

# Graphical GenoTypes (GGT) software for visualization and analysis of genetic data

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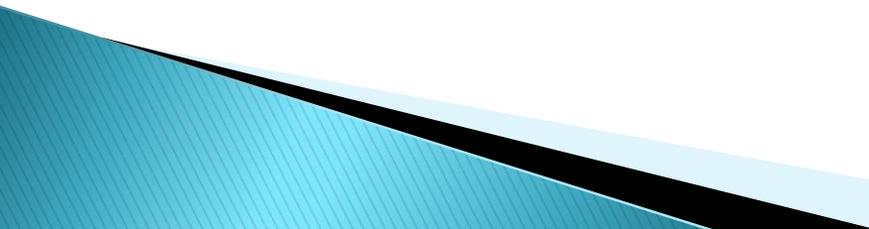
# Purpose of this tutorial

- ▶ To demonstrate how to download and install Graphical GenoTypes (GGT) software.
  - ▶ Explain how to organize and input data.
  - ▶ Explain the uses of GGT to visualize and analyze genetic data.
- 

# GGT 2.0 Graphical Genotypes

- ▶ Version 1 was released in 1999 as a free software package for visualization of molecular marker data (van Berloo, R., 1999).
- ▶ The concept of graphical genotypes was developed for plant breeding and plant genetics (Young, N. D. and S. D. Tanksley. 1989).
- ▶ The latest version (2010) has expanded options for genetic analysis of populations including diversity analyses and simple association studies.

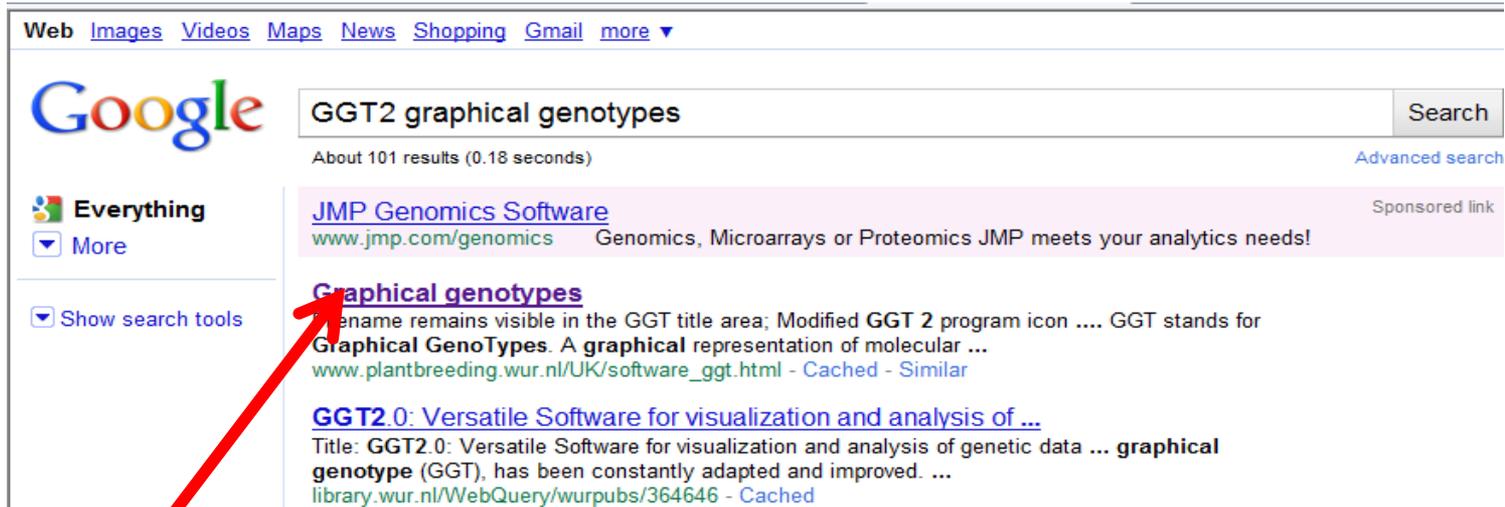
# Why GGT ?

- ▶ A graphical representation of molecular marker data can be an important tool in the process of selection and evaluation of plant material.
  - ▶ It enables the representation of molecular marker data by simple chromosome drawing in several ways.
- 

# Requirements

- ▶ Software is in English, developed by Laboratory of Plant Breeding, Wageningen University, The Netherlands (Van Berloo, R., 1999).
- ▶ System requirements
  - Computer running Windows
  - Will take 5 - 10 MB of hard disk space.

# Where to find...



The image shows a screenshot of a Google search results page. The search query is "GGT2 graphical genotypes". The search results include a sponsored link for "JMP Genomics Software" and a search result for "Graphical genotypes" with a red arrow pointing to the title. Below the search results, the URL "www.plantbreeding.wur.nl/UK/software\_ggt.html" is displayed.

Web Images Videos Maps News Shopping Gmail more ▾

Google

GGT2 graphical genotypes Search

About 101 results (0.18 seconds) Advanced search

Everything More

Show search tools

**JMP Genomics Software** Sponsored link  
[www.jmp.com/genomics](http://www.jmp.com/genomics) Genomics, Microarrays or Proteomics JMP meets your analytics needs!

**Graphical genotypes**  
... name remains visible in the GGT title area; Modified GGT 2 program icon .... GGT stands for **Graphical GenoTypes**. A **graphical** representation of molecular ...  
[www.plantbreeding.wur.nl/UK/software\\_ggt.html](http://www.plantbreeding.wur.nl/UK/software_ggt.html) - Cached - Similar

**GGT2.0: Versatile Software for visualization and analysis of ...**  
Title: GGT2.0: Versatile Software for visualization and analysis of genetic data ... **graphical genotype** (GGT), has been constantly adapted and improved. ...  
[library.wur.nl/WebQuery/wurpubs/364646](http://library.wur.nl/WebQuery/wurpubs/364646) - Cached

[www.plantbreeding.wur.nl/UK/software\\_ggt.html](http://www.plantbreeding.wur.nl/UK/software_ggt.html)

Plant Breeding

Education

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Work at

Phone book

Links

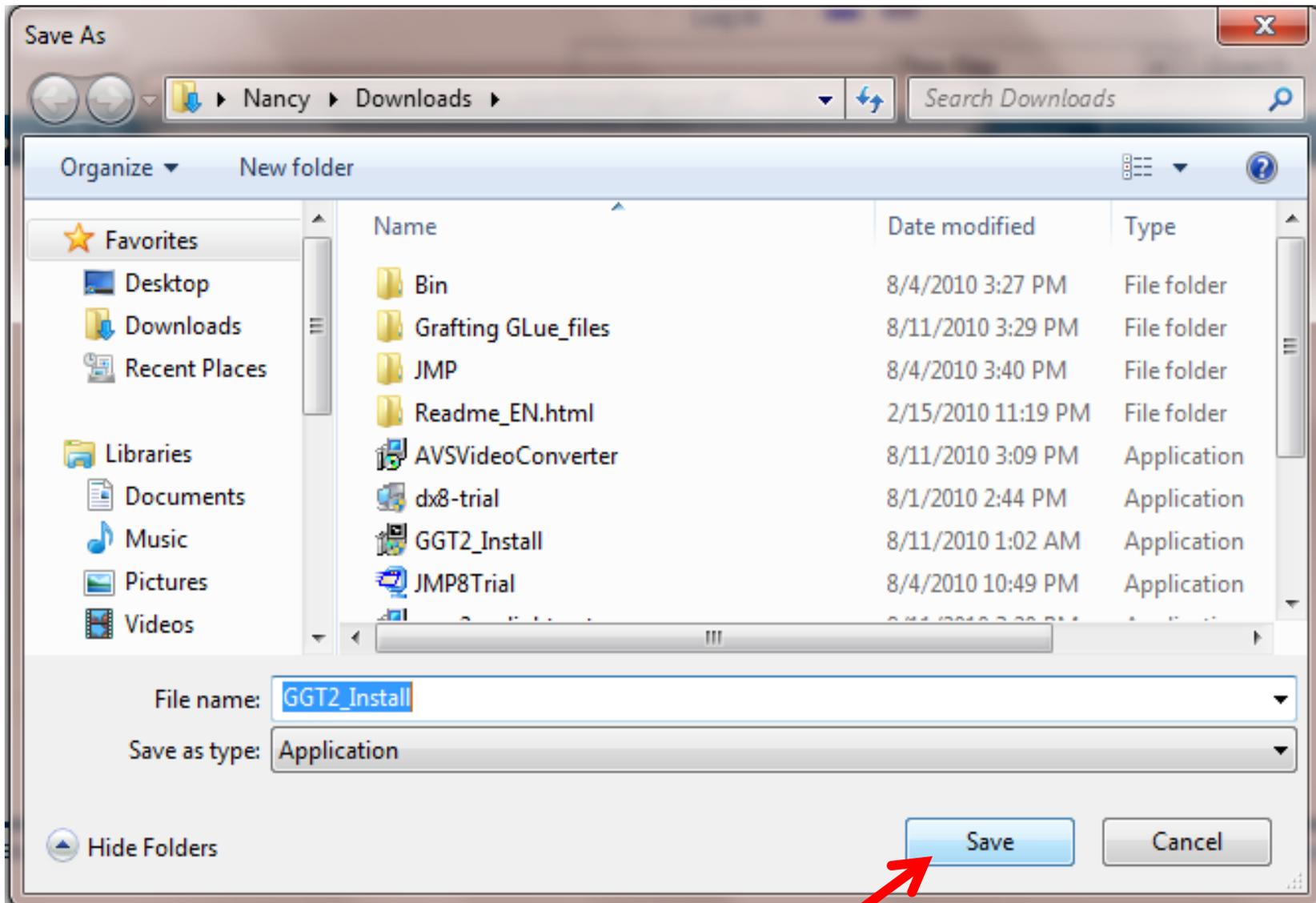
Contact

# GGT 2.0: graphical genotypes

please click [this link](#)  to download the GGT 2.0 install package (2.5 MB)

[back to GGT homepage](#)

Click here to download the software



Save to file 'Downloads'

Download complete



Download Complete

GGT2\_Install.exe from www.plantbreeding.wur.nl



Downloaded: 107KB in 12 sec

Download to: C:\Users\Nancy\Downloads\GGT2\_Install.exe

Transfer rate: 8.99KB/Sec

Close this dialog box when download completes

Run

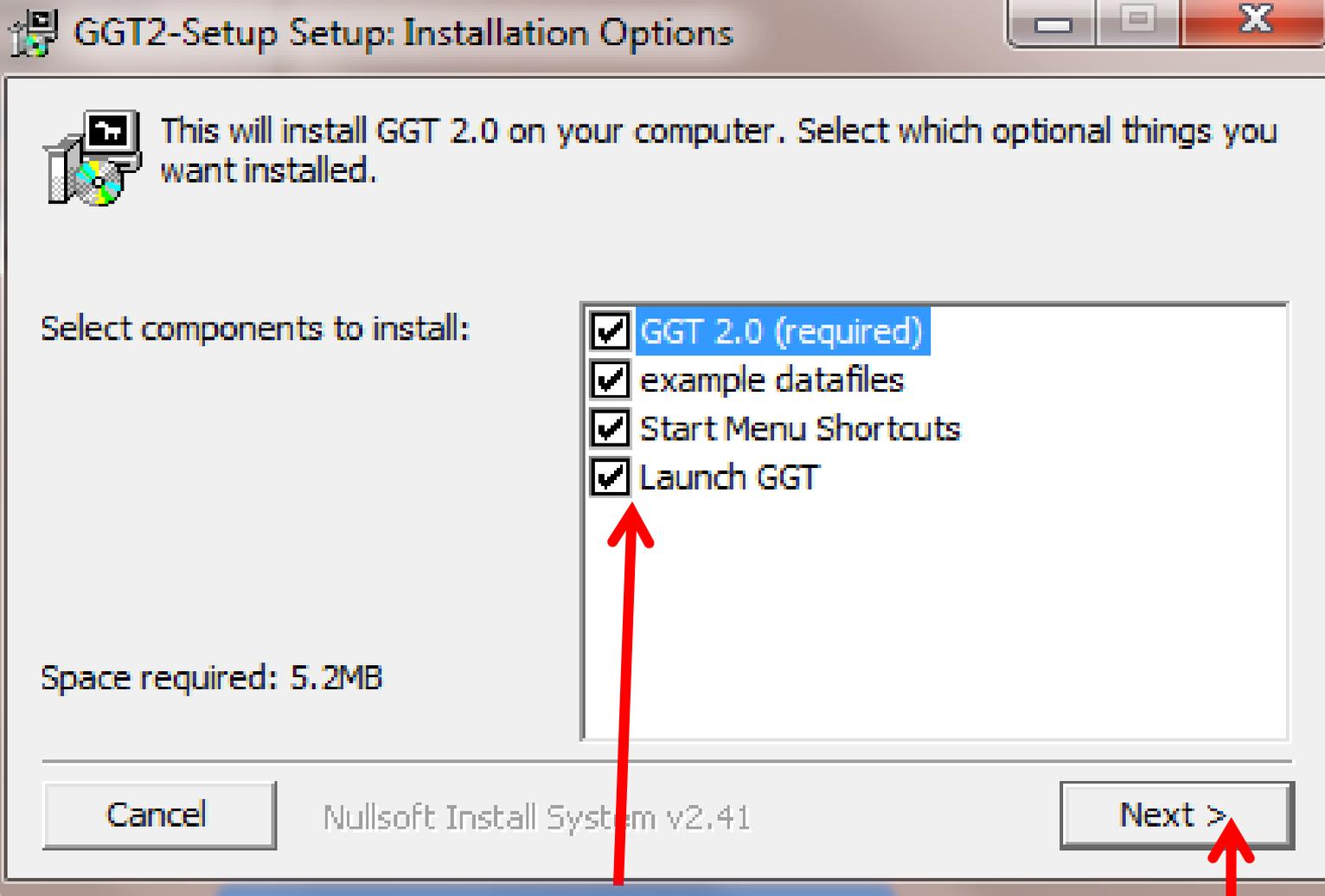
Open Folder

Close



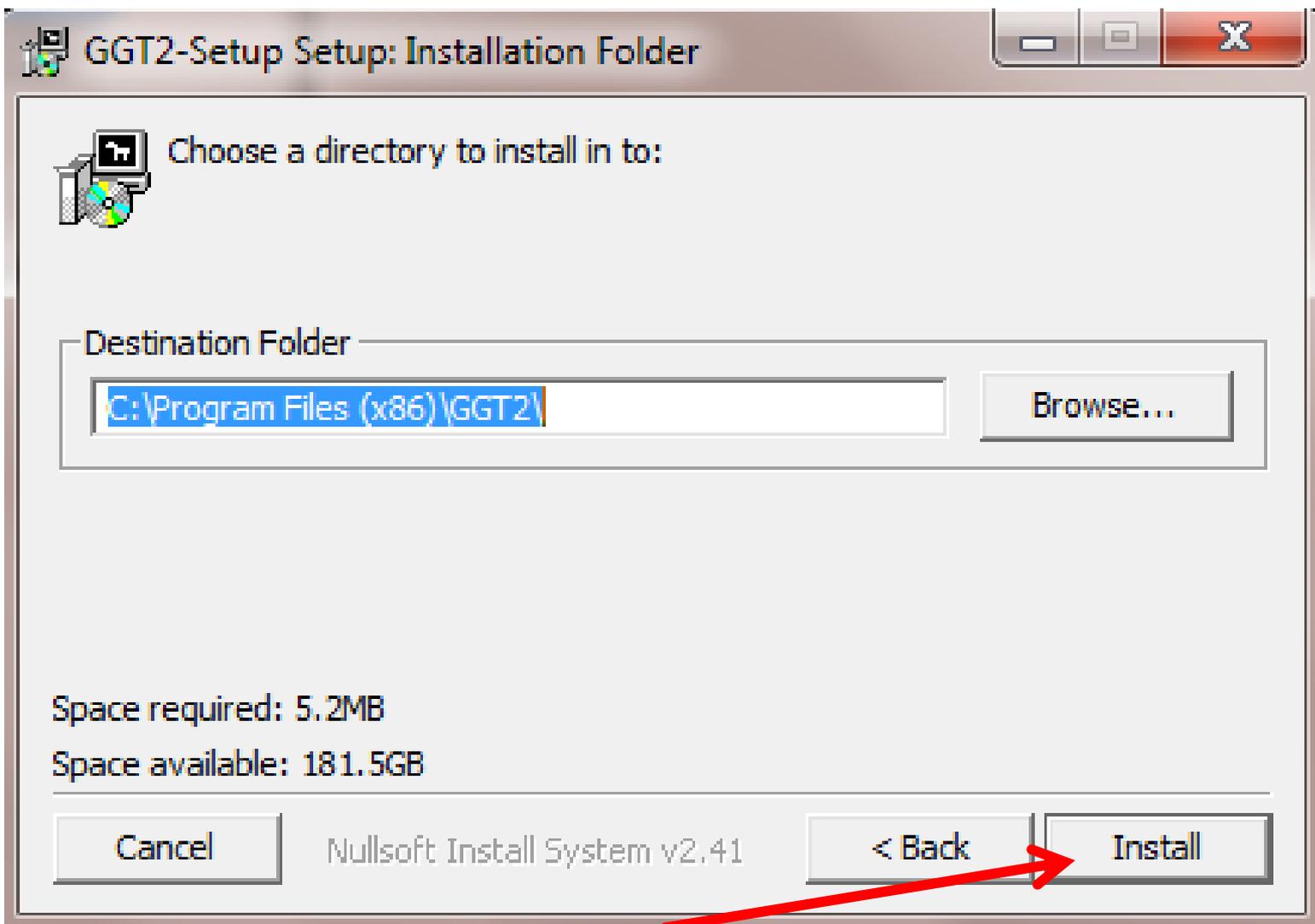
SmartScreen Filter checked this download and did not report any threats. [Report an unsafe download.](#)

Click on run to start the installation!



Check all boxes

Click here!



Last step click here!

# What files should you get ?

The screenshot shows a Windows Explorer window with the address bar set to 'Computer > Local Disk (C:) > Program Files (x86) > GGT2'. The window title is 'Computer > Local Disk (C:) > Program Files (x86) > GGT2'. The menu bar includes 'Organize', 'Include in library', 'Share with', 'Burn', 'Compatibility files', and 'New folder'. The left sidebar shows 'Favorites' (Desktop, Downloads, Recent Places) and 'Libraries' (Documents, Music, Pictures, Videos). The main pane displays a list of files and folders with columns for Name, Date modified, Type, and Size.

| Name        | Date modified     | Type                  | Size     |
|-------------|-------------------|-----------------------|----------|
| examples    | 8/11/2010 7:18 AM | File folder           |          |
| example     | 3/28/2007 4:41 AM | Graphical Genoty...   | 1 KB     |
| ggt         | 8/15/2010 1:23 PM | Configuration sett... | 1 KB     |
| ggt2_manual | 3/28/2007 4:41 AM | Adobe Acrobat D...    | 2,100 KB |
| Ggt32       | 2/4/2010 5:44 PM  | Application           | 2,458 KB |
| LISTER_all  | 3/28/2007 4:41 AM | Graphical Genoty...   | 42 KB    |
| uninstall   | 8/15/2010 1:23 PM | Application           | 35 KB    |
| whatsnew    | 2/4/2010 5:05 PM  | Text Document         | 15 KB    |

# Example Data

er ▶ Local Disk (C:) ▶ Program Files (x86) ▶ GGT2 ▶ examples

Library ▼ Share with ▼ Burn Compatibility files New folder

| Name   | Date modified     | Type                  | Size   |
|--|-------------------|-----------------------|--------|
|  alternative      | 3/28/2007 4:41 AM | Microsoft Office E... | 15 KB  |
|  CHROM1           | 3/28/2007 4:41 AM | Graphical Genoty...   | 11 KB  |
|  CHROM1.LOC       | 3/28/2007 4:41 AM | LOC File              | 12 KB  |
|  chrom1.map       | 3/28/2007 4:41 AM | MAP File              | 3 KB   |
|  CHROM2           | 3/28/2007 4:41 AM | Graphical Genoty...   | 13 KB  |
|  CHROM2.LOC       | 3/28/2007 4:41 AM | LOC File              | 14 KB  |
|  chrom2.map       | 3/28/2007 4:41 AM | MAP File              | 3 KB   |
|  CHROM3           | 3/28/2007 4:41 AM | Graphical Genoty...   | 9 KB   |
|  CHROM3.LOC      | 3/28/2007 4:41 AM | LOC File              | 9 KB   |
|  chrom3.map     | 3/28/2007 4:41 AM | MAP File              | 2 KB   |
|  Democp1        | 3/28/2007 4:41 AM | Graphical Genoty...   | 2 KB   |
|  LISTER.LOC     | 3/28/2007 4:41 AM | LOC File              | 39 KB  |
|  LISTER.MAP     | 3/28/2007 4:41 AM | MAP File              | 6 KB   |
|  LISTER_all     | 8/11/2010 7:18 AM | Graphical Genoty...   | 41 KB  |
|  listerdean_ggt | 3/28/2007 4:41 AM | Microsoft Office E... | 595 KB |
|  smallggt       | 3/28/2007 4:41 AM | Microsoft Office E... | 14 KB  |

# How to prepare data?

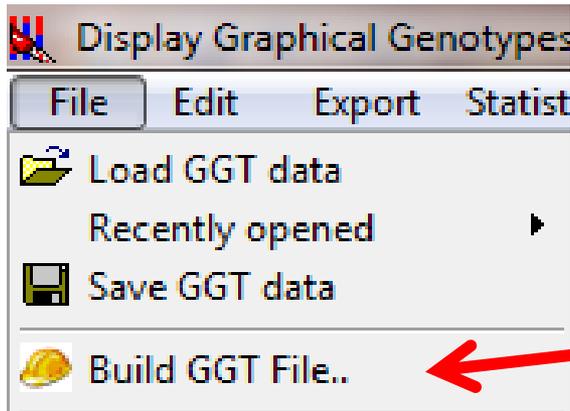
- ▶ There are many options to prepare data:
  - 1) Build GGT from two sources, locus and map data.
  - 2) Export using an EXCEL spreadsheet.
  - 3) Alternative layout (for further information see the manual)

# 1. Input Data – Building GGT files

▶ From two sources:

a) Locus Data

b) Map Data



Build GGT file

# a) Locus Data

```
; This file was used as input for the JOINMAP mapping software
; use the BUIL GGT FILE option to merge '.loc' and '.map' files into a
'.ggt' file
;
; Fri, 10 Jan 1997, 11:54
; grouping file: mylvuniq.grp
; original file: mylvuniq.loc
; linkage group: 1

name = lvuniq-1|
popt = RI9
nloc = 72
nind = 103

E42M32-231#1
aaaaa -ca-a caccc aacca cacac caaca aaaca cccca accaa accca
caaac aaaaa accaa acccc accaa cccac acaaa caccc caaaa ccaac
ccc
E33M61-740
aaaaa aaaca caccc aacca aacac caaca caaca acaaa acacc accaa
cacaa acaaa accca ccccc accaa accac accaa caaca caaaa caaac
```

- ▶ *The locus file is a plain text file (txt).*
- ▶ *A = Parent 1; B = Parent 2; H = heterozygote; C = B/H; D = A/H (MAPMAKER FORMAT)*

## b) Map Data

```
; Genetic map file of a Barley RIL population
; chromosome 1

chrom 1

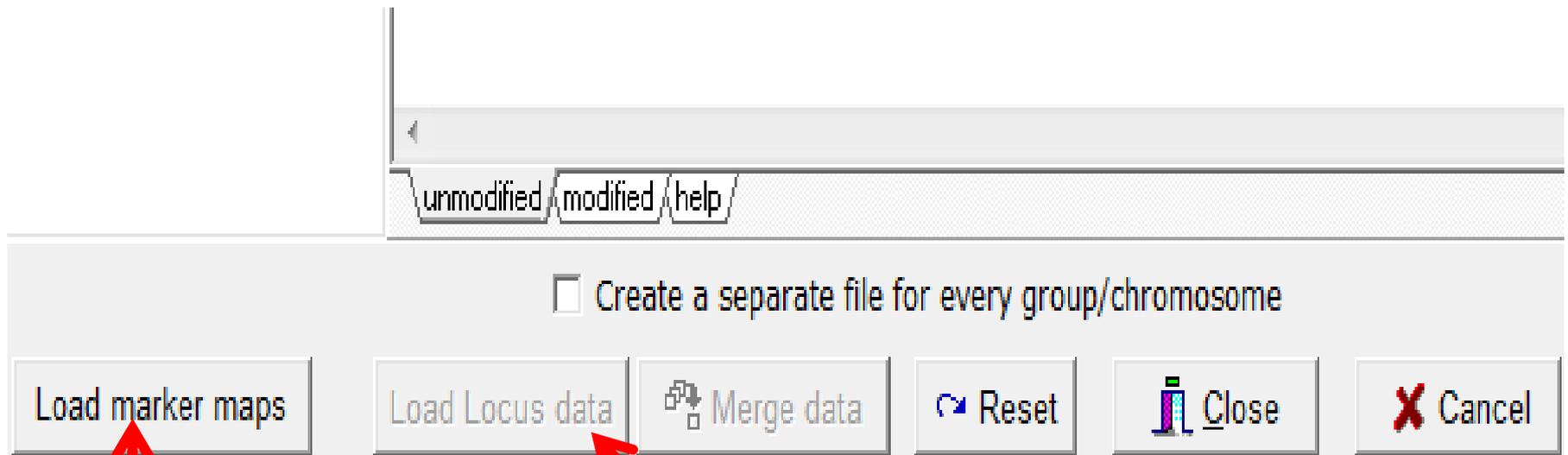
E33M55-508      0.0
E39M61-574      1.8
E35M48-228      4.0
E33M61-740      14.6
E35M54-93       14.6
E41M40-112      20.7
E42M51-267      23.3
E42M32-231#1    26.5
E42M40-287      28.5
E33M61-120      29.2
E37M32-99       38.0
```

Marker

Position

- ▶ The map file is a plain text file as well (MAPMAKER Output). It lists, in two columns, markers and their map positions.

# To merge both sources of data



Load marker maps

Load Locus data

Merge data

Reset

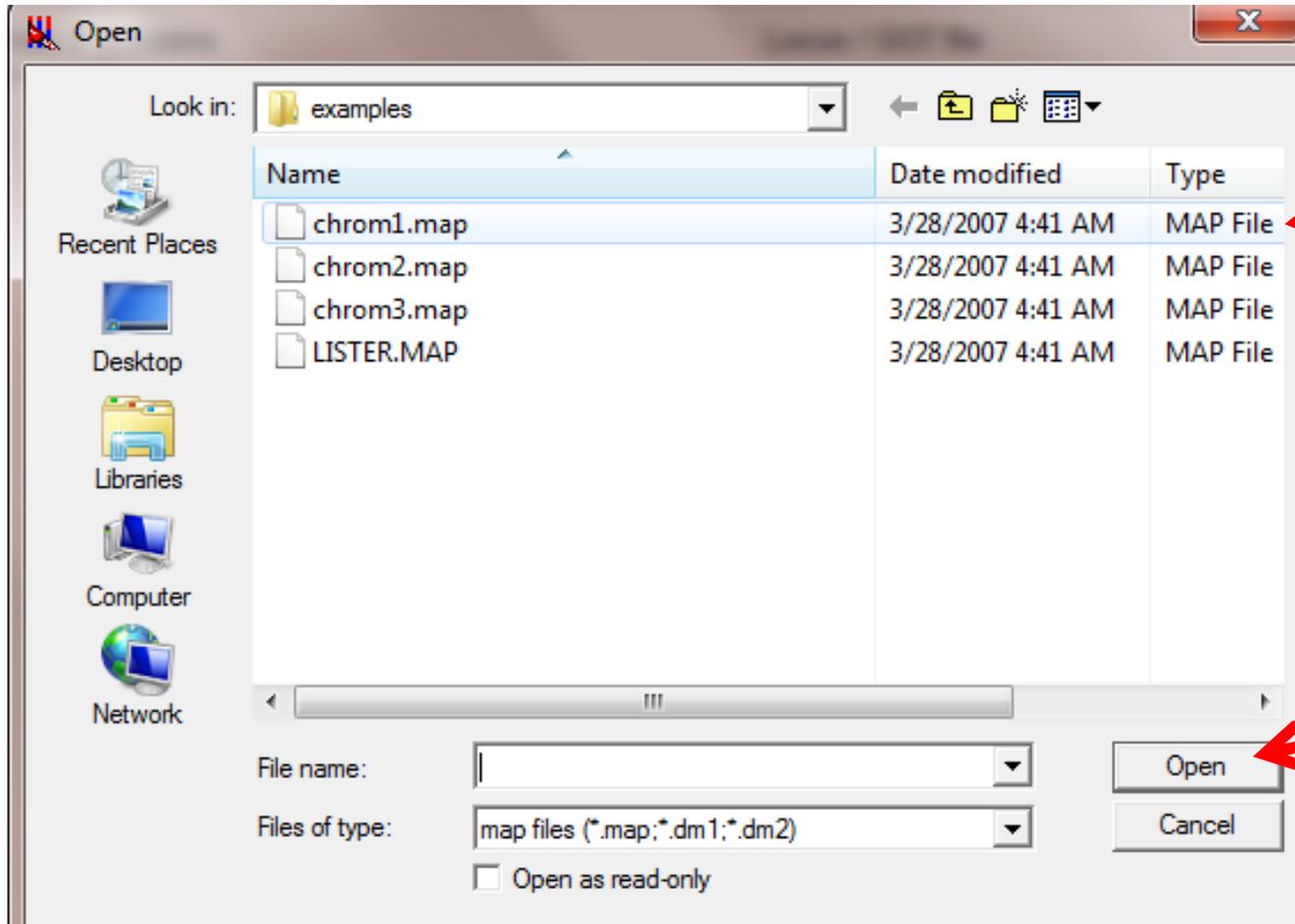
Close

Cancel

Click here to insert map data

Click here to insert locus data

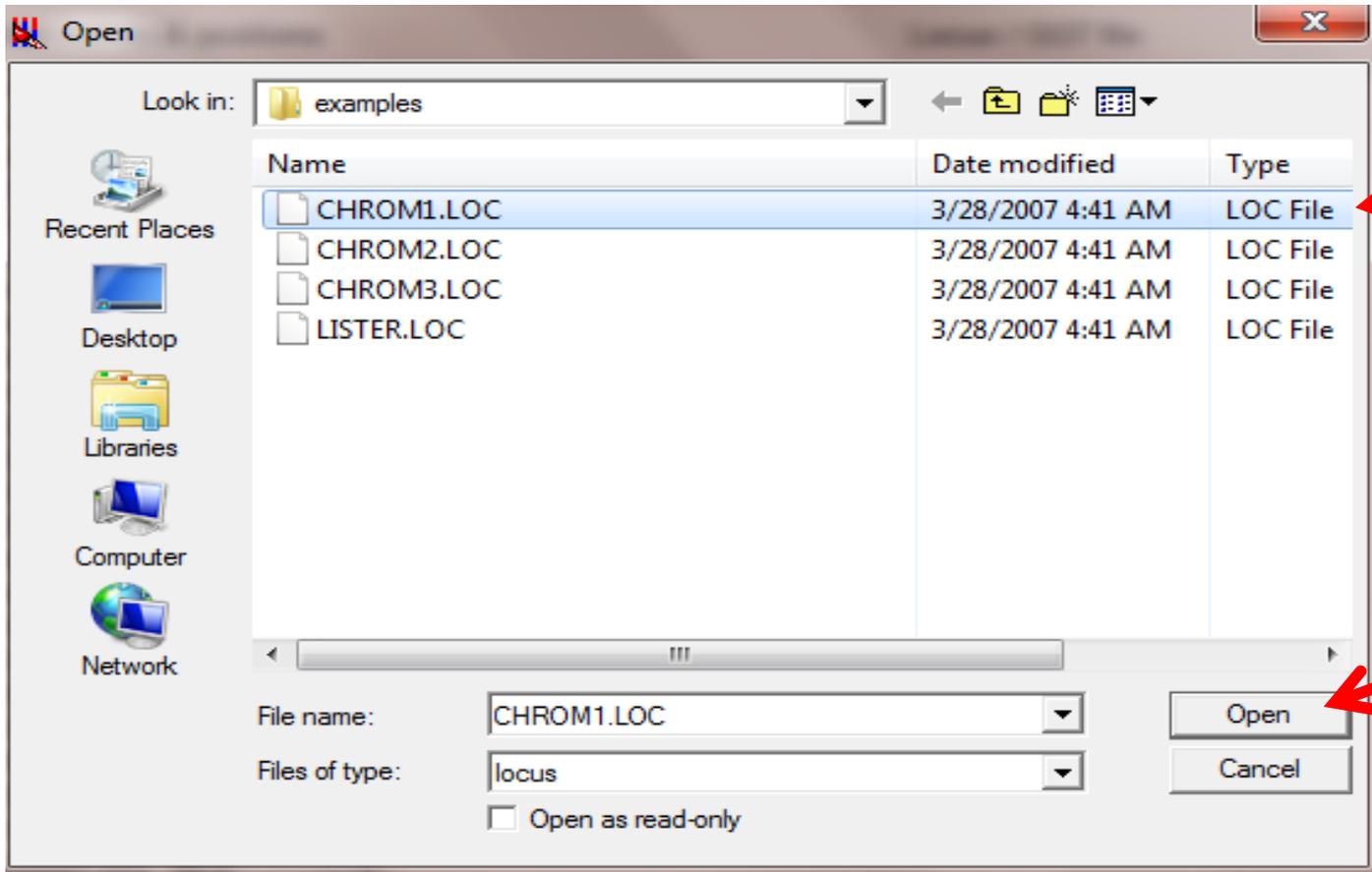
# Loading marker maps



Select  
one file

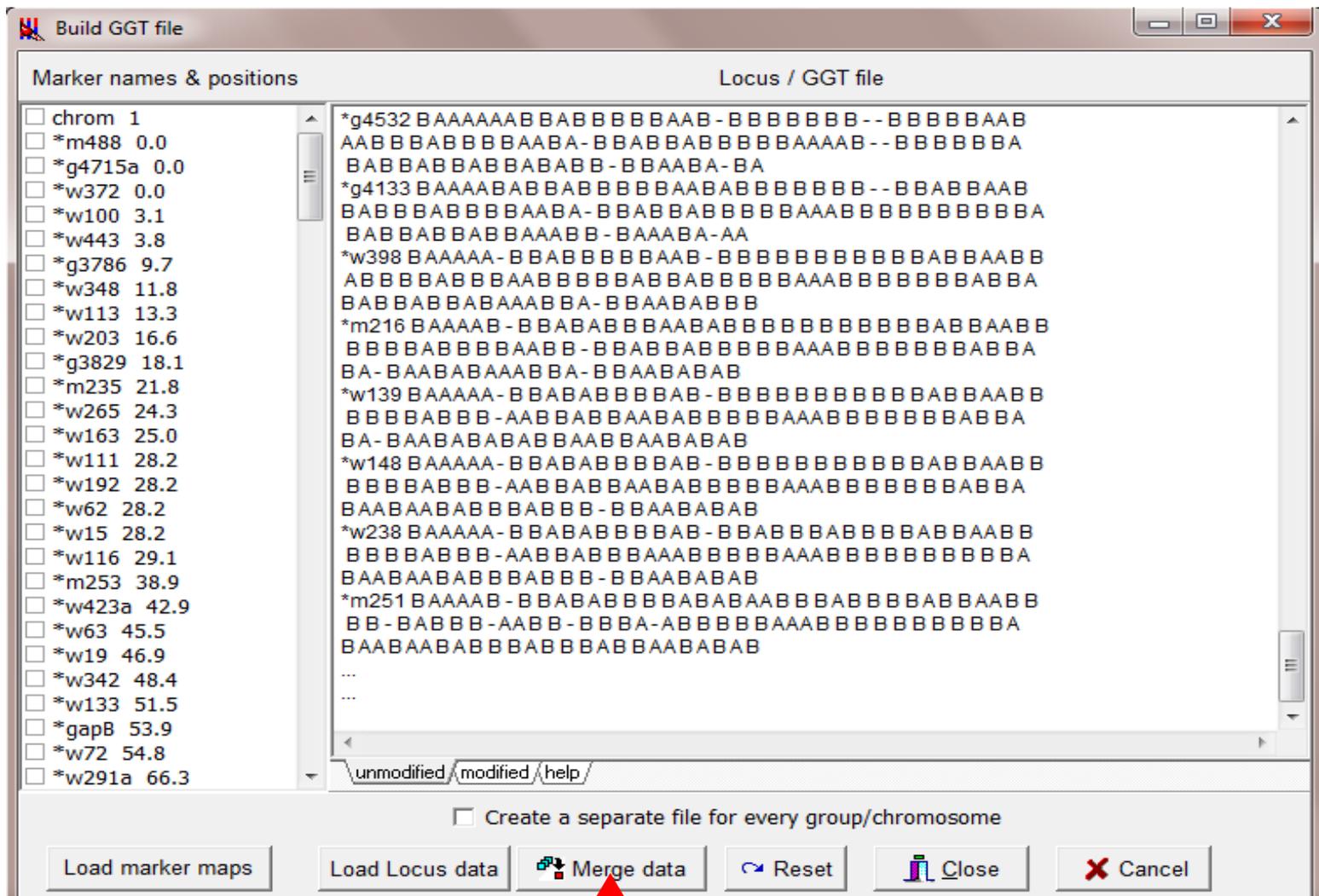
click on  
open

# Loading locus data

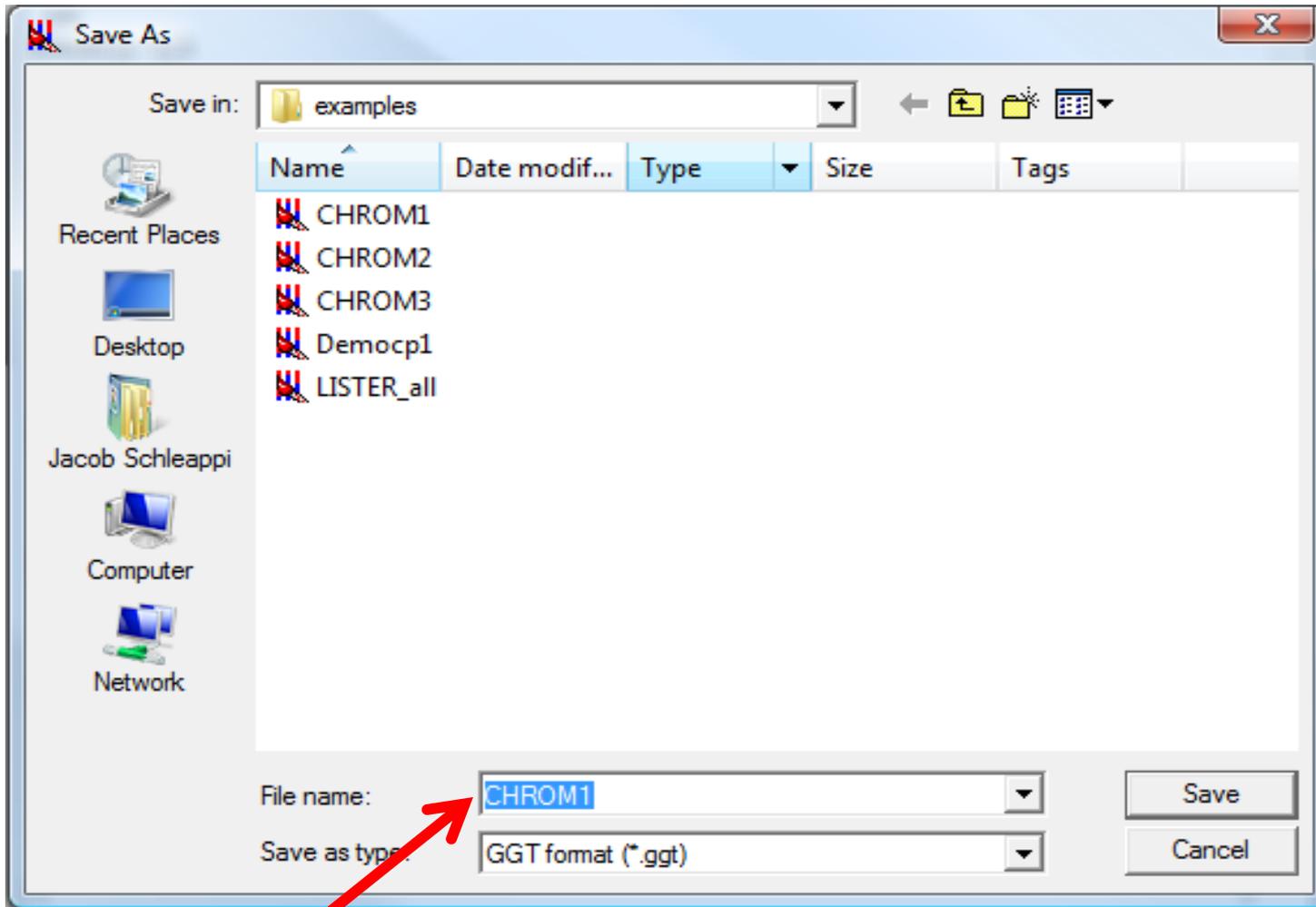


Select one file

And click on open



Click on merge data



Save in the same folder as your original data files using \*.ggt format

Build GGT file

Marker names & positions      Locus / GGT file

|   |   |
|---|---|
| <input checked="" type="checkbox"/> chrom 1           | nchrom=1  |
| <input checked="" type="checkbox"/> E33M55-508 0.0    | nind=103  |
| <input checked="" type="checkbox"/> E39M61-574 1.8    | popt=ri9  |
| <input checked="" type="checkbox"/> E35M48-228 4.0    |   |
| <input checked="" type="checkbox"/> E33M61-740 14.6   | name= 1   |
| <input checked="" type="checkbox"/> E35M54-93 14.6    | nloc=72   |
| <input checked="" type="checkbox"/> E41M40-112 20.7   |   |
| <input checked="" type="checkbox"/> E42M51-267 23.3   | E33M55-508 0.0  |
| <input checked="" type="checkbox"/> E42M32-231#1 26.5 | dddbd bdddd bdbbb ddbbb dbddb bddbd bddbd bddbd bbbbb dbddb |
| <input checked="" type="checkbox"/> E42M40-287 28.5   | bddbd dbddd ddbbb bdbbb bddbd dbbdb dbddd bdbbd bdbdd bddbd |
| <input checked="" type="checkbox"/> E33M61-120 29.2   | dbd   |
| <input checked="" type="checkbox"/> E37M32-99 38.0    | E39M61-574 1.8  |
| <input checked="" type="checkbox"/> e37m32-555#1 38.6 | d-dbd bd-bd bdbbb ddbbb ddbbd bddbd bddbd dbddd bbbbb dbddd |
| <input checked="" type="checkbox"/> E35M61-432 44.0   | bddbd dbddd ddbbb bdbbb bddbd dbbdb dbddd bdbbd bdbdd bddbd |
| <input checked="" type="checkbox"/> E42M32-195 71.7   | dbd   |
| <input checked="" type="checkbox"/> E38M54-618 79.3   | E35M48-228 4.0  |
| <input checked="" type="checkbox"/> E33M61-210 79.3   | dddb- bddbd bdbbb ddbbb dd-db b-dbd bddbd dbddd bbbbb dbddd |
| <input checked="" type="checkbox"/> e37m33-154 81.0   | bdbdd dbddd ddb-b bdbbb bd-dd dbbdb dbddd bdbbd bdbdd bddbd |
| <input checked="" type="checkbox"/> E37M33-311 81.0   | bbd   |
| <input checked="" type="checkbox"/> E33M54-261 81.6   | E33M61-740 14.6   |
| <input checked="" type="checkbox"/> E45M55-510 81.6   | aaaaa aaaca caccc aacca aacac caaca caaca acaaa acacc accaa |
| <input checked="" type="checkbox"/> E35M55-458 84.0   | cacaa acaaa accca ccccc accaa accac accaa caaca caaaa caaac |
| <input checked="" type="checkbox"/> E33M61-353 85.3   | cca   |
| <input checked="" type="checkbox"/> e33M54-201 86.0   |   |
| <input checked="" type="checkbox"/> e33M54-202 86.0   |   |
| <input checked="" type="checkbox"/> e42M40-472 86.0   |   |
| <input checked="" type="checkbox"/> e37M33-439 86.6   |   |
| <input checked="" type="checkbox"/> e33M61-718 86.6   |   |

unmodified modified help

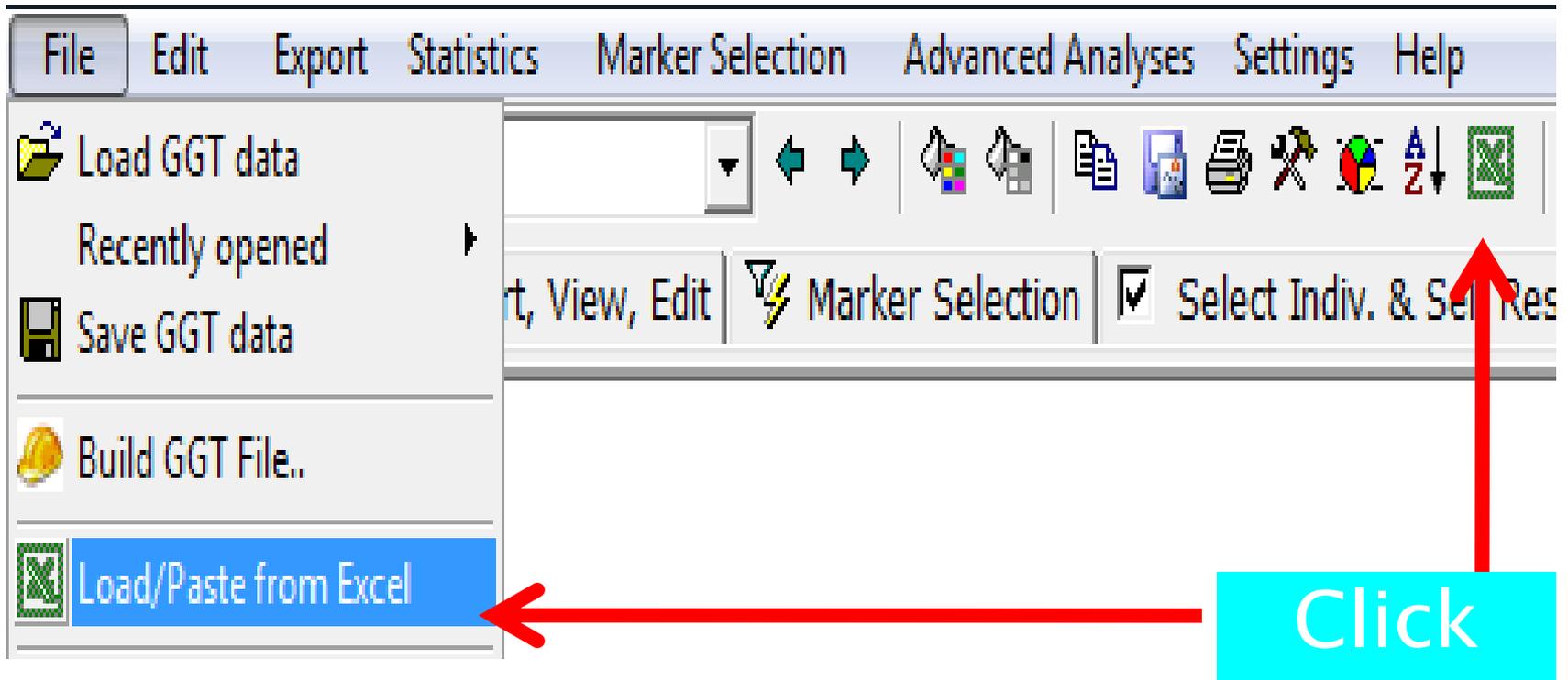
Create a separate file for every group/chromosome

Load marker maps    Load Locus data    Merge data    Reset    **Close**    Cancel



Click here!

## 2) Input Data using EXCEL

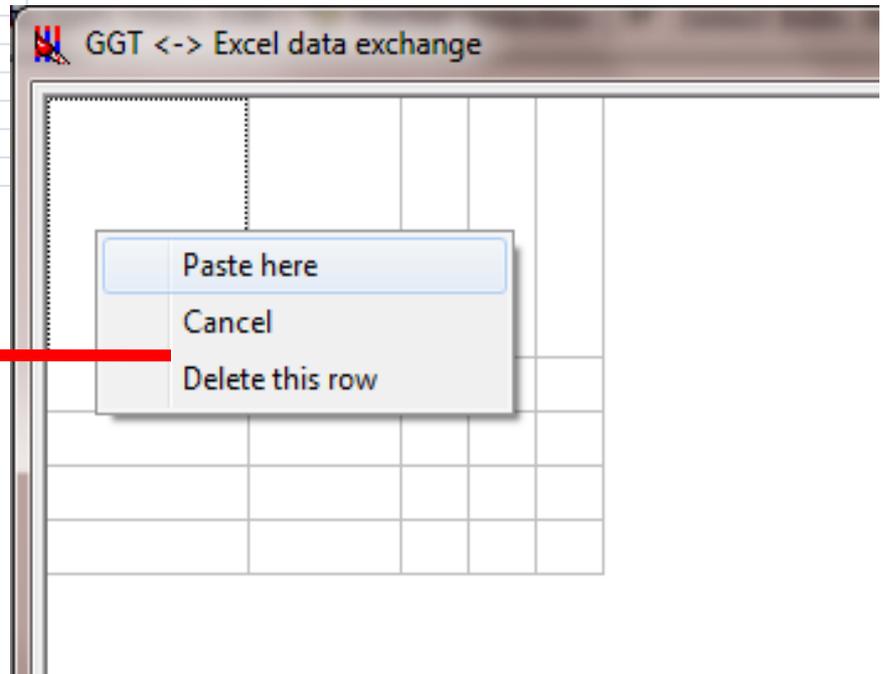




|    | A           | B     | C     | D     | E     | F     | G     | H |
|----|-------------|-------|-------|-------|-------|-------|-------|---|
| 1  | alias       |       | geno1 | geno2 | geno3 | geno4 | geno5 |   |
| 2  |             |       |       |       |       |       |       |   |
| 3  | nchrom      | 2     |       |       |       |       |       |   |
| 4  |             |       |       |       |       |       |       |   |
| 5  | popt        | F2    |       |       |       |       |       |   |
| 6  | locus       | pos   |       |       |       |       |       |   |
| 7  |             |       |       |       |       |       |       |   |
| 8  | name=group1 |       |       |       |       |       |       |   |
| 9  | marker1     | 0     | 33    | 40    | 33    | 56    | 33    |   |
| 10 | marker2     | 25.8  | A     | ?     | A     | H     | B     |   |
| 11 | marker3     | 76.9  | all1  | all2  | ?     | all2  | all3  |   |
| 12 | marker4     | 101.3 | A     | B     | H     | A     | A     |   |
| 13 |             |       |       |       |       |       |       |   |
| 14 | name=group2 |       |       |       |       |       |       |   |
| 15 | marker21    | 15.5  | H     | B     | A     | H     | A     |   |
| 16 | marker22    | 43.7  | all1  | all2  | all3  | all4  | all2  |   |
| 17 | marker23    | 81    | A     | ?     | A     | H     | B     |   |
| 18 |             |       |       |       |       |       |       |   |
| 19 |             |       |       |       |       |       |       |   |
| 20 |             |       |       |       |       |       |       |   |

This is how to organize your data in an Excel spreadsheet.

Right Click



|      |       |   |   |   |   |   |   |   |   |   |   |   |   |
|------|-------|---|---|---|---|---|---|---|---|---|---|---|---|
| w265 | 11.00 | A | A | A | A | A | A | A | A | A | A | A | A |
| w163 | 12.00 | A | A | A | A | A | A | A | A | A | A | A | A |

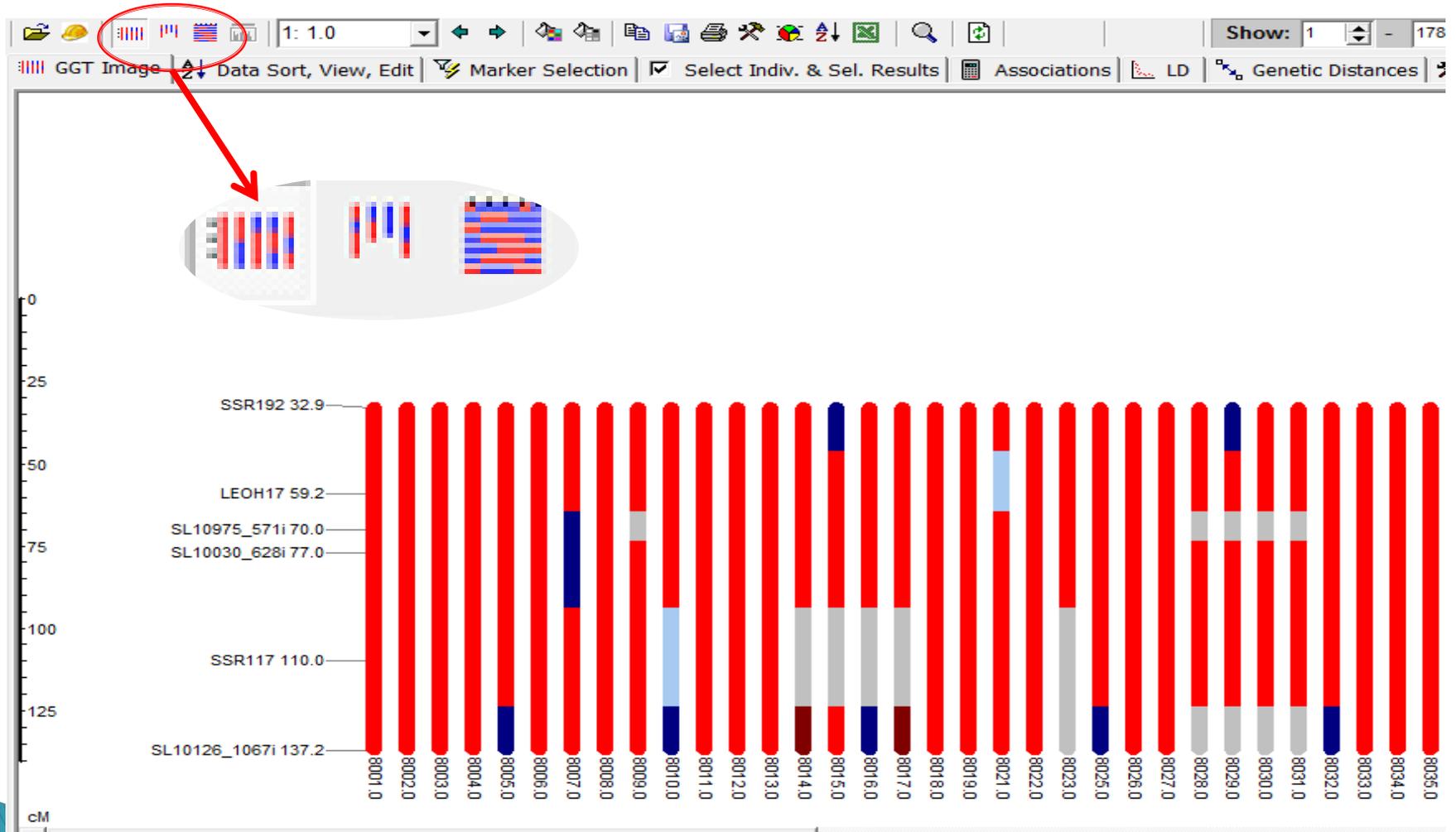
Show Headers:  Yes  No  Impute map positions

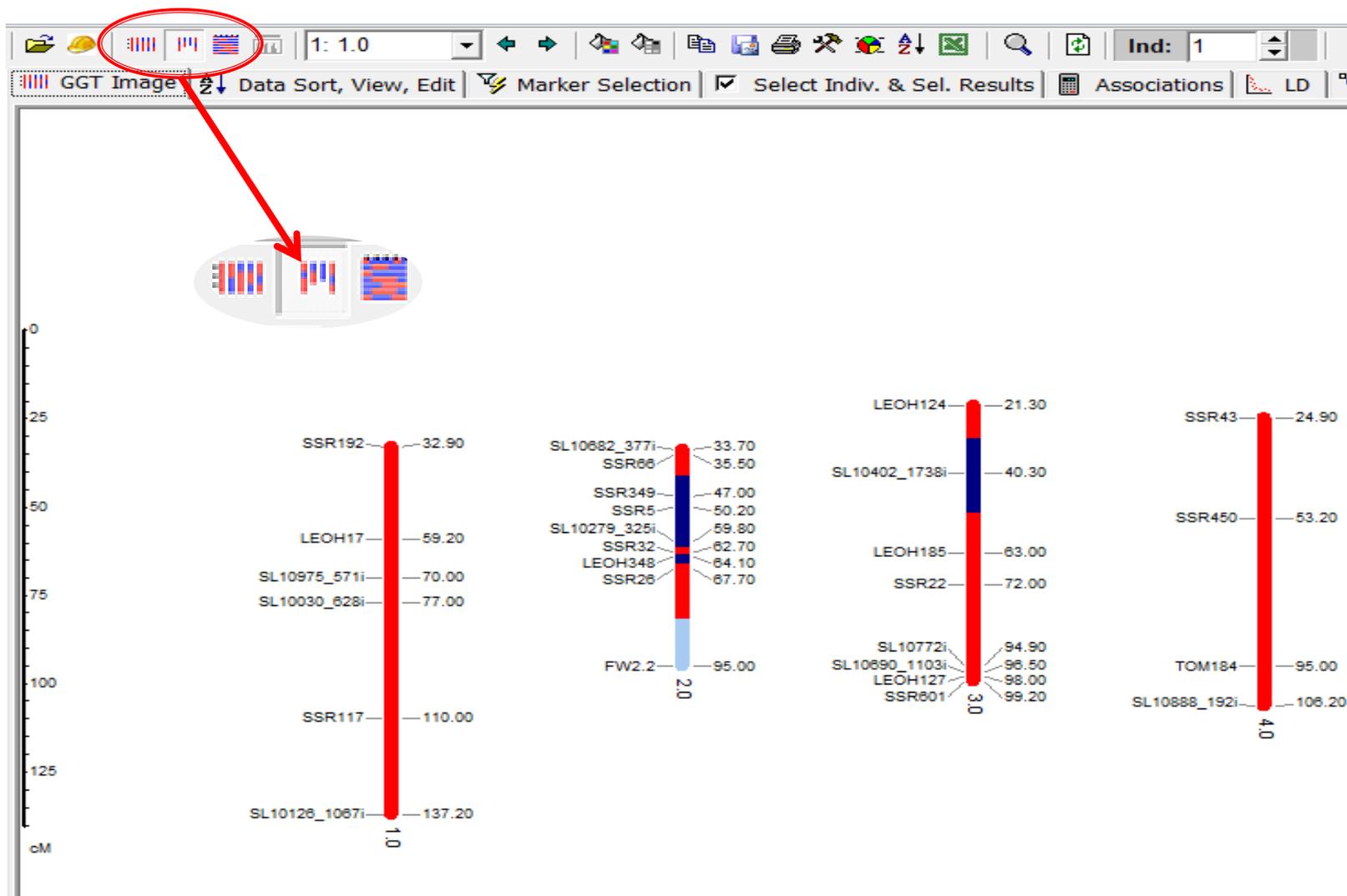
Open file or paste. Either way works

Import

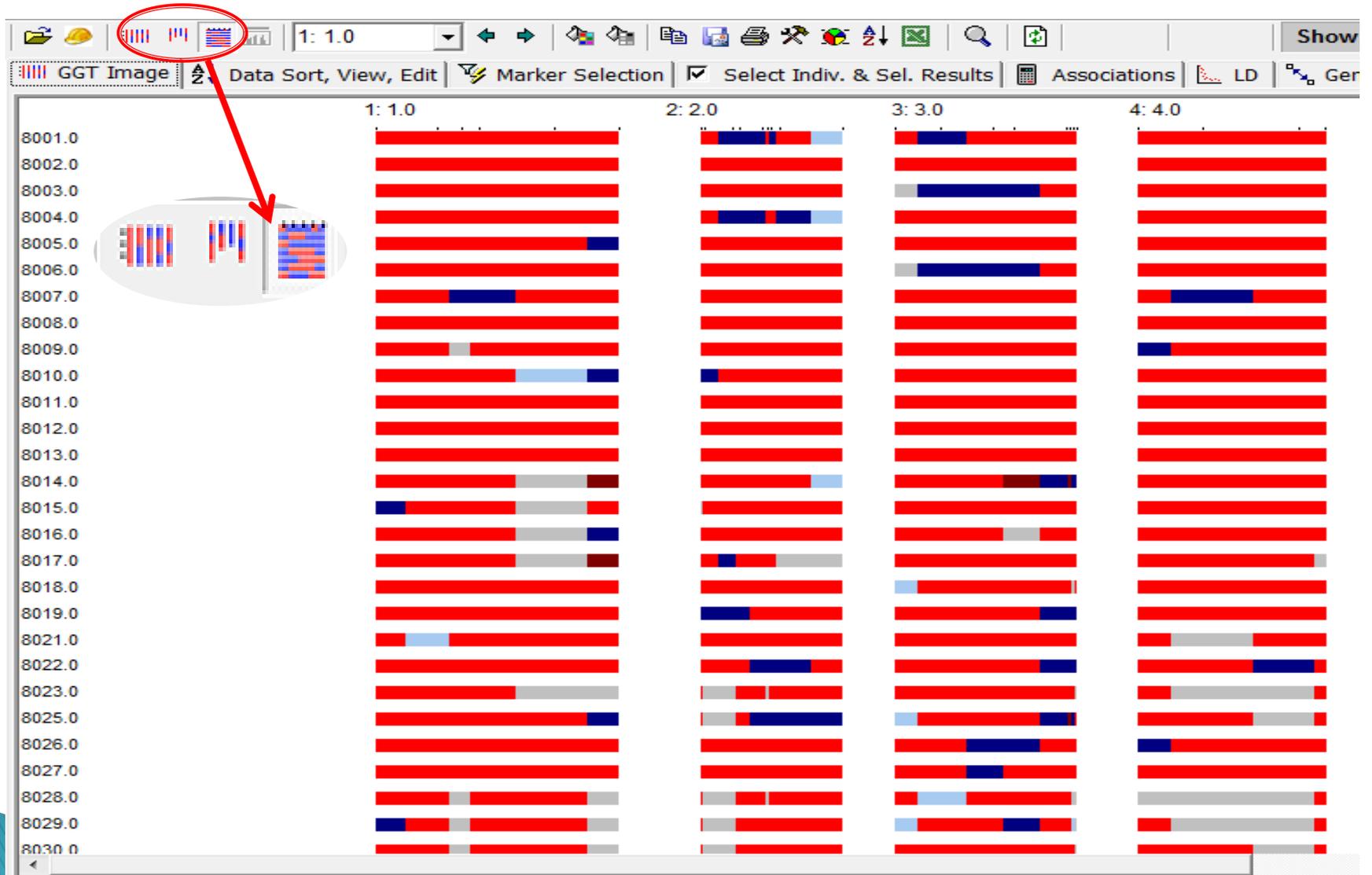
# Output for all individuals for one chromosome



# Output for one individual all chromosomes



# Output all individuals all chromosomes



# Manipulation of data – sorting data

File Edit Export Statistics Marker Selection Advanced Analyses Settings Help

GGT Image **Data Sort, View, Edit** Marker Selection Select Individ. & Sel. Results

Show & edit data in gridview

genome

- group 1: "1.0"
  - "SSR192" (1: 32.9)
  - "LEOH17" (1: 59.2)
  - "SL10975\_571i" (1: 70.0)
  - "SL10030\_628i" (1: 77.0)
  - "SSR117" (1: 110.0)
  - "SL10126\_1067i" (1: 137.2)
- group 2: "2.0"
- group 3: "3.0"
- group 4: "4.0"
- group 5: "5.0"
- group 6: "6.0"
- group 7: "8.0"
- group 8: "10.0"
- group 9: "11.0"
- group 10: "12.0"

Sort individuals

- No sort /undo sort
- All markers
- Selected marker
- Selected group
- Alias
- overall allele content: choose..

Note: Updates will be visible

Markername  
LEOH17

Position (cM)  
59.2

QTL interval  
- -

Sort!

Refresh tree

Update

Options to view and edit data

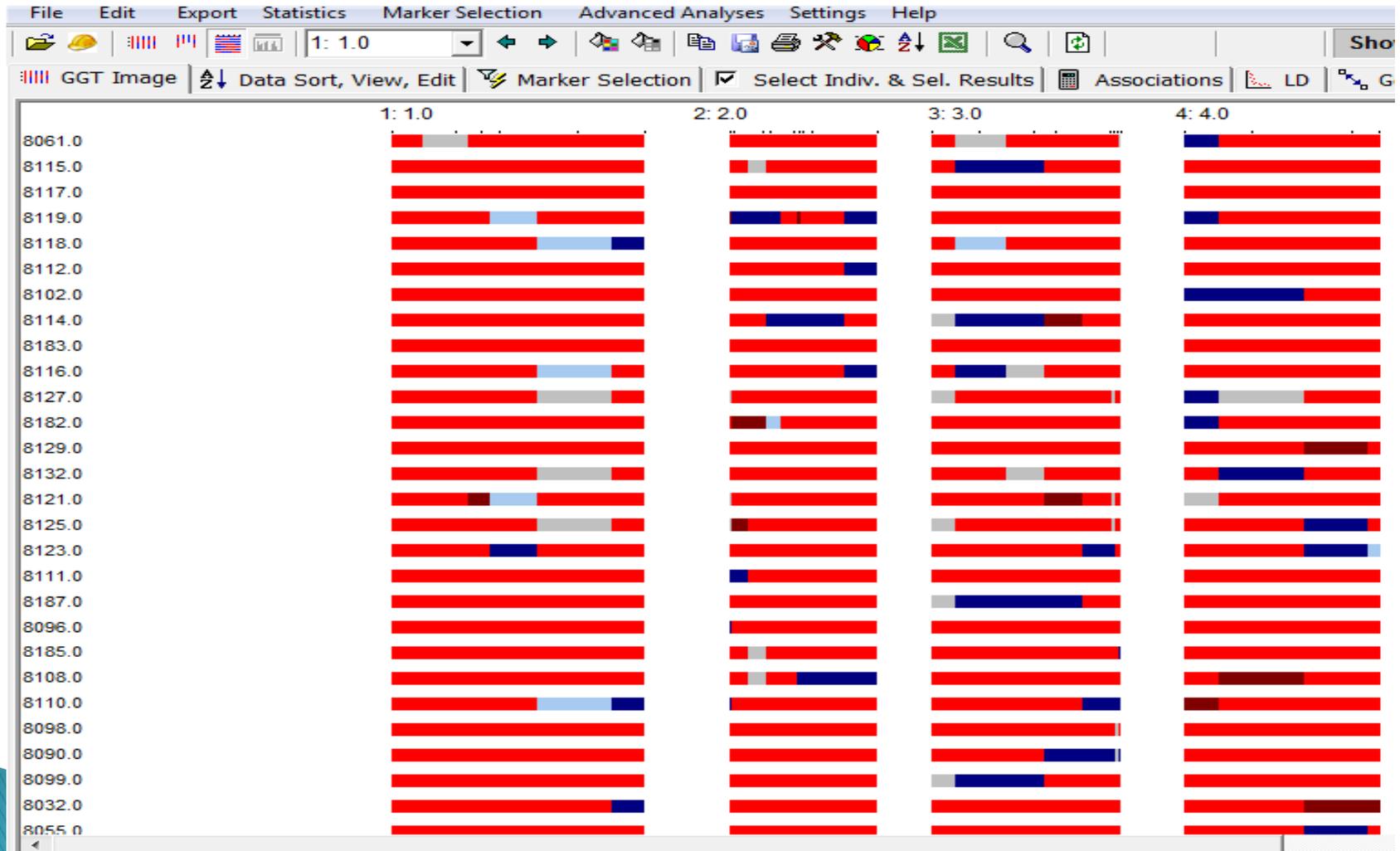
First, decide how you want to sort data

Second, choose allele to sort by

Three, sort

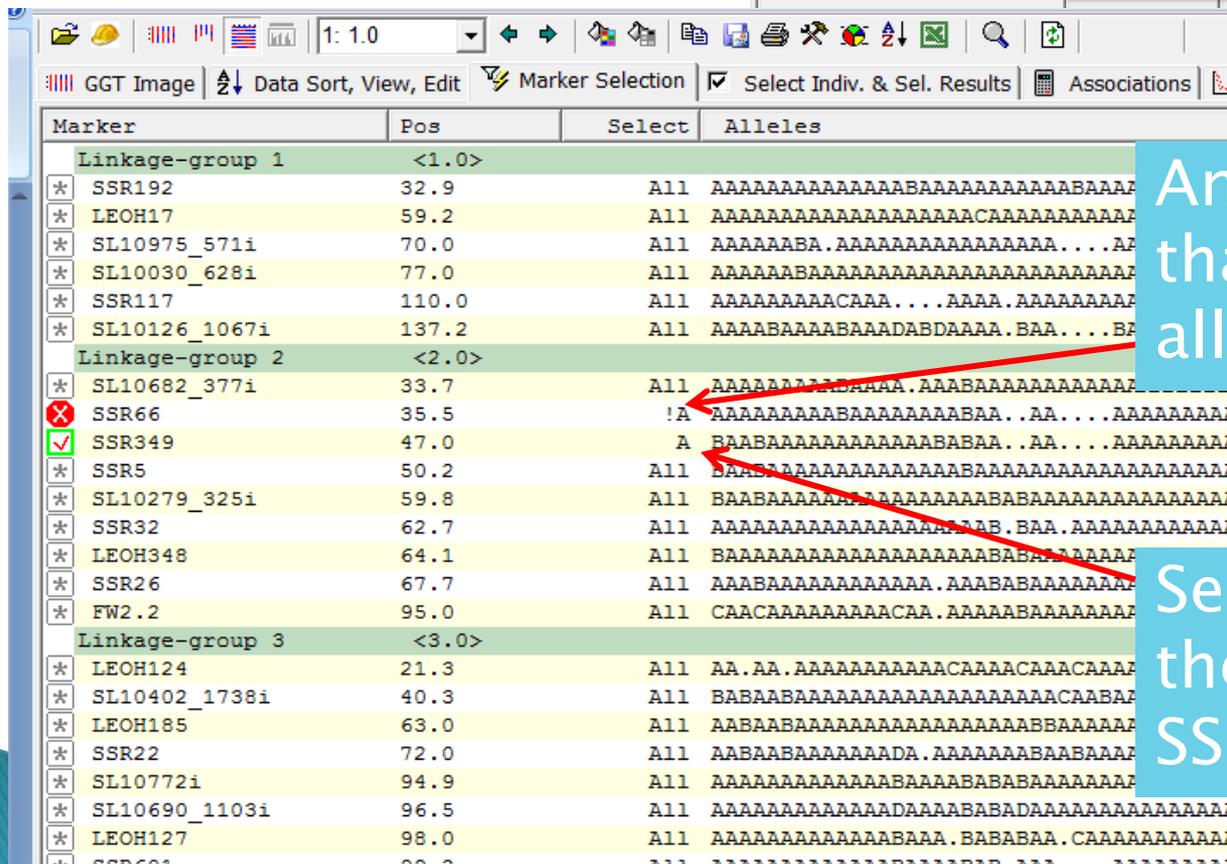
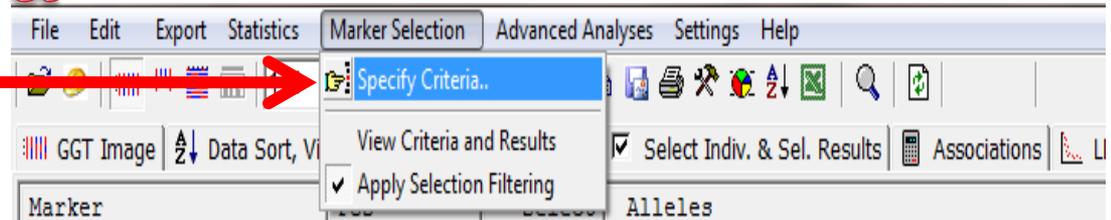
Last, Refresh

# Output after data are sorted by allele content of marker LEOH17



# How to select individuals using specific criteria

Setting selection criteria



A screenshot of the software's main window showing a table of markers and alleles. The table has columns for Marker, Pos, Select, and Alleles. The 'Select' column contains checkboxes. A red 'X' is in the checkbox for marker SSR66, and a green checkmark is in the checkbox for marker SSR349. Red arrows point from the 'Specify Criteria..' menu option to the 'Select' column and from the 'Apply Selection Filtering' menu option to the 'Alleles' column.

| Marker                | Pos   | Select | Alleles                                      |
|-----------------------|-------|--------|--|
| Linkage-group 1 <1.0> |       |        |  |
| * SSR192              | 32.9  | All    | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA            |
| * LEOH17              | 59.2  | All    | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA            |
| * SL10975_571i        | 70.0  | All    | AAAAAABA.AAAAAAAAAAAAAAAAAA...A              |
| * SL10030_628i        | 77.0  | All    | AAAAAABAAAAAAAAAAAAAAAAAAAAAAAA              |
| * SSR117              | 110.0 | All    | AAAAAAAAACAAA...AAAA.AAAAAAAAA               |
| * SL10126_1067i       | 137.2 | All    | AAAAAABAAAABAAADABDAAAA.BAA...B              |
| Linkage-group 2 <2.0> |       |        |  |
| * SL10682_377i        | 33.7  | All    | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA            |
| ✗ SSR66               | 35.5  | !      | AAAAAAAAAAAAAAAAAAAAAAAAABAA..AA...AAAAAAAAA |
| ☑ SSR349              | 47.0  | A      | BAABAAAAAAAAAAAAAAAAABABAA..AA...AAAAAAAAA   |
| * SSR5                | 50.2  | All    | BAABAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA        |
| * SL10279_325i        | 59.8  | All    | BAABAAAAAAAAAAAAAAAAABABAAAAAAAAAAAAAAAAA    |
| * SSR32               | 62.7  | All    | AAAAAAAAAAAAAAAAAAAAAAAAAB.BAA.AAAAAAAAAA    |
| * LEOH348             | 64.1  | All    | BAAAAAAAAAAAAAAAAAAAAAAAAAABAAAAAAAAA        |
| * SSR26               | 67.7  | All    | AAABAAAAAAAAAAAAA.AAABAAAAAAAAA              |
| * FW2.2               | 95.0  | All    | CAACAAAAAAAAAACAA.AAAAAA                     |
| Linkage-group 3 <3.0> |       |        |  |
| * LEOH124             | 21.3  | All    | AA.AA.AAAAAAAAAAAAAACAAACAAACAA              |
| * SL10402_1738i       | 40.3  | All    | BABAABAAAAAAAAAAAAAAAAAAAAAABAA              |
| * LEOH185             | 63.0  | All    | AABAABAAAAAAAAAAAAAAAAAAAAA                  |
| * SSR22               | 72.0  | All    | AABAABAAAAAADA.AAAAAAABAA                    |
| * SL10772i            | 94.9  | All    | AAAAAAAAAAAAAAAAABAAAABABAAAAAAAAA           |
| * SL10690_1103i       | 96.5  | All    | AAAAAAAAAAAAAAAAADAAAABABADAAAAAAAAA         |
| * LEOH127             | 98.0  | All    | AAAAAAAAAAAAAAAAABAAA.BABABAA.CAAAAAAAAA     |

And select individuals that do not have the A allele at marker SSR66

Select individuals with the A allele at markers SSR349

# Manipulation of data (continued)

The screenshot shows the 'Display Graphical Genotypes' software interface. The window title is 'H:\Spot genotyping\IBC LD analysis\IBC data.ggt'. The menu bar includes File, Edit, Export, Statistics, Marker Selection, Advanced Analyses, Settings, and Help. The toolbar contains various icons for file operations and analysis. The main window is divided into several sections:

- Selected individuals:** A list of individuals from 8001.0 to 8057.0. Individual 8010.0 is checked.
- Selection criteria, results, subsize selection logging:** A panel with two sub-sections:
  - Selection Criteria:** Lists criteria 1.0 through 8.0. A red arrow points from the 'Criteria selected' callout to this section.
  - Selection Results:** Shows '5 individuals selected:' with a list: Nr. 10 [8010.0], Nr. 94 [8101.0], Nr. 103 [8111.0], Nr. 116 [8125.0], and Nr. 121 [8130.0]. A red arrow points from the 'Individual selected' callout to this section.
- Bottom Panel:** Contains buttons for 'Save..', 'Print', 'Select core set of size: 20', 'Compare Individuals', and 'Use criterion: Max (Diversity Sum)'. A red arrow points from the 'And Click here!' callout to the 'Compare Individuals' button. It also includes a 'Method' section with 'Simulated annealing' selected and 'Iterative optimization' unselected, and a 'selection cycles' section with '100' cycles and '50' iterations/cycle.

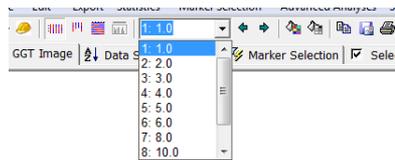
At the bottom of the window, the status bar displays: '178 individuals/ 6 loci/ Pop:unknown [1] 8001.0 selection criteria set zoom:100%'.

Criteria selected

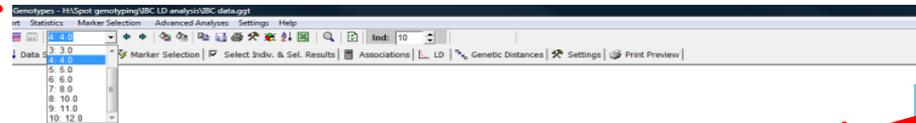
Individual selected

And Click here!

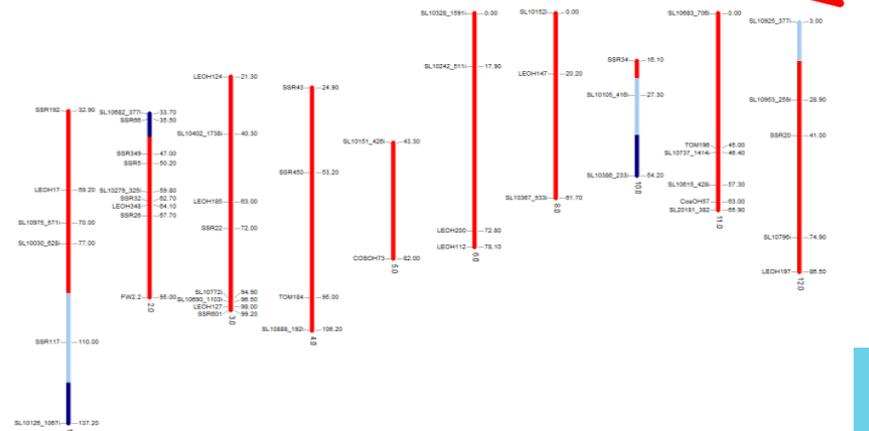
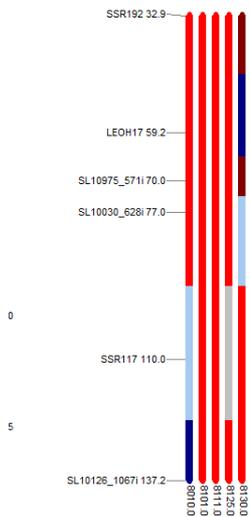
# Results after selected the criteria



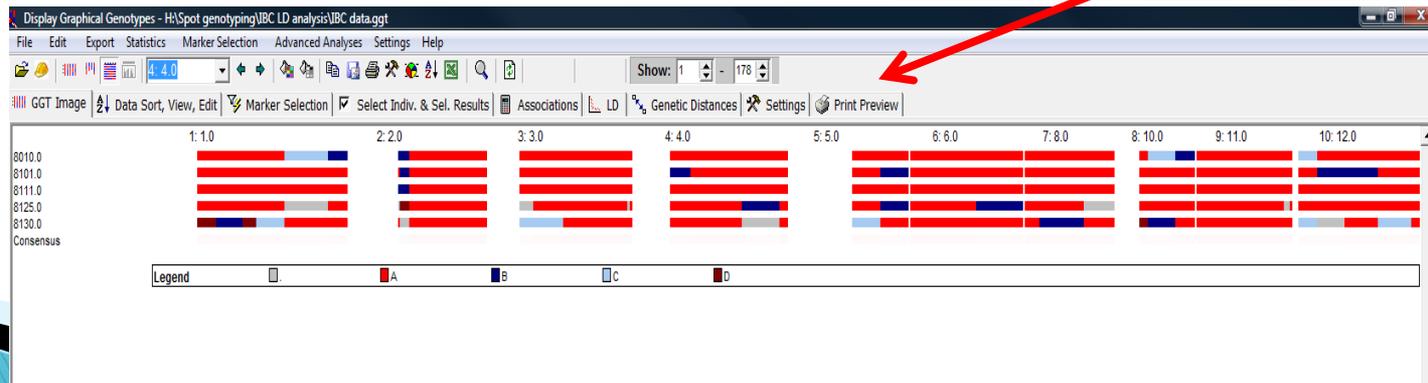
All individuals selected for one chromosome



one individual all chromosomes



All individuals for all chromosome



# Conclusions

- ▶ In many cases the GGT software package can assist in the exploration, visualization and analysis of molecular marker data in applications in plant (and animal) science.

# What else can GGT do

- ▶ Genetic distance
  - ▶ Linkage disequilibrium (LD)
  - ▶ Summary statistics by individual or marker (background genome selection)
- 

# References

- ▶ Van Berloo, R. 1999. GGT: software for the display of graphical genotypes. *Journal of Heredity* 90:328–329.
- ▶ Van Berloo, R. 2008. GGT 2.0: Versatile software for visualization and analysis of genetic data. *Journal of Heredity* 99:232–236.
- ▶ Young, N. D. and S. D. Tanksley. 1989. Restriction fragment length polymorphisms maps and the concept of graphical genotypes. *Theoretical and Applied Genetics* 77:95–101.

# External Link

- ▶ Wageningen UR. GGT2.0: Graphical genotypes [Online]. Wageningen UR Plant Breeding. Available at:  
[www.plantbreeding.wur.nl/UK/software\\_ggt.html](http://www.plantbreeding.wur.nl/UK/software_ggt.html)  
(verified 23 Nov 2010).

# Acknowledgement

- ▶ Genotypic data was provided by Matthew Robbins, The Ohio State University.