

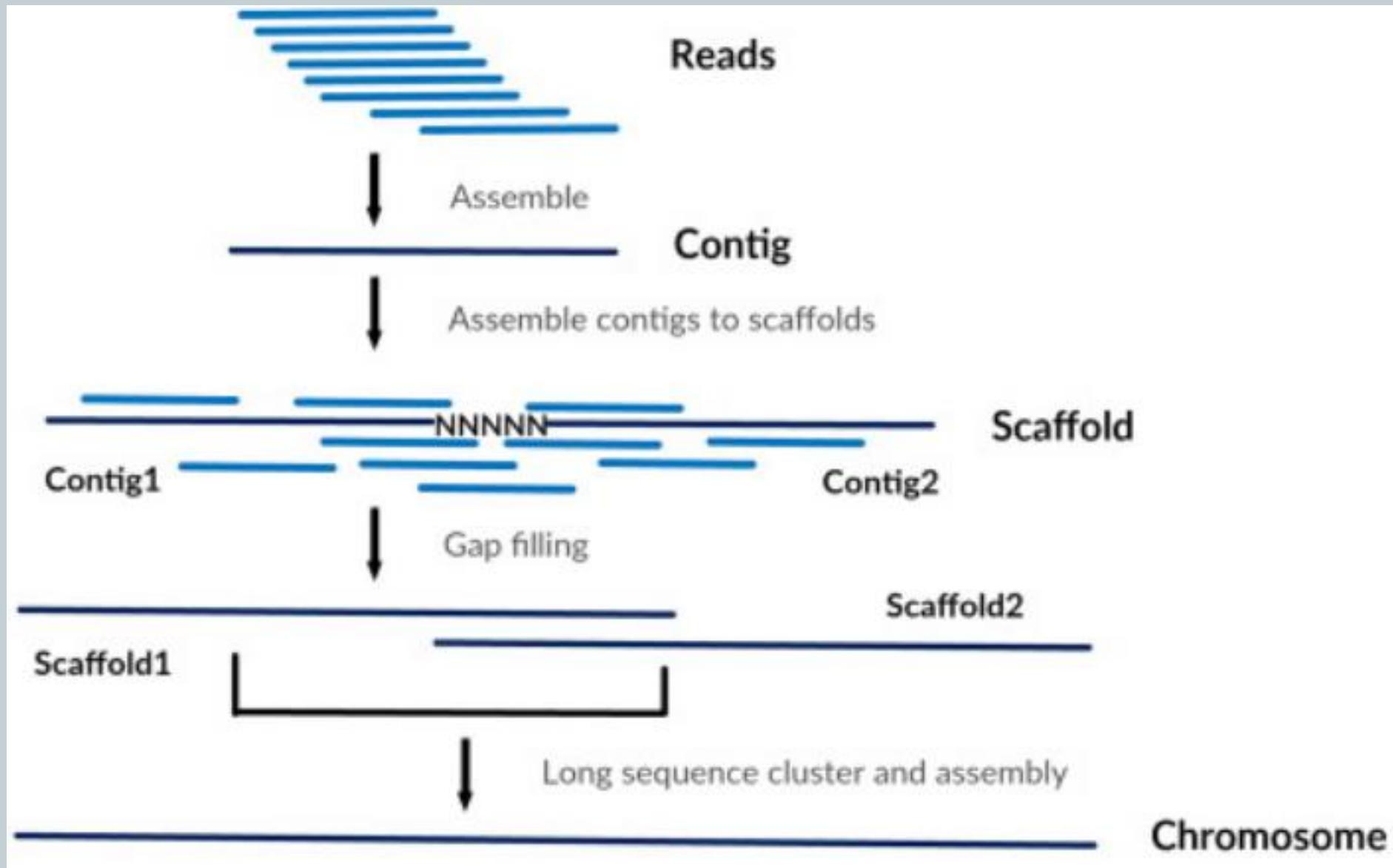
LINKAGE MAPPING

**Sujan Mamidi &
Divyashree Nageswaran**

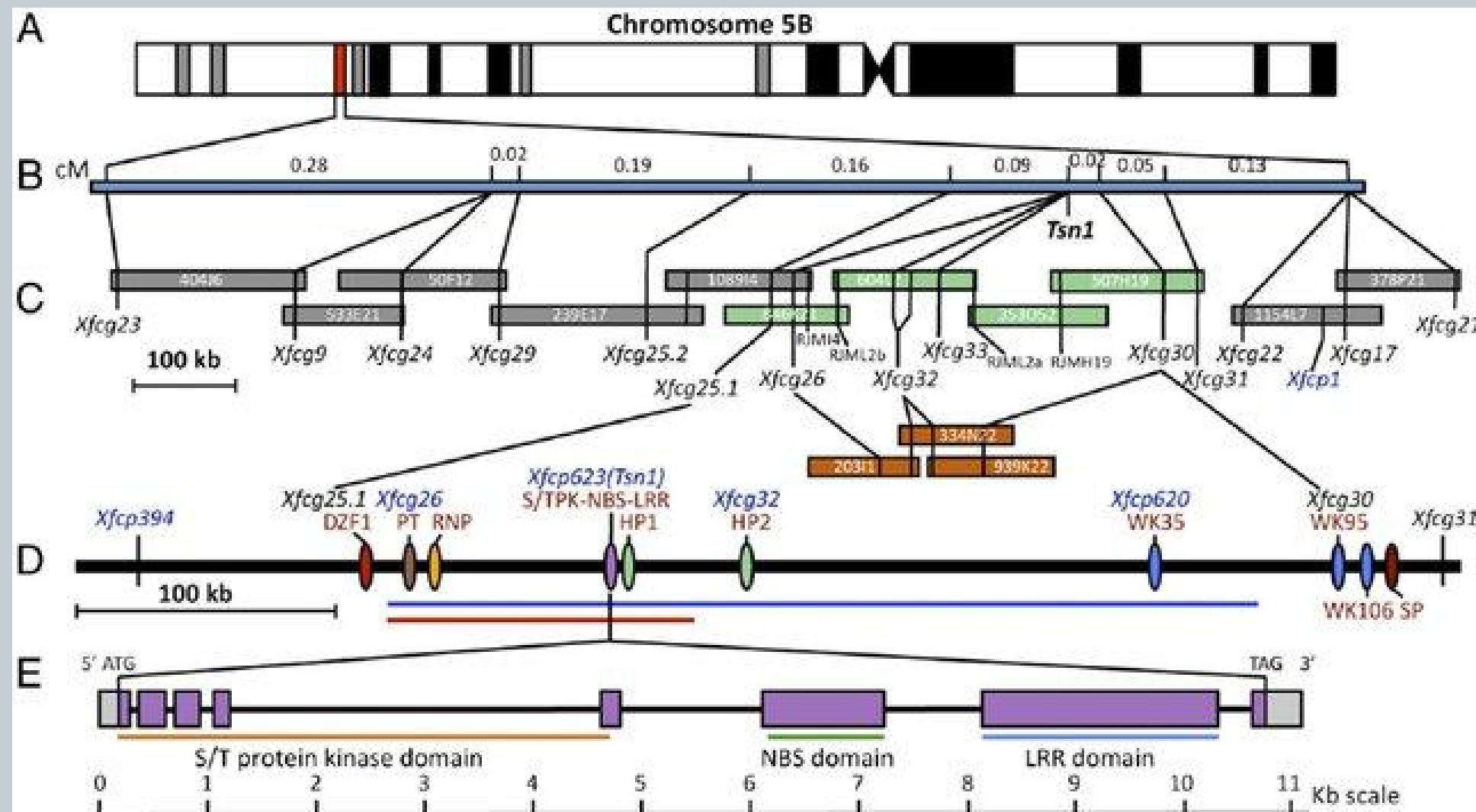
Applications/Uses of Linkage Maps:

- Genome Assembly
- Map based cloning
- Studying genome structure, organization and evolution – Synteny.
- QTL analysis
 - Identify genes responsible for traits of interest
 - Estimation of gene effects of important agronomic traits
 - Tagging genes of interest to facilitate marker assisted selection (MAS) programs.

Genome assembly

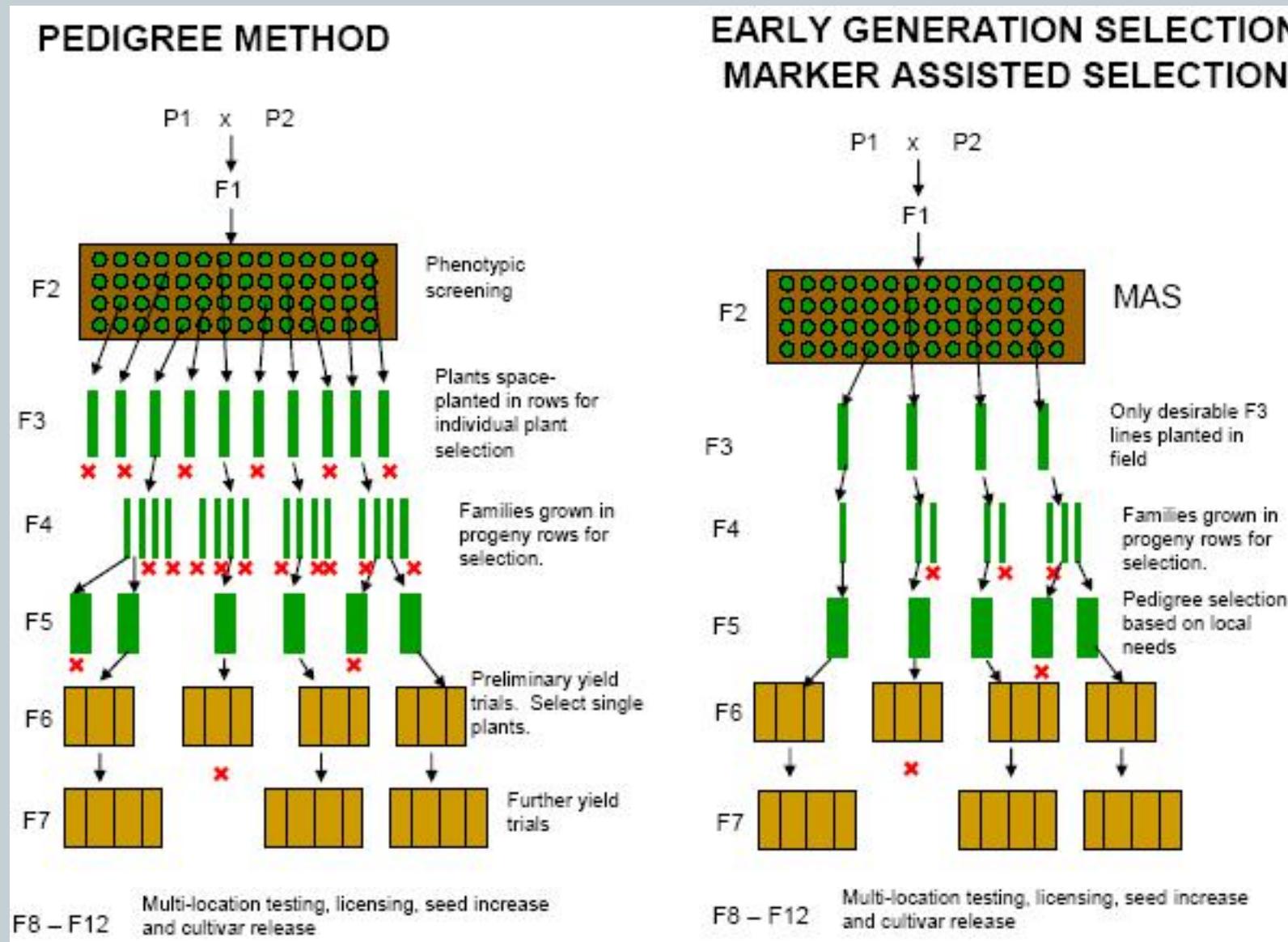


Map based cloning :



Faris et.al 2010: A unique wheat disease resistance-like gene confers toxin-induced susceptibility to necrotrophic pathogens

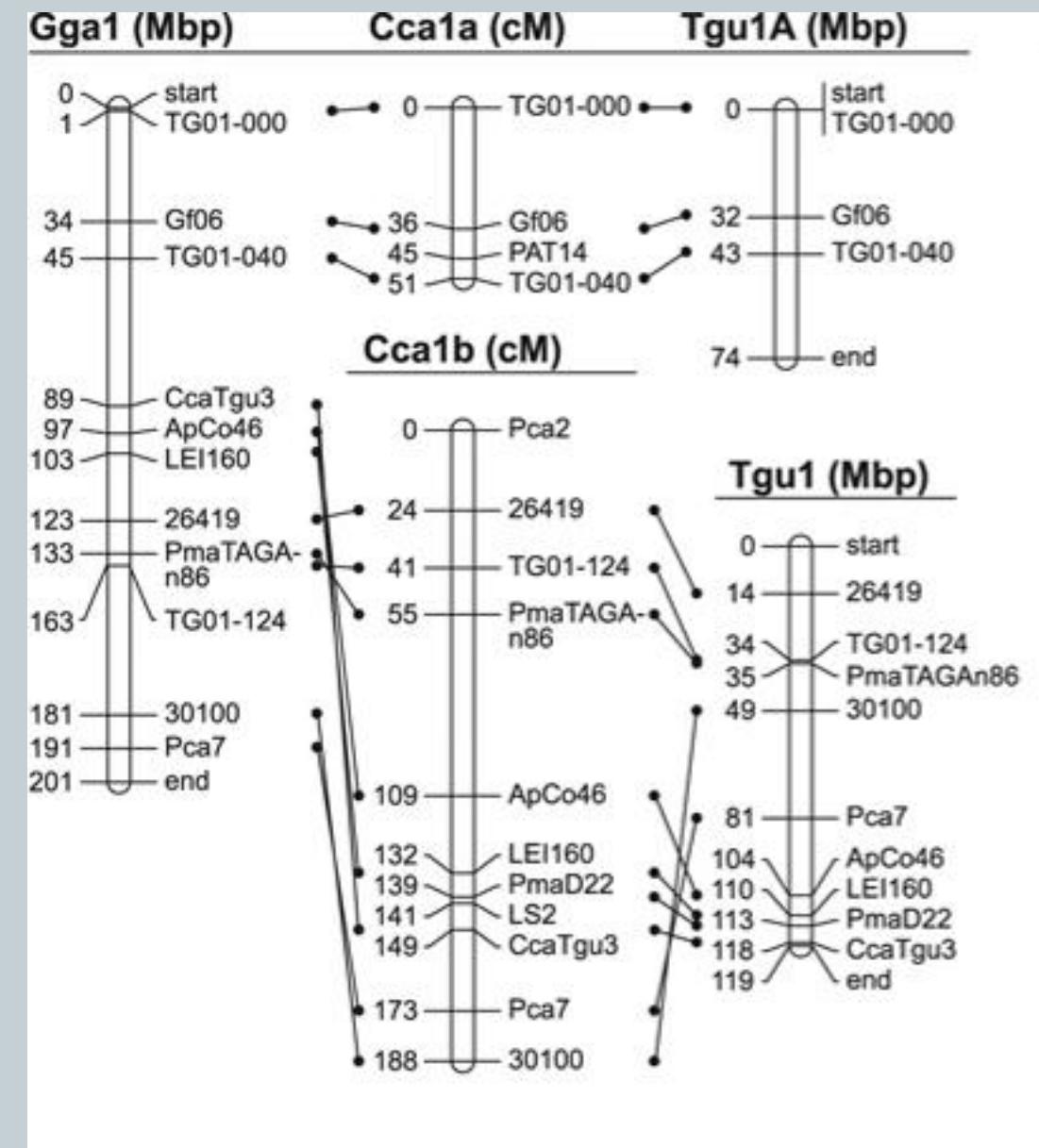
Marker assisted selection



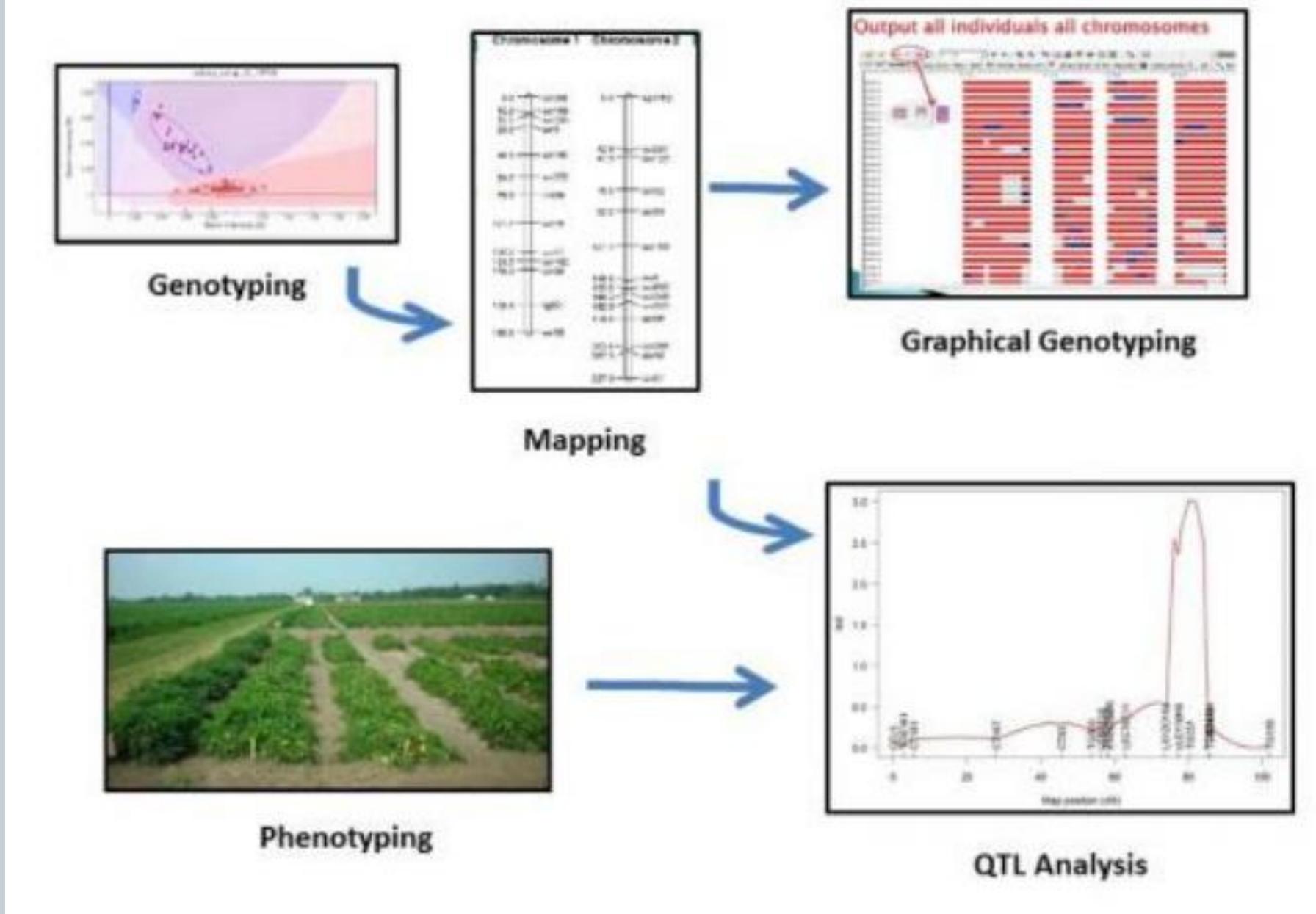
Genome evolution

Blue tit (*Cyanistes caeruleus*; *Cca*) in cM

Orthologs loci
Chicken *Gga*) and zebra finch genomes
(*Tgu* in Mbp).



QTL analysis



Steps in Genetic Linkage Mapping

- Development of The Mapping Population
- Genotyping of Mapping Population (Molecular Markers)
- Map Construction (Linkage Map)

I) Mapping Populations

Parents:

- Contrasting for trait of interest.

Develop a Segregating population

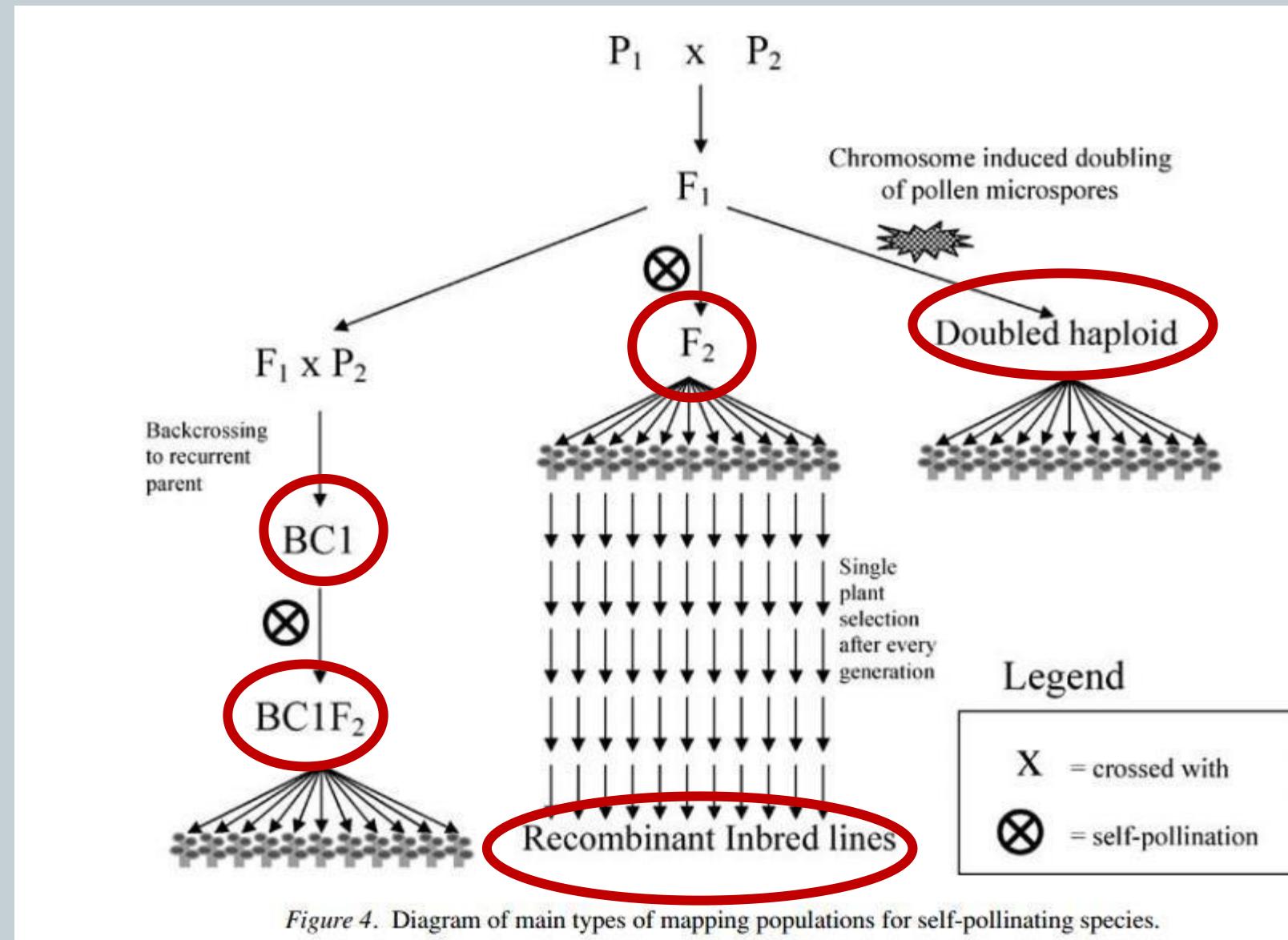
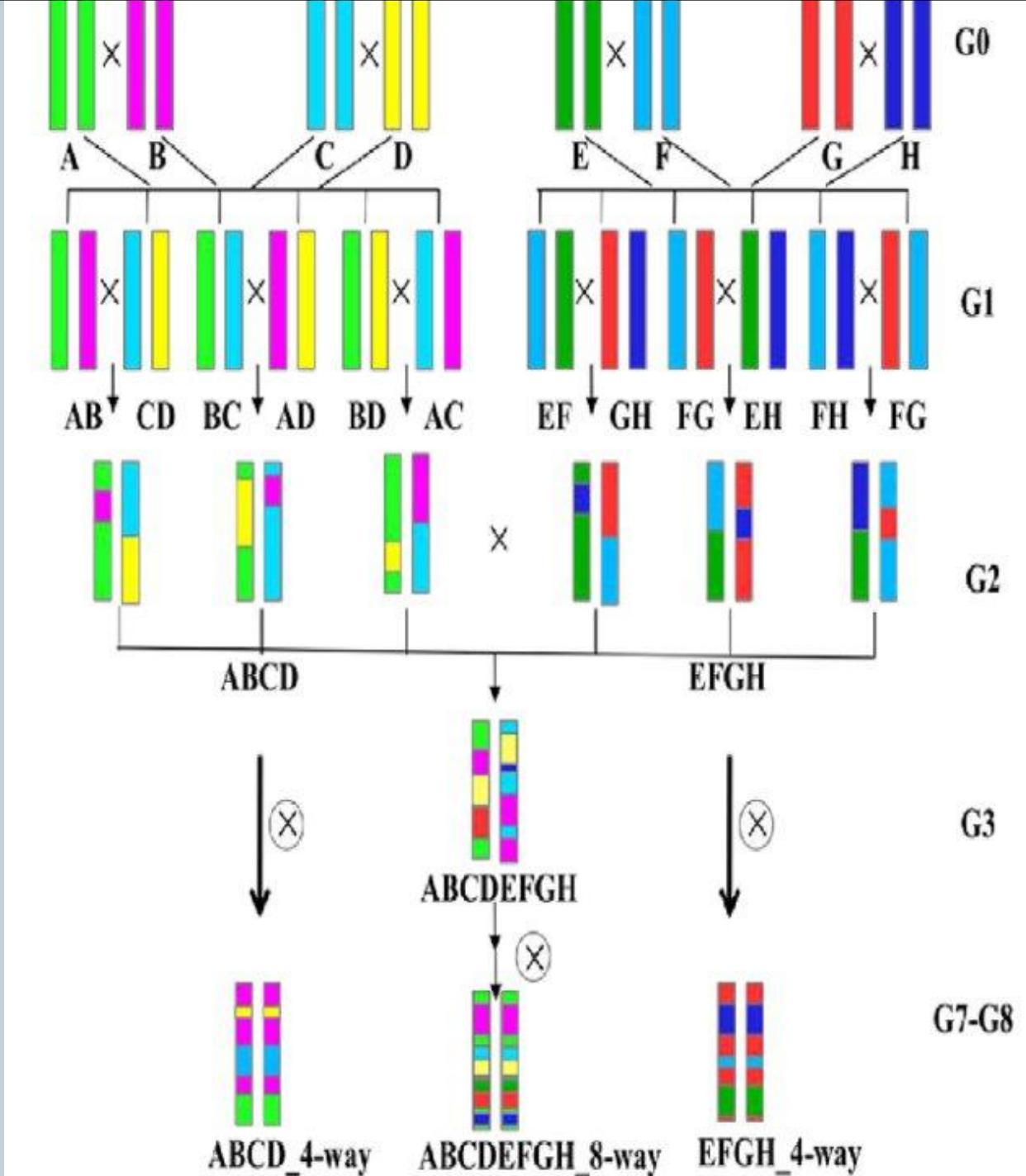


Figure 4. Diagram of main types of mapping populations for self-pollinating species.

MAGIC Populations

4-way and 8-way populations



Meng et al. 2016 - Characterization of Three Rice Multiparent Advanced Generation Intercross (MAGIC) Populations for Quantitative Trait Loci Identification

POLYPLOIDS

- Possess more than two complete sets of chromosome
 - **Auto polyploids** - Arise within a species
 - Homozygous at every locus in the genome
 - **Allo polyploids**- Arise due to the hybridization of two distinct species
 - Varying degrees of heterozygosity
 - Depends on the divergence of the parental genomes
 - **Advantages**
 - Hybrid vigor and better adaptation
 - Gene redundancy
- Canola
 - Grape
 - Switchgrass
 - Wheat
 - Tobacco
 - Banana
 - Strawberry
 - Sugarcane
 - Alfa-alfa
 - Potato

- For highly heterozygous crops, we can map in **F₁ populations**,
- Parents (or at least one of them) carry several alleles
- segregate in the F₁ progeny.

Parent genotypes	Expected gamete ratios		Expected progeny phenotype ratios*	
	Disomic-digenic	Tetrasomic	Disomic-digenic	Tetrasomic
a ₁ a ₁ a ₂ a ₂ × A ₁ a ₁ a ₂ a ₂	(aa) × (1Aa:1aa)	(aa) × (1Aa:1aa)	1:1	1:1
a ₁ a ₁ a ₂ a ₂ × A ₁ A ₁ a ₂ a ₂	(aa) × (Aa)	(aa) × (1AA:4Aa:1aa)	1:0	5:1
a ₁ a ₁ a ₂ a ₂ × A ₁ a ₁ A ₂ a ₂	(aa) × (1AA:2Aa:1aa)	(aa) × (1AA:4Aa:1aa)	3:1	5:1
a ₁ a ₁ a ₂ a ₂ × A ₁ a ₁ A ₂ A ₂	(aa) × (1Aa:1Aa)	(aa) × (1Aa:1aa)	1:1	1:1
a ₁ a ₁ a ₂ a ₂ × A ₁ A ₁ A ₂ A ₂	(aa) × (AA)	(aa) × (AA)	1:0	1:0
a ₁ a ₁ A ₂ a ₂ × a ₁ a ₁ A ₂ a ₂	(1aa:1Aa) × (1aa:1Aa)	(1aa:1Aa) × (1aa:1Aa)	3:1	3:1
a ₁ a ₁ A ₂ A ₂ × a ₁ a ₁ A ₂ A ₂	(Aa) × (Aa)	(1AA:4Aa:1aa) × (1A:4Aa:1aa)	1:0	35:1
A ₁ a ₁ A ₂ a ₂ × A ₁ a ₁ A ₂ a ₂	(1AA:2Aa:1aa) × (1AA:2Aa:1aa)	(1AA:4Aa:1aa) × (1AA:4Aa:1aa)	15:1	35:1
A ₁ A ₁ A ₂ a ₂ × A ₁ A ₁ A ₂ a ₂	(1AA:1Aa) × (1AA:1Aa)	(1AA:1Aa) × (1AA:1aa)	3:1	3:1

* Assuming complete dominance of allele A.

Disomic in Allotetraploids

Tetrasomic in Auto-tetraploids

2) Markers

Dominant – 2 states

Co-dominant – 3 states

- SSR
- SNP
 - Illumina chips
 - GBS
 - NGS
- Indels
- kmers

Segregating Ratios
I:I RILs
I:2:I – F2

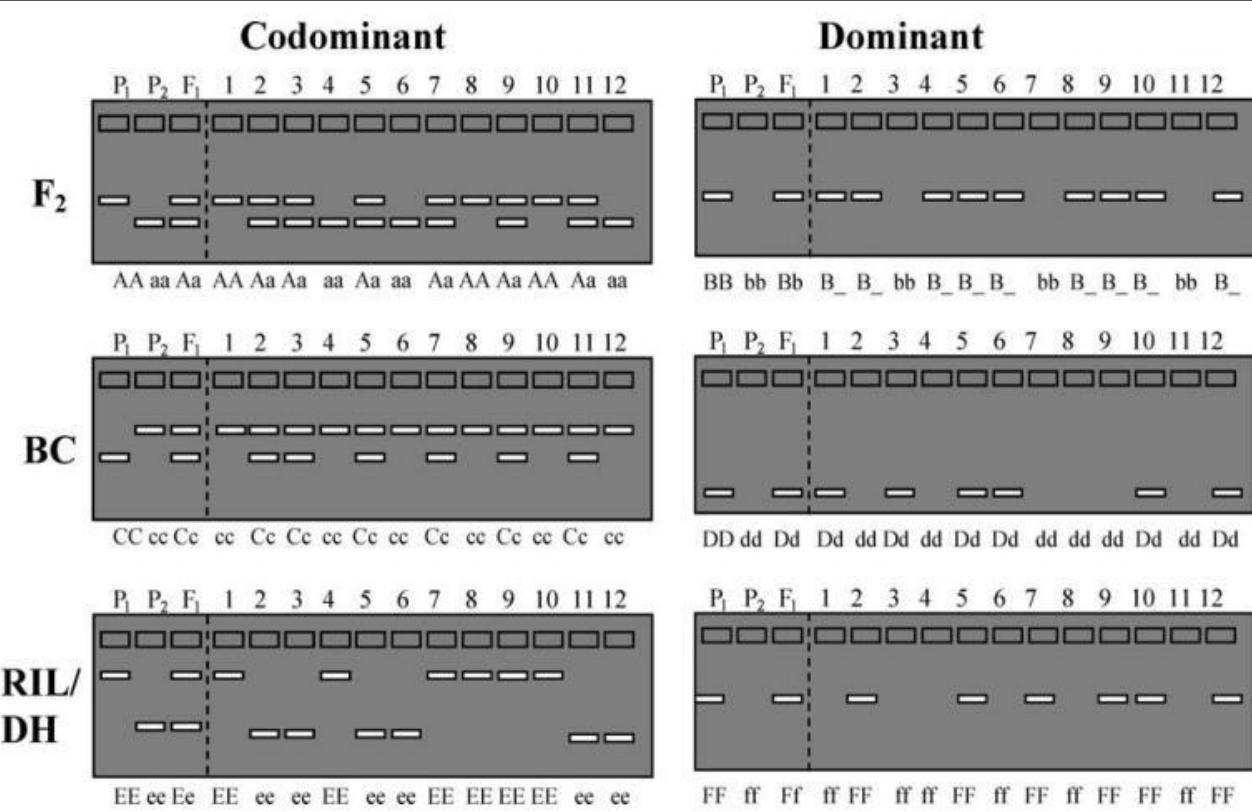
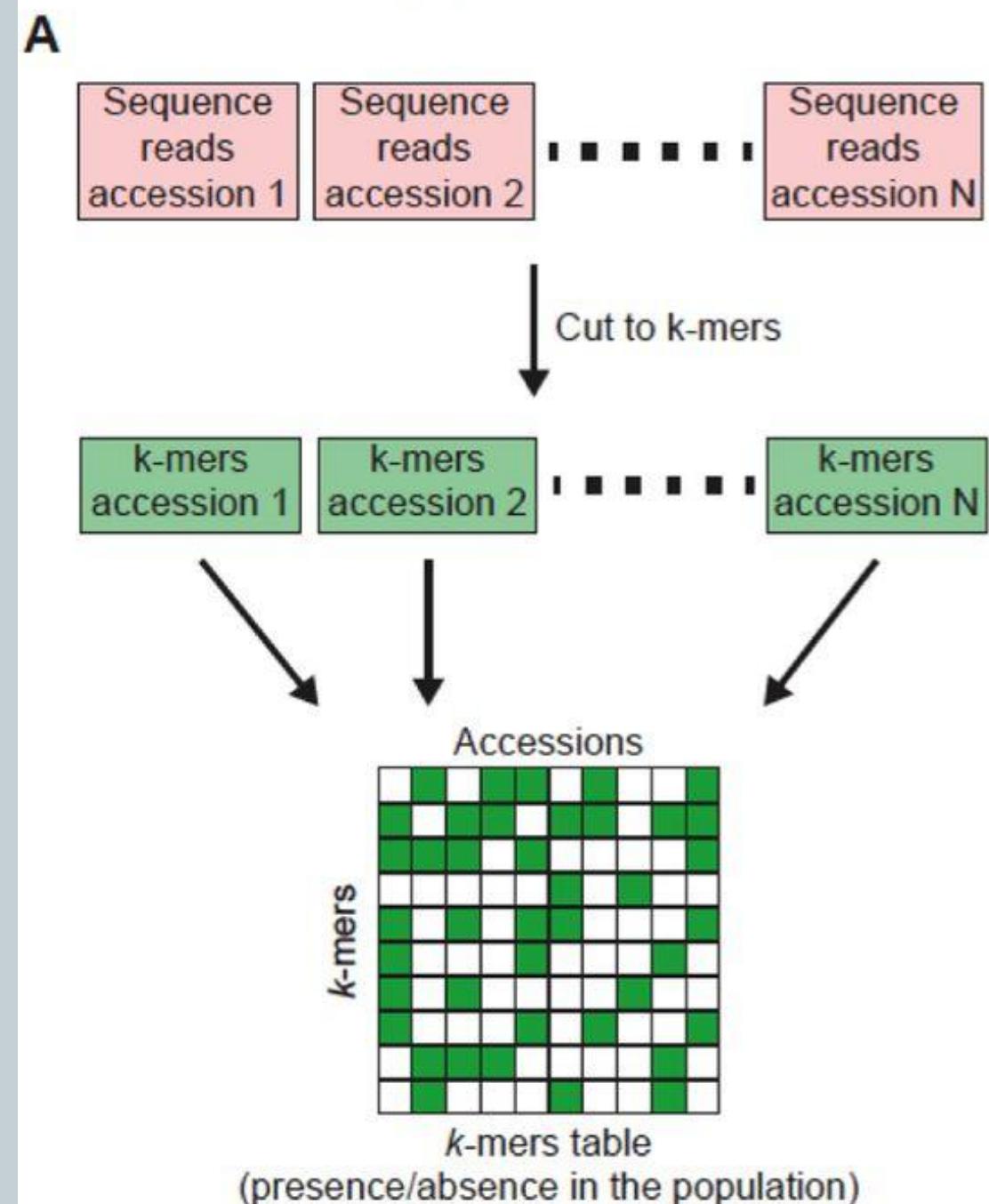
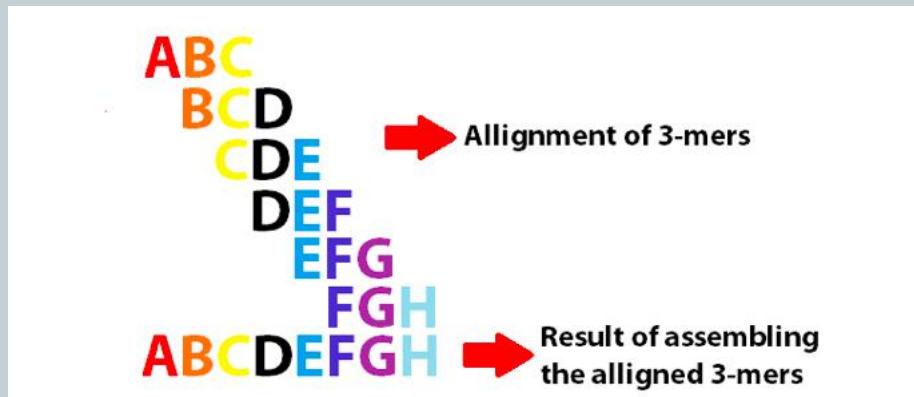


Figure 5. Hypothetical gel photos representing segregating codominant markers (left-hand side) and dominant markers (right-hand side) for typical mapping populations. Codominant markers indicate the complete genotype of a plant. Note that dominant markers cannot discriminate between heterozygotes and one homozygote genotype in F₂ populations. The segregation ratios of markers can be easily understood by using Punnett squares to derive population genotypes.

Kmers

Short fragment of sequences



Polyploids

Type	Parent 1	Parent 2
Null (N)	AAAA	BBBB
Simplex (S)	AAAA	AAAB
Simplex (S)	ABBB	BBBB
Triplex (T)	AAAA	ABBB
Triplex (T)	AAAB	BBBB
Duplex (D)	AAAA	AABB
Duplex (D)	AABB	BBBB
Double-simplex (SS)	AAAB	AAAB
Double-simplex (SS)	ABBB	ABBB
X-double-simplex (XSS)	AAAB	ABBB
Simplex-duplex (SD)	AAAB	AABB
Duplex-simplex (DS)	AABB	ABBB
Double-duplex (DD)	AABB	AABB
Total		

Genotype classes ; [Ferreira](#) et al. 2019. Genetic Mapping With Allele Dosage Information in Tetraploid *Urochloa decumbens* (Stapf) R. D. Webster Reveals Insights Into Spittlebug (*Notozulia enteriana* Berg) Resistance

Software for polyploid linkage map

- polymapR
- TetraploidSNPMap
- netgwas

Autotetraploid Segregation

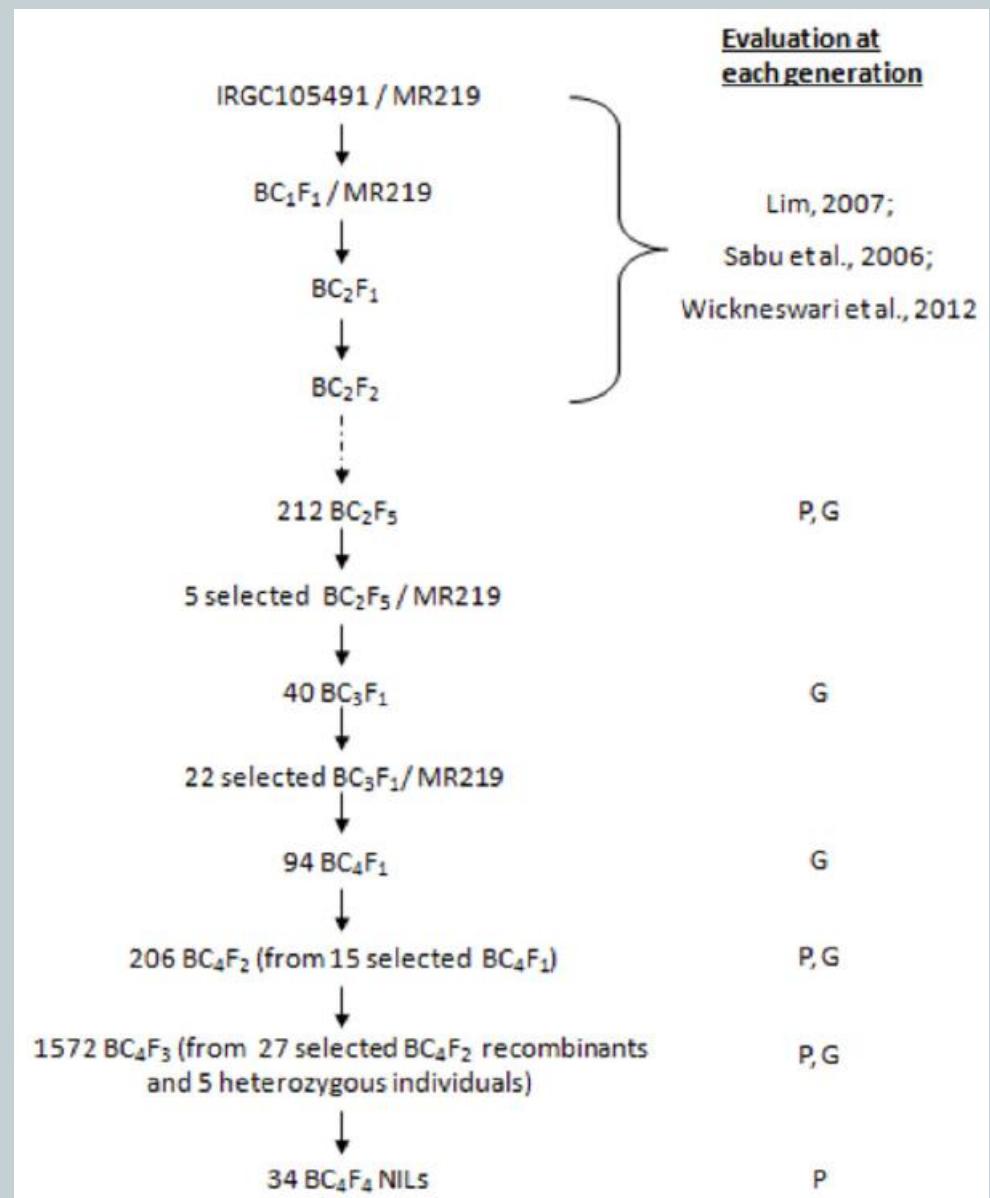
Cross	Nulliplex (aaaa)				
Nulliplex (aaaa)	All N	Simplex (Aaaa)			
Simplex (Aaaa)	1S:1N	1D:2S:1N	Duplex (AAaa)		
Duplex (AAaa)	1D:4S:1N	1T:5D:5S: 1N	1Q:8T:18D: 8S:1N	Triplex (AAAa)	Quad'plex (AAAA)
Triplex (AAAa)	1D:1S	1T:2D:1S	1Q:5T:5D: 1N	1Q:2T:1D	
Quad'plex (AAAA)	All D	1T:1D	1Q:4T:1D	1Q:1T	All Q

https://www.webpages.uidaho.edu/jbrown/plsc546/class_notes/class-15-Qualitative%20Genetics%20III-2008.pdf

Map saturation

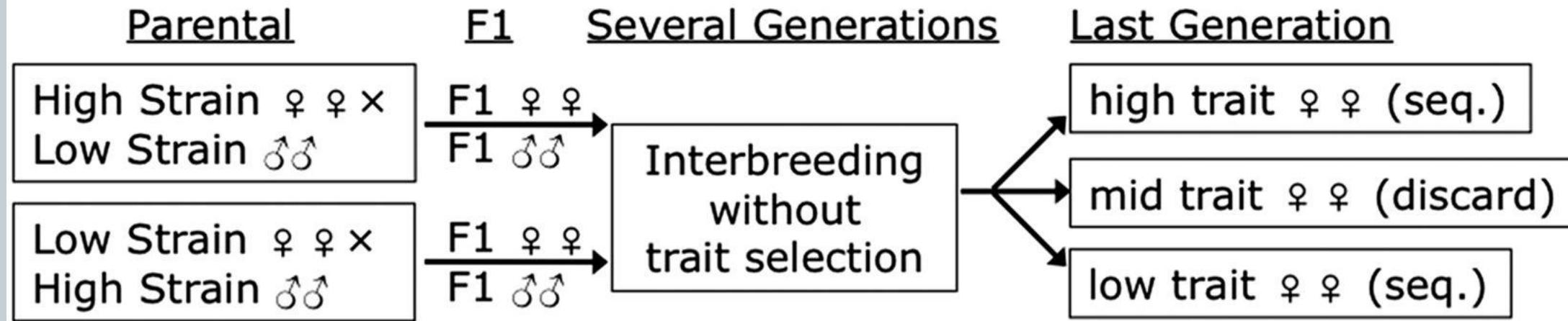
Ex: A region of interest is about 5cM with about 200 genes. To narrow the interval

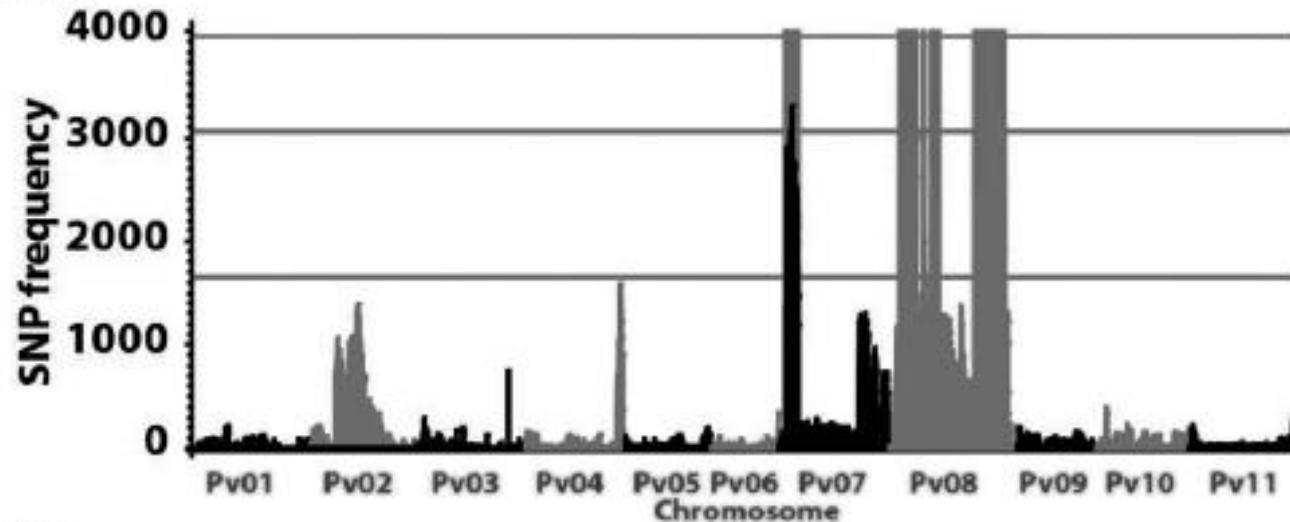
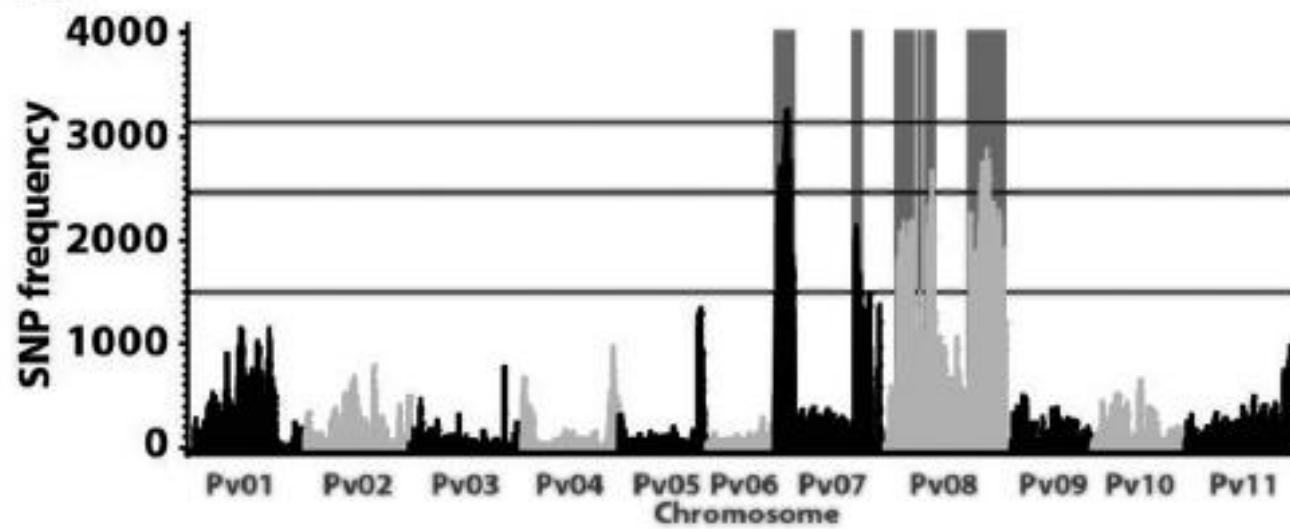
- i. **Nearly isogenic lines (NIL)**: for targeting regions with a gene of interest
- a) Backcrossing a particular gene into desirable cultivar e.g., Williams, - cultivar in soybean
- Williams 79, and Williams 82 soybeans-- phytophthora genes introgressed)
- b) NILs have homogeneous genetic background, except in the location of the gene.



ii. Bulk segregant analysis (BSA):

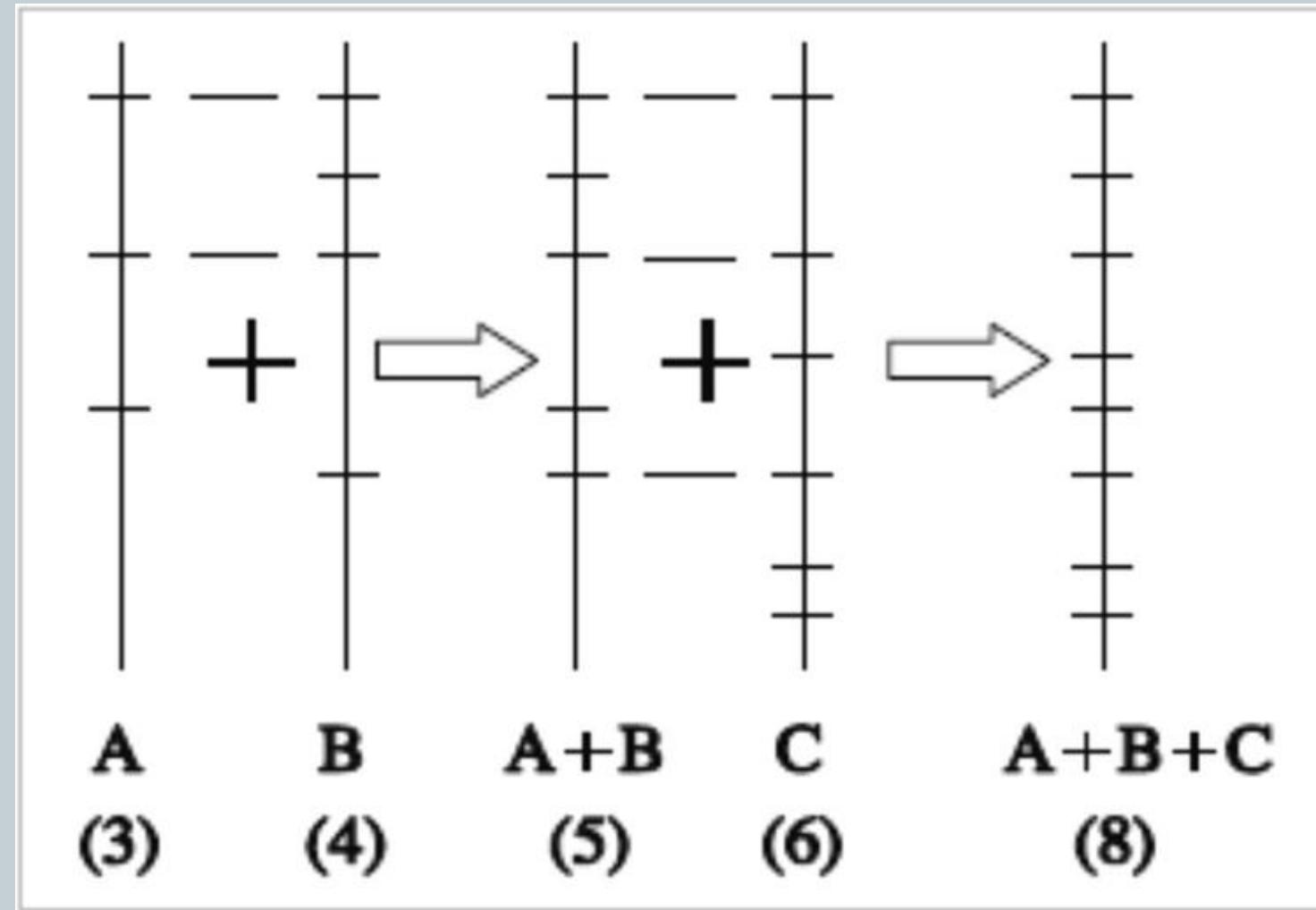
BULK SEGREGANT ANALYSIS (BSA):

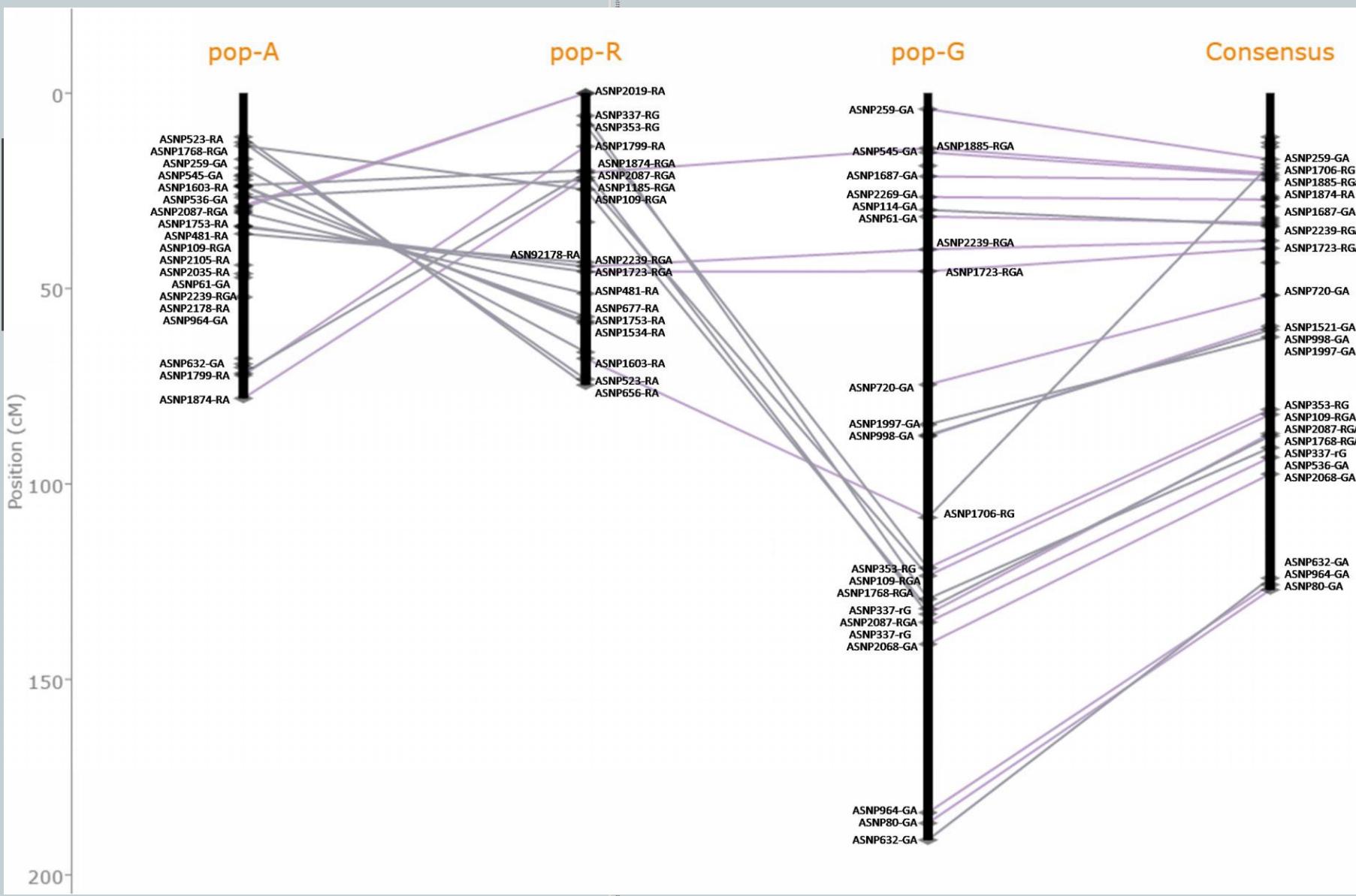


A.**B.**

Map Merging

- Lpmerge
- AMap – R
- MergeMap





Aurora et al. 2017: A high-density intraspecific SNP linkage map of pigeonpea (*Cajanas cajan* L. Millsp.)

Data cleaning

- Parents:
 - Polymorphic
 - Parent 1 is A allele, Parent 2 is B allele (always)
- Duplicate Marker Names
- Missing
- Check for ratios – Chi square test
- No parents for mapping software

INPUT – CARTHAGENE/MAPMAKER FORMAT

The very first line of your raw data file

data type xxxx

where xxxx is one of the allowed data types, either:

f2 intercross

f2 backcross

f3 self

ri self

ri sib

The second line of the raw file should contain a **list of three numbers, separated by spaces**, such as:

46 362 0

The first value - The number of progeny (46) for which data are included in the file

The second value - Number of genetic loci for which data are supplied (362).

The third indicates the number of quantitative traits in the data set (0)

Additional information may be optionally supplied at the end of second line

Ex: **46 362 2 symbols I=A 2=B 0=-.**

After the first two header lines,

For each locus, you list

- (1) the name of the locus, preceded by an asterisk ("*");
- (2) one or more spaces (or tabs etc.); and
- (3) the genotypic data for all individuals, in order.

example:

***m234 AB-ABBABABABABABA---BABABABA**

Carthagene useful commands

help - to get all commands

Type '<command-name> -H' for more help with a particular command.

To change the defaults, edit the '.carthagenerc'

Manipulate data sets :

dsload Load a Biological Data Set.

dsinfo Summarize the current data sets.

dsmergen Merge two Biological Data Sets.

dsget Get a list of the current data sets description.

Manipulate groups :

group Identify linkage groups.

groupget Get a group by markers ID.

- **Manipulate loci :**

- mrkdoubleget Retrieve a list of pairs of markers with compatible typing.
- mrklod2p Print the two points LOD matrix.
- mrkselget Return the loci selection into a list.
- mrkselset Set the marker list(by Id).
- mrkdist2p Print the two points distance matrix.
- mrkmerge Merges two compatible markers.
- mrkdouble Identifies pairs of markers with compatible typing.
- mrkmerget Retrieve a list of merged markers.

Search for good maps :

- **greedy** Find good maps using the greedy algorithm.
- **buildfw** Build a framework map.
- **nicemapd** Provide quickly a (nice) map, using the 2-points distances.
- **annealing** Find good maps using the annealing algorithm.
- **build** Build maps with two-points information
- **Verify maps**
- **flips** Try to improve the best map by flipping.
- **polish** Try to improve the best map by polishing.

Manipulate the heap :

- **heaprintd** Display the heap in detail, sorted.
- **heaprint** Display the heap sorted.
- **bestprint** Print the best map in the heap.
- **bestprintd** Print the best map in the heap, in detail.

To manipulate a map :

- `maprint` Print a map.
 - `maprintdr` Print a map reverse, in detail.
 - `mapget` Get a map, in a list.
 - `maprintd` Print a map, in detail.
-
- **Graphical commands :**
 - `maprintg` Draw a map into a graphical display.
-
- **Miscellaneous :**
 - `cgresstart` Reset the application.
 - `cgstop` To stop a running command, type `ctrl-c`.
 - `cgsave` Save the state of the current session.
 - `cgexport` Save the state of the current session.

Carthagene Main steps

Load - select the file

Data/info - To get information on data file

Marker merge - optional

Loci/config

Loci/Identify Groups

For each linkage group (>3 markers) - REPEAT for each group

Loci/select a group

Loci/Dist2pt (if duplicates- merge 2 locus)

Buildfw & Detail

* Other algorithms - ALGORITHM & Detail

flips & Detail

polish & Detail

“bestprint”; “bestprintd”

Copy into a file

DATA CLEANING

Parents
highlight

Sujan ... Go Premium

WPS Office Linkage_mapping_data.xlsx

Home Insert Page Layout Formulas Data Review View Tools Cli... +

Cut Copy Format Painter Calibri 12 A+ A- Merge and Center Wrap Text General Conditional Formatting AutoSum AutoFilter Sort Format Fill Rows Color

B1	P1	P1	D	E	F	G	H	I	J	K	L	M	N
Marker	P1	P2	samp1	samp2	samp3	samp4	samp5	samp6	samp7	samp8	samp9	samp10	samp1
*A8ag	A	B	A	A	B	A	A	-	A	A	A	A	B
*abi3	A	B	A	A	A	B	B	B	-	A	A	A	B
*adh	A	B	-	A	A	-	-	B	-	-	-	-	-
*ASA1	A	B	-	A	B	-	-	B	-	-	-	-	-
*CD3-42	A	B	-	B	-	-	-	-	-	-	A	-	B
*dfr	A	B	-	-	B	-	-	B	-	-	-	-	-
*DHS1	A	B	-	-	B	-	-	A	-	-	-	-	-
*EG17G9L	A	B	B	B	A	B	B	-	-	B	A	B	A
*er	A	B	B	A	A	A	A	-	-	B	B	A	B
*g10086	A	B	A	A	B	A	A	-	A	A	A	A	B
*G11	A	B	-	A	A	-	-	B	-	-	-	-	-
*g17288	A	B	B	A	A	A	A	B	A	B	B	A	B
*g19838	A	B	-	-	-	-	-	-	-	-	-	-	-
*g2368	A	B	B	B	B	B	A	B	-	A	B	A	B
*g2486	B	A	A	B	A	B	B	A	A	B	B	A	A
*g2616	B	A	B	A	A	B	B	A	-	B	A	B	A
*g2778	B	A	B	A	A	A	B	A	-	B	A	B	A
*g3088	B	A	B	B	B	B	B	A	-	B	B	A	A
*g3713	B	A	A	B	A	B	B	B	-	B	B	A	A

1.raw_data 2.Parents 3.missing_chisquare 4.Final_datasheet +

Sum=0 Average=0 Count=284

Search for anything

3:18 PM 11/23/2020

Parents - Polymorphic

WPS Office Linkage_mapping_data.xlsx

Home Insert Page Layout Formulas Data Review View Tools Cli... +

Cut Copy Format Painter Calibri 12 A A Merge and Center Wrap Text General Conditional Formatting AutoSum AutoFilter Sort Format Fill Rows Color

SUM ✓ fx =EXACT(C2,D2)

	Parents-Polymorphic	Marker	P1	P2	samp1	samp2	samp3	samp4	samp5	samp6	samp7	samp8	samp9
1			A	B	A	A	B	A	A	-	A	A	A
2	=EXACT(C2,D2)	*A8ag	A	B	A	A	B	B	B	-	A	A	A
3		*ab13	A	B	A	A	A	-	-	B	-	A	-
4		*adh	A	B	-	A	A	-	-	B	-	-	-
5		*ASA1	A	B	-	A	B	-	-	B	-	-	-
6		*CD3-42	A	B	-	B	-	-	-	-	-	-	A
7		*dfr	A	B	-	-	B	-	-	B	-	-	-
8		*DHS1	A	B	-	-	B	-	-	A	-	-	-
9		*EG17G9LE	A	B	B	B	A	B	B	-	-	B	A
10		*er	A	B	B	A	A	A	A	-	-	B	B
11		*g10086	A	B	A	A	B	A	A	-	A	A	A
12		*G11	A	B	-	A	A	-	-	B	-	-	-
13		*g17288	A	B	B	A	A	A	A	B	A	B	B
14		*g19838	A	B	-	-	-	-	-	-	-	-	-
15		*g2368	A	B	B	B	B	B	A	B	-	A	B
16		*g2486	B	A	A	B	A	B	B	A	A	B	B
17		*g2616	B	A	B	A	A	B	B	A	-	B	A
18		*g2778	B	A	B	A	A	A	B	A	-	B	A
19		*g3088	B	A	B	B	B	B	B	A	-	B	B
20		*g3713	B	A	A	B	A	B	B	B	-	B	B

Parents - PI - A; P2 - B

WPS Office Linkage_mapping_data.xlsx

Home Insert Page Layout Formulas Data Review View Tools Cli... 1 sujan ... Go Premium

Cut Copy Format Painter Calibri 12 Merge and Center Wrap Text General Conditional Formatting Format as Table AutoSum AutoFilter Sort Format Fill Rows Columns

B140 *SNP4

1 2

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y		
111	*um579D	A	B	B	A	B	A	B	A	A	-	B	B	A	A	B	B	B	B	B	B	B	A	A	B		
112	*um596A	A	B	B	A	-	A	-	-	-	-	A	A	B	-	-	B	A	B	-	A	A	A	A	-		
113	*um713B	A	B	-	A	-	-	-	-	-	-	A	A	B	B	-	-	B	B	-	A	-	A	A	B		
114	*g2486	A	B	B	A	B	A	A	B	B	A	A	B	B	B	B	-	-	B	B	B	B	B	A	A	B	
115	*g2616	A	B	A	B	B	A	A	B	-	A	A	B	B	B	B	A	A	A	A	B	B	B	A	A	A	
116	*g2778	A	B	A	B	B	B	A	B	-	A	B	A	B	B	B	A	A	A	A	A	A	B	B	A	A	
117	*g3088	A	B	A	A	A	A	A	B	-	A	A	B	B	B	B	A	A	A	B	B	B	-	A	-	B	
118	*g3713	A	B	B	A	B	A	A	A	-	B	B	A	B	B	B	A	A	A	B	B	B	B	B	A	B	
119	*g3715	A	B	A	A	B	A	B	B	-	B	B	A	B	B	B	A	A	B	B	A	B	B	B	A	B	
120	*g3786	A	B	B	B	B	B	B	A	-	B	A	B	B	B	B	A	A	A	B	B	B	B	A	A	A	
121	*g3829	A	B	B	B	B	B	B	A	-	B	A	B	B	B	B	A	A	B	A	A	A	B	-	A	B	A
122	*g3837	A	B	A	A	B	B	B	B	-	B	B	A	B	B	B	A	A	B	B	A	A	B	B	A	A	B
123	*g3843	A	B	A	B	B	A	A	B	-	A	B	B	B	B	B	A	A	A	B	A	B	A	A	A	A	A
124	*g3845	A	B	A	A	B	A	A	A	-	A	A	A	B	B	B	B	B	A	B	B	B	-	A	A	A	A
125	*g3883	A	B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
126	*g4014	A	B	A	B	-	-	-	B	A	A	B	A	B	B	B	A	A	A	A	A	A	A	A	A	A	A
127	*g4026	A	B	A	A	A	A	B	B	B	B	A	A	B	A	A	A	A	A	A	A	A	B	B	A	A	A
128	*g4028	A	B	B	A	A	A	B	B	-	B	A	B	B	B	B	A	A	A	B	A	B	A	B	A	A	A
129	*g4108	A	B	A	A	B	A	A	A	-	-	A	A	A	B	B	B	A	A	A	A	A	A	A	A	A	A
130	*pCITd99	A	B	B	A	A	A	A	-	B	B	A	A	B	B	B	A	A	A	B	B	B	B	A	-	B	
131	*pCITf117	A	B	A	A	A	A	A	B	A	B	A	A	B	A	A	A	A	A	A	A	A	B	B	A	A	A
132	*pCITf3	A	B	A	A	B	-	A	-	-	A	A	A	B	B	B	B	A	B	B	B	B	B	A	A	-	A
133	*pv4	A	B	B	A	B	B	B	A	B	B	B	B	B	B	B	B	B	B	B	B	B	B	A	B	B	
134	*SNP7	A	B	B	B	A	-	B	-	-	B	B	B	A	A	A	A	B	A	A	A	A	B	B	-		
135	*SNP8	A	B	A	A	B	A	B	A	-	B	A	A	A	A	A	B	A	A	A	A	A	B	A	A	B	
136	*SNP9	A	B	A	A	B	B	-	B	-	B	B	A	B	A	A	B	B	A	A	A	-	B	A	A	A	B
137	*SNP1	A	B	A	A	A	A	A	B	B	A	A	B	-	-	A	A	B	A	B	B	B	A	A	A	B	
138	*SNP2	A	B	B	B	A	B	B	B	A	B	B	B	B	B	B	B	B	A	B	B	B	B	A	B	B	
139	*SNP3	A	B	A	A	B	A	A	-	-	A	A	A	B	B	B	A	B	B	B	B	B	B	A	A	A	
140	*SNP4	A	B	B	A	A	A	A	-	B	A	A	B	B	B	B	A	A	B	A	B	B	B	-	A	B	B
141	*SNP5	A	B	A	B	B	B	B	B	A	-	A	A	B	B	A	A	B	B	B	A	A	B	-	A		
142	*SNP6	A	B	B	B	B	B	B	B	A	B	B	A	B	B	B	A	B	B	B	A	B	B	A	A	B	B

1.raw_data 2.Parents 3.missing_chisquare 4.Final_datasheet +

Sum=0 Average=0 Count=312

Search for anything

Windows Search icon Task View Taskbar Icons Chrome Edge 3:32 PM 11/23/2020

Duplicate markers?

Screenshot of WPS Office showing a spreadsheet titled "Linkage_mapping_data.xlsx". The Data tab is selected, and the ribbon shows various options like PivotTable, AutoFilter, Advanced, Sort, Highlight Duplicates, Manage Duplicates, and Remove Duplicates.

The formula bar displays "=EXACT(B2,B1)". A red box highlights the range A1:A2, which contains the text "Marker" and the formula "=EXACT(B2 , B1)".

The spreadsheet contains 29 rows of data, starting with "Marker" and "EXACT (Text, Text)". The columns are labeled A through R, and the data consists mostly of "A", "B", or "-" values.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	Marker	P1		P2	samp1	samp2	samp3	samp4	samp5	samp6	samp7	samp8	samp9	samp10	samp11	samp12	samp13	samp14	samp15
2	=EXACT(B2 , B1)	A		B	A	A	B	A	A	-	A	A	A	B	B	B	A	A	A
3	EXACT (Text, Text)	A		B	A	A	A	B	B	B	-	A	A	A	B	B	B	A	B
4				B	-	A	A	-	-	B	-	-	-	-	-	-	-	-	-
5				B	-	A	B	-	-	B	-	-	-	-	-	-	-	-	-
6				B	-	B	-	-	-	B	-	-	-	-	-	-	-	-	B
7				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
8				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
9				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
10				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
11				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
12				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
13				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
14				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
15				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
16				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
17				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
18				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
19				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
20				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
21				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
22				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
23				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
24				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
25				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
26				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
27				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
28				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-
29				B	-	-	B	-	-	B	-	-	-	-	-	-	-	-	-

The bottom navigation bar shows tabs: 1.raw_data, 2.Parents, 3.missing_chisquare, 4.Final_datasheet, and +.

The taskbar at the bottom includes icons for Windows, Search, Task View, File Explorer, Edge, Google Chrome, and WPS Office.

The system tray shows the date and time as 3:36 PM, 11/23/2020.

Counts - Alleles, Missing

Screenshot of WPS Office showing a spreadsheet titled "Linkage_mapping_data.xlsx". The formula bar displays the formula `=FLOOR(((E2+F2)/2),1)`. The spreadsheet contains data for marker alleles across various samples.

Notes	Chi-sq	expected-A	expected-B	A-allele	B-Allele	Missing-alleles	Parents-missing	Marker	P1	P2	samp1	samp2	samp3	samp4	samp5	samp6	samp7
		47		54	40	7	0	*A8ag	A	B	A	A	B	A	A	-	A
							0	*abi3	A	B	A	A	A	B	B	B	-
							0	*adh	A	B	-	A	A	-	-	B	-
							0	*ASA1	A	B	-	A	B	-	-	B	-
							0	*CD3-42	A	B	-	B	-	-	-	-	-
							0	*dfr	A	B	-	-	B	-	-	B	-
							0	*DHS1	A	B	-	-	B	-	-	-	A
							0	*EG17G9LE	A	B	B	A	B	B	-	-	-
							0	*er	A	B	B	A	A	A	-	-	-
							0	*g10086	A	B	A	A	B	A	-	-	A
							0	*G11	A	B	-	A	A	-	-	B	-
							0	*g17288	A	B	B	A	A	A	A	B	A
							0	*g19838	A	B	-	-	-	-	-	-	-
							0	*g2368	A	B	B	B	B	B	A	B	-
							0	*g2486	A	B	B	A	B	A	A	B	B
							0	*g2616	A	B	A	B	B	A	A	A	B
							0	*g2778	A	B	A	B	B	B	A	B	-
							0	*g3088	A	B	A	A	A	A	A	B	-
							0	*g3713	A	B	B	A	B	A	A	A	-
							0	*g3715	A	B	A	A	B	A	B	B	-
							0	*g3786	A	B	B	B	B	B	B	A	-
							0	*g3829	A	B	B	B	B	B	B	A	-
							0	*g3837	A	B	A	A	B	B	B	B	-
							0	*g3843	A	B	A	B	B	A	A	B	-
							0	*g3845	A	B	A	A	B	A	A	A	A
							0	*g3883	A	B	-	-	-	-	-	-	-
							0	*g4014	A	B	A	B	-	-	-	B	A
							0	*e4026	A	B	A	A	A	A	B	R	R

The formula bar shows the formula `=FLOOR(((E2+F2)/2),1)` entered in cell C2.

Bottom navigation bar: 1.raw_data, 2.Parents, 3.missing_chisquare (selected), 4.Final_datasheet, +

Bottom right corner: 3:43 PM, 11/23/2020, 1 notification

Chisq test

Sujan ... Go Premium

WPS Office Linkage_mapping_data.xlsx Day2-Linkage_mapping.pptx

Home Insert Page Layout Formulas Data Review View Tools

Cut Copy Format Painter Calibri 12 Merge and Center Wrap Text General Conditional Formatting AutoSum AutoFilter Sort Format Fill Rows Color

Notes Chi-sq expected-A expected-B A-allele B-Allele Missing-alleles Parents-miss Marker P1 P2 samp1 samp2 samp3 samp4 samp5 samp6 samp7

=CHITEST(E2:F2,c2:d2) 47 54 40

Marker P1 P2 samp1 samp2 samp3 samp4 samp5 samp6 samp7

*A8ag A B A A B A B B A A - A

*abi3 A B A A A B B B B B B -

*adh A B - A A A B B B B B B -

*ASA1 A B - A A B B B B B B -

*CD3-42 A B - B B B B B B B B -

*dfc A B - - B B B B B B B -

*DHS1 A B - - B B B B B B B -

*EG17G9LE A B B B A B B B B B -

*er A B B A A A A A A A A -

*g10086 A B A A B A A A A A A -

*G11 A B - A A A A A A A A -

*g17288 A B B A A A A A A A A -

*g19838 A B - - - - - - - -

*g2368 A B B B B B B B B B -

*g2486 A B B A B A A A A A B -

*g2616 A B A B B B A A A A B -

*g2778 A B A B B B B B B A B -

*g3088 A B A A B A A A A A B -

*g3713 A B B A A B A A A A A -

*g3715 A B A A B A A B A B B -

*g3786 A B B B B B B B B B A -

*g3829 A B B B B B B B B B A -

*g3837 A B A A B A B B B B B -

*g3843 A B A B B B B B A A B -

*g3845 A B A B A A B B A A A -

*g3883 A B - - - - - - - -

*g4014 A B A B B B B B B B B -

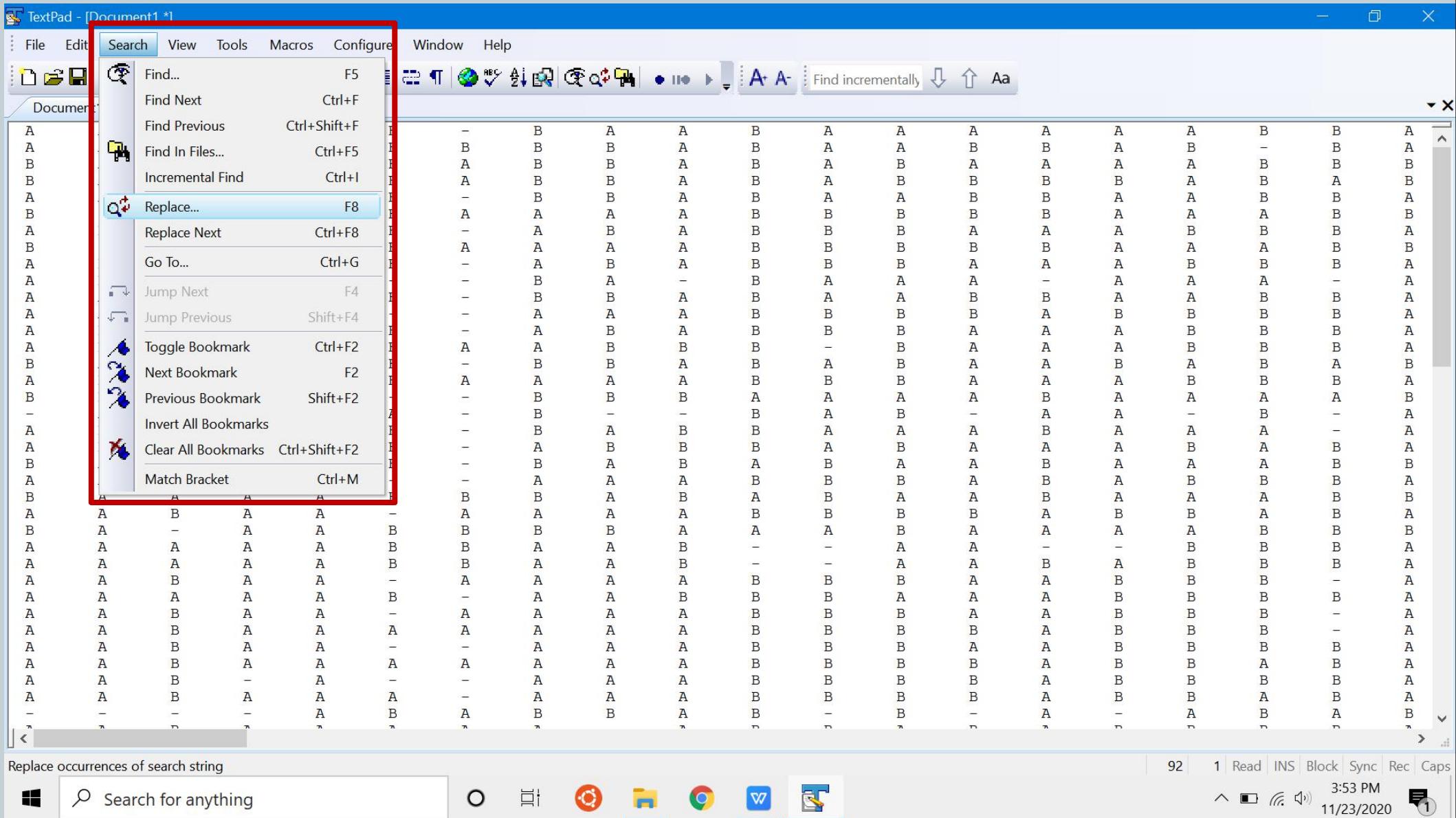
*e4026 A R A A A A A A B B B -

1.raw_data 2.Parents 3.missing_chisquare 4.Final_datasheet

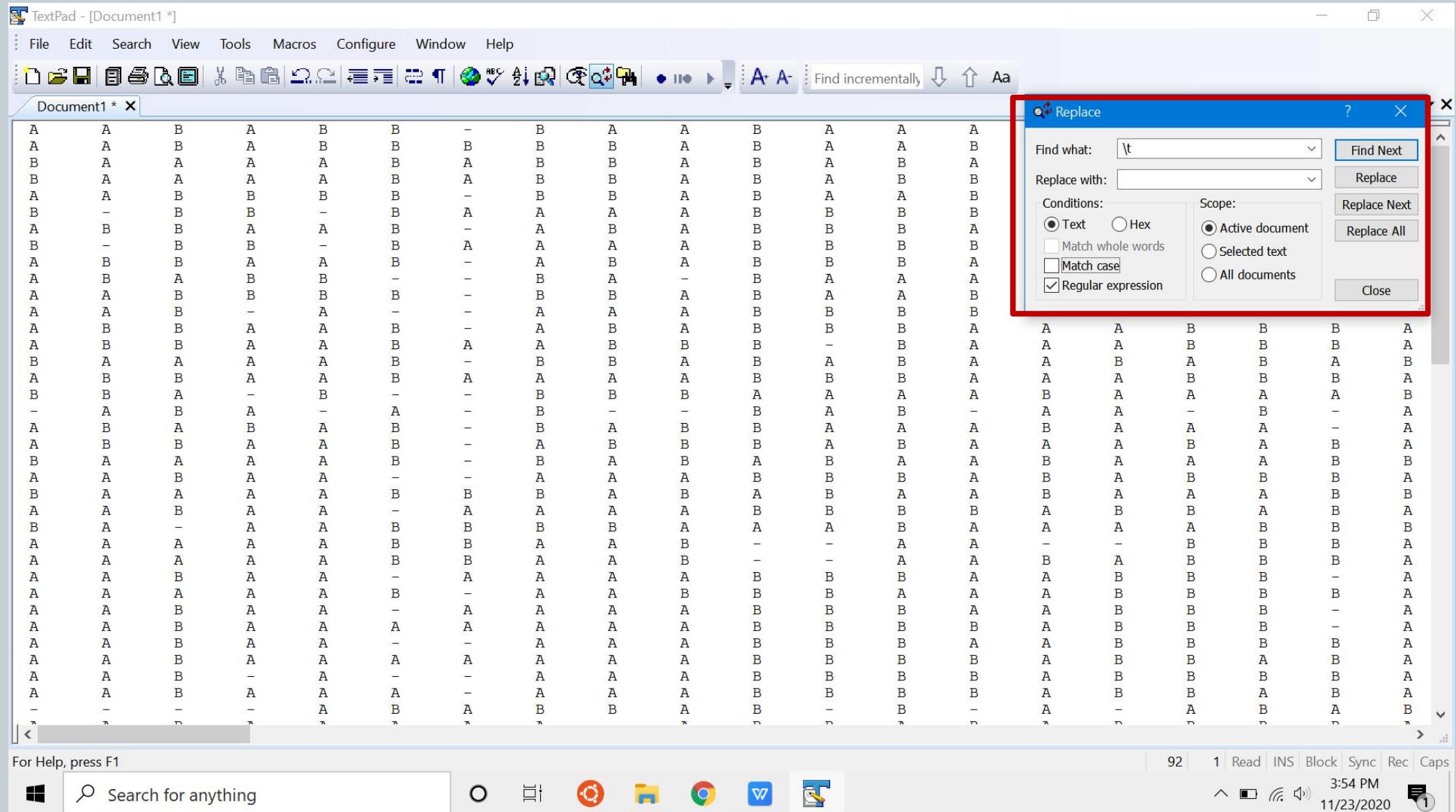
Search for anything

3:44 PM

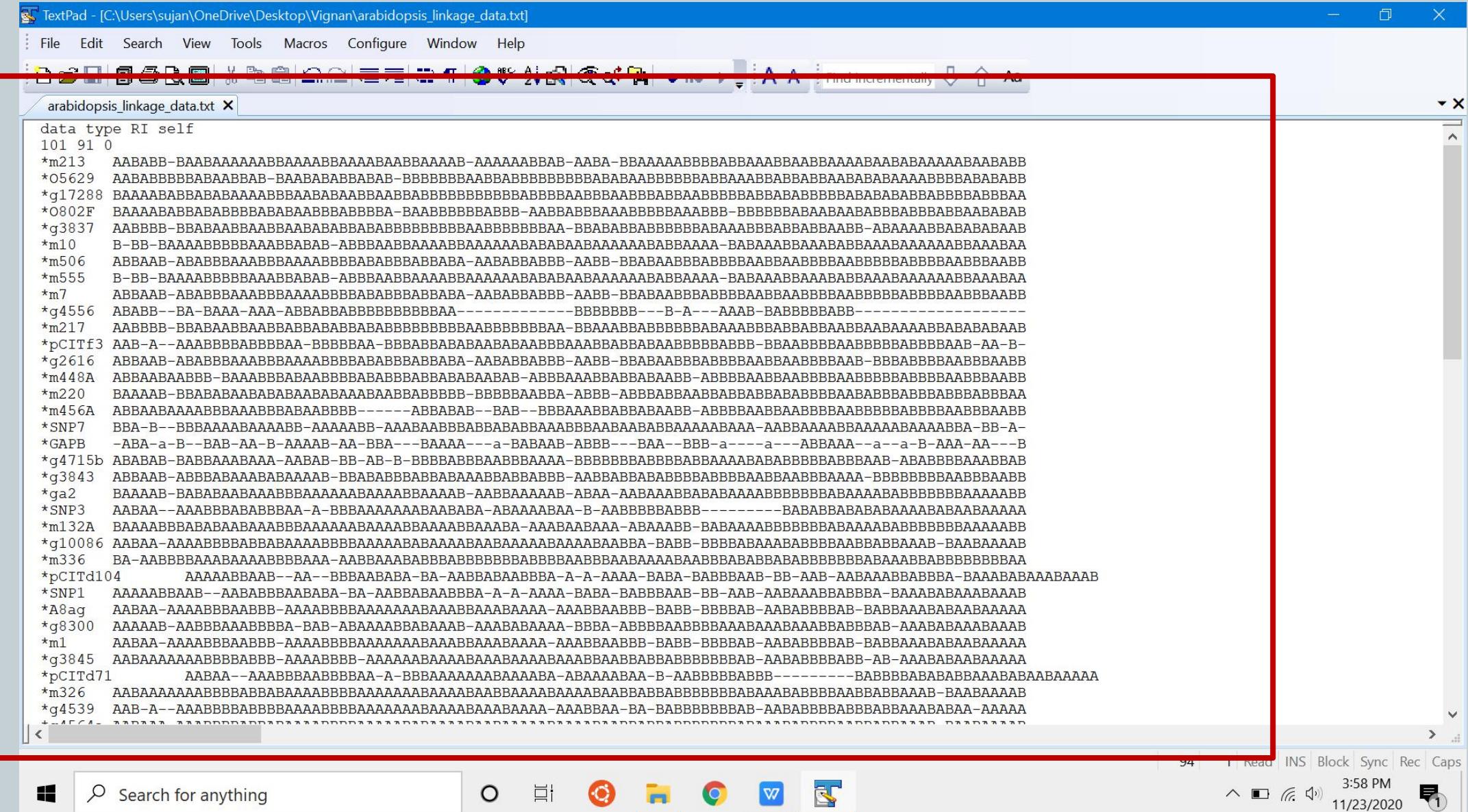
Concatenate



Concatenate



Final Input file

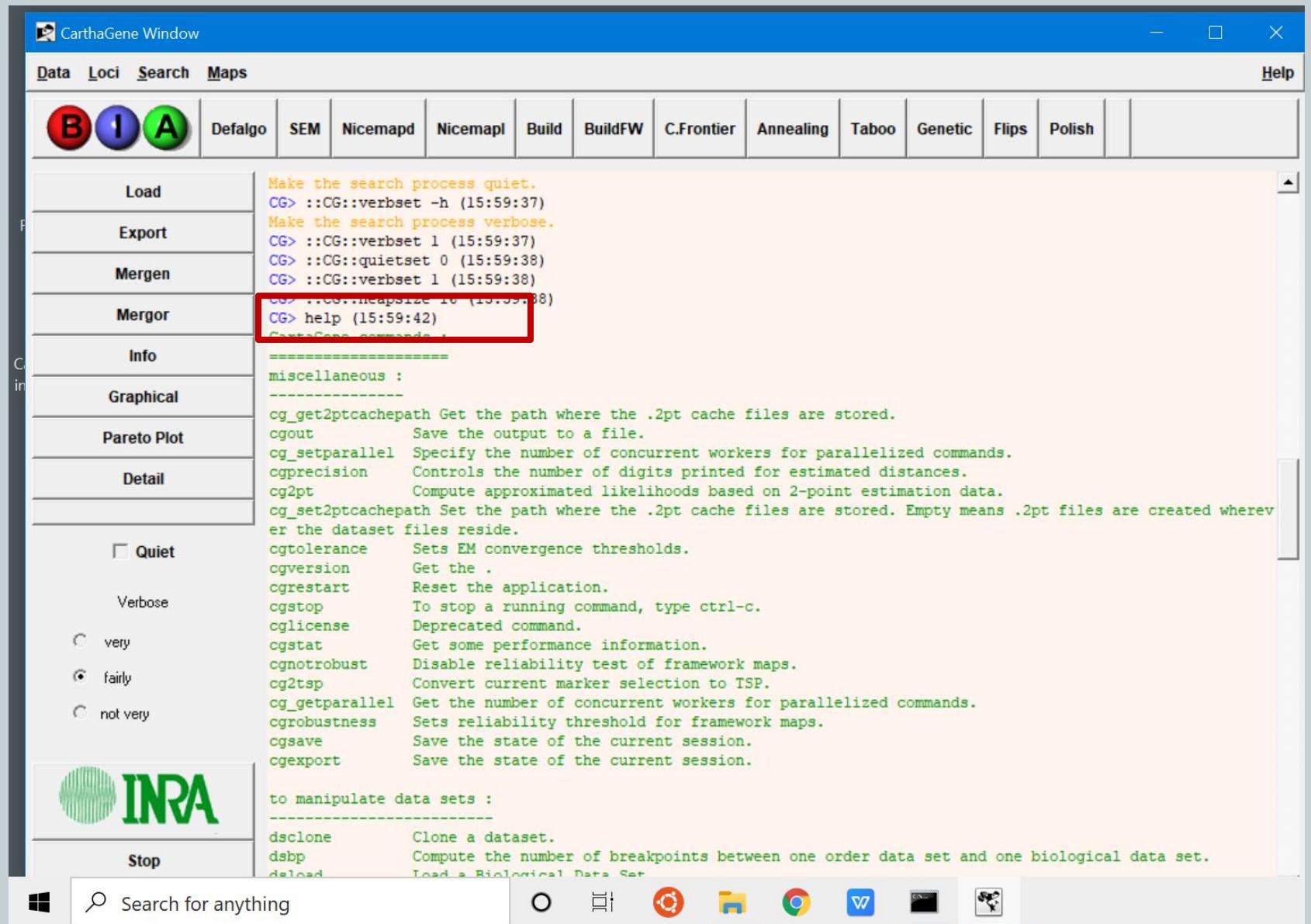


The screenshot shows a Windows desktop environment with a TPad text editor window open. The window title is "TextPad - [C:\Users\sujan\OneDrive\Desktop\Vignan\arabidopsis_linkage_data.txt]". The menu bar includes File, Edit, Search, View, Tools, Macros, Configure, Window, and Help. The toolbar contains various icons for file operations like Open, Save, Print, and Find. The main text area is titled "arabidopsis_linkage_data.txt" and contains a large block of DNA sequence data. The data consists of multiple lines of text, each starting with a marker (* or *) followed by a unique identifier and a long sequence of A's, T's, C's, and G's. A red rectangular box highlights the entire content of the text area. The status bar at the bottom shows "94" files, "Read" mode, and the date/time "3:58 PM 11/23/2020". The taskbar at the bottom includes icons for File Explorer, Task View, Start, and several application windows.

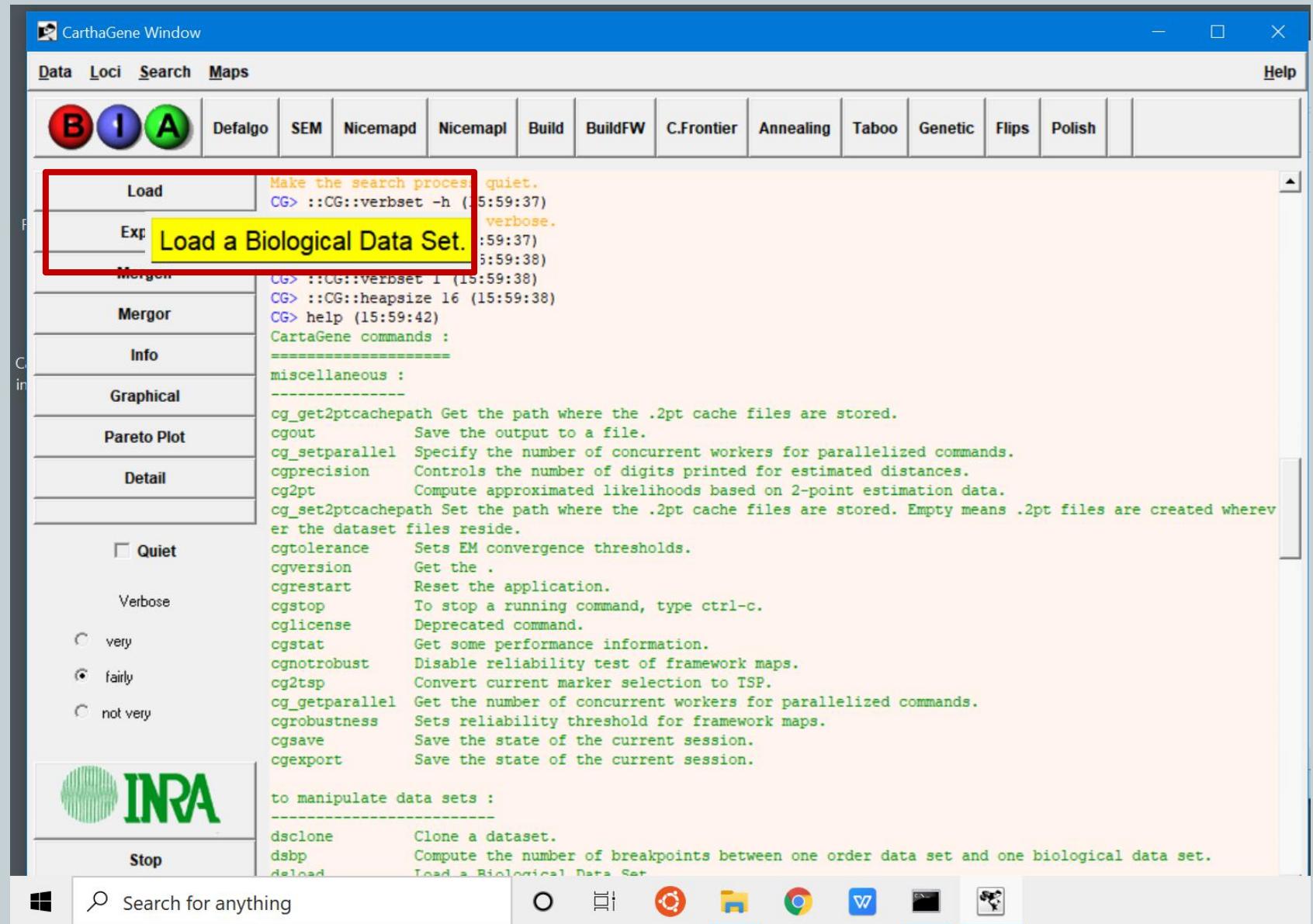
```
data type RI self
101 91 0
*m213 AABABB-BAABAAAAAABAAAABAABAAAAB-AAAAABBAB-AABA-BBAAAABBBBABAABBAABAAAABAABAAAABAABBB
*05629 AABBBBBBABAABBAB-BAABABBBABAB-BBBBBBBAABB BBBBBAABAABBBBABAABBAABABAABAAAABBBBABAABBB
*g17288 BAAABABBAABAAAABBAABABAABBAABBABBBBBAABBBABAABBBABAABBBBABAABBAABABAABAAAABBBBABAABBB
*0802F BAAABABBAABBBBABAABBAABBBBABA-BAABBBBBBABA-AABBABBBAAABBBBABAABBBBABAABBAABBAABABAAB
*g3837 AABBB-BBABAABBAABBAABABBAABBBBBAABBBBABA-BBABAABBBBBAABBBBABAABBAABBAAB-ABAAAABBAABABAAB
*m10 B-B-BAAAABBBBAAABBAAB-BBABAABBBAAABAAAABAABAAAABAABAAAABAABAAAABAABAAAABAABAAAABAABAAA
*m506 ABBAB-ABBBBBAAABBBBABAABBBBABA-AABBBBABA-AAB-BBABAABBBBABAABBAABBBBABAABBBBABAABBB
*m555 B-BB-BAAAABBBBAAABBAAB-BBABAABBBAAABAAAABAABAAAABAABAAAABAABAAAABAABAAAABAABAAAABAABAAA
*m7 ABBAAB-ABBBBBAAABBBBABAABBBBABAABBAABBAABBAABBBBABAABBBBABAABBBBABAABBBBABAABBB
*g4556 ABABB--BA-BAAA-AAA-ABBABBABBBBBBBBAA-----BBBBBBB---B-A--AAAB-BABBBBBBAA----B
*m217 AABBB-BBABAABBAABBAABBAABBBBBBBBAA-BBAAAABBBBABAABBAABBAABAAAABAABBAABABAAB
*pCITf3 AAB-A-AAABBBBABAAB-BBBBBAABBAABABAABBBBABAABBBBABAAB-BBAABBBBABAABBBBABAAB-AA-B-
*g2616 ABBAAB-ABBBBBAAABBAABBBBABAABBAABBAABBAABBAABBAABBAABBAABBBBABAABBBBABAABBBBABAAB
*m448A ABBAABAABBB-BAAABBBBABAABBBBABAABBAABBAABBAABBAABBBBABAABBBBABAABBBBABAABBBBABAAB
*m220 BAAAAB-BBABAABABAABABAABBAABBBB-BBBBBAABBA-ABBB-ABBBABAABBBBABAABBBBABAABBBBABAABBB
*m456A ABBAABAAAABBBBABAABBBB-----ABBABAB-BAB--BBAAABBBBABAAB-BBBBABAABBAABBBBABAABBBBABAAB
*SNP7 BBA-B-BBBAAAABAAAAB-BAAAAB-AAAABAABBBBABAABBAABBAABBAABAAAABAAA-AABBAABBAABAAAABBA-BB-A-
*GAPB -ABA-a-B-B-BAA-B-AAAAB-AA-BBA--BAAA--a-BABAAB-BBBB-BAA-B-BB-a---a---ABAAA--a--a-B-AAA-AA--B
*g4715b ABABAB-BBABAABAAA-AABAB-BB-B-BBBBABAABBBAAA-BBBBBAABBBBABAABBAABBBBABAABBBBABAAB
*g3843 ABBAAB-ABBBBABAABAAAAB-BBABAABBBBABAABBAABBBBABAABBAABBBBABAABBAABBBBABAABBBBABAAB
*ga2 BAAAAB-BBABAABAAAABAAAABAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
*SNP3 AABAA-AAABBBBABAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
*m132A BAAAABBBBABAABAAAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
*g10086 AABAA-AAAABBBBABAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
*m336 BA-AABBBBABAABAAAABBBBAAA-AABBAABBBBABAABBBBABAABBAABBAABBAABBAABBAABBAABBAABBAAB
*pCITd104 AAAAABBAAB--AA-BBABAABA-BA-AABBABAABBB-A-A-AAAA-BABA-BBBBABAAB-BB-AAB-AABAABBBBABA-BAAABABAABAAAB
*SNP1 AAAAABBAAB--AABBBBABAABA-BA-AABBABAABBB-A-A-AAA-BABA-BBBBABAAB-BB-AAB-AABAABBBBABA-BAAABABAABAAAB
*A8ag AABAA-AAAABBBBABAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
*g8300 AAAAAB-AABBBBABAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
*m1 AABAA-AAAABBBBABAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
*g3845 AABAAAABBBBABAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
*pCITd71 AABA--AAABBBBABAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
*m326 AABAAAABBBBABAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
*g4539 AAB-A-AAABBBBABAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAABBAAB
```

Carthagene

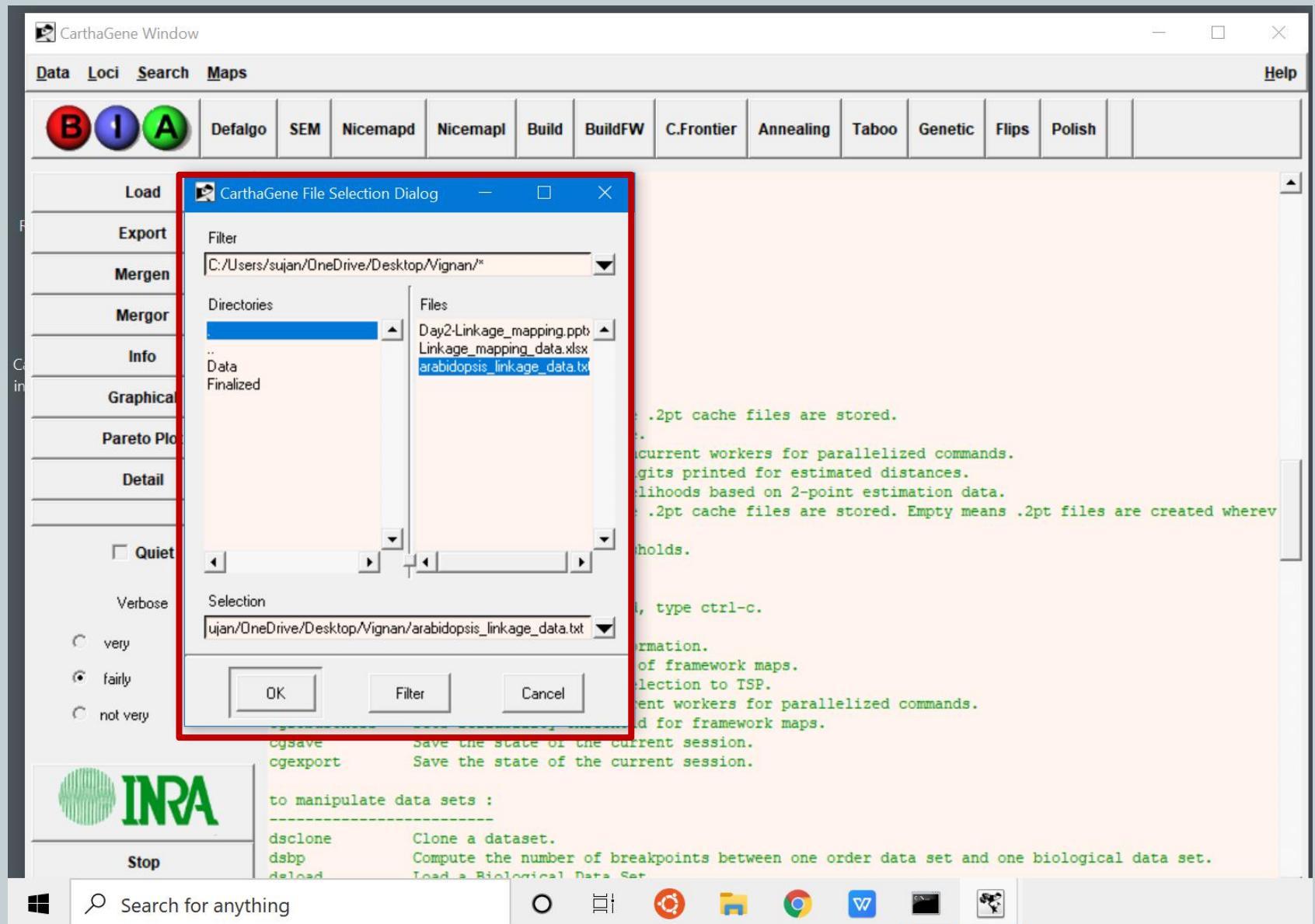
Help command



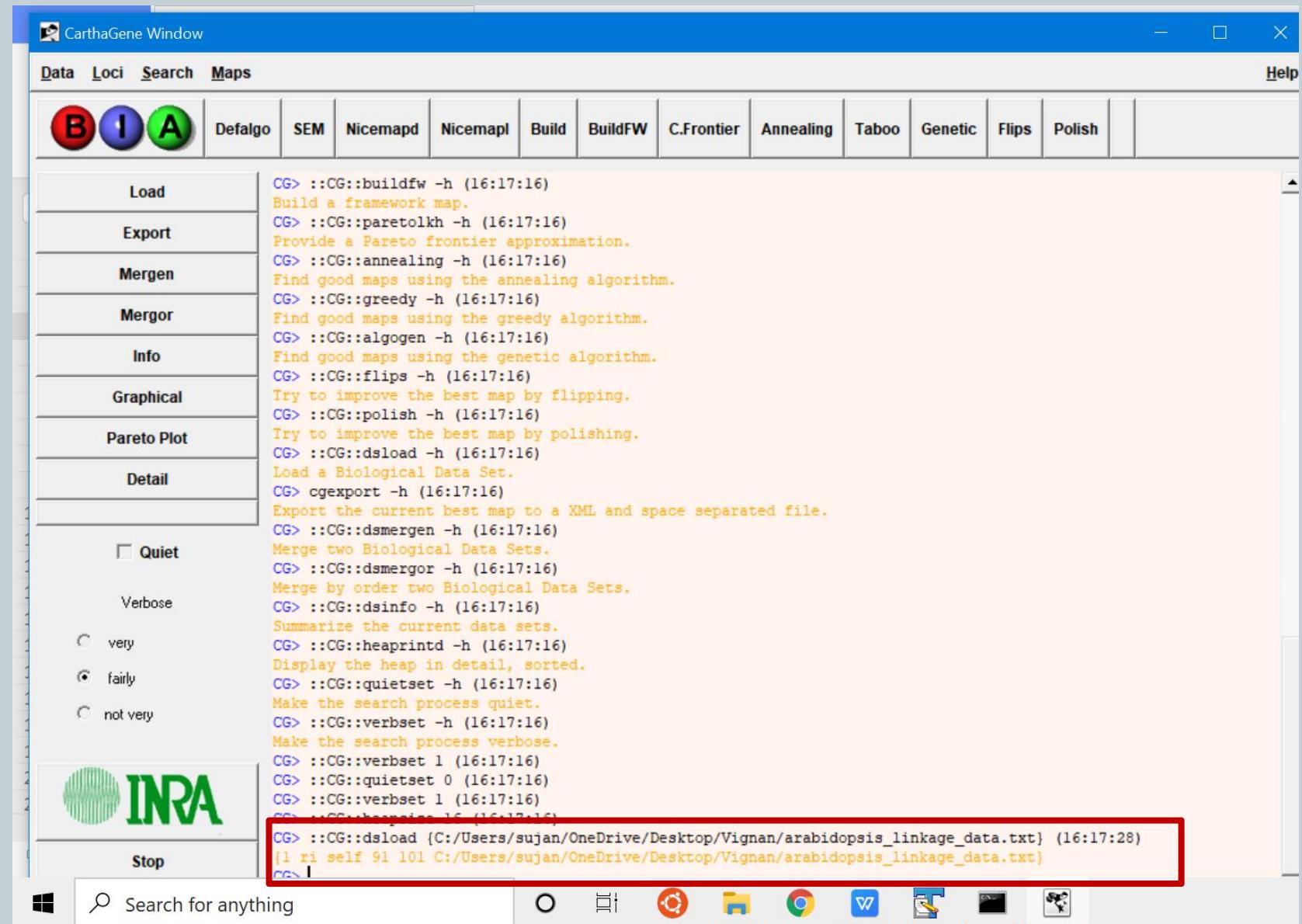
Load Button



select file - Path



File loaded successfully



Data/Info

WPS Office | Linkage_mapping_data.xlsx | +

CarthaGene Window

Data Loci Search Maps Help

B I A Defalgo SEM Nicemapd Nicemapl Build BuildFW C.Frontier Annealing Taboo Genetic Flips Polish

Load Export Merge Merge by order two Biological Data Sets. CG> ::CG::dsmergen -h (16:17:16)
Merge two Biological Data Sets. CG> ::CG::dsmergor -h (16:17:16)
Mergen CG> ::CG::dsinfo -h (16:17:16)
Summarize the current data sets. CG> ::CG::heaprintd -h (16:17:16)
Mergor CG> ::CG::quietset -h (16:17:16)
Display the heap in detail, sorted. CG> ::CG::verbset -h (16:17:16)
Info CG> ::CG::quietset 0 (16:17:16)
Make the search process quiet. CG> ::CG::verbset 1 (16:17:16)
Graphical Make the search process verbose.
CG> ::CG::verbset 1 (16:17:16)
CG> ::CG::quietset 0 (16:17:16)
Pareto Plot CG> ::CG::verbset 1 (16:17:16)
CG> ::CG::heapspace 16 (16:17:16)
Detail CG> ::CG::dsload {C:/Users/sujan/OneDrive/Desktop/Vignan/arabidopsis_linkage_data.txt} (16:17:28)
CG> ::CG::dsinfo (16:17:53)

Quiet
 Quiet
Verbose
 very
 Quite

Data Sets :
-----:
ID Data Type markers individuals filename constraints merging
1 ri self 91 101 arabidopsis_linkage_data.txt

20	*GAPB	-ABA-a-B--BAB-AA-B-AA-	A	B	A	-	A	-	B	-		
21	*g4715b	ABABAB-BABBAABAA/A	B	A	B	A	B	-	B	A	B	A

1.raw_data 2.Parents 3.missing_chisquare 4.Final_datasheet +

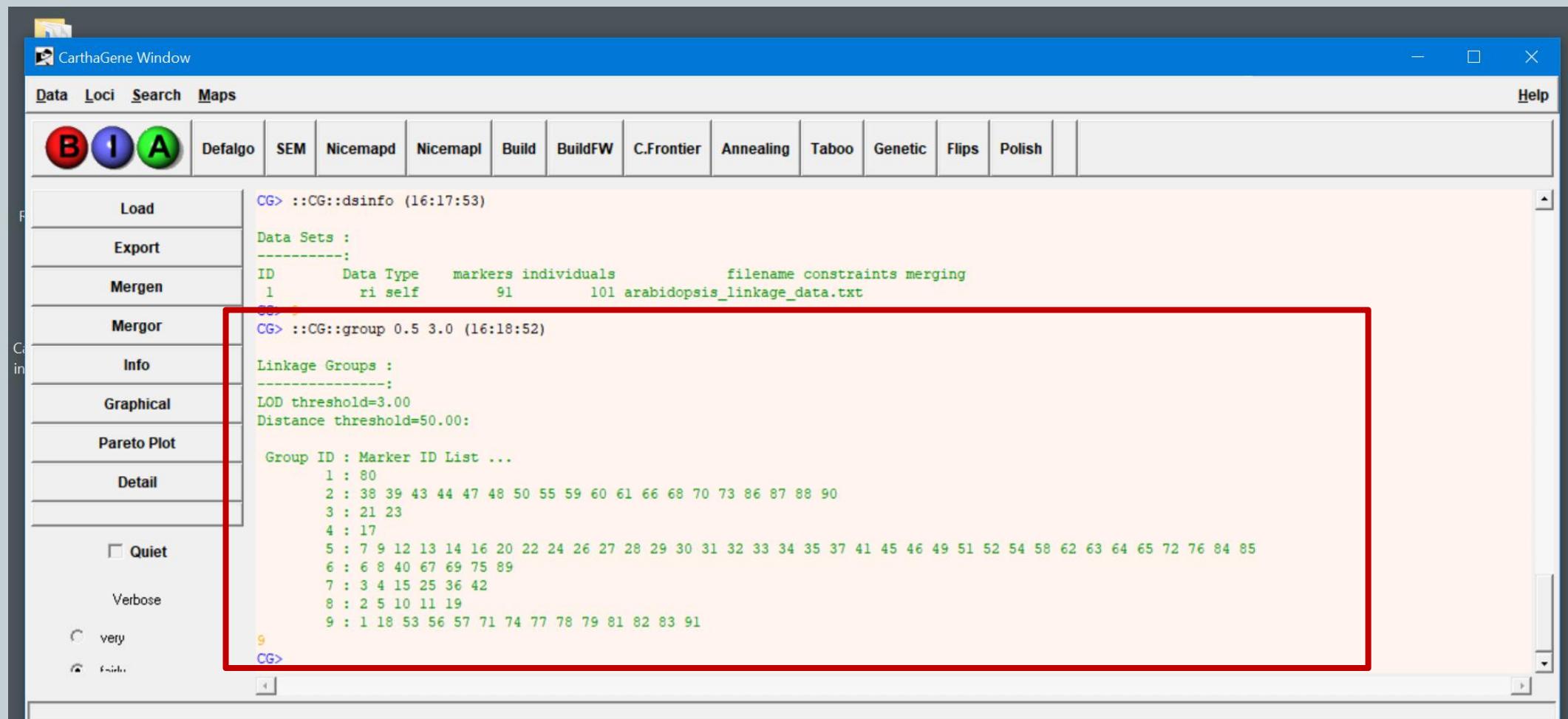
AutoFilter Sort Format Fill Rows and Columns

	L	M
1	A	B
2	A	B
3	A	B
4	A	B
5	A	B
6	A	B
7	A	B
8	A	B
9	A	B
10	A	B
11	A	B
12	A	B
13	A	B
14	-	B
15	A	B
16	A	B
17	A	B
18	A	B
19	A	B
20	B	B
21	A	B
22	A	B
23	B	B
24	-	B
25	A	B
26	A	B
27	B	B
28	-	B
29	A	B
30	B	A
31	B	A
32	-	B
33	B	A
34	A	B
35	B	A
36	-	B
37	B	A
38	A	B
39	B	A
40	-	B
41	B	A
42	A	B
43	B	A
44	-	B
45	B	A
46	A	B
47	B	A
48	-	B
49	B	A
50	A	B
51	B	A
52	-	B
53	B	A
54	A	B
55	B	A
56	-	B
57	B	A
58	A	B
59	B	A
60	-	B
61	B	A
62	A	B
63	B	A
64	-	B
65	B	A
66	A	B
67	B	A
68	-	B
69	B	A
70	A	B
71	B	A
72	-	B
73	B	A
74	A	B
75	B	A
76	-	B
77	B	A
78	A	B
79	B	A
80	-	B
81	B	A
82	A	B
83	B	A
84	-	B
85	B	A
86	A	B
87	B	A
88	-	B
89	B	A
90	A	B
91	B	A
92	-	B
93	B	A
94	A	B
95	B	A
96	-	B
97	B	A
98	A	B
99	B	A
100	-	B

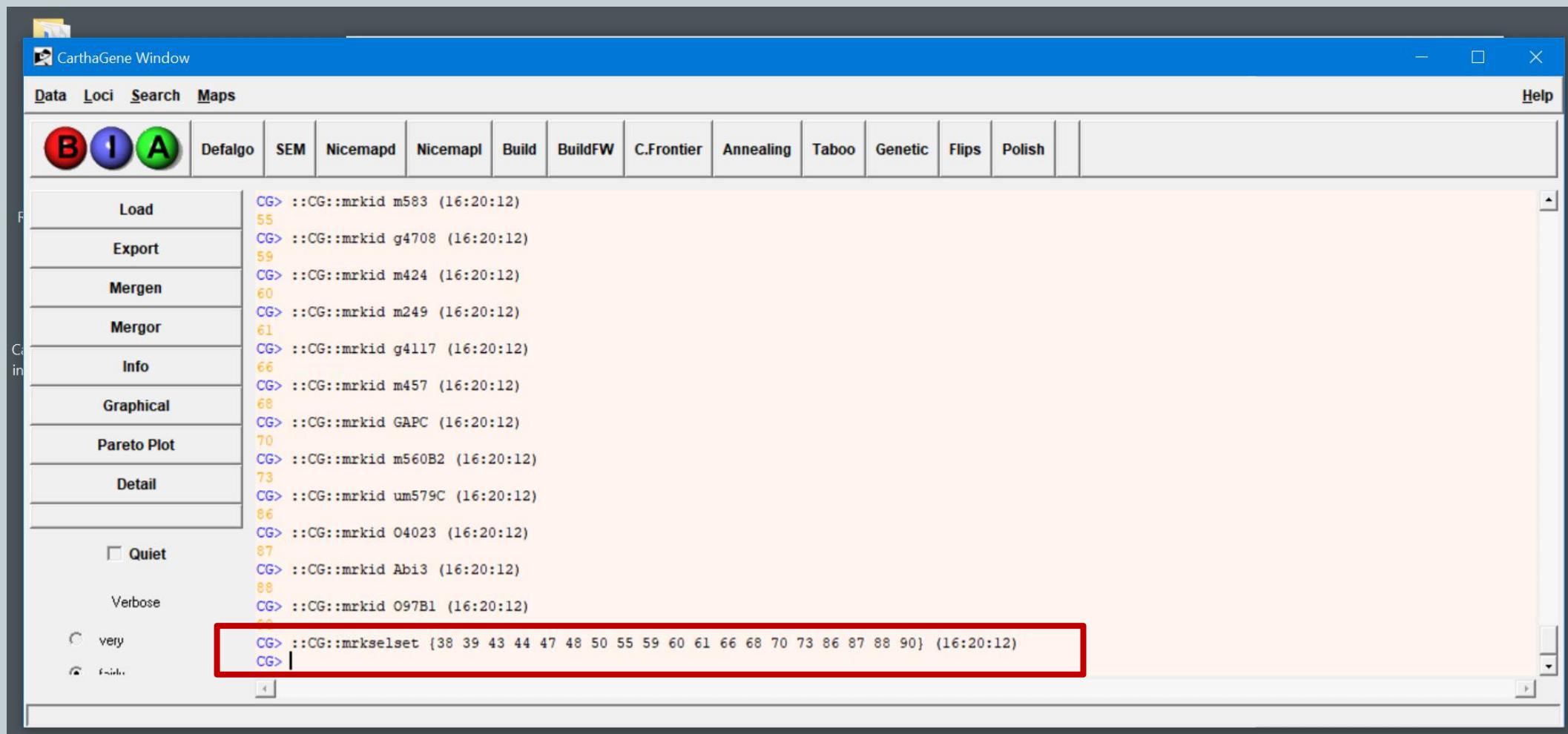
Search for anything

4:18 PM 11/23/2020

Loci/Identify groups



Loci/select a group



Loci/Dist2pt

The screenshot shows the CarthaGene Window software interface. The menu bar includes Data, Loci, Search, Maps, and Help. The toolbar contains buttons for SEM, Nicemapd, Nicemapl, Build, BuildFW, C.Frontier, Annealing, Taboo, Genetic, Flips, and Polish. On the left, a sidebar menu lists options: Identify groups, Select a group, Config, select by Locus, merge two loci, Info, Lod2pt, Dist2pt (which is highlighted with a red box), Fr2pt, Graphical, Pareto Plot, Detail, Quiet (unchecked), Verbose, very (radio button), and Fstida (radio button). The main window displays a command-line interface with the following text:
Print two points distance matrices of the loci selection :
Data Set Number 1 :
g4014 m228 g2778 m105 g4564 m2 g4523 m583 g4708 m424 m249 g4117 m457 GACP m560B um579 O4023 Abi3 O97B1

g4014 |----- 41.5 7.0 34.1 2.6 2.6 44.8 43.4 41.5 11.0 5.9 5.8 3.7 69.8 35.0 22.2 28.2 30.6 8.1
m228 | 41.5 ----- 66.6 4.3 38.0 38.0 6.4 6.4 0.0 84.2 29.8 29.8 72.0 8.0 7.3 20.7 7.0 12.4 44.8
g2778 | 7.0 66.6 ----- 48.6 12.2 12.2 72.5 85.3 57.8 4.1 11.5 11.5 5.4 172.7 43.9 24.8 38.3 35.2 12.3
m105 | 34.1 4.3 48.6 ----- 25.4 25.4 11.2 11.8 4.0 49.7 24.1 23.7 45.3 16.4 1.7 19.4 1.3 8.8 30.2
g4564b | 2.6 38.0 12.2 25.4 ----- 0.0 40.2 40.2 35.2 18.2 3.5 3.5 7.7 50.6 25.8 18.4 24.3 20.6 6.4
m2 | 2.6 38.0 12.2 25.4 0.0 ----- 40.2 40.2 35.2 18.2 3.5 3.5 7.7 50.6 25.8 18.4 24.3 20.6 6.4
g4523 | 44.8 6.4 72.5 11.2 40.2 40.2 ----- 0.5 6.7 172.7 37.7 37.7 65.2 4.1 15.7 32.0 14.8 20.5 50.0
m583 | 43.4 6.4 85.3 11.8 40.2 40.2 0.5 ----- 7.3 172.7 39.2 38.3 65.7 5.1 16.3 33.7 14.6 21.7 46.1
g4708 | 41.5 0.0 57.8 4.0 35.2 35.2 6.7 7.3 ----- 68.8 27.5 27.5 52.0 7.5 6.2 21.0 6.8 13.1 37.1
m424 | 11.0 84.2 4.1 49.7 18.2 18.2 172.7 172.7 68.8 ----- 16.3 16.3 10.1 172.7 45.1 24.9 36.0 39.7 16.3
m249 | 5.9 29.8 11.5 24.1 3.5 3.5 37.7 39.2 27.5 16.3 ----- 0.0 10.7 47.7 24.4 13.9 22.3 17.6 5.8
g4117 | 5.8 29.8 11.5 23.7 3.5 3.5 37.7 38.3 27.5 16.3 0.0 ----- 10.5 51.5 24.0 13.9 21.8 17.6 5.7
m457 | 3.7 72.0 5.4 45.3 7.7 7.7 65.2 65.7 52.0 10.1 10.7 10.5 ----- 100.2 41.3 22.1 28.8 33.4 8.3
GACP | 69.8 8.0 172.7 16.4 50.6 50.6 4.1 5.1 7.5 172.7 47.7 51.5 100.2 ----- 15.1 27.5 16.8 23.9 94.0
m560B | 35.0 7.3 43.9 1.7 25.8 25.8 15.7 16.3 6.2 45.1 24.4 24.0 41.3 15.1 ----- 19.1 0.6 12.8 30.2
um579C | 22.2 20.7 24.8 19.4 18.4 18.4 32.0 33.7 21.0 24.9 13.9 13.9 22.1 27.5 19.1 ----- 16.9 10.1 15.7
O4023 | 28.2 7.0 38.3 1.3 24.3 24.3 14.8 14.6 6.8 36.0 22.3 21.8 28.8 16.8 0.6 16.9 ----- 11.7 26.8
Abi3 | 30.6 12.4 35.2 8.8 20.6 20.6 20.5 21.7 13.1 39.7 17.6 17.6 33.4 23.9 12.8 10.1 11.7 ----- 22.6
O97B1 | 8.1 44.8 12.3 30.2 6.4 6.4 50.0 46.1 37.1 16.3 5.8 5.7 8.3 94.0 30.2 15.7 26.8 22.6 -----

CG> Print the two points distance matrix.

Duplicates can be identified here

“Nicemapd” button

CarthaGene Window

Data Loci Search Maps Help

B I A Defalgo SEM Nicemapd Nicemapl Build BuildFW C.Frontier Annealing Taboo Genetic Flips Polish

Load Export Mergen Mergor Info Graphical Pareto Plot Detail

Map -1 : log10-likelihood = -205.95

```
-----  
Set : Marker List ...  
1 : m424 g2778 m457 g4014 g4564b m2 m249 g4117 097B1 um579C Abi3 m105 04023 m560B2 g4708 m228 m583 g4523 GAPC  
27.5 16.3 0.0 ----- 10.5 51.5 24.0 13.9 21.8 17.6 5.7  
m457 | 3.7 72.0 5.4 45.3 7.7 7.7 65.2 65.7 52.0 10.1 10.7 10.5 ----- 100.2 41.3 22.1 28.8 33.4 8.3  
GAPC | 69.8 8.0 172.7 16.4 50.6 50.6 4.1 5.1 7.5 172.7 47.7 51.5 100.2 ----- 15.1 27.5 16.8 23.9 94.0  
m560B2 | 35.0 7.3 43.9 1.7 25.8 25.8 15.7 16.3 6.2 45.1 24.4 24.0 41.3 15.1 ----- 19.1 0.6 12.8 30.2  
um579C | 22.2 20.7 24.8 19.4 18.4 18.4 32.0 33.7 21.0 24.9 13.9 13.9 22.1 27.5 19.1 ----- 16.9 10.1 15.7  
04023 | 28.2 7.0 38.3 1.3 24.3 24.3 14.8 14.6 6.8 36.0 22.3 21.8 28.8 16.8 0.6 16.9 ----- 11.7 26.8  
Abi3 | 30.6 12.4 35.2 8.8 20.6 20.6 20.5 21.7 13.1 39.7 17.6 17.6 33.4 23.9 12.8 10.1 11.7 ----- 22.6  
097B1 | 8.1 44.8 12.3 30.2 6.4 6.4 50.0 46.1 37.1 16.3 5.8 5.7 8.3 94.0 30.2 15.7 26.8 22.6 -----
```

```
CG> CG> ::CG::heaptintd (16:24:00)
```

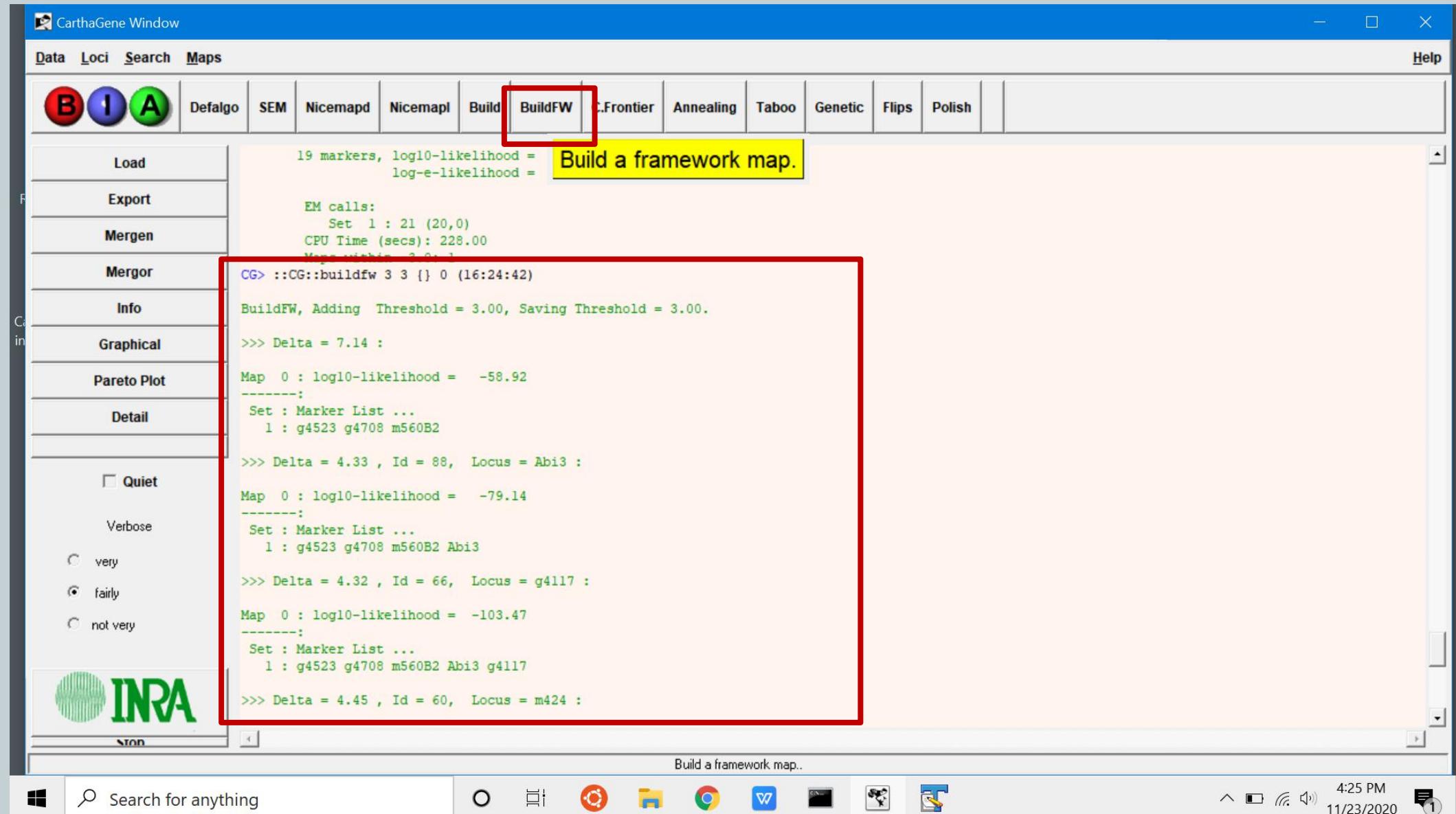
Map 0 : log10-likelihood = -205.95, log-e-likelihood = -474.22

```
-----  
Data Set Number 1 :  
Quiet  
Verbose  
Very  
Fairly  
Not very  
INRA
```

Pos	Id	name	Markers	Distance Haldane	Cumulative Haldane	Distance Kosambi	Theta (\$%age)	2pt LOD
1	60	m424		4.1 cM	0.0 cM	4.0 cM	4.0 %	16.9
2	43	g2778		5.5 cM	4.1 cM	5.2 cM	5.2 %	14.9
3	68	m457		4.3 cM	9.6 cM	4.2 cM	4.2 %	16.7
4	38	g4014		3.0 cM	13.9 cM	3.0 cM	3.0 %	17.7
5	47	g4564b		0.0 cM	17.0 cM	0.0 cM	0.0 %	27.4
6	48	m2		3.8 cM	17.0 cM	3.7 cM	3.7 %	17.8
7	61	m249		0.0 cM	20.8 cM	0.0 cM	0.0 %	29.5
8	66	g4117		6.8 cM	20.8 cM	6.4 cM	6.4 %	12.3
9	90	097B1		22.6 cM	27.6 cM	19.0 cM	18.2 %	3.9
10	86	um579C		11.3 cM	50.2 cM	10.3 cM	10.1 %	7.6

4:24 PM 11/23/2020

buildfw



Last map is the best

Search/config

CarthaGene Window

Data Loci Search Maps Help

B I A Defalgo SEM Nicemapd Nicemapl Build BuildFW C.Frontier Annealing Taboo Genetic Flips Polish

Load : 5 5 7 8 8 6 4 3 6 4 6
: 0 9 3 8 6 6 7 8 8 3 0

Export

Mergen

Mergor

Info

Graphical

Pareto Plot

Detail

Quiet

Verbose

fairly

not very

INRA

CarthaGene Search Config

Specific parameter of the method BuildFW

keepthres: 3

addthres: 3

Build

BuildFW

C.Frontier

Annealing

Greedy

Genetic_A

Flips

OK Try Cancel

```
Ab 50.9 g4014 53.6 m457 57.8 g2778 63.0 m424 66.9]) {8 -1  
1 g4014 59.8 m457 64.0 g2778 69.2 m424 73.2}) {10 -175.62  
2.8 g4523 62.6 g4708 69.2 m560B2 75.4}) {15 -176.86 {1 -1  
560B2 59.6 g4708 65.4 g4523 72.0}) {12 -176.92 {1 -176.92  
58.6 Abi3 80.4 um579C 90.4}) {11 -177.77 {1 -177.77 m424  
560B2 70.8 Abi3 82.8}) {7 -177.98 {1 -177.98 g4523 0.0 g4  
.3 um579C 84.6}) {5 -178.07 {1 -178.07 g4117 0.0 g4564b 3  
um579C 243.8}) {13 -178.25 {1 -178.25 m424 0.0 g2778 4.0  
2 81.3}) {9 -179.15 {1 -179.15 g4708 0.0 g4523 6.6 m560B2  
.})
```

CG> ::CG::asget (16:28:20)
{1 "ri self" "C:/Users/sujan/OneDrive/Desktop/Vignan/arabidopsis_linkage_data.txt" 91 101}
CG>

Search for anything

4:29 PM 11/23/2020

Best map -

Last in heap (or)

bestprint; bestprintd
commands

CarthaGene Window

Data Loci Search Maps

B I A Defalgo SEM Nicemapd Nicemapl Build BuildFW C.Frontier Annealing Taboo Genetic Flips Polish

Load

Maps within -3.0: 1

CG> bestmap (16:29:51)
invalid command name "beatman"
CG> bestprint (16:30:33)

Map 14 : log10-likelihood = -171.17

Set : Marker List ...
1 : g4523 g4708 m560B2 Abi3 um579C g4117 g4564b g4014 m457 g2778 m424

14

CG> bestprintd (16:30:40)

Map 14 : log10-likelihood = -171.17, log-e-likelihood = -394.13

Data Set Number 1 :

Pos	Id	name	Markers	Distance Haldane	Cumulative Distance Haldane	Theta Kosambi (%)	2pt LOD
1	50	g4523	7.0 cM	0.0 cM	6.6 cM	6.6 %	13.6
2	59	g4708	6.2 cM	7.0 cM	5.9 cM	5.8 %	13.7
3	73	m560B2	13.1 cM	13.2 cM	11.7 cM	11.5 %	7.5
4	88	Abi3	10.8 cM	26.4 cM	9.9 cM	9.7 %	7.6
5	86	um579C	15.2 cM	37.2 cM	13.4 cM	13.1 %	5.7
6	66	g4117	3.5 cM	52.4 cM	3.4 cM	3.4 %	17.8
7	47	g4564b	2.8 cM	55.9 cM	2.7 cM	2.7 %	17.7
8	38	g4014	4.4 cM	58.6 cM	4.2 cM	4.2 %	16.7
9	68	m457	5.5 cM	63.0 cM	5.2 cM	5.2 %	14.9
10	43	g2778	4.1 cM	68.5 cM	4.0 cM	4.0 %	16.9
11	60	m424	-----	72.6 cM	-----	66.9 cM	

INRA

Search for anything

