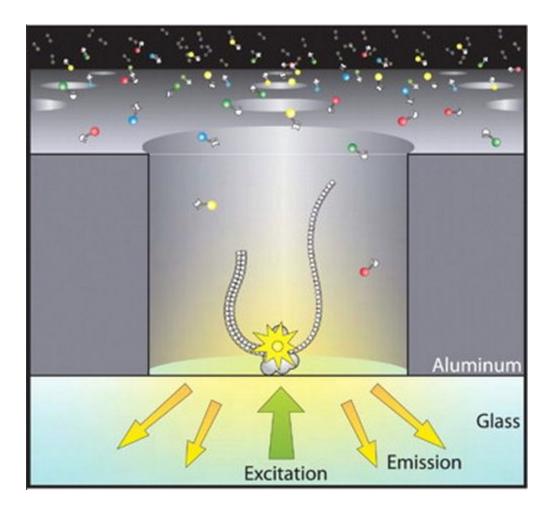
# Single Molecule Real Time (SMRT)





National Center for Genome Resources

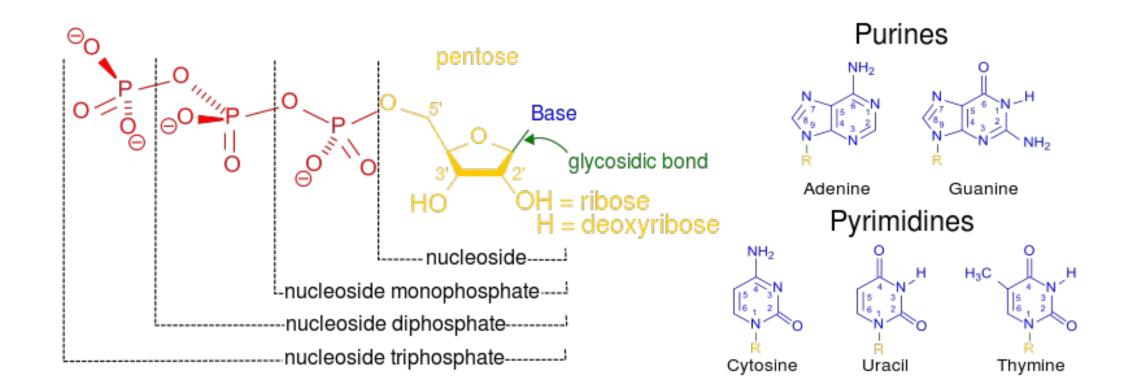
# Zero Mode Waveguide







# Fluorescence

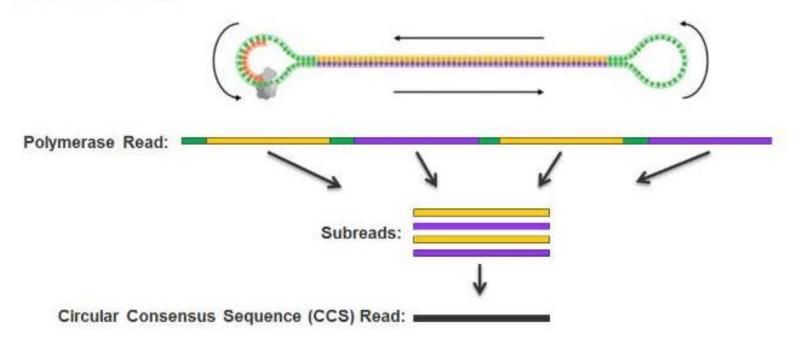






# PacBio Terminology

Read Terminology



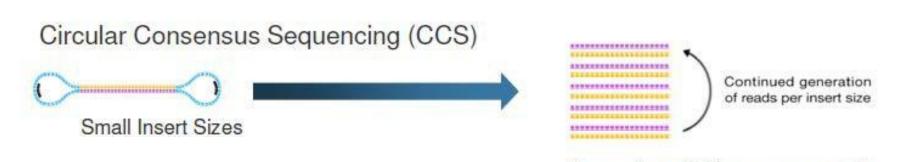




# PacBio Terminology

Standard Sequencing for Continuous Long Reads (CLR)





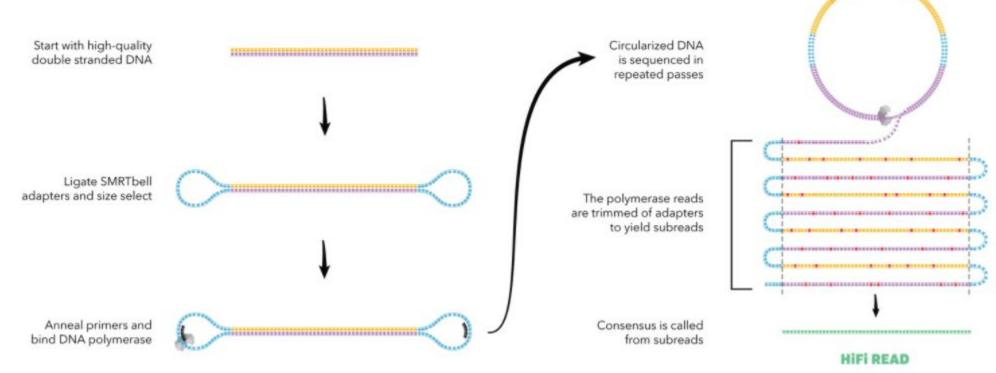
Generates multiple passes on each molecule sequenced





# PacBio Terminology

#### How are HiFi Reads Generated?



>99.9% accuracy

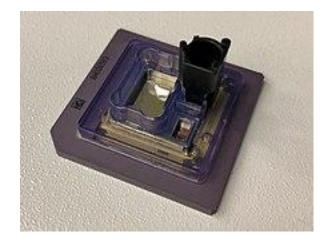




# PacBio development



RS II

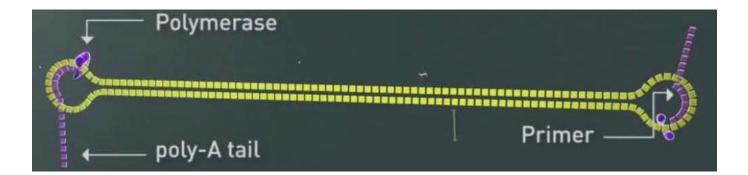


Sequel



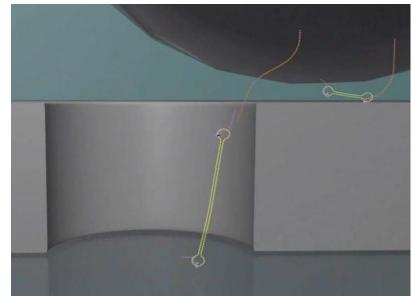


# Magnetic bead loading



http://www.youtube.com/watch?v=1b7UeGu9xa8

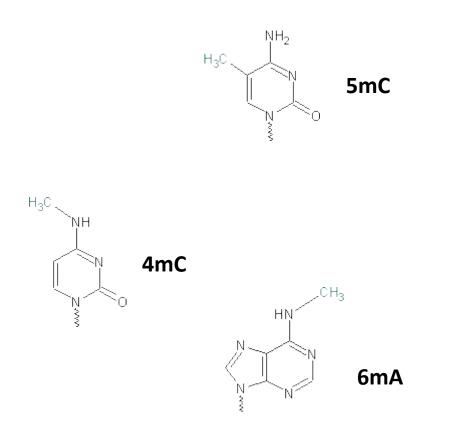








#### Base modification detection



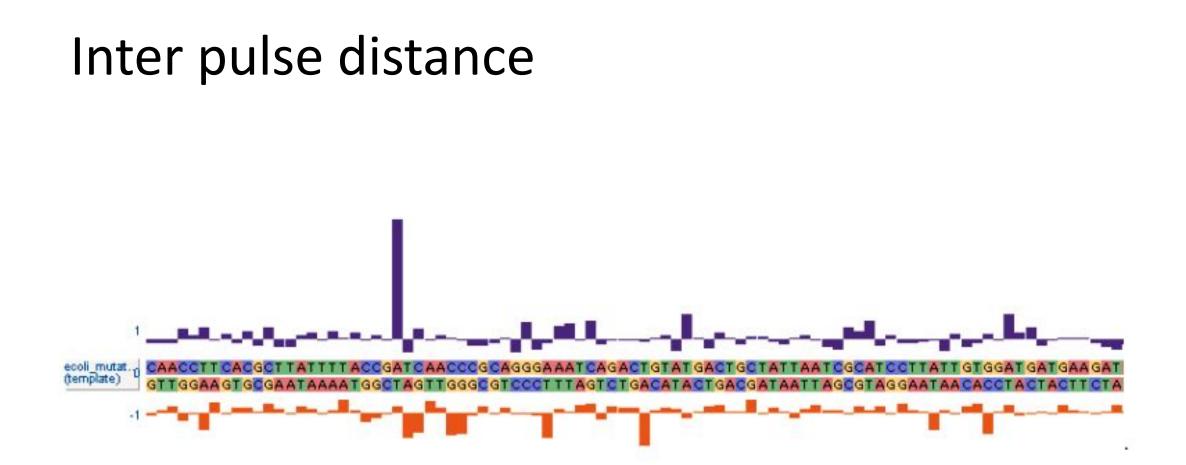
**Chemical Modifications:** •5mC •5hmC •4mC •5fC •6mA DNA Damage: •8oxoG •06mG •5hC



•04mT



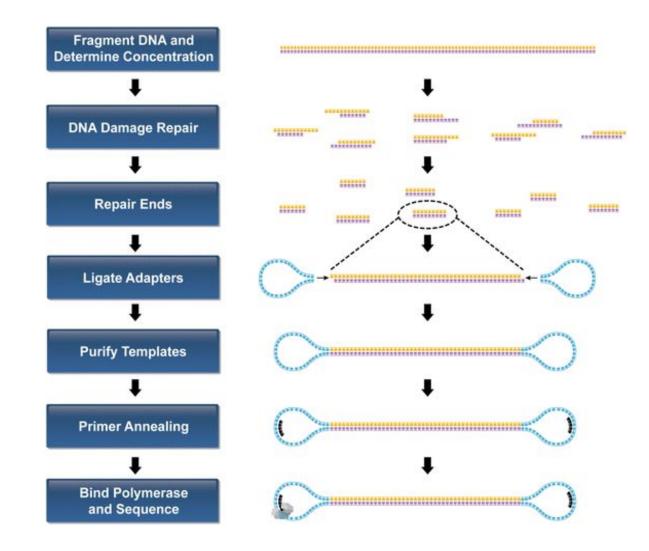








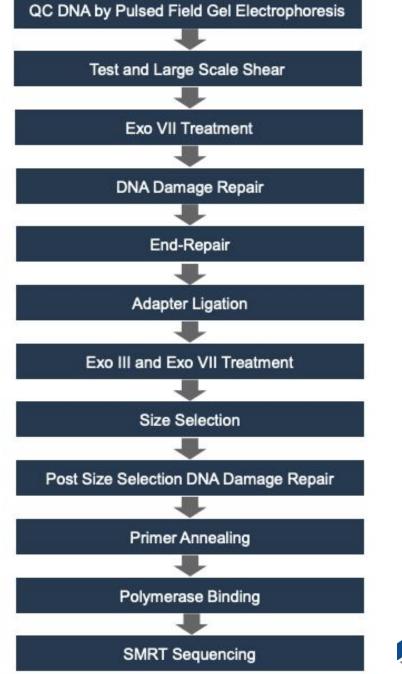
# Library construction







#### More recent example

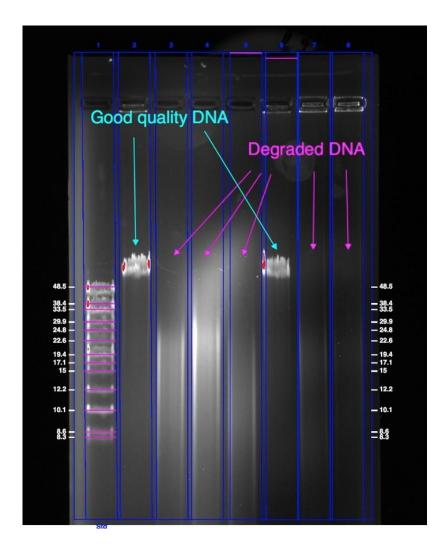






# Verify quality of DNA

- Qubit
  - Accurate quantification
- Field Inversion Gel
  - Verify DNA integrity

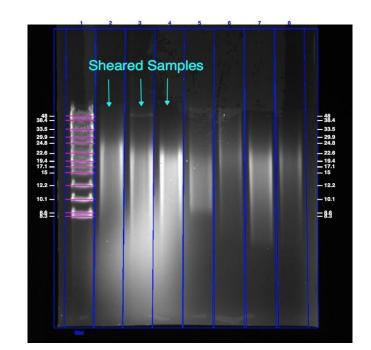






# **DNA** Shearing

- Covaris g-tube
- Centrifugation
- Synthetic ruby pore
- 4-20 kb









# **DNA** Shearing

- Diagenode megaruptor
- Hydropore
- Controlled flow rate
- 20-75 kb





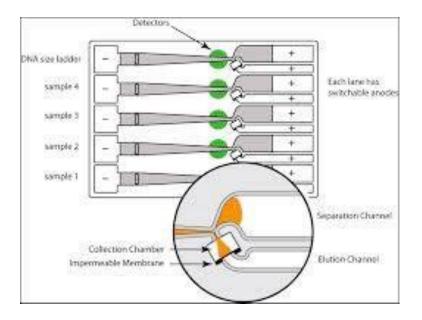


# Size Selection

- Sage Sciences Blue Pippin
- Automated sample collection
- Replaced gel purification



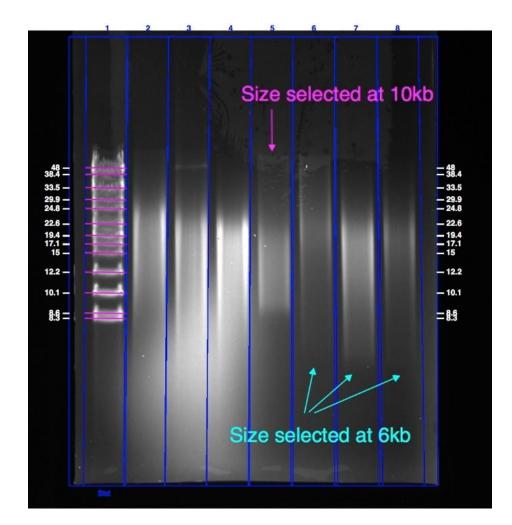








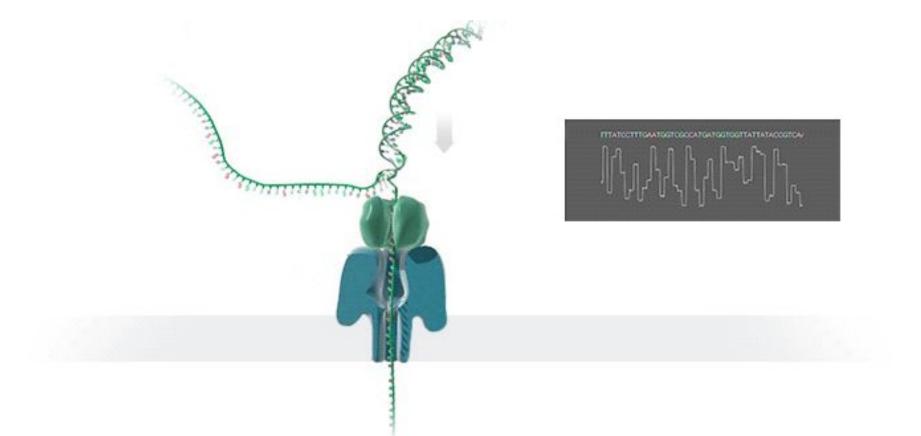
#### Before and after size selection







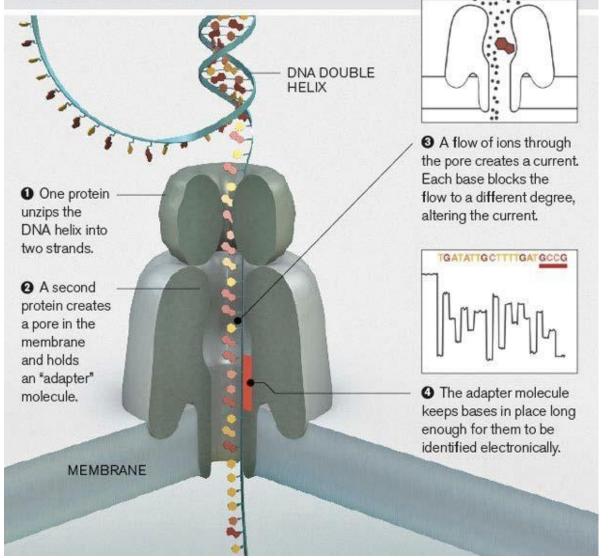
#### **Oxford Nanopore Technologies**







DNA can be sequenced by threading it through a microscopic pore in a membrane. Bases are identified by the way they affect ions flowing through the pore from one side of the membrane to the other.



https://youtu.be/GUb1TZ vMWsw

https://www.youtube.co m/watch?v=CGWZvHIi3i0





# Minlon

#### MinION SEQUENCER - USB DEVICE AND FLOWCELL



"The MinION *FlowCell* contains the proprietary sensor array which includes the Nanopores that are needed to perform a complete single-molecule sensing experiment. It also has the *Application-Specific Integrated Circuit* (*ASIC*) used to capture the Nanopore signal used for base calling in the sequencing application."





#### MinION MK1C







# **ONT** features

- Introduced 2012
- Sequencing is real time. Can analyze as the sequence is read
- No amplification
- Scalability
- Use in the field
- Essentially eliminates capital cost





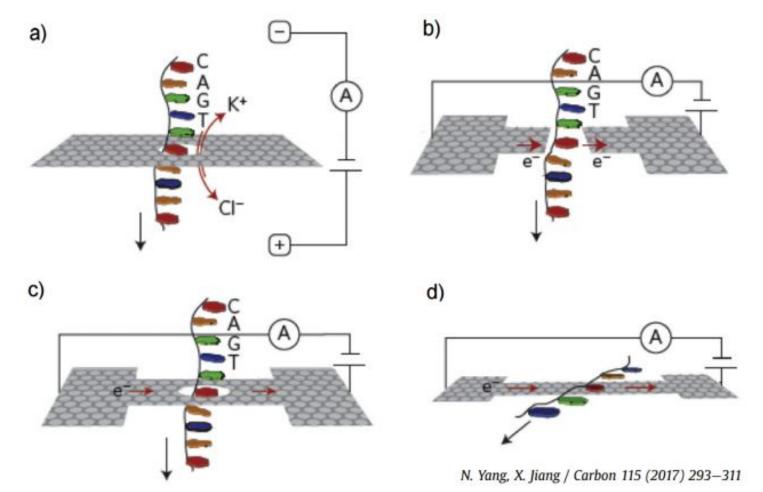
### Scalability







#### Solid State Nanopores



https://mappingignorance.org/2017/01/23/graphene-nanopore-dna-sequencing/





Short read vs long read sequencing What are the advantages and disadvantages? What applications are best for each technology?



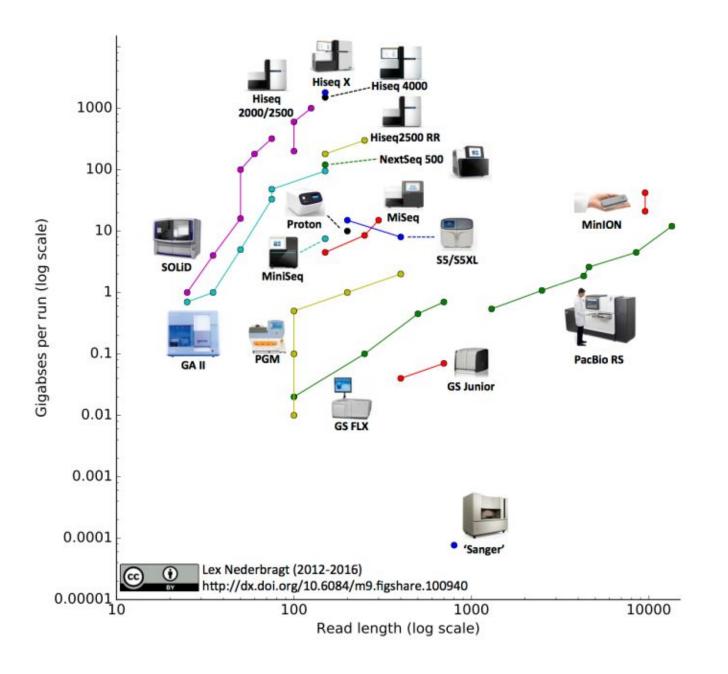
NovaSeq 6000













CGR

# Matching the library and sequencing technology to the project mRNA

- 1. Expression-related
- 2. What are the samples?
- 3. How many samples?
- 4. How many replicates?
- 5. What library prep strategies?
- 6. What sequencing technology?
- 7. How much sequencing?
- 8. What analysis tools?
- 9. Conclusions?

mRNA Full-length mRNA Isoforms Nascent transcription miRNA or small RNAs Single cell Spatial transcriptomics Methylation and other DNA modifications Histones and histone modifications Open chromatin Transcription Factor Binding Sites Stranded RNA

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