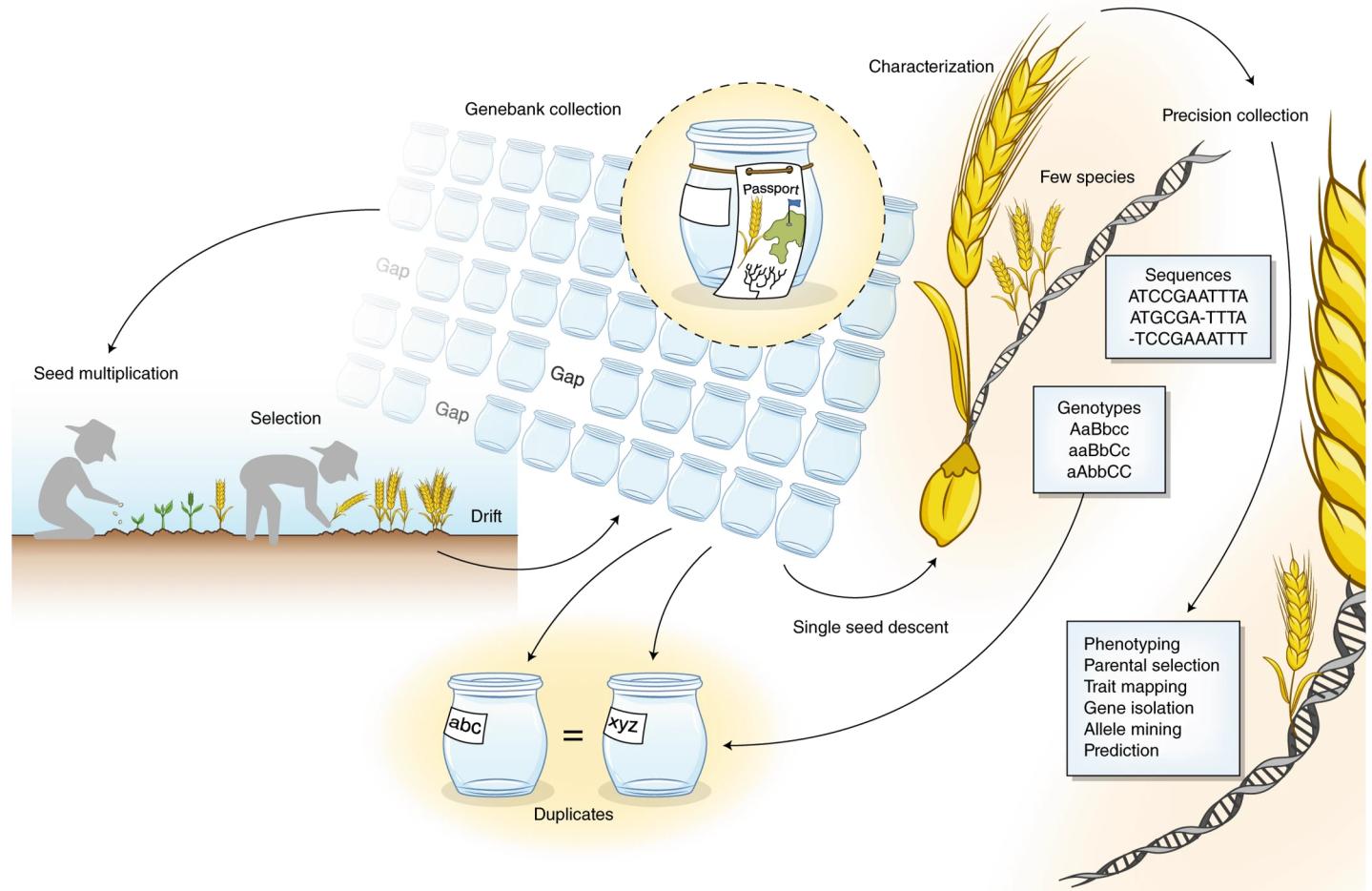


# Genomic Selection Workshop

Day 1

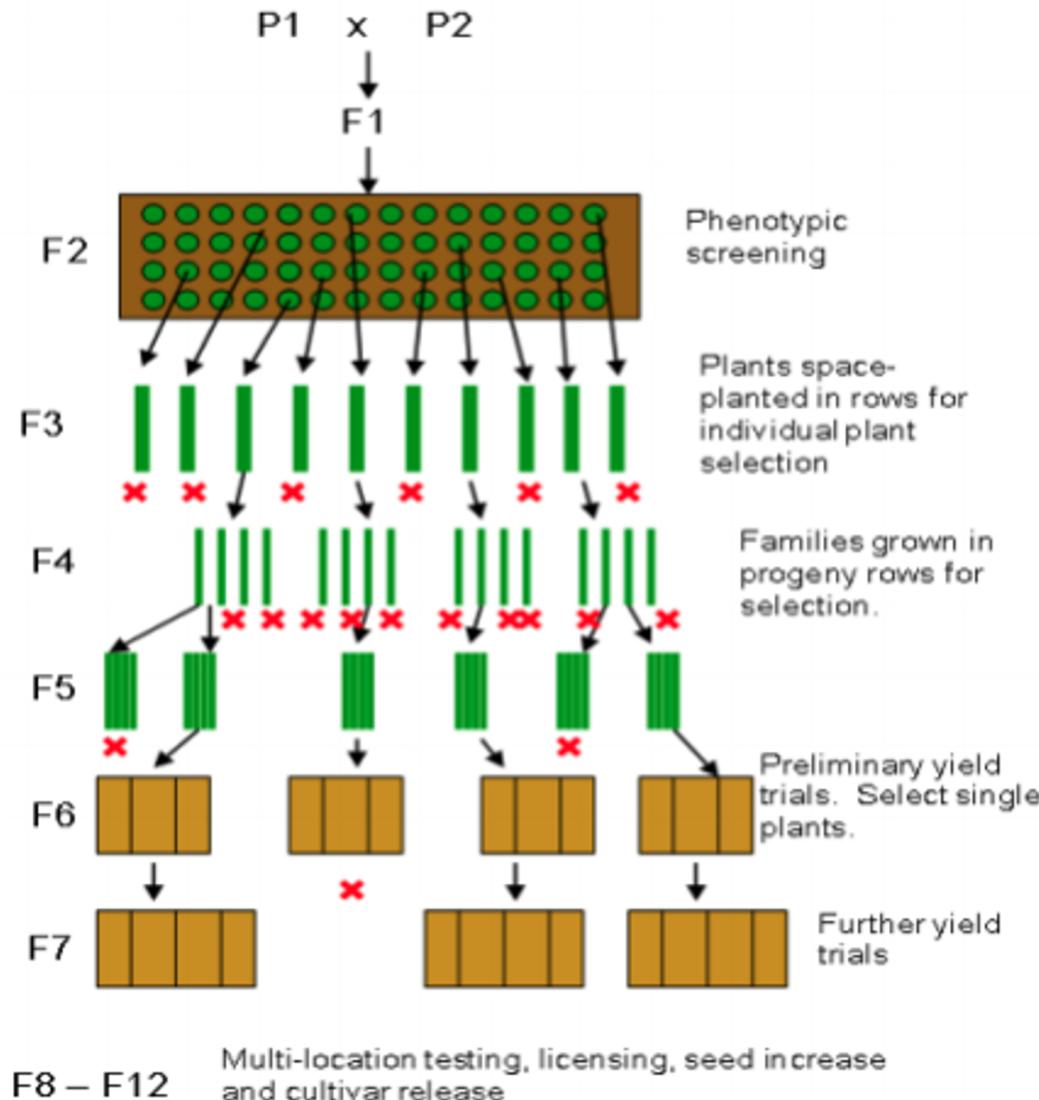
# Where are we and where do we want to go?

- Conventional breeding
- Marker Assisted Selection
- Genomic Selection

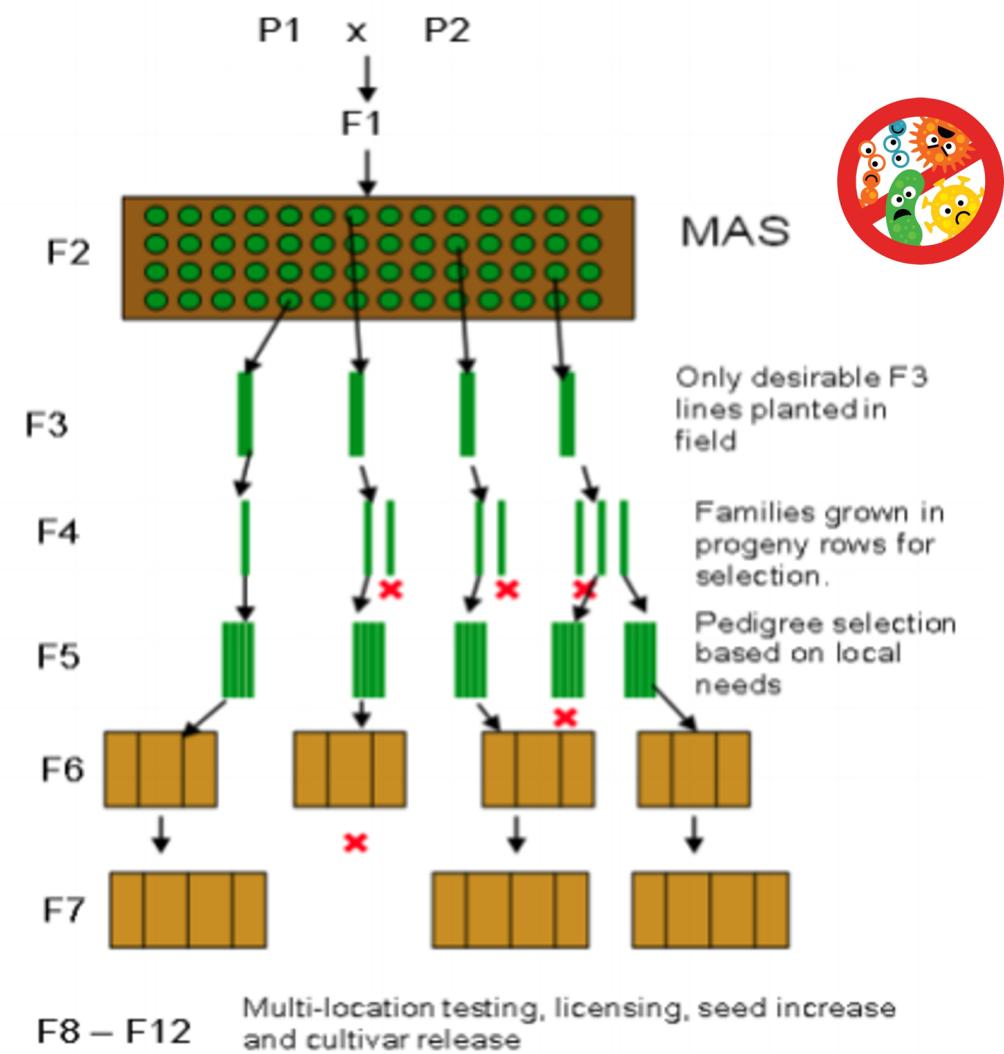


Mascher et al 2019

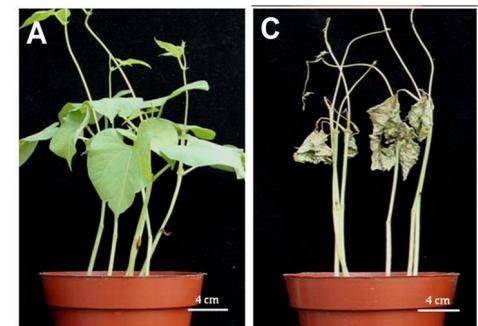
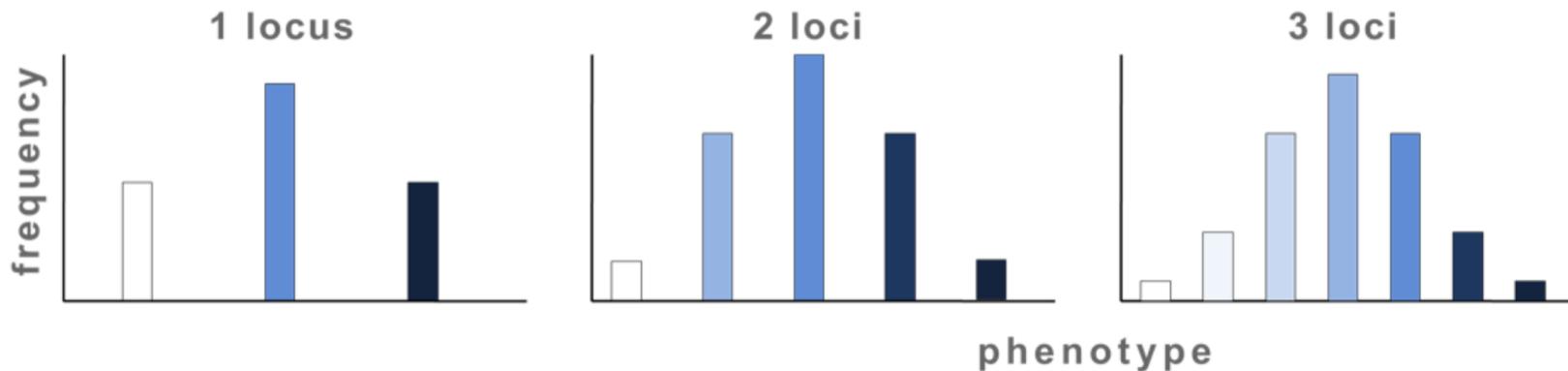
# Conventional Plant Breeding



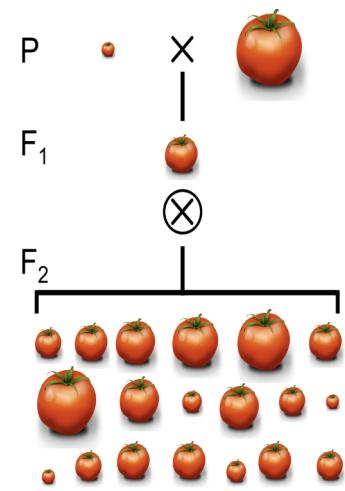
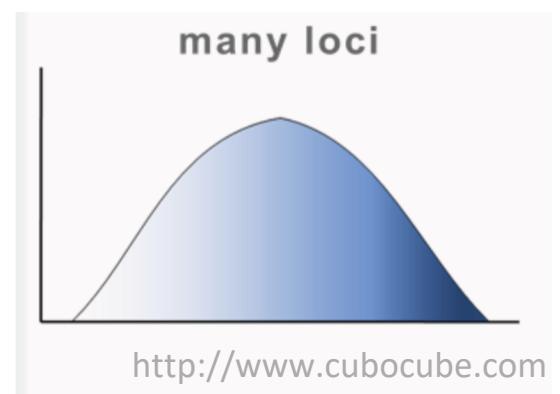
# Marker Assisted Selection



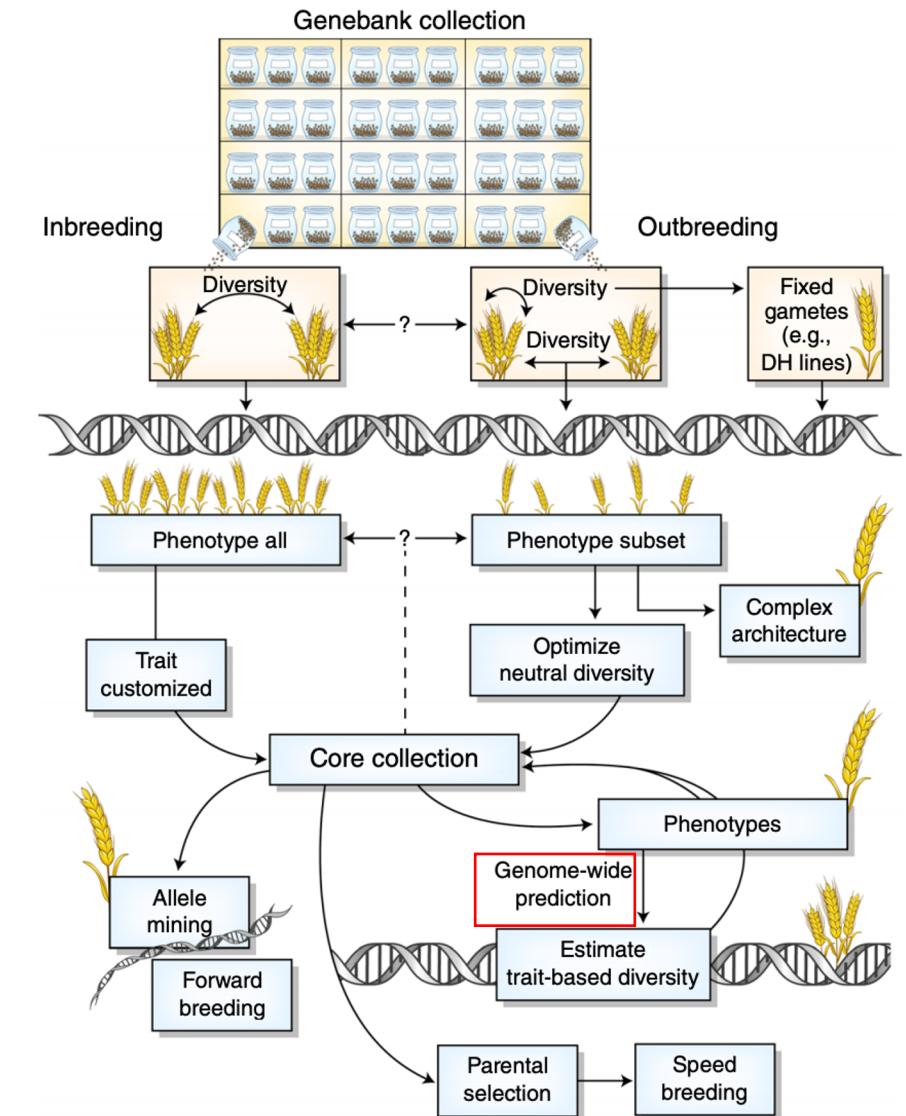
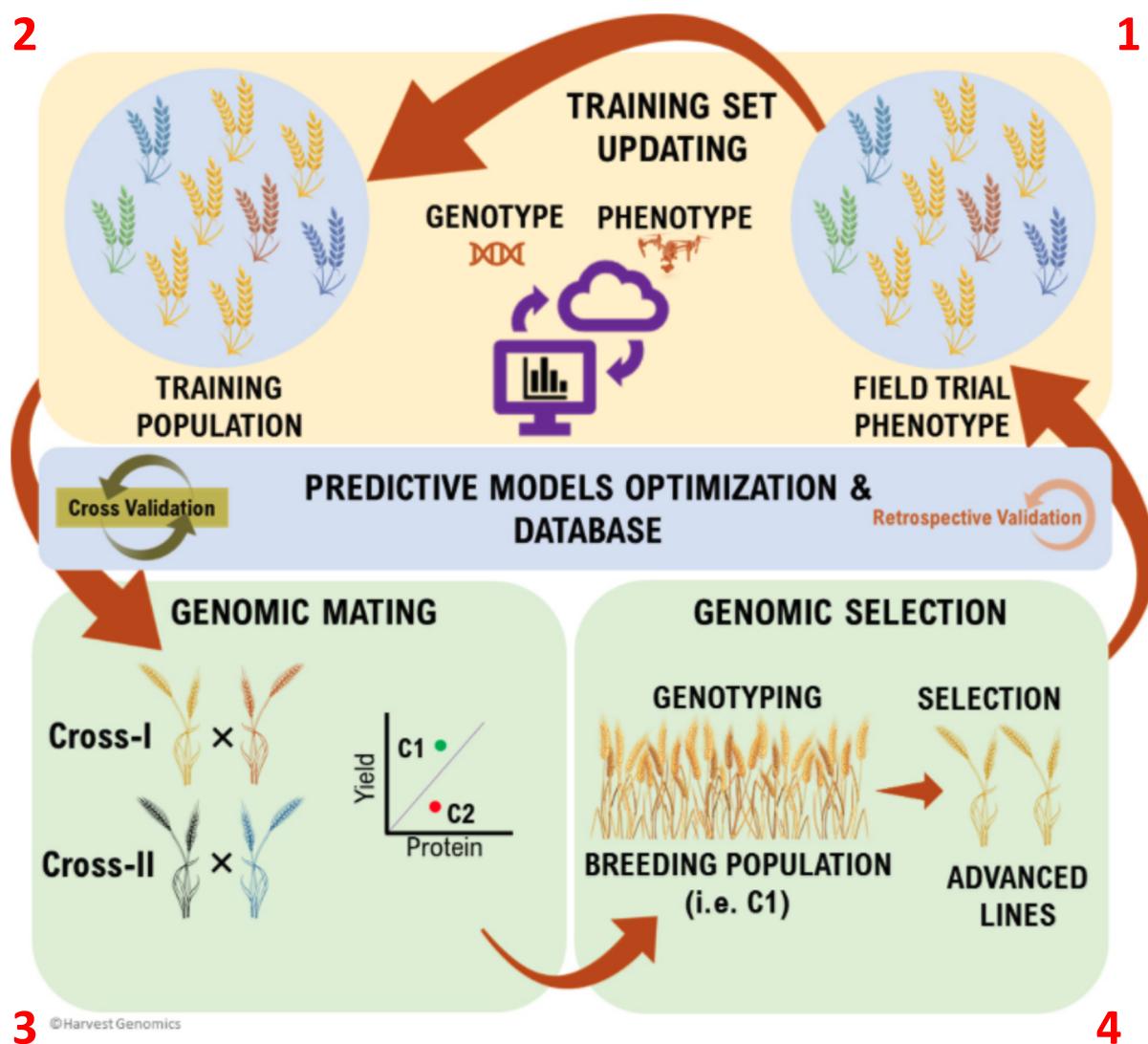
# What are quantitative traits?



Chen et al 2017



# Genomic Selection Workshop



# **Genomic Selection Workshop**

**The molecular basis of genetics**

# The Molecular Basis of Genetics

1. Genome
2. Chromosomes
3. Genes
4. Mitosis
5. Meiosis
  - a. Crossing over



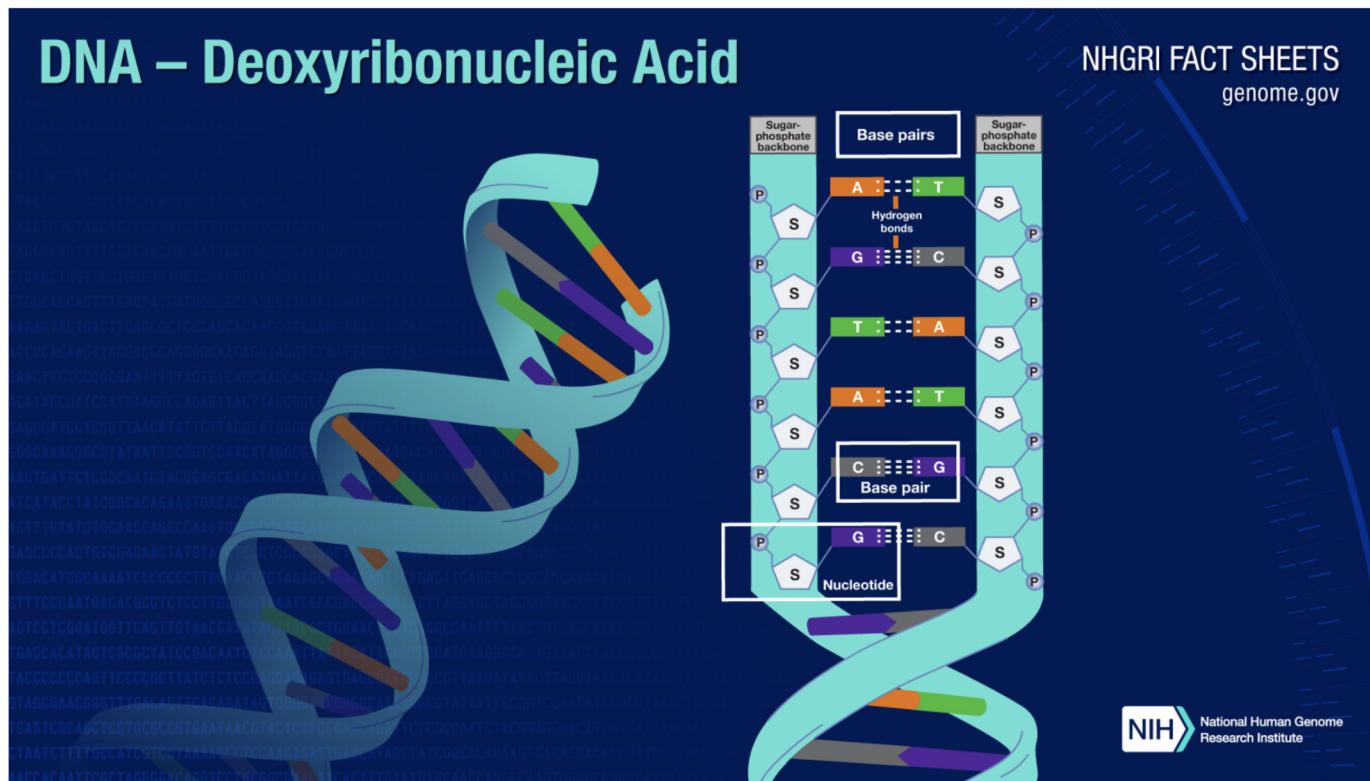
greenhousegrower.com

# 1. The Genome

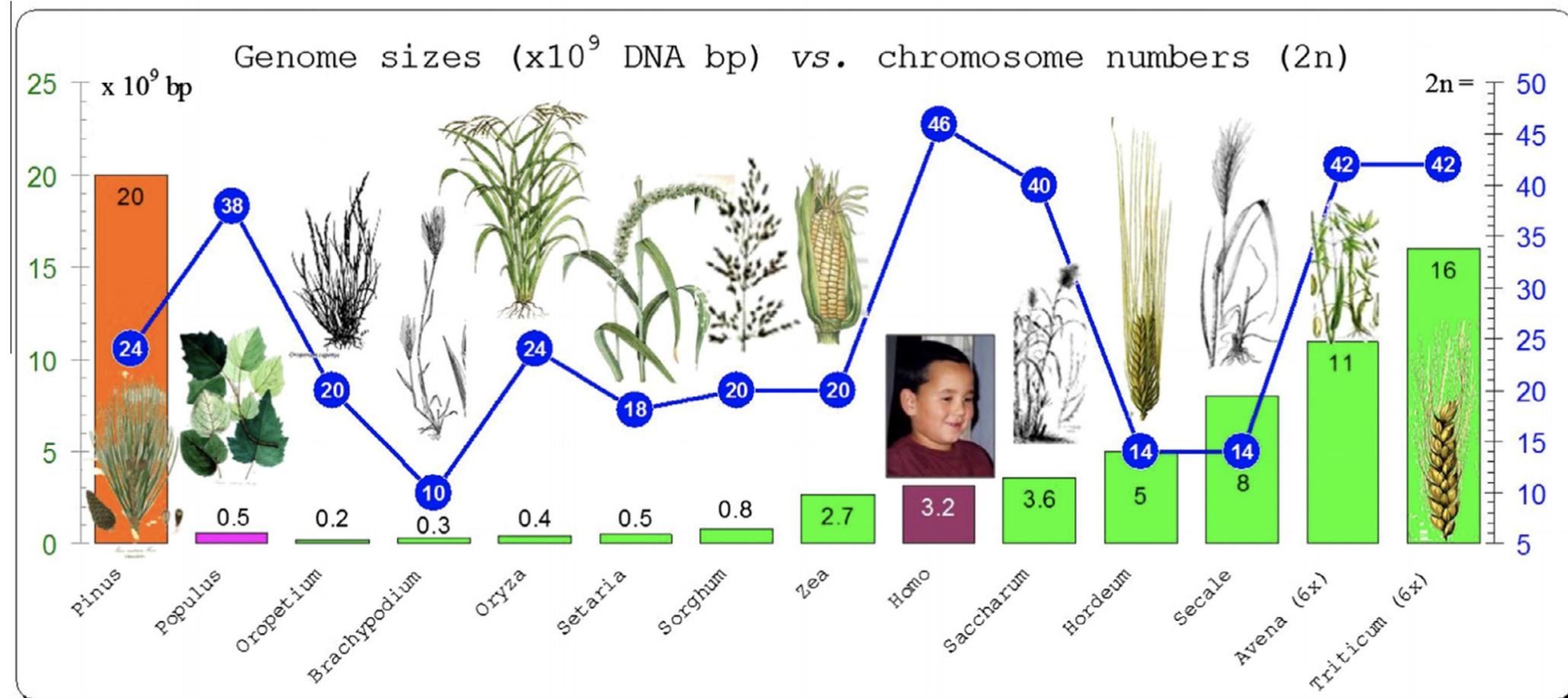
**Deoxyribonucleic acid (DNA)** is a molecule that contains the genetic instructions for the development, functioning, growth and reproduction of nearly all living organisms.

**DNA** is made of four chemical units, called nucleotide bases (adenine (A), thymine (T), guanine (G), and cytosine (C)).

A - T  
C - G



# Genome sizes



**Figure 1** Sizes of plant genomes. Sizes (bp) vs. chromosome numbers ( $2n$ ) of plant genomes from different taxa and compared to human genome size ( $3.2 \times 10^9$  bp).

Ali et al 2014

# *Phaseolus vulgaris* genome



~540 Millions bases!

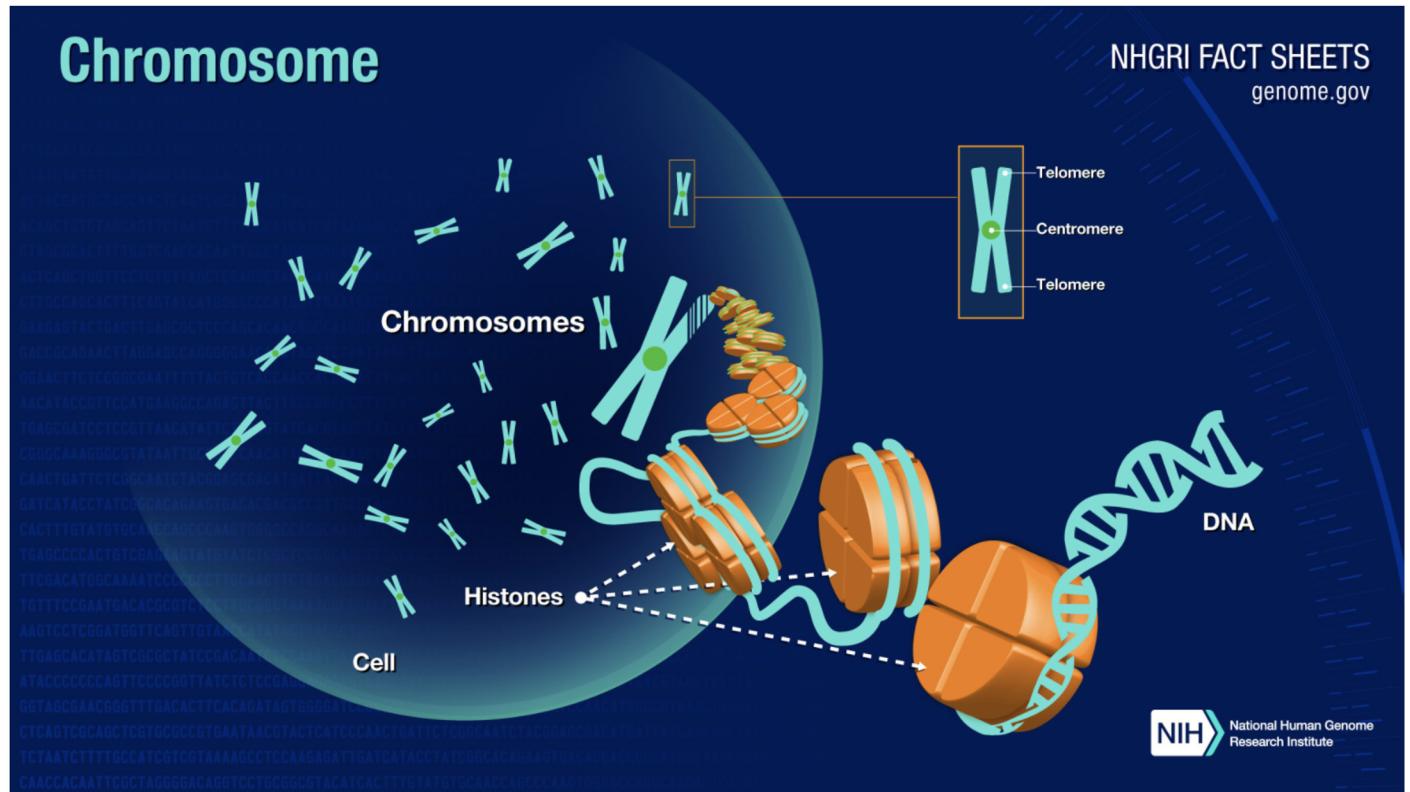


Image Credit: fotohunter / Shutterstock

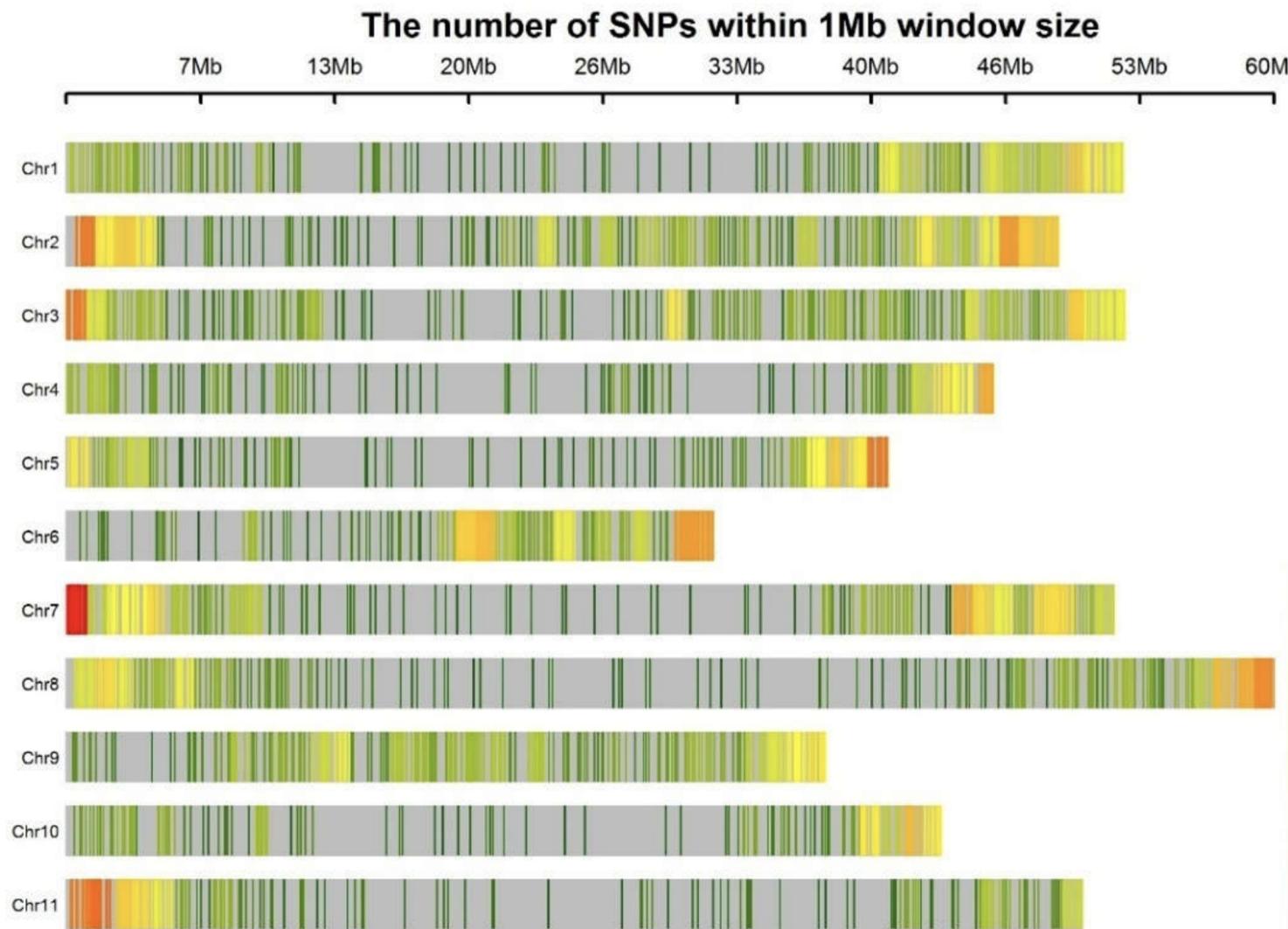
# 2. Chromosomes

Chromosomes house the genetic material (DNA).

Chromosomes keep DNA wrapped around proteins called **histones** which bind to and condense the DNA molecule to maintain its integrity.



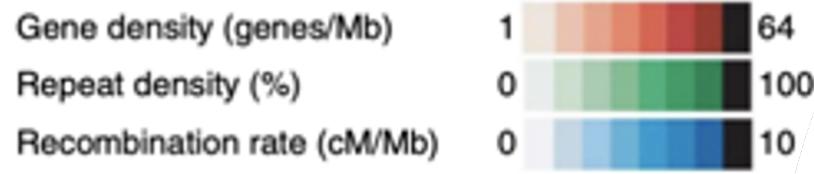
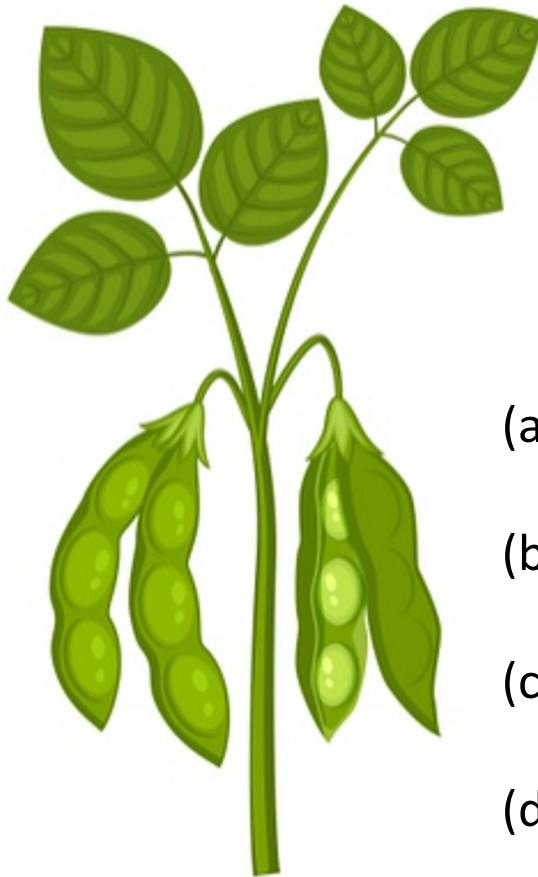
# *Phaseolus vulgaris* has 11 chromosomes



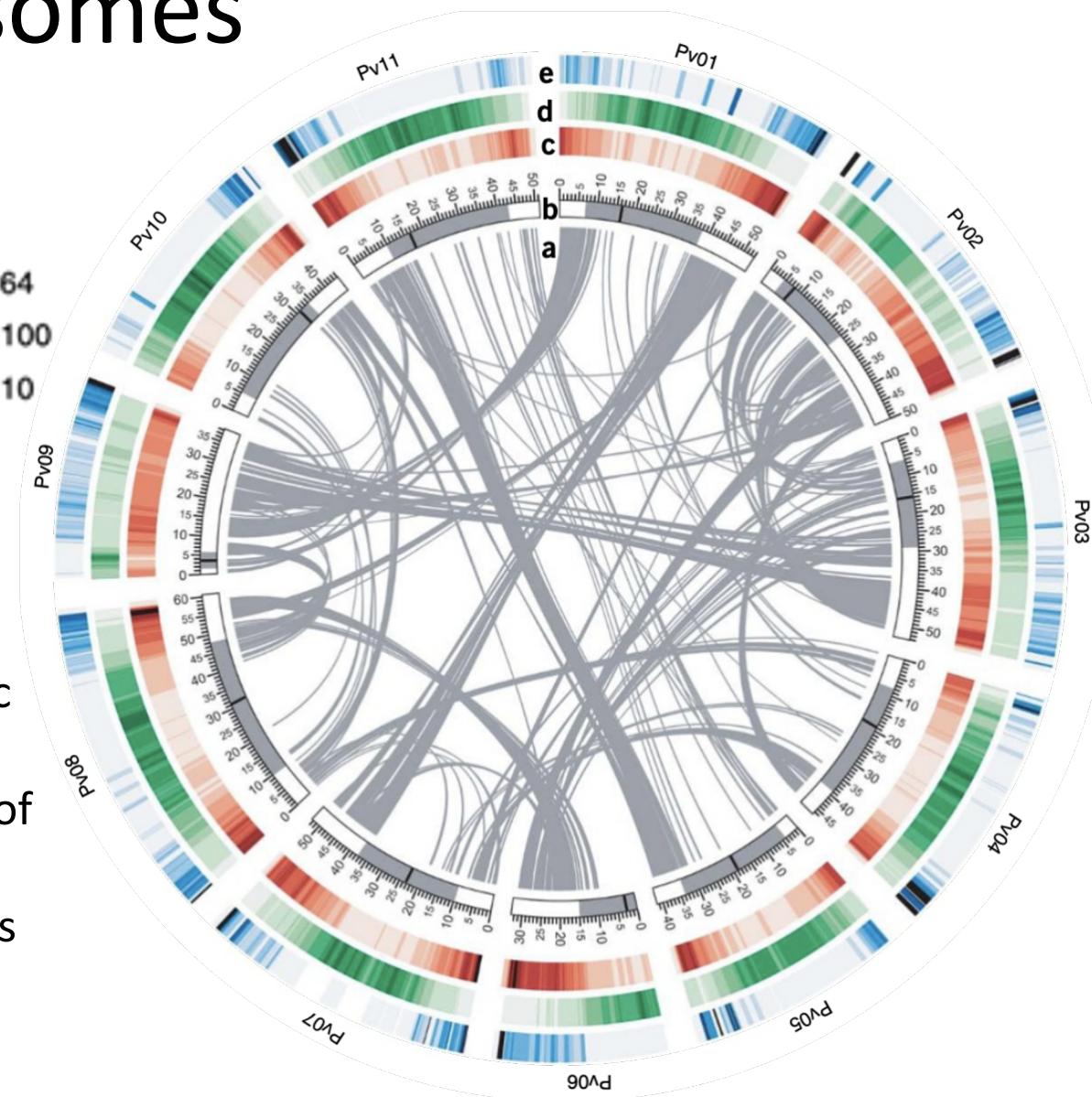
0  
3  
6  
9  
12  
15  
18  
21  
24  
27  
30  
>30

Campa et al 2018

# *Phaseolus vulgaris* chromosomes

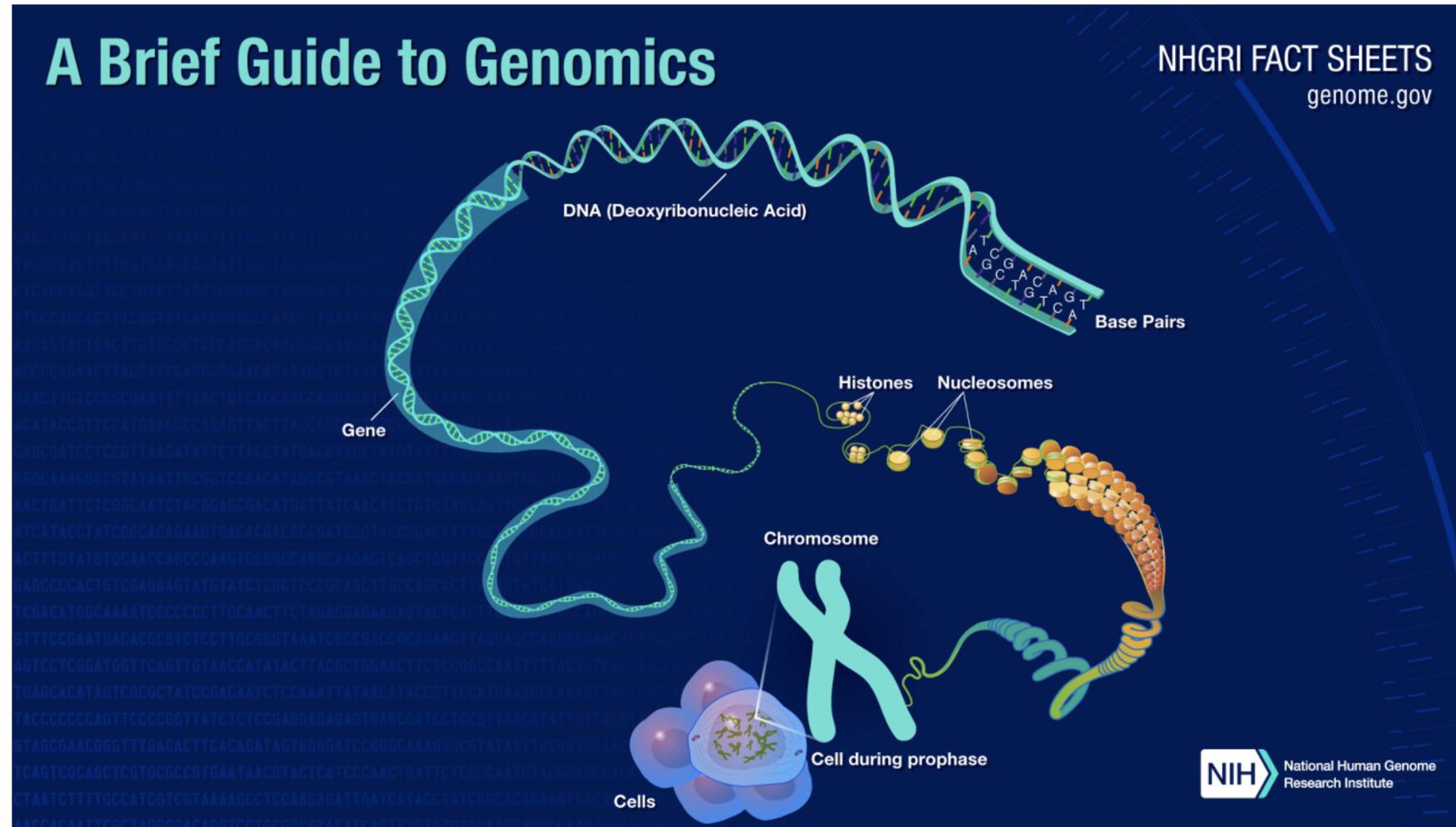


- (a) Gray lines connect duplicated genes.
- (b) Centromeric and pericentromeric regions in black and gray.
- (c) Gene density in sliding windows of 1 Mb.
- (d) Repeat density in sliding windows of 1 Mb
- (e) Recombination rate



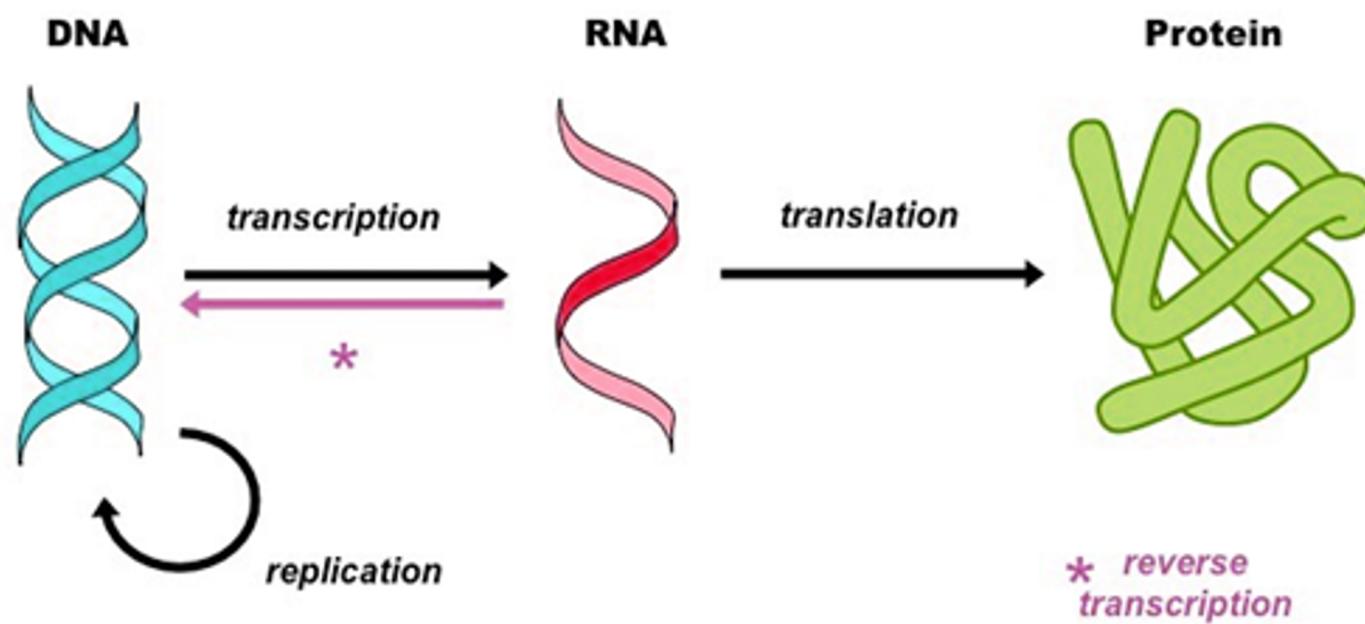
# 3. Genes

The gene is the basic physical unit of inheritance and contains the information needed to specify traits.



# Central dogma

## CENTRAL DOGMA

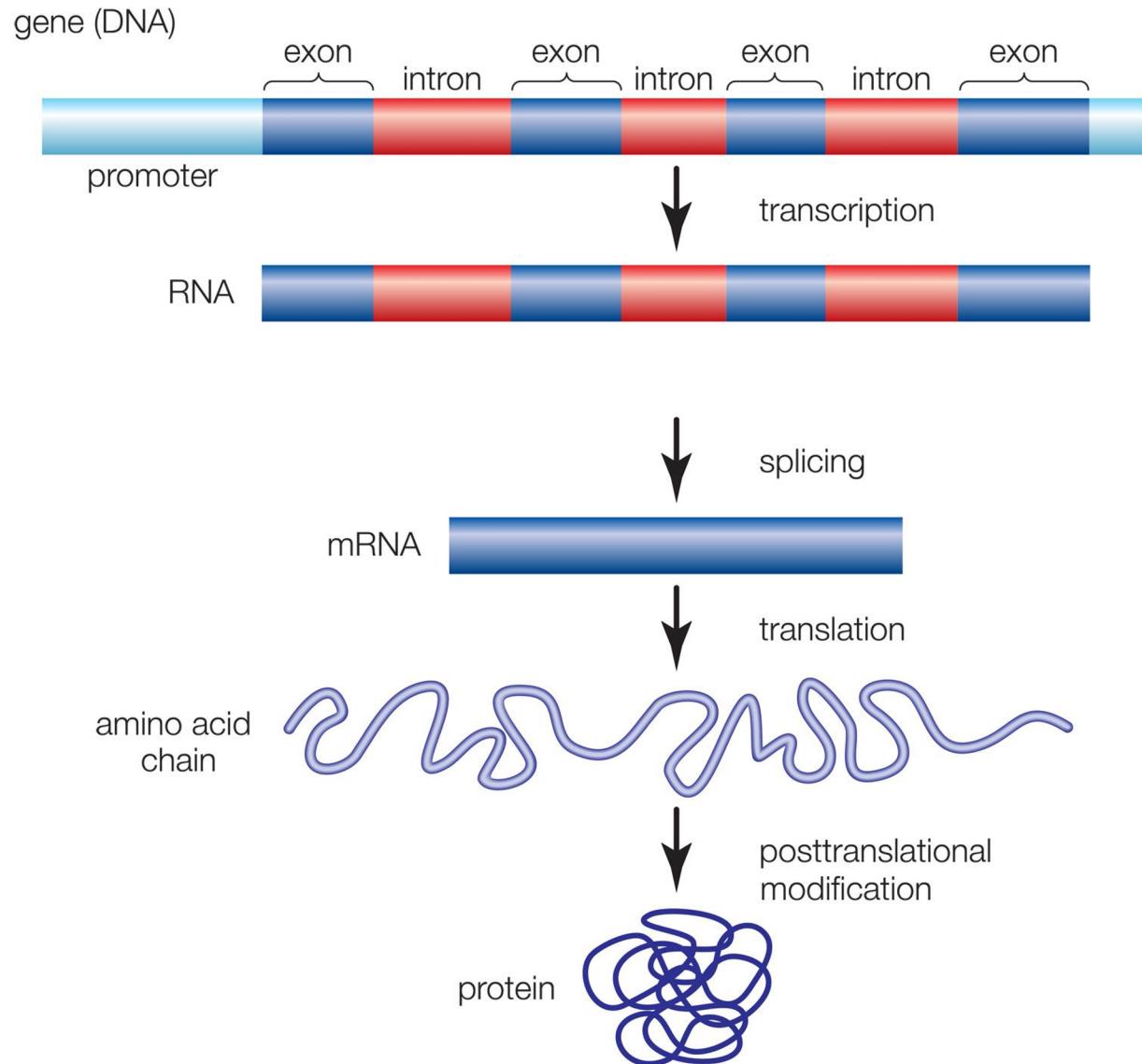


# Gene Structure

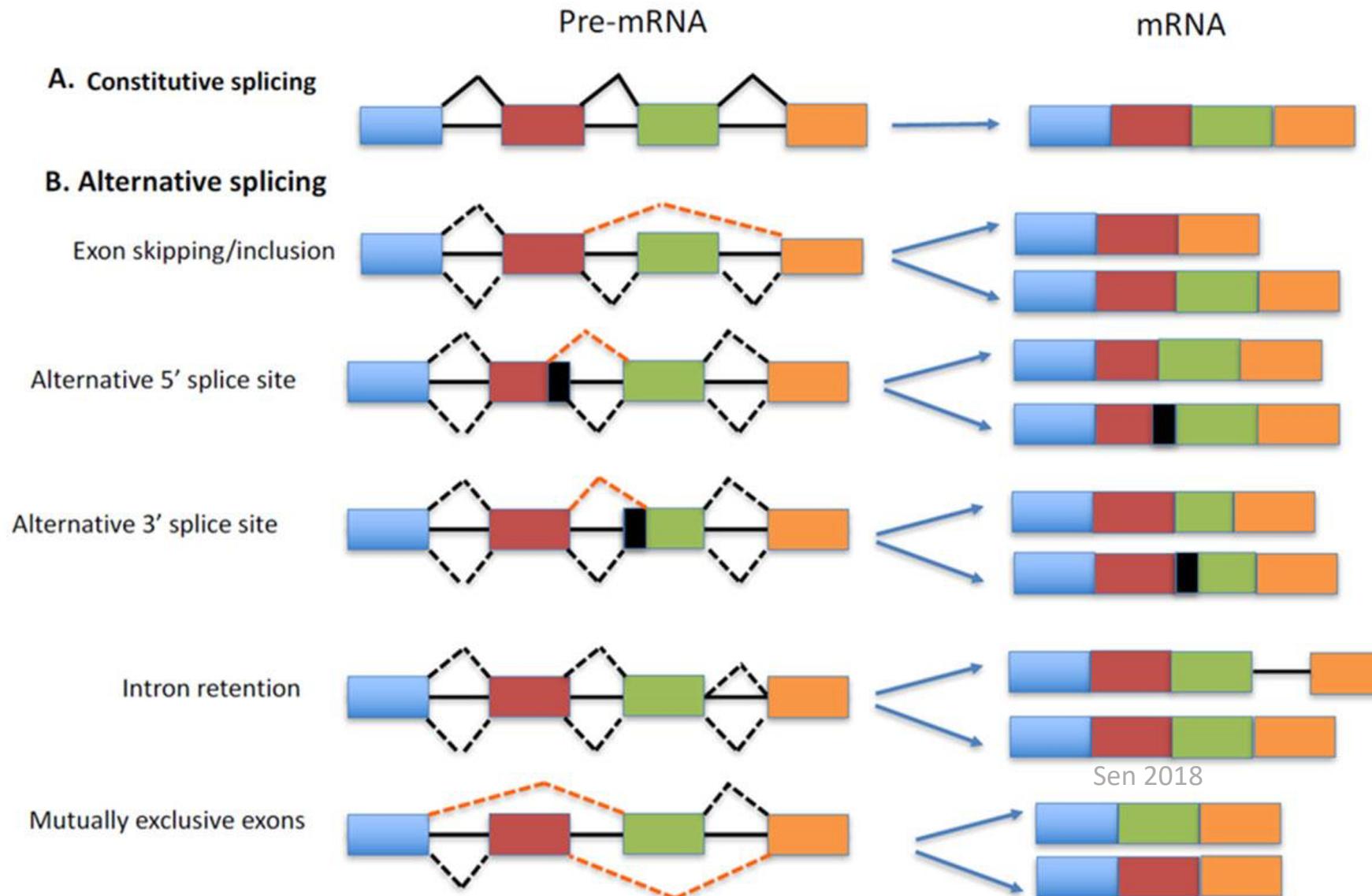
**Promoter:** sequence of DNA needed to turn a gene on or off.

**Exons:** parts of the gene sequence that are expressed in the protein.

**Introns:** parts of the gene sequence that are not expressed in the protein.

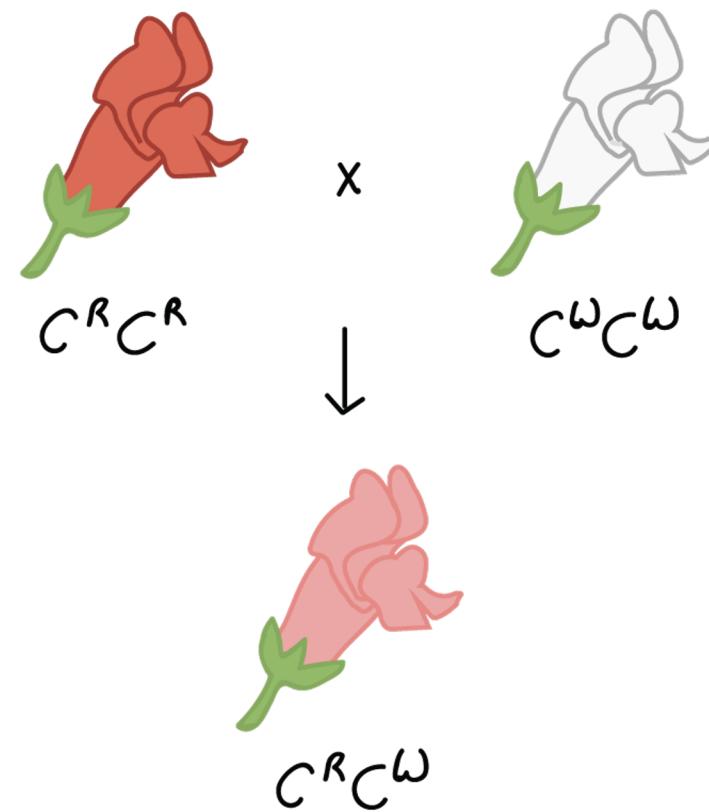


# DNA to RNA



# Alleles

- An allele is one of **two or more versions** of a gene.
- For diploids, such as *P. vulgaris*, If the two alleles are the same, the individual is homozygous for that gene.
- If the alleles are different, the individual is heterozygous.
- The use of the allele also refers to variation among non-coding DNA sequences.



# *Phaseolus vulgaris* Gene Number

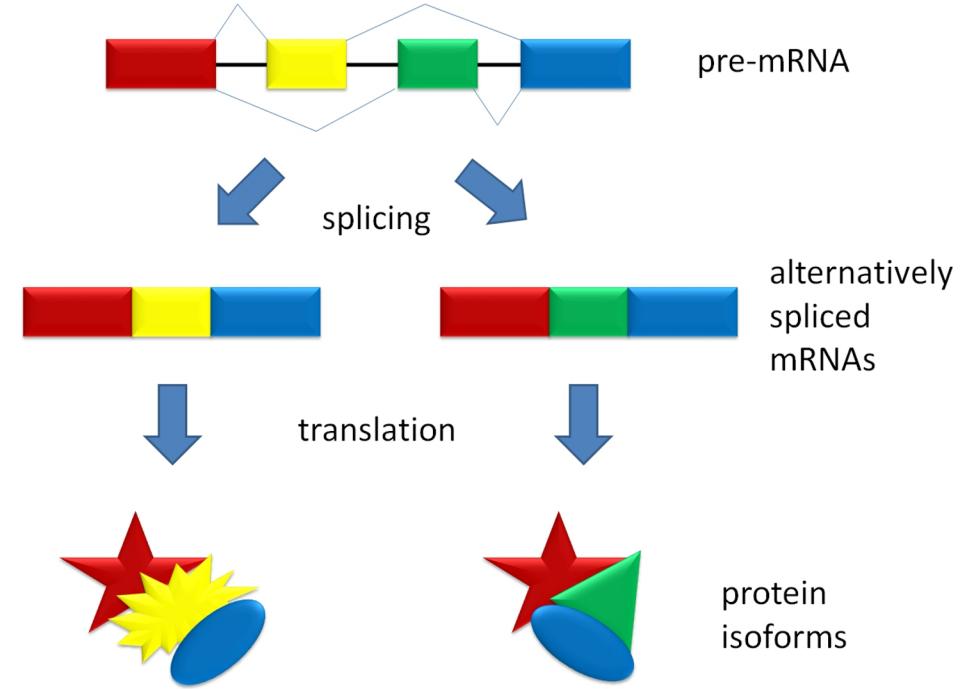


## Loci

27,433 total loci  
containing 36,995  
protein-coding  
transcripts

## Alternative Transcripts

$36,995 - 27,433 =$   
**9,562 total  
alternatively spliced  
transcripts**



wikipedia.org

# 4. Mitosis

Mitosis occurs in the somatic cells, and it is meant for the multiplication of cells.

- Development and growth
- Cell replacement
- Regeneration
- Asexual reproduction

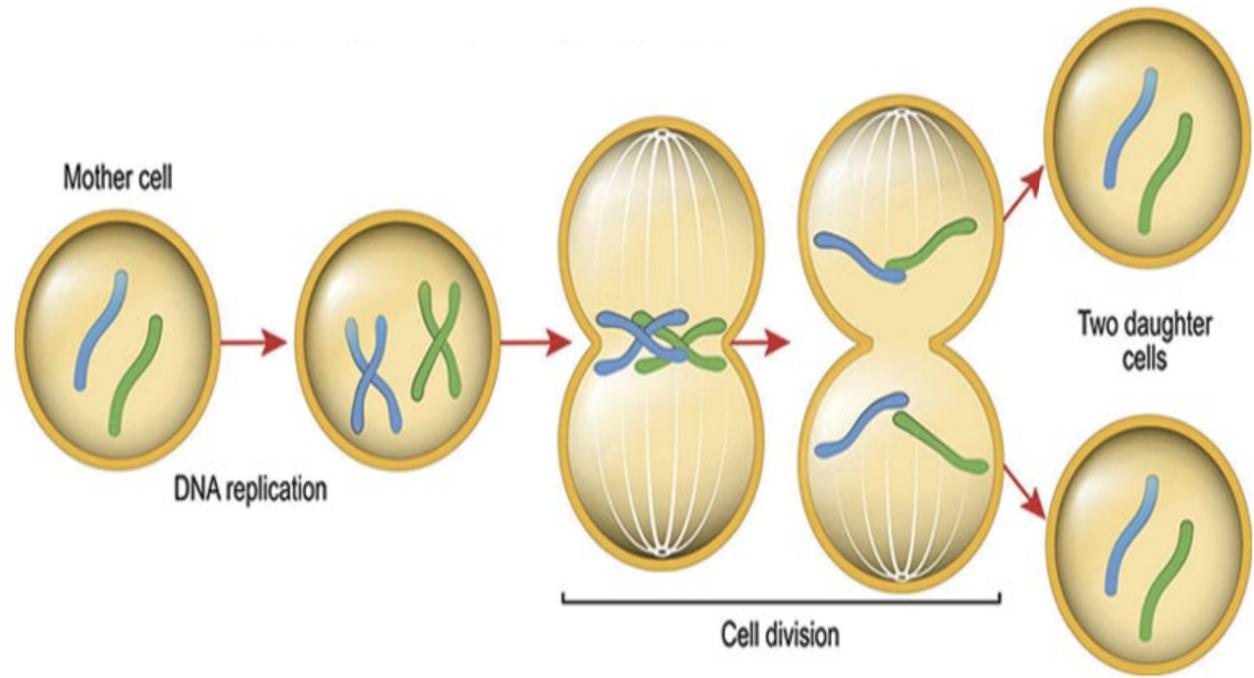


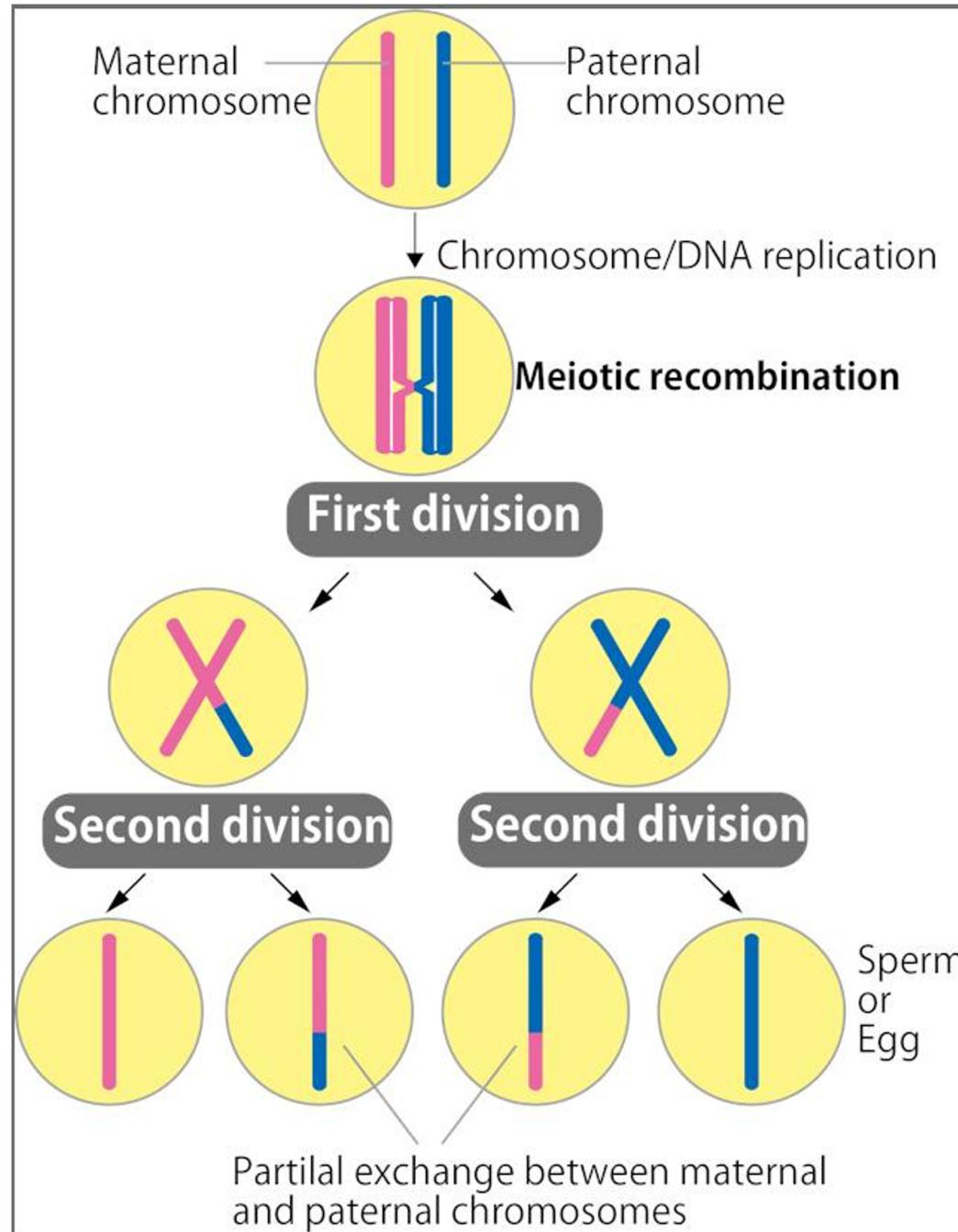
Image Source: [Biology Wise](#).

# 5. Meiosis

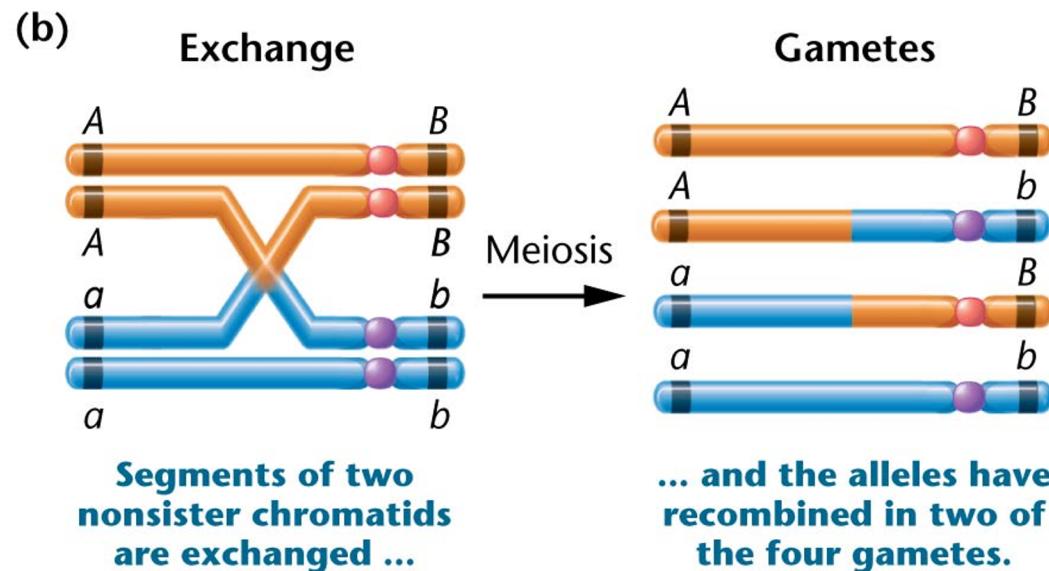
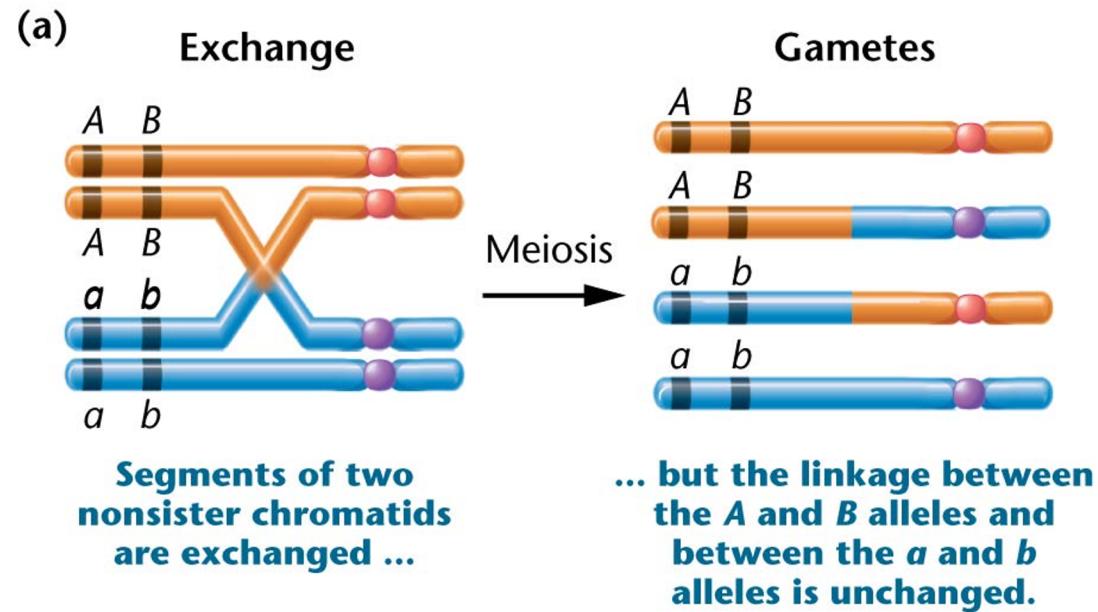
During meiosis, diploid cells undergo DNA replication, followed by two rounds of cell division in germ cells, producing four haploid sex cells.

Meiosis maintains genetic continuity from generation to generation and gives rise to genetic variation in gametes through:

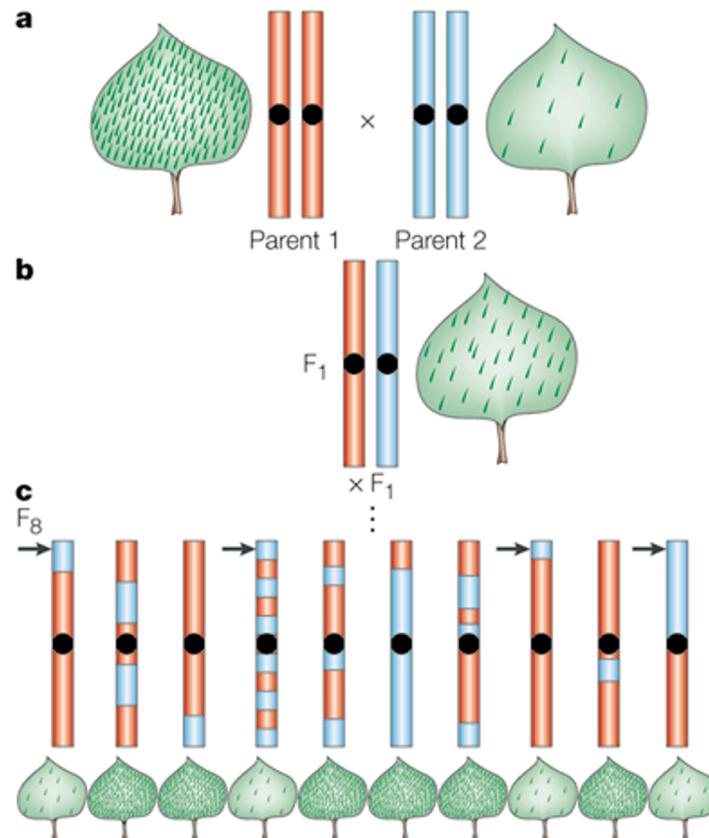
- Crossing over of homologous chromosomes.
- Unique combinations of maternal/paternal chromosomes.



# Crossing Over

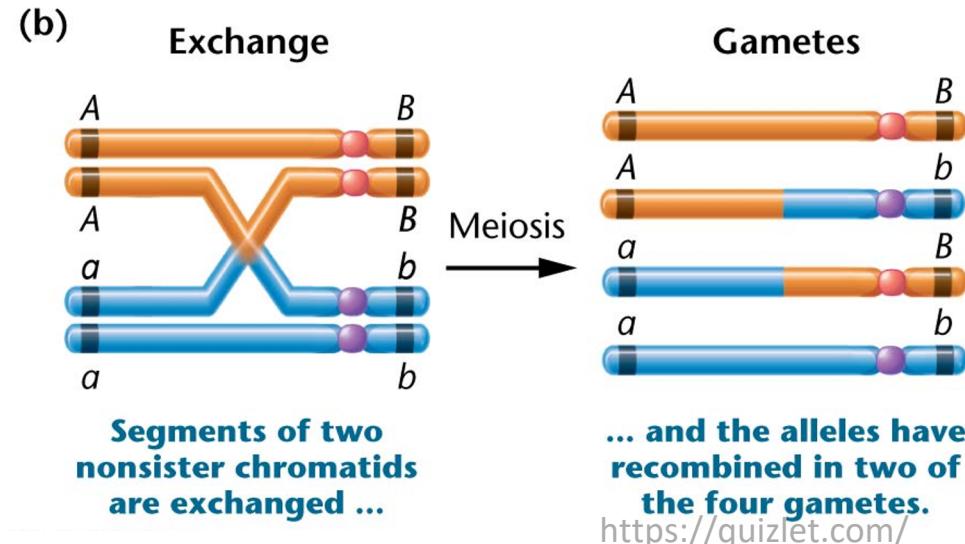
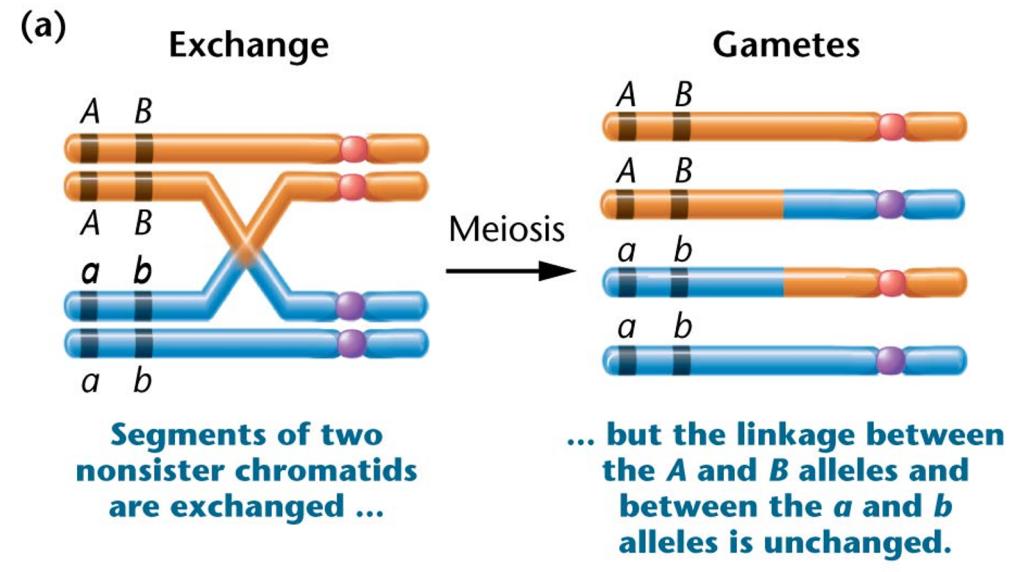


# Crossing Over

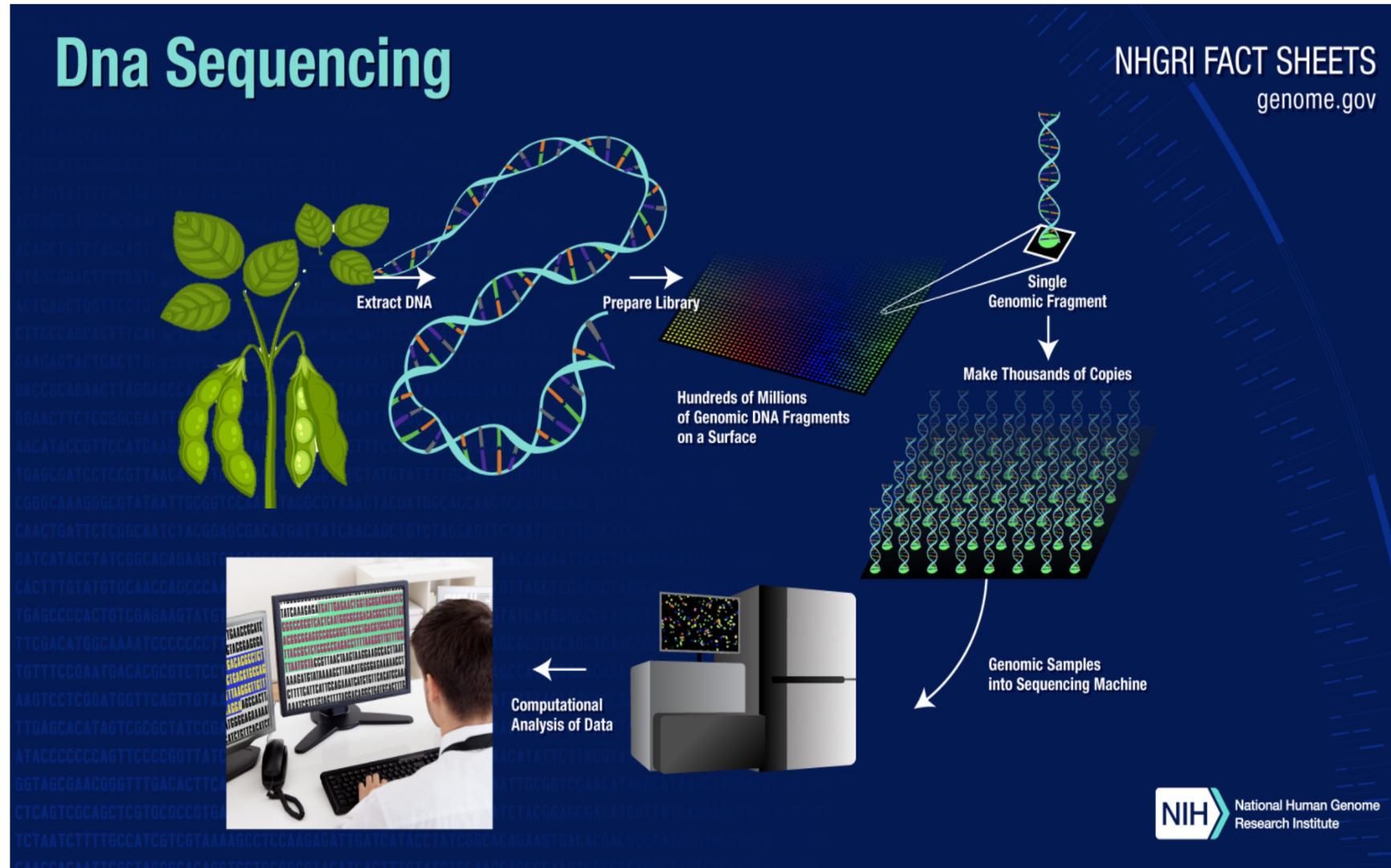


Nature Reviews | Genetics

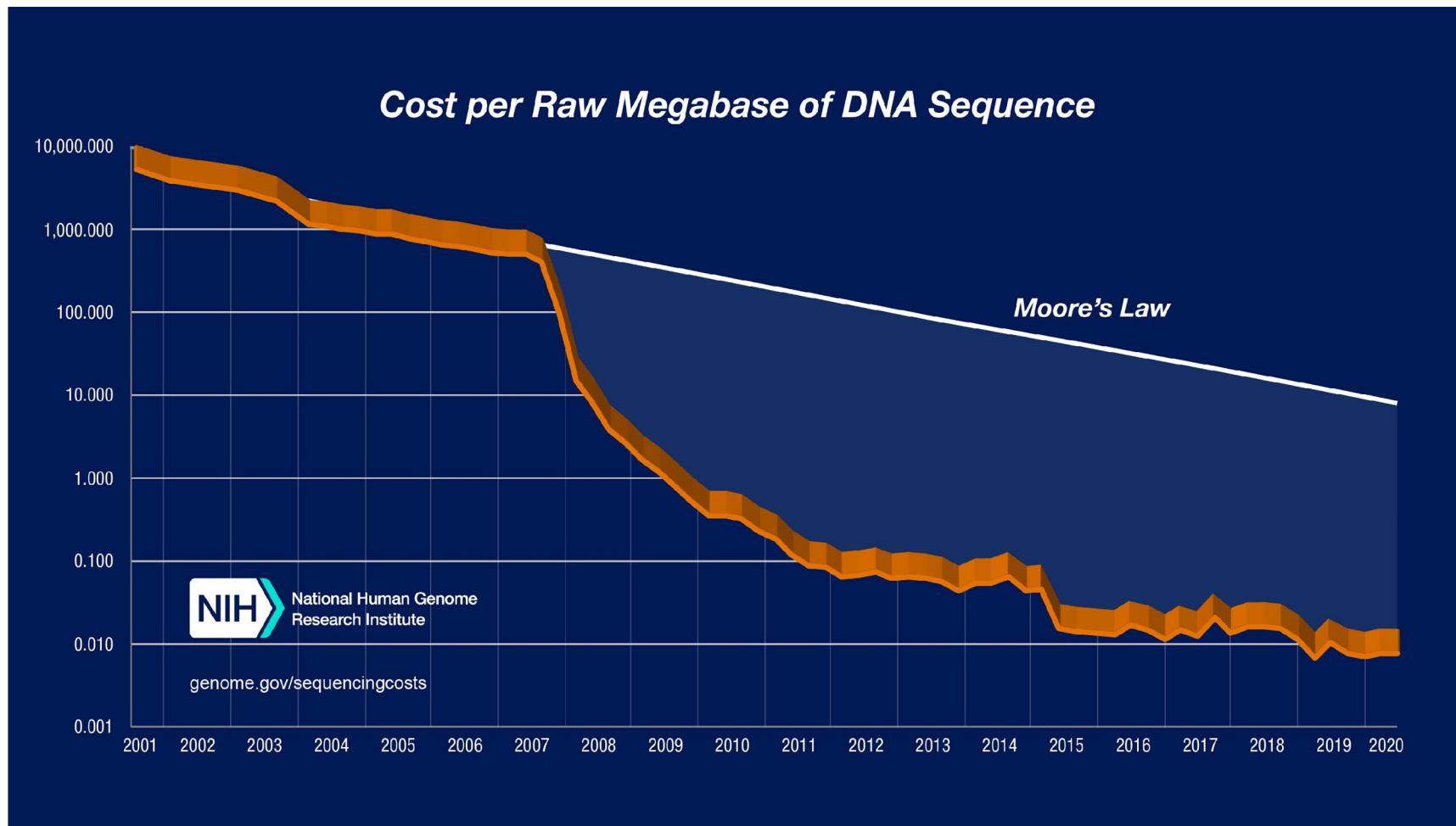
Mauricio  
2001



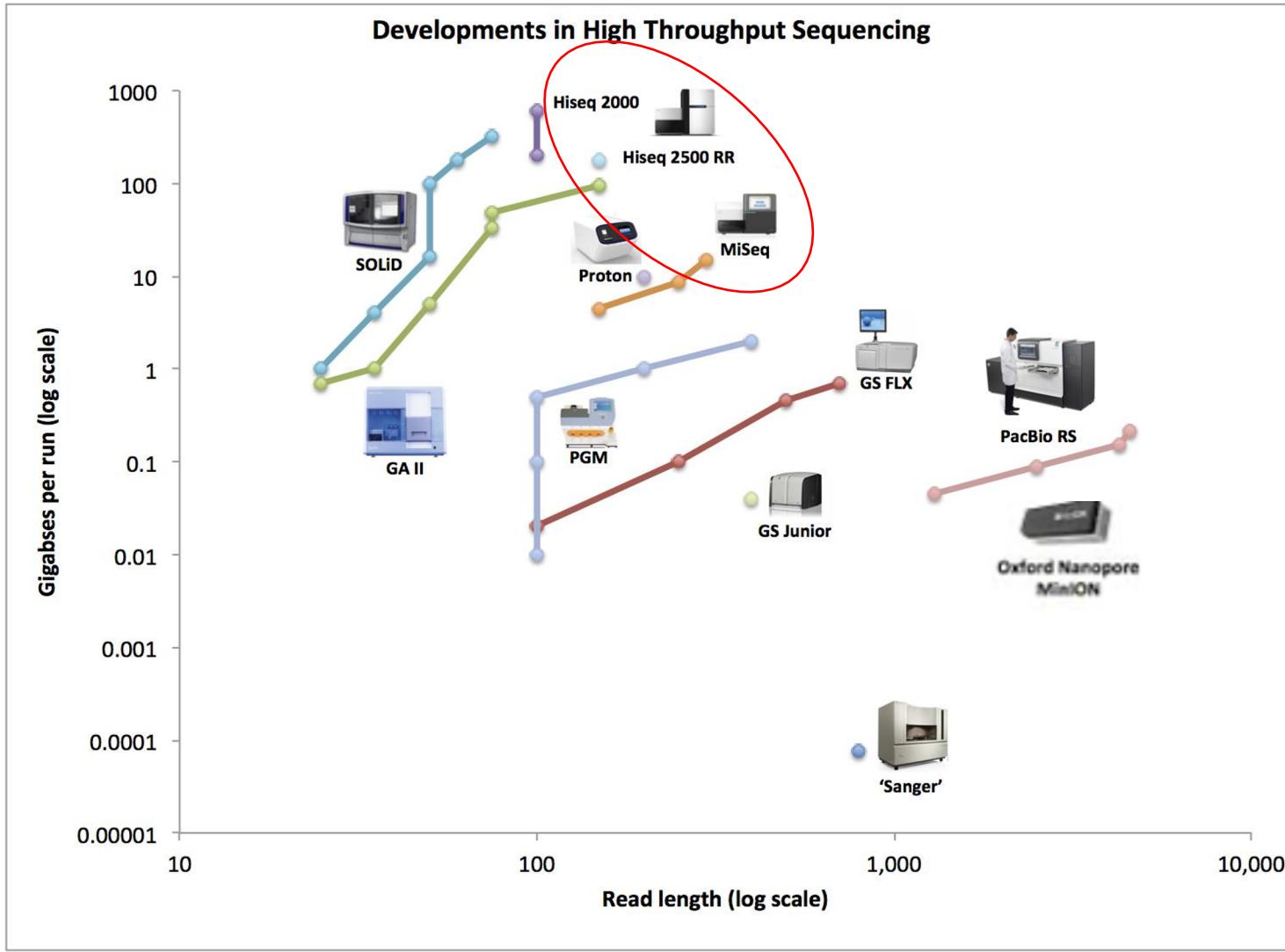
# Essential Genomics Tool: DNA Sequencing



# DNA Sequencing- Cost



# DNA Sequencing-Technology



# Whole Genome Sequencing



JGI Home JGI Data Portal Login Tools ▾ Projects ▾ Genomes ▾ Cart

Welcome to Phytozome ▾

Overview

Release Notes

## Recent Genome Releases

Genome	Common name	Release Date
Hydrangea quercifolia 'HQ6' v1.1	Oakleaf Hydrangea	Feb 3, 2021
Zostera marina v3.1	common eelgrass	Feb 3, 2021
Phaseolus acutifolius Frijol Bayo v1.0	tepary bean	Nov 6, 2020
Phaseolus acutifolius W6 15578 v2.0	tepary bean	Nov 6, 2020
Poncirus trifoliata v1.3.1	hardy orange	Oct 30, 2020
Joinvillea ascendens v1.1	'Ohe	Oct 30, 2020
Acorus americanus v1.1	American sweet flag	Oct 30, 2020

Phytozome, the Plant Comparative Genomics portal of the Department of Energy's Joint Genome Institute, provides JGI users and the broader plant science community a hub for accessing, visualizing and analyzing JGI-sequenced plant genomes, as well as selected genomes and datasets that have been sequenced elsewhere. By integrating this large collection of plant genomes into a single resource and performing comprehensive and uniform annotation and analyses, Phytozome facilitates accurate and insightful comparative genomics studies.

As of release v13, Phytozome hosts 224 assembled and annotated genomes, from 128 Archaeplastida species, and contains both the 54 Brachypodium

1. Choose genomes by selecting from tree or type genus/species/common name  
0 genomes selected ▾

2. find genes by keyword search by BLAST get standard data files build custom data sets

The screenshot shows a list of genomes categorized by genus. The highlighted section, enclosed in a red box, lists various Phaseolus species with their version numbers and download links. Other genera listed include Glycine, Lotus, Lupinus, Malus, Medicago, Prunus, Trifolium, and Vigna. Each entry includes a green 'info' icon, a 'RST' button, and a 'JGI' button.

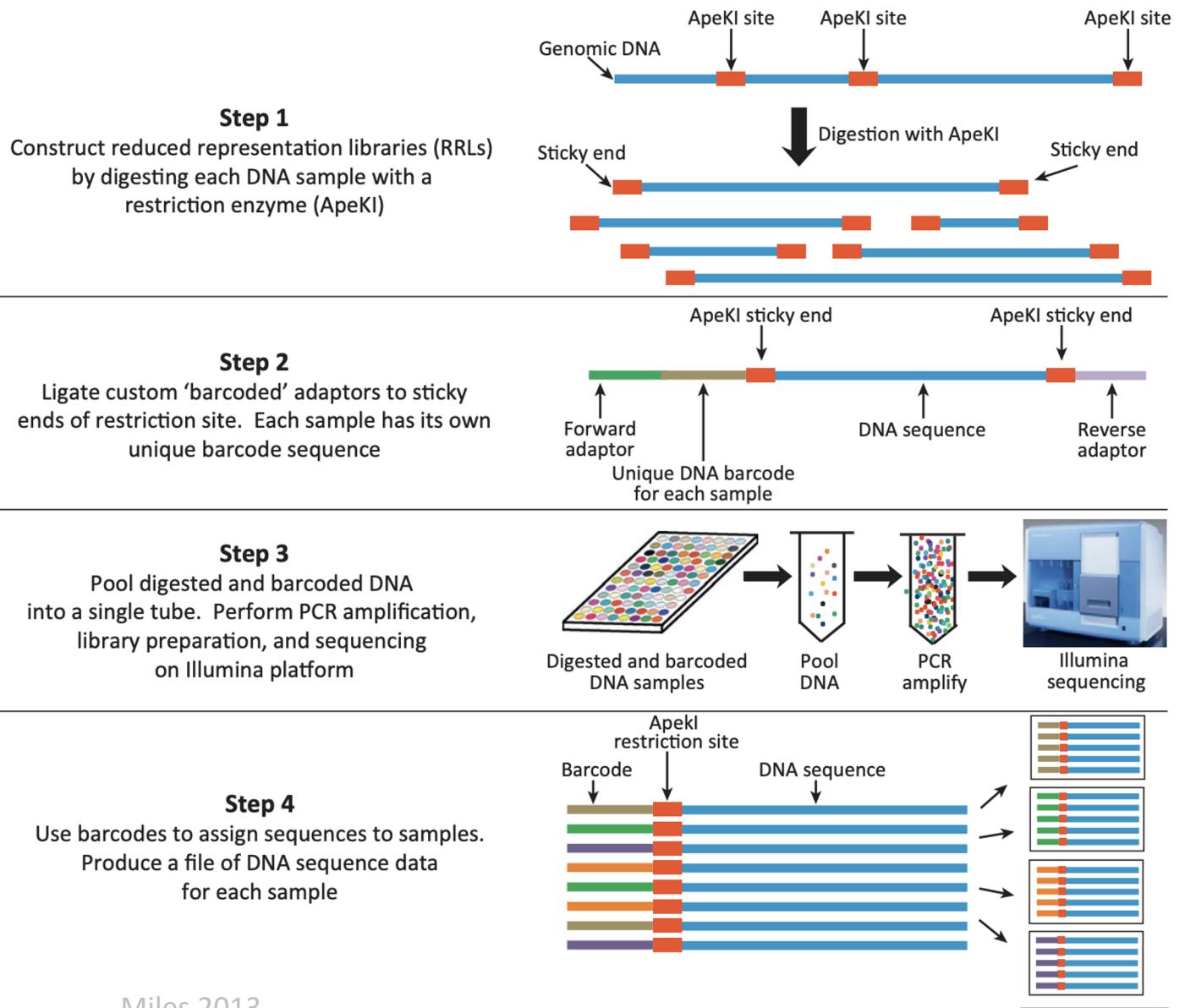
- Glycine max Lee v1.1 ⓘ RST JGI
- Glycine soja v1.1 ⓘ RST JGI
- Lotus japonicus Lj1.0v1 ⓘ UNRST EXT
- Lupinus albus v1 ⓘ UNRST EXT
- Malus domestica v1.1 ⓘ RST EXT
- Medicago truncatula Mt4.0v1 ⓘ UNRST EXT
- Phaseolus acutifolius v1.0 ⓘ RST EXT
- Phaseolus acutifolius WLD v2.0 ⓘ RST EXT
- Phaseolus lunatus V1 ⓘ RST EXT
- Phaseolus vulgaris v2.1 ⓘ RST JGI
- Phaseolus vulgaris UI111 v1.1 ⓘ RST JGI
- Prunus persica v2.1 ⓘ UNRST JGI
- Trifolium pratense v2 ⓘ RST EXT
- Vigna unguiculata
  - Vigna unguiculata v1.1 ⓘ UNRST COWPEAPAN JGI
  - Vigna unguiculata v1.2 ⓘ RST COWPEAPAN JGI
  - Vigna unguiculata CB5-2 v1.1 ⓘ RST COWPEAPAN JGI
  - Vigna unguiculata Sanzi v1.1 ⓘ RST COWPEAPAN JGI
  - Vigna unguiculata Suvita2 v1.1 ⓘ RST COWPEAPAN JGI
  - Vigna unguiculata TZ20 v1.2 ⓘ RST COWPEAPAN JGI

As of release v13, Phytozome hosts 224 assembled and annotated genomes! <https://phytozome-next.jgi.doe.gov/>

# Genotyping-by-Sequencing (GBS)

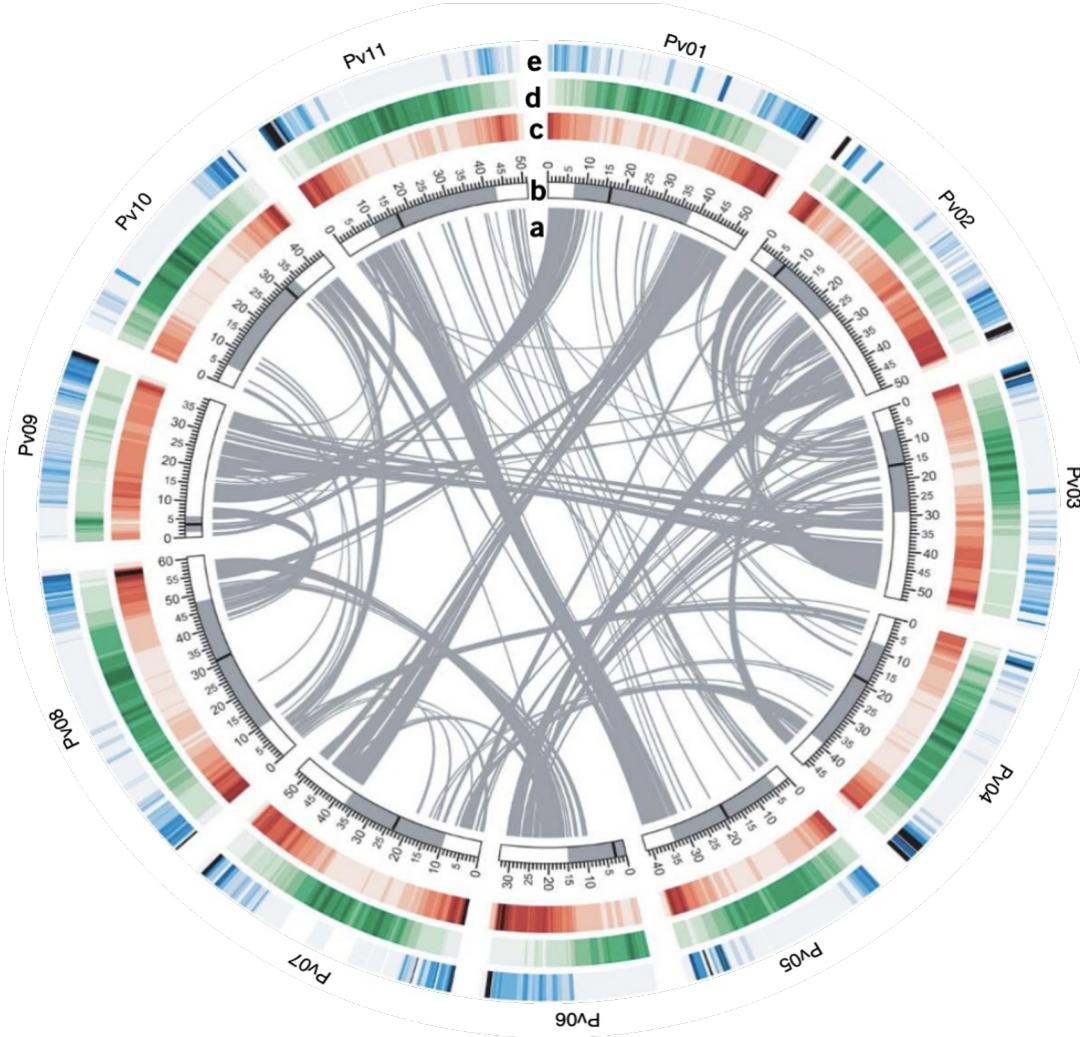
This approach is simple, quick, specific, highly reproducible, and may reach important regions of the genome

Elshire *et al.* 2011



# Review

- Big picture of GS
- Genome
- Chromosomes
- Genes (alternative splicing)
- Mitosis and meiosis
- Crossing over
- DNA sequencing
- GBS



**Genome**  
~537.2 Mb

**Loci**  
27,433 total loci containing  
36,995 protein-coding  
transcripts

**Alternative Transcripts**  
9,562 total alternatively  
spliced transcripts

