



# Beyond the Genome

Chandler Sutherland

Krasileva Lab, Department of Plant  
and Microbial Biology, UC Berkeley



Letter

**Nucleotide:** building block of DNA, consisting of sugar molecule and a nucleotide base

Word

**Sequence:** a string of nucleotides

Book

**Genome:** the complete set of genetic material (DNA) in an organism

Library

**Genomics:** study of the structure, function, evolution, and editing of genomes



1869: Discovery and Isolation of DNA

1953: Structure of DNA determined

1965: First DNA Sequence

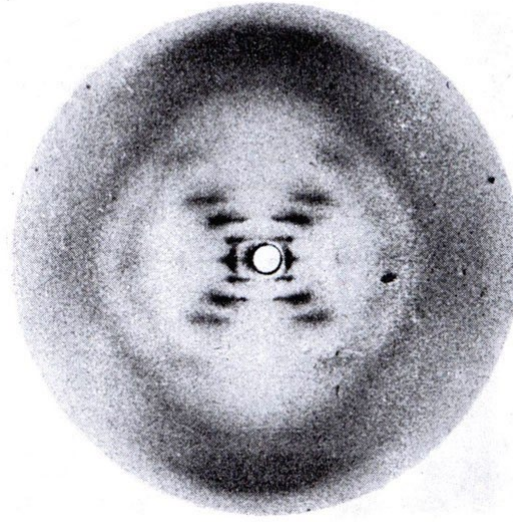
1977: First genome

1996: Sequencing by fluorescently labeled dyes

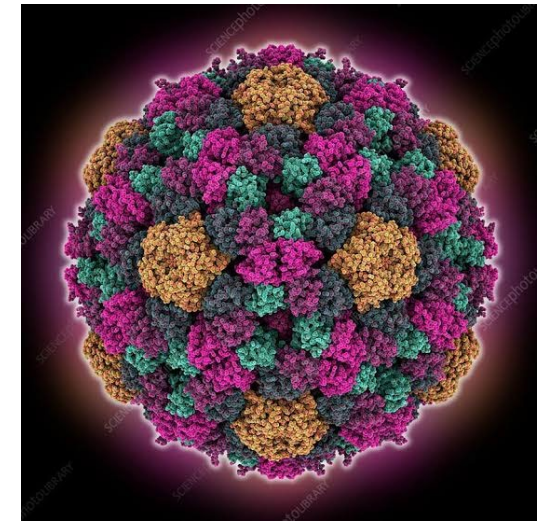
2000: First plant genome sequenced

2014: Nanopore long read sequencing

2021: Human genome finished end to end

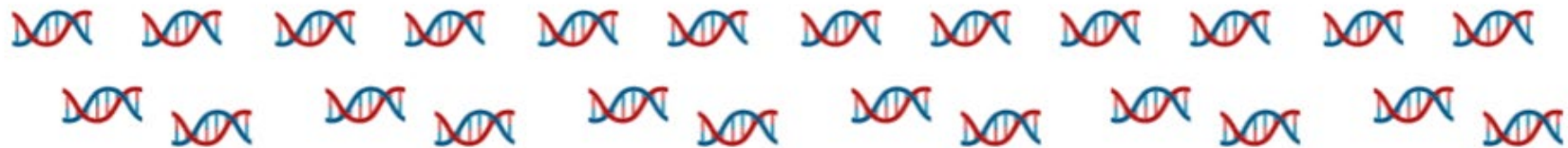


## Brief History of Sequencing

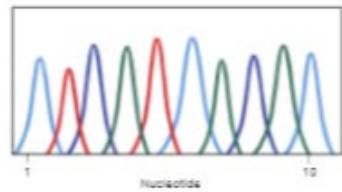




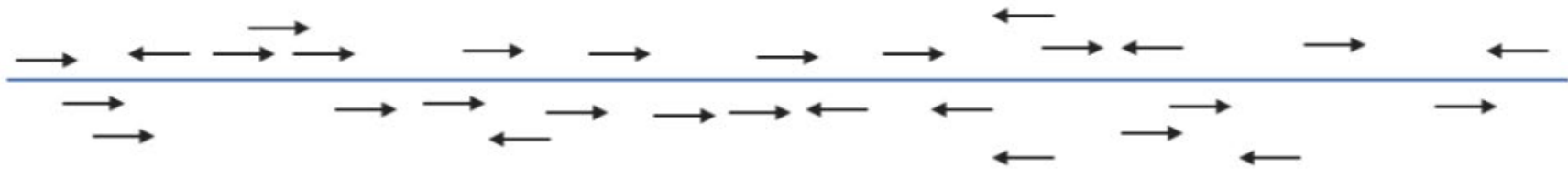
Fragment DNA



Sequence each fragment



Reconstruct original sequence from smaller fragments





# Dominant Sequencing Technologies

1

## Short read sequencing by synthesis (Illumina)

- >90% of world's sequencing data
- Each read (sequence-able fragment of DNA) is only 100-350 nucleotides long
- Very accurate

2

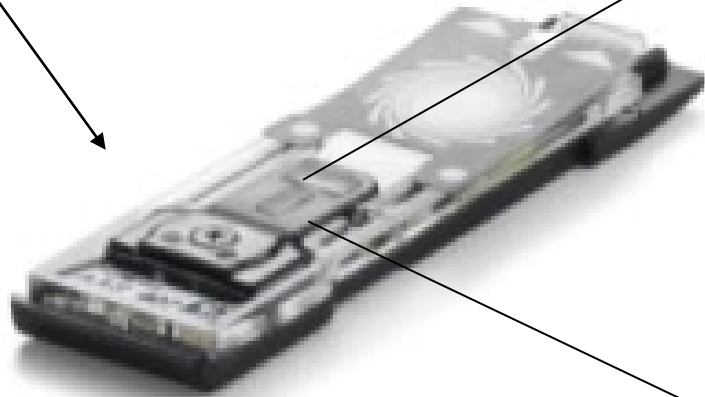
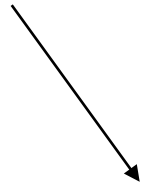
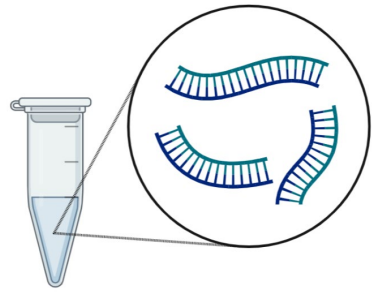
## Long read sequencing (PacBio)

- Rapid sequencing (3 DNA molecules per second)
- Long reads – up to 20,000 nucleotides
- Somewhat accurate

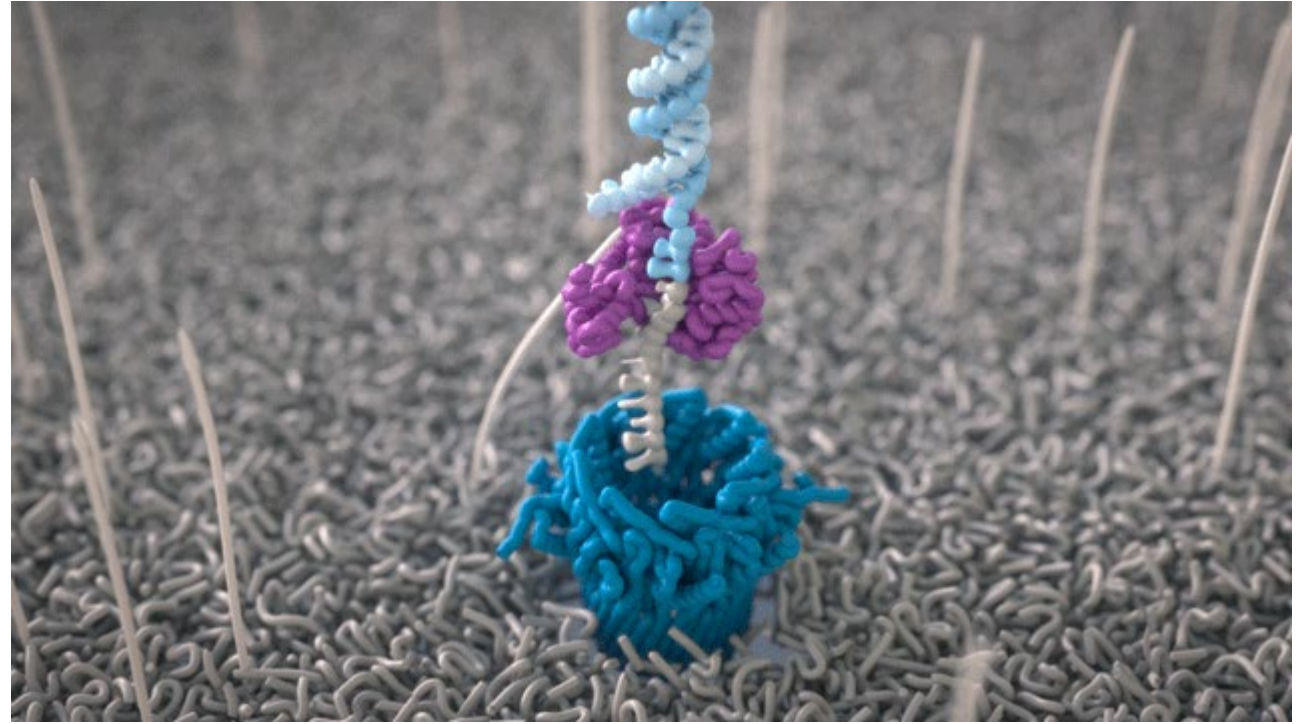
3

## Long read sequencing (Oxford Nanopore)

- Small, portable, USB-powered
- Long reads (up to 1,000,000s nucleotides)
- Field applications, including missions in space



Flow Cell

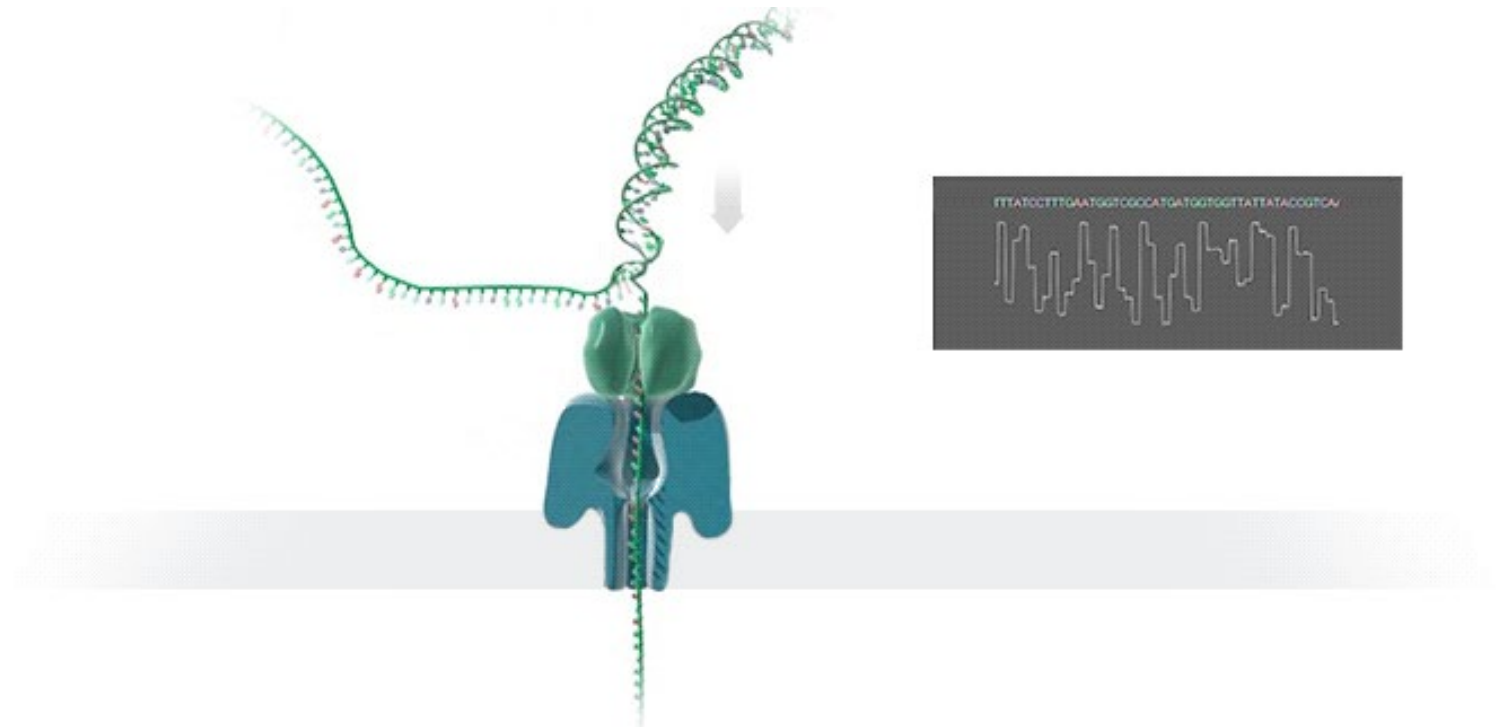


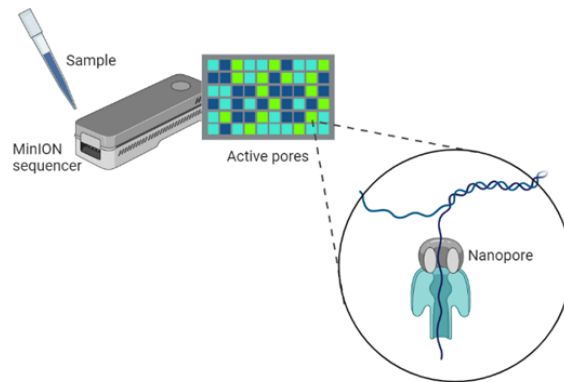
Nanopores





As each strand of DNA is passed through a nanopore, an electrical signal is recorded that can be used to decode the sequence



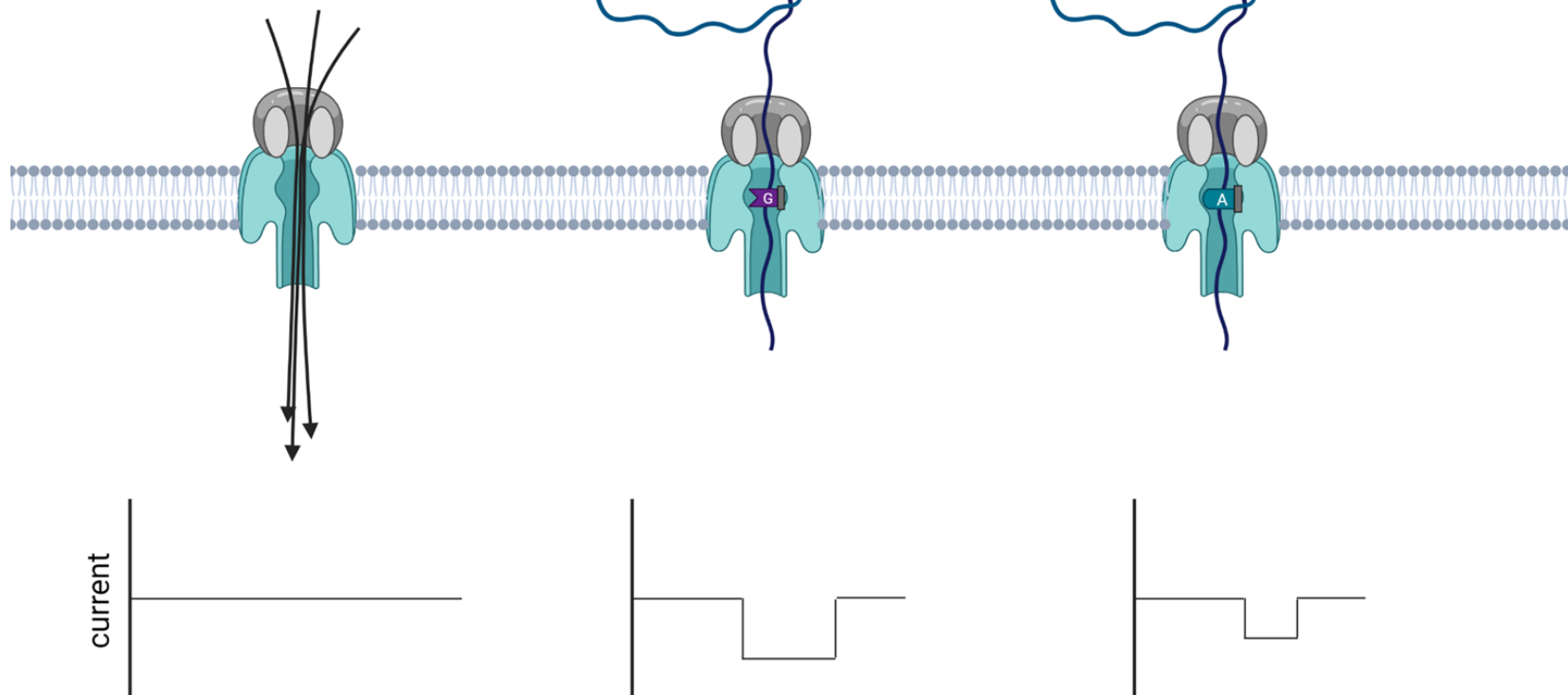


# Nanopore sensing

As a DNA sequence passes through the pore, disruptions are characterized by a distinct electrical signal

Current disruption is interpreted to understand the identity of the base pair

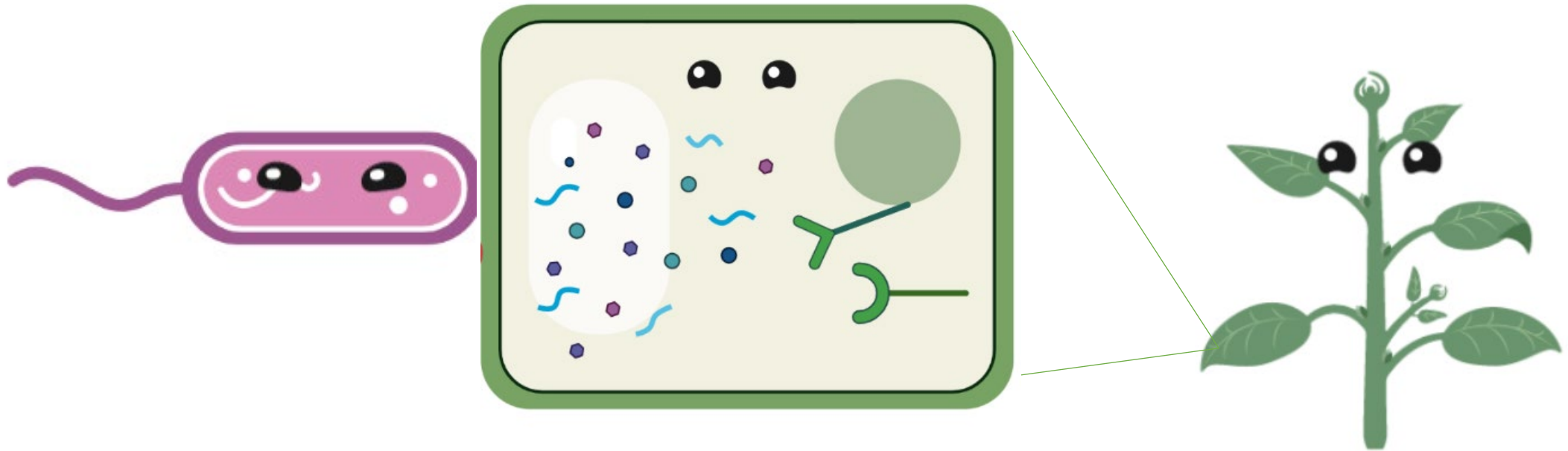
Nanopores create holes in the membrane, allowing current to pass through

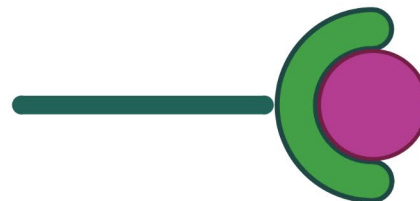
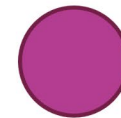
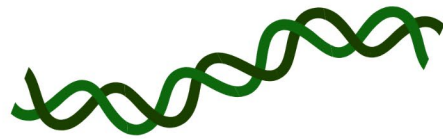




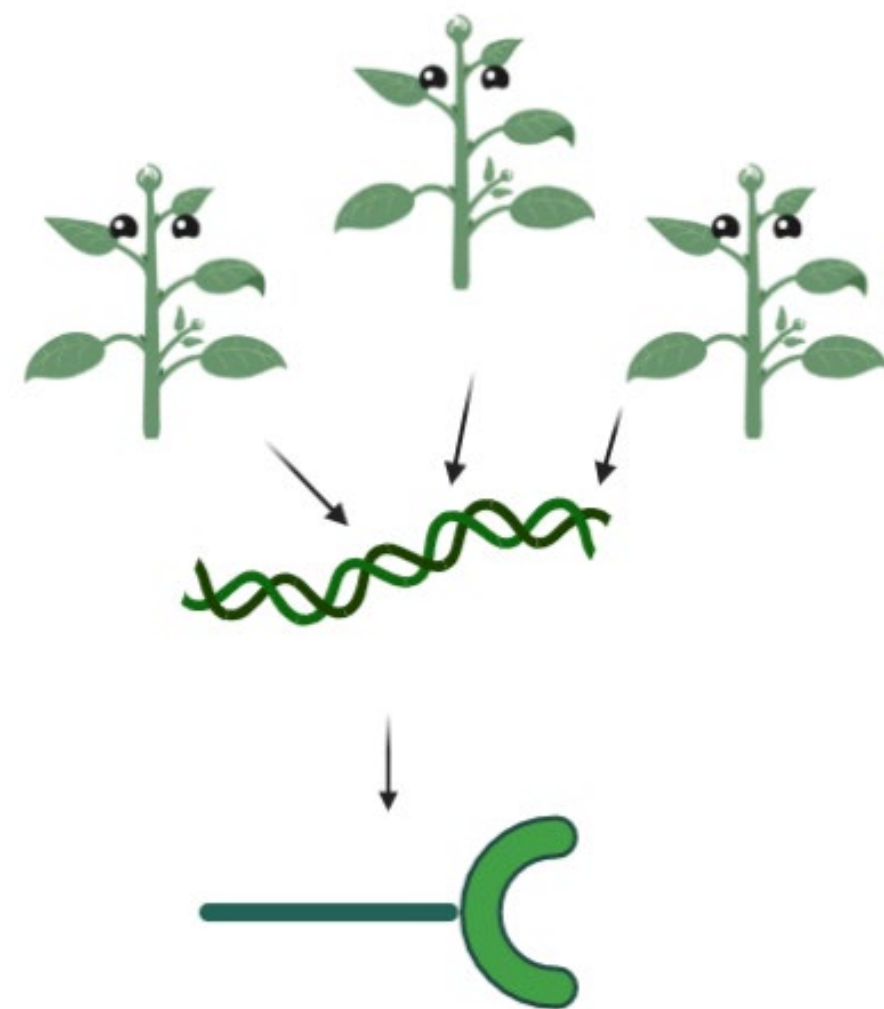
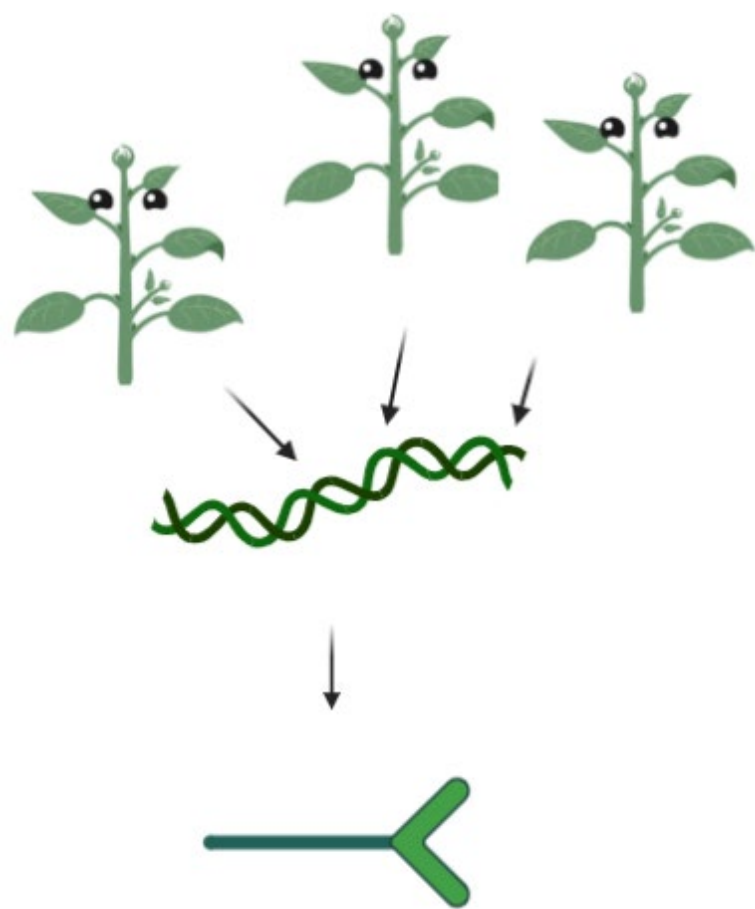


# Plant Recognition of Pathogens

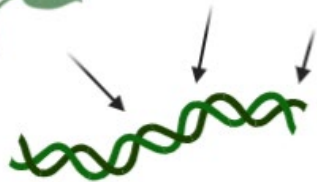




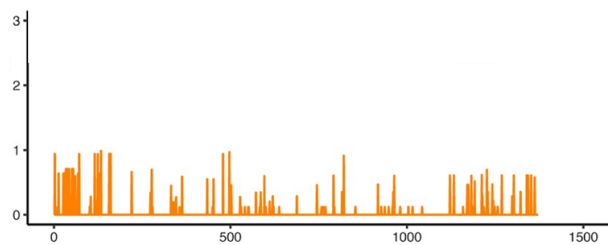
Recognition =  
Immunity!



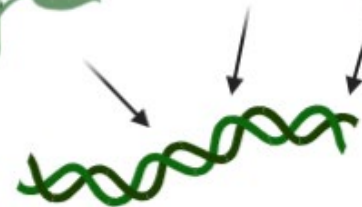




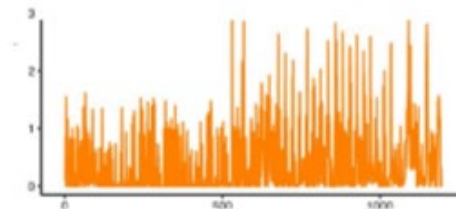
Diversity



DNA sequence



Diversity



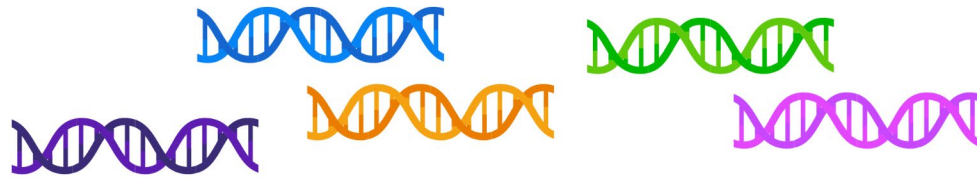
DNA sequence



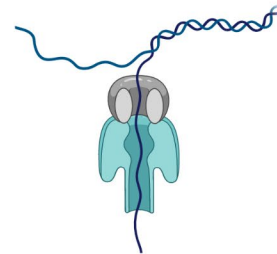
Amplify Genes  
of Interest

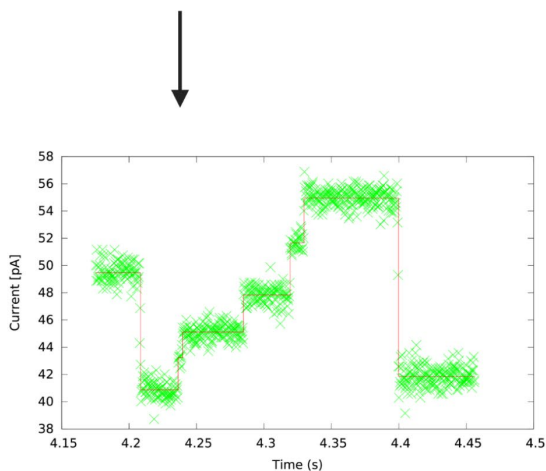


pool



Nanopore  
Sequence





.fast5

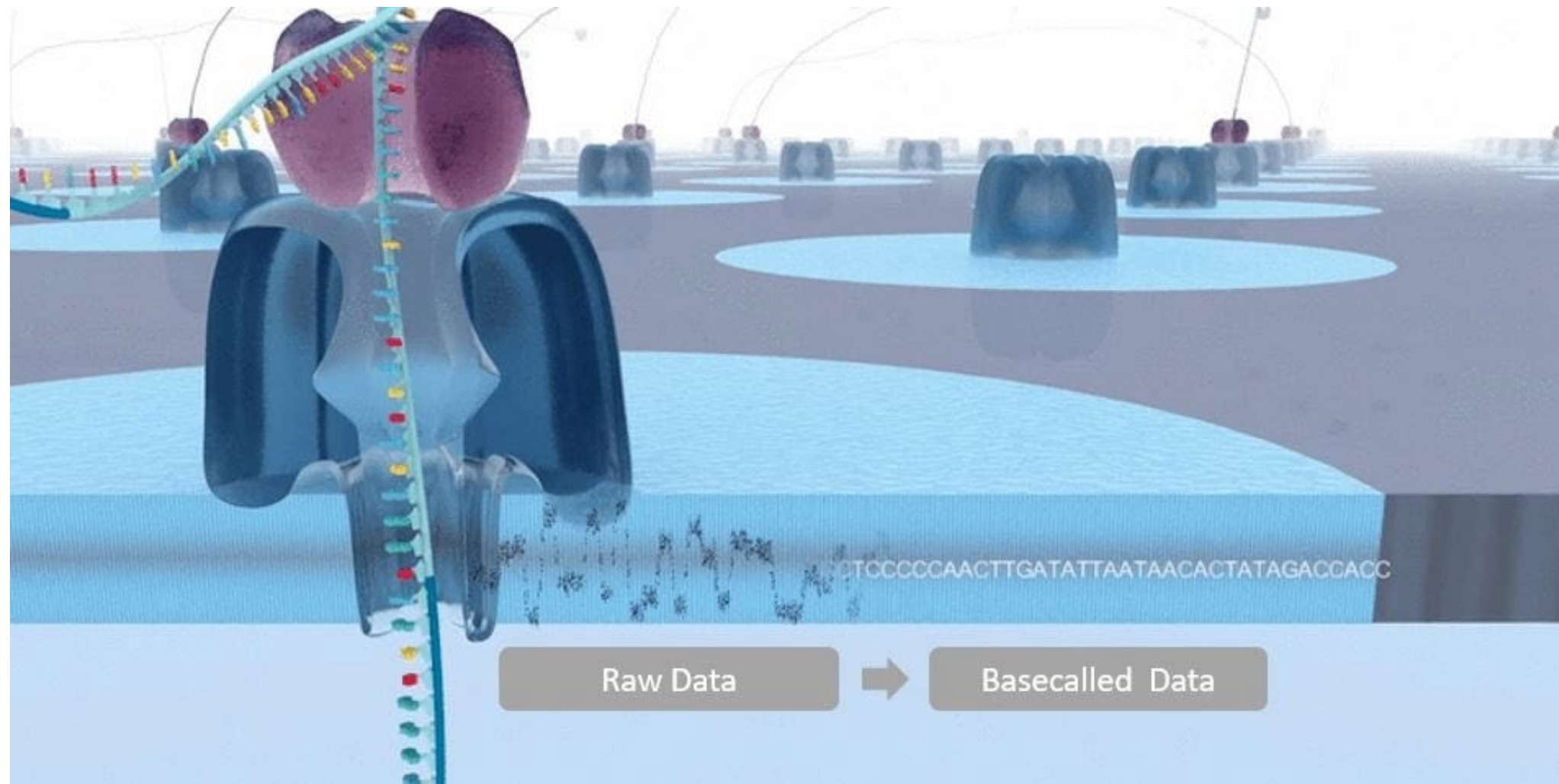
## Basecalling

.fastq

chr1:chr3:chr6:chr7 chr10:chr11:chr12:chr13 chr14:chr15:chr16:chr17 chr18:chr19:chr20:chr21 chr22:chr23:chr24:chr25 chr26:chr27:chr28:chr29 chr30:chr31:chr32:chr33 chr34:chr35:chr36:chr37 chr38:chr39:chr40:chr41 chr42:chr43:chr44:chr45 chr46:chr47:chr48:chr49 chr50:chr51:chr52:chr53 chr54:chr55:chr56:chr57 chr58:chr59:chr60:chr61 chr62:chr63:chr64:chr65 chr66:chr67:chr68:chr69 chr70:chr71:chr72:chr73 chr74:chr75:chr76:chr77 chr78:chr79:chr80:chr81 chr82:chr83:chr84:chr85 chr86:chr87:chr88:chr89 chr90:chr91:chr92:chr93 chr94:chr95:chr96:chr97 chr98:chr99:chr100:chr101 chr102:chr103:chr104:chr105 chr106:chr107:chr108:chr109 chr110:chr111:chr112:chr113 chr114:chr115:chr116:chr117 chr118:chr119:chr120:chr121 chr122:chr123:chr124:chr125 chr126:chr127:chr128:chr129 chr130:chr131:chr132:chr133 chr134:chr135:chr136:chr137 chr138:chr139:chr140:chr141 chr142:chr143:chr144:chr145 chr146:chr147:chr148:chr149 chr150:chr151:chr152:chr153 chr154:chr155:chr156:chr157 chr158:chr159:chr160:chr161 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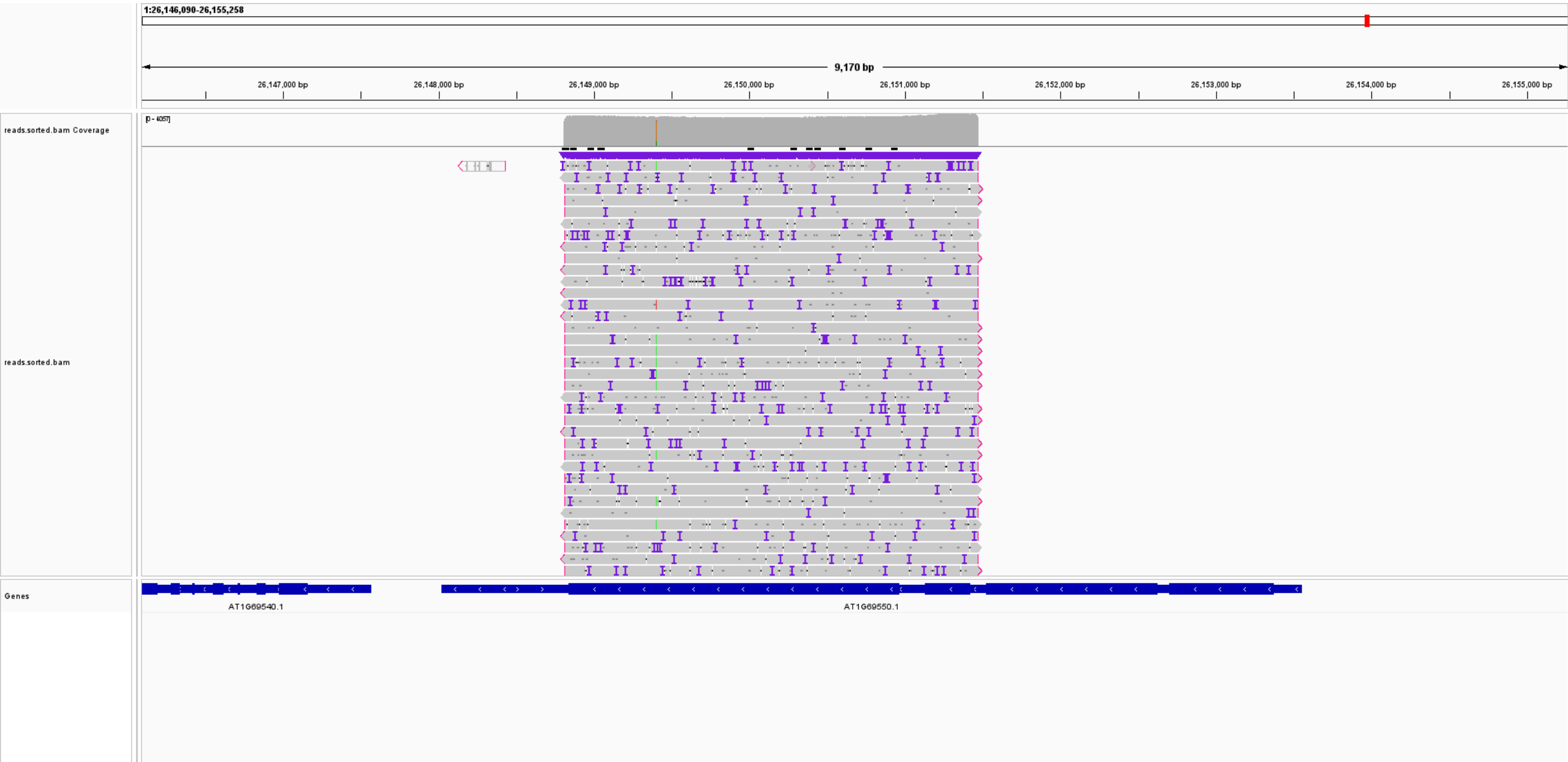


# Basecalling

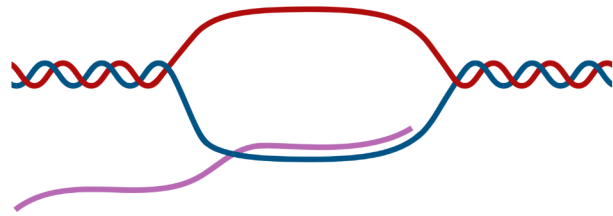


# Time to process some sequenced reads!

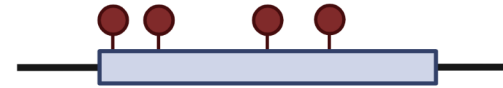
[tinyurl.com/nuevagenome](https://tinyurl.com/nuevagenome)



# What other information can we evaluate?



Transcription



Methyl groups

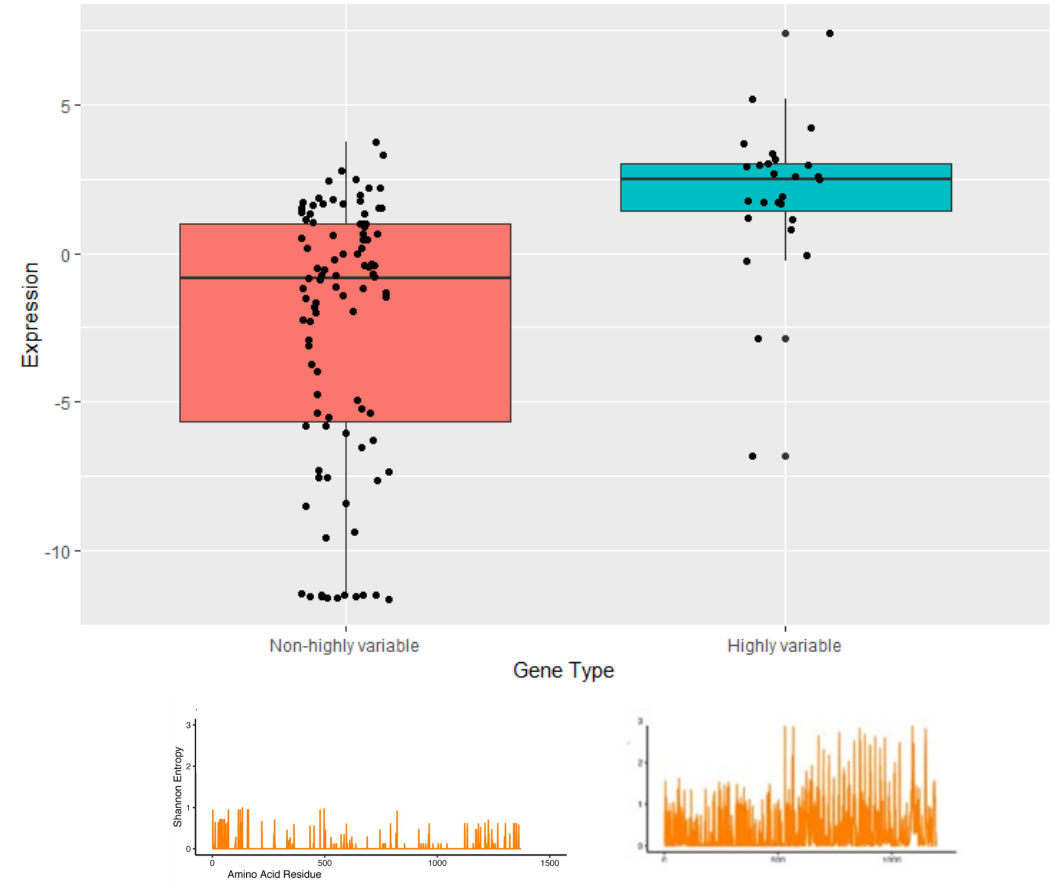
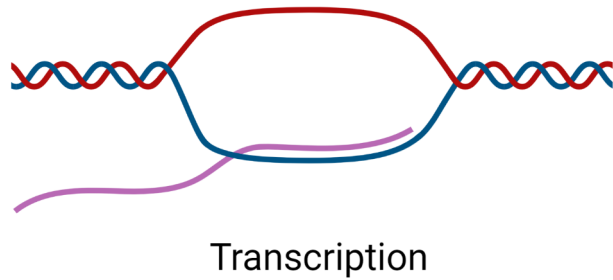


Mutation rate

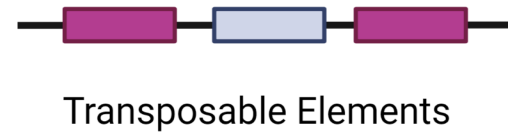
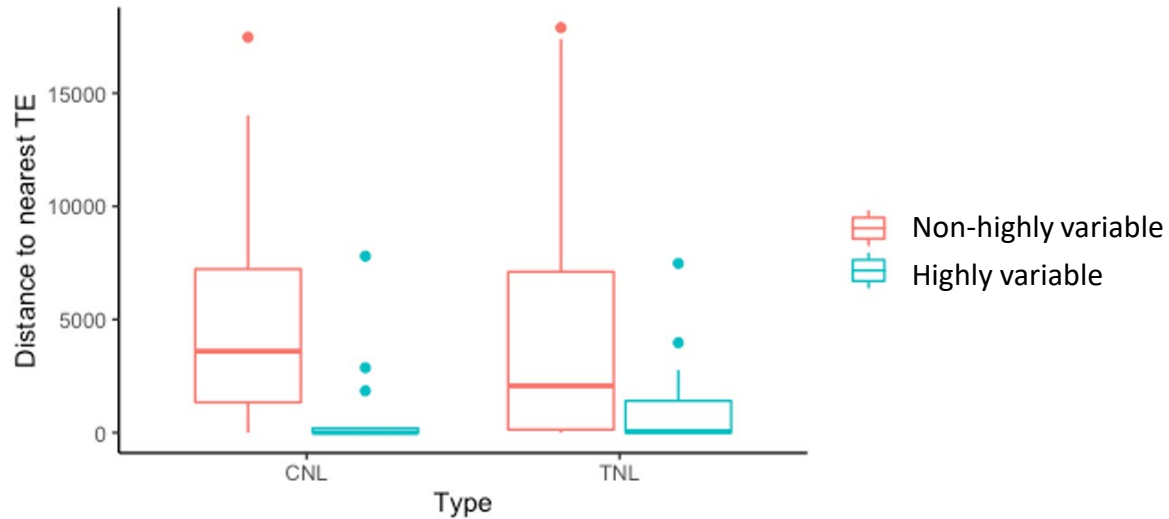


Transposable Elements

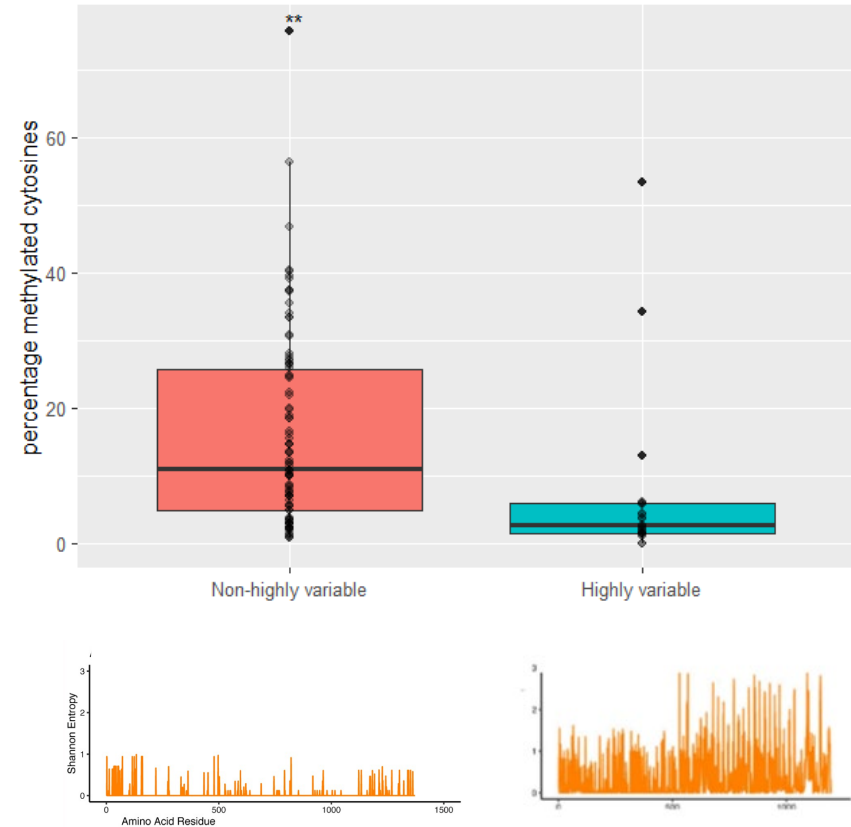
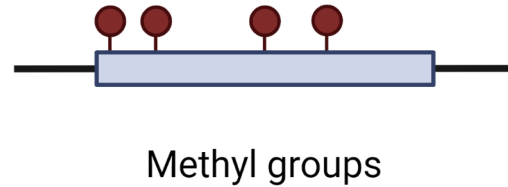
# Highly variable immune receptors are expressed more than non-highly variable immune receptors



# Highly variable immune receptors are closer to transcriptional elements than non-highly variable immune receptors



# Highly variable immune are more methylated than non-highly variable immune receptors

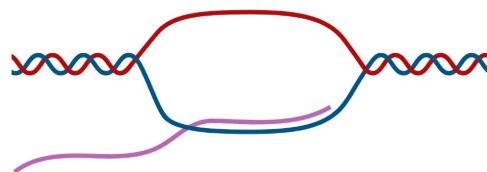




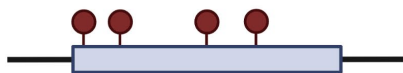
An individual's methylation status, expression, and TE distance are correlated with intraspecies allelic diversity.



Allelic Diversity



Transcription

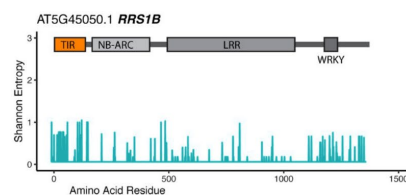


Methyl groups

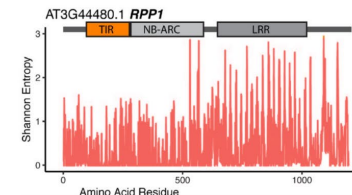


Distance to Transposable Elements

Non-Highly Variable NLR



Highly Variable NLR



# Berkeley Plant & Microbial Biology



@chandler\_suth



chandersutherland@berkeley.edu

