

# *Genotype Matrix Mapping*

The logo for Genotype Matrix Mapping (GMM) is displayed in white on a red background. It features the letters 'GMM' in a stylized, outlined font. The 'G' is a simple circle with a horizontal bar. The 'M's are formed by two vertical lines connected at the top by a horizontal bar, with a small 'TM' trademark symbol to the right. The logo is reflected below it on a gradient background.

*Ver. 2.1*

**Manual**

2009/8/27

## **Trademarks**

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## **Acknowledgments**

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This product includes JFreeChart.

This product includes software developed at The Apache Software Foundation (<http://www.apache.org/>).

# GMM Manual

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## Introduction

## About GMM

GMM (Genotype Matrix Mapping) is a computer program for the detection of QTLs (Quantitative Trait Loci) and QTL interactions in genetic variation from comparisons of genotypic and phenotypic data. The central approach in GMM is the following:

- Each tested marker is given a virtual matrix (GM) containing intersecting lines and rows equal to the total number of alleles for the marker in the population analyzed.
- QTL interactions are then estimated and compared through virtual networks among the GMs.

## Reference

S. Isobe, A. Nakaya and S. Tabata. Genotype Matrix Mapping (GMM): Searching for QTL interactions in genetic variation in complex traits. (2007) DNA Research 14:217-225.

Hardware requirements are listed in Table 1-1.

Table 1-1 Hardware requirements

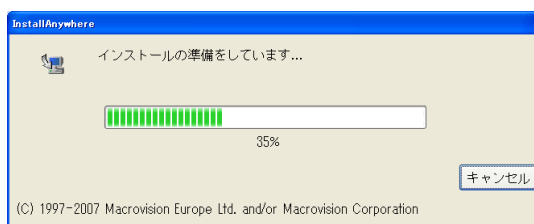
	<b>Windows</b>	<b>Mac OS X</b>
CPU	Pentium4 or later version	PPC or Intel
Memory	>512 MB	
Hard disk	>100 MB	
OS Version	XP or later version	10.4 or later version

Large scale data analysis by Windows 32 bit often causes to stop program execution because of running out of memory. We recommend using Windows 64 bit or Mac for large scale data analysis.

# Chapter 1 Installation

## 1-1. Windows

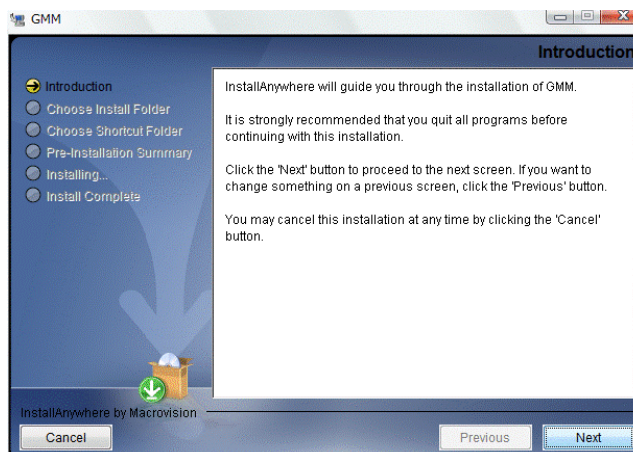
1. Start up the downloaded file (install.exe) by double-clicking on the icon.



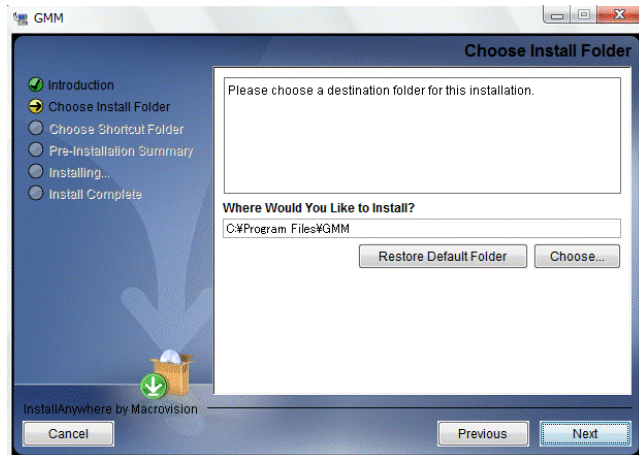
2. After the installation preparation is finished, the screen at right is displayed. Click on the [OK] button, and then go to the next step.



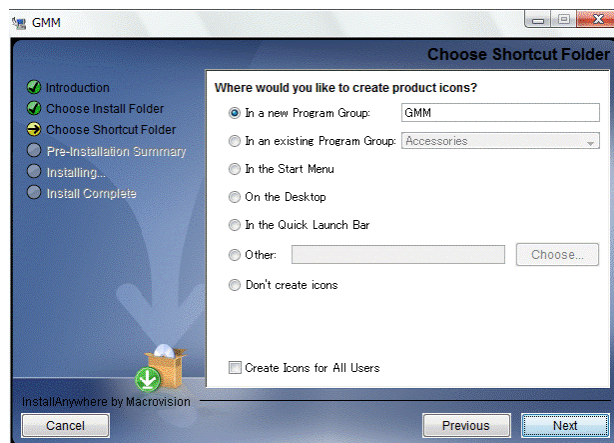
3. The Introduction is displayed. Click on the [Next] button to go to the next step.



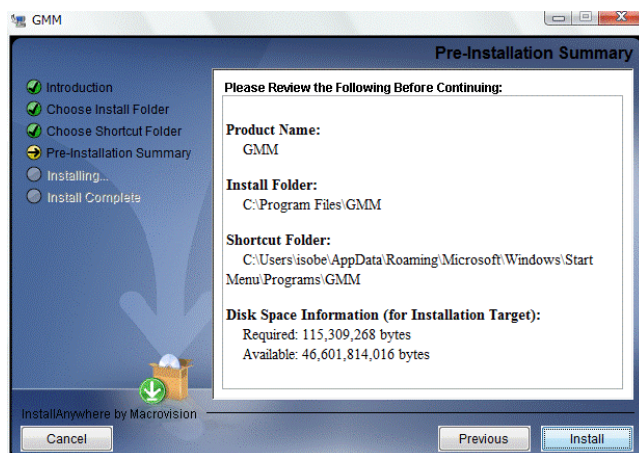
4. Choose the install folder. To change the folder from the default setting, click on the [Choose] button.



5. Choose the shortcut folder.



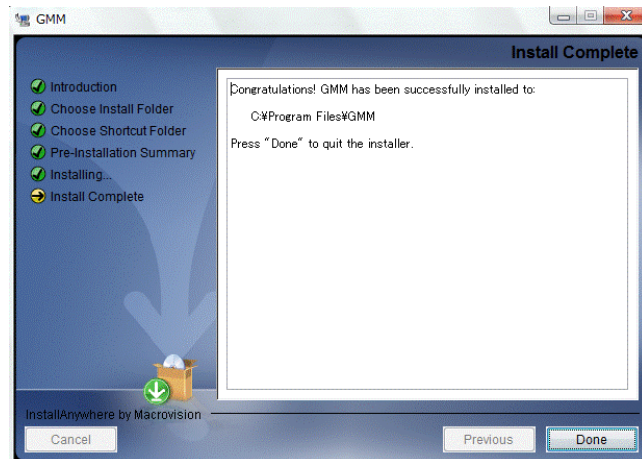
6. The Pre-installation summary is displayed. Confirm that the summary details are correct, and then start installation by clicking on the [Install] button.



7. The installation progress is displayed.



8. After the installation is finished, the screen at right is displayed. Click on the [Done] button to complete the installation.



## 1-2. Mac OS X

1. Unpack the downloaded file [install.zip] by double clicking. Then start the generated installer by double clicking.



2. After the installation preparation is finished, the screen at right is displayed. Click on the [OK] button to go to the next step.

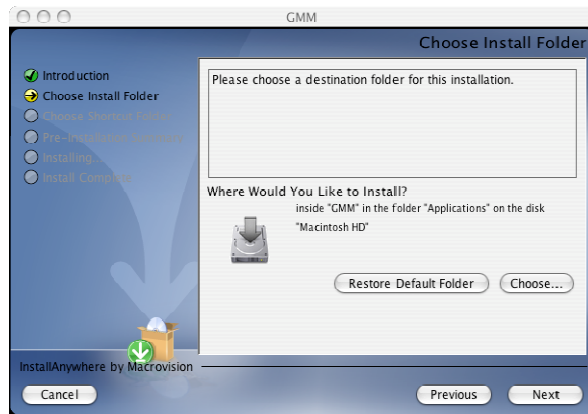


3. The Introduction is displayed. Click on the [Next] button to go to the next step.

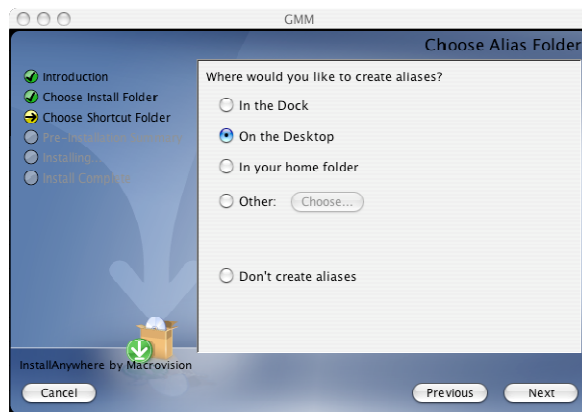




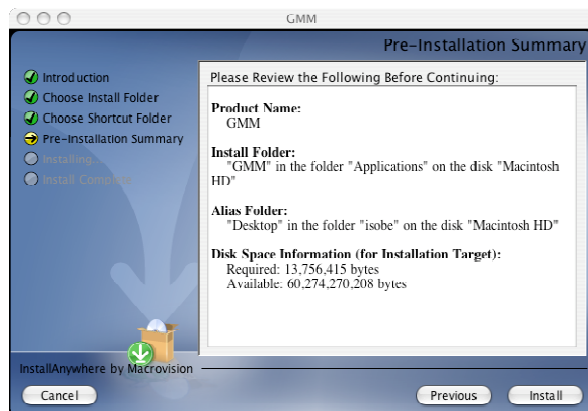
4. The Introduction is displayed. Click on the [Next] button to go to the next step.



5. Choose the alias folder.



6. The pre-installation summary is displayed. Confirm that the summary details are correct, and then start installation by clicking on the [Install] button.



7. The installation progress is displayed.



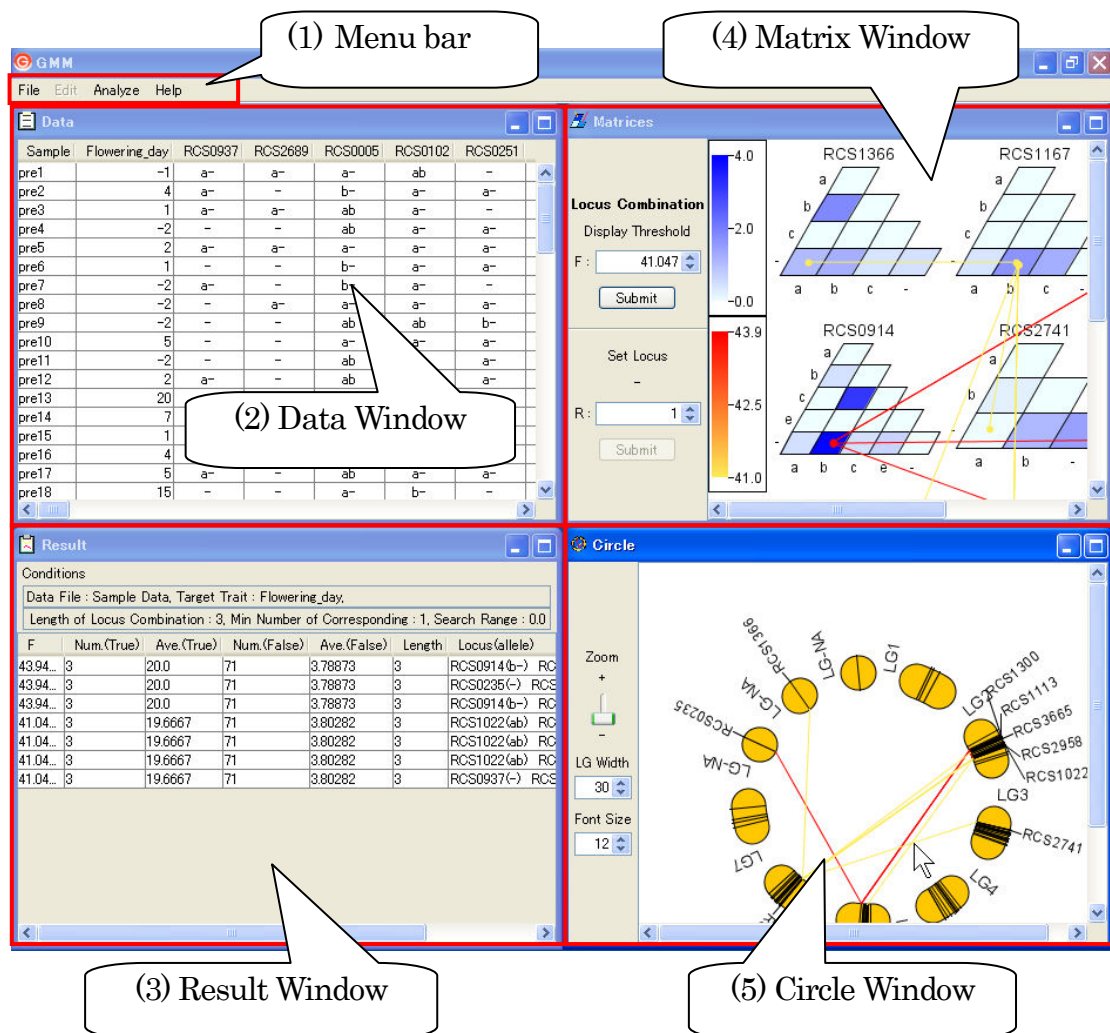
8. After the installation is finished, the screen at right is displayed. Click on the [Done] button to complete the installation.



## Chapter 2 Using GMM

### 2-1. General

The GMM display consists of the following five components:

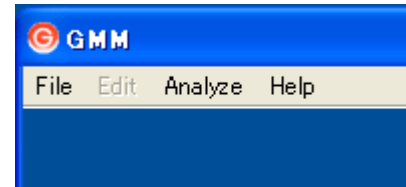


- (1) The Menu bar contains the operations menu.
- (2) The Data Window contains a loaded data set.
- (3) The Result Window contains a list of analysis results.
- (4) The Matrix Window contains analysis results in the form of Genetic Matrixes.
- (5) The Circle Window contains analysis results on linkage groups.

## 2-2. Menu bar

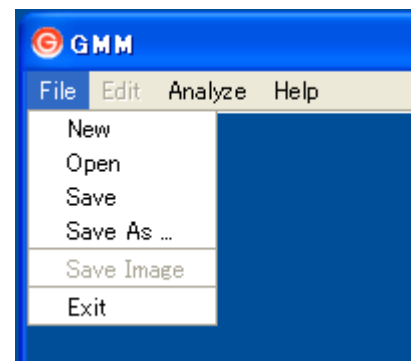
The menu consists of the following three components. Edit menu is not available now.

1. File menu
2. Analyze menu
3. Help menu



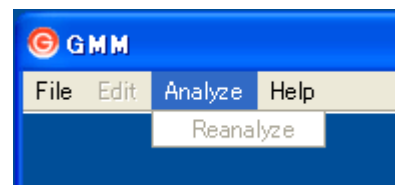
### 1. File menu

- |            |   |
|------------|---|
| New        | Load and analyze a new data set.  |
| Open       | Open an existing file.  |
| Save       | Save contents as a GMM file.  |
| Save As    | Save contents with a new file name.   |
| Save Image | Save a screen image of a Matrix or Circle window as an image file (PNG or EPS). |
| Exit       | Close the GMM program.  |



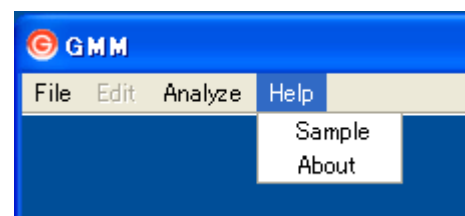
### 2. Analyze Menu

- |           |  |
|-----------|--|
| Reanalyze | Reanalyze the uploaded data with different conditions. |
|-----------|--|



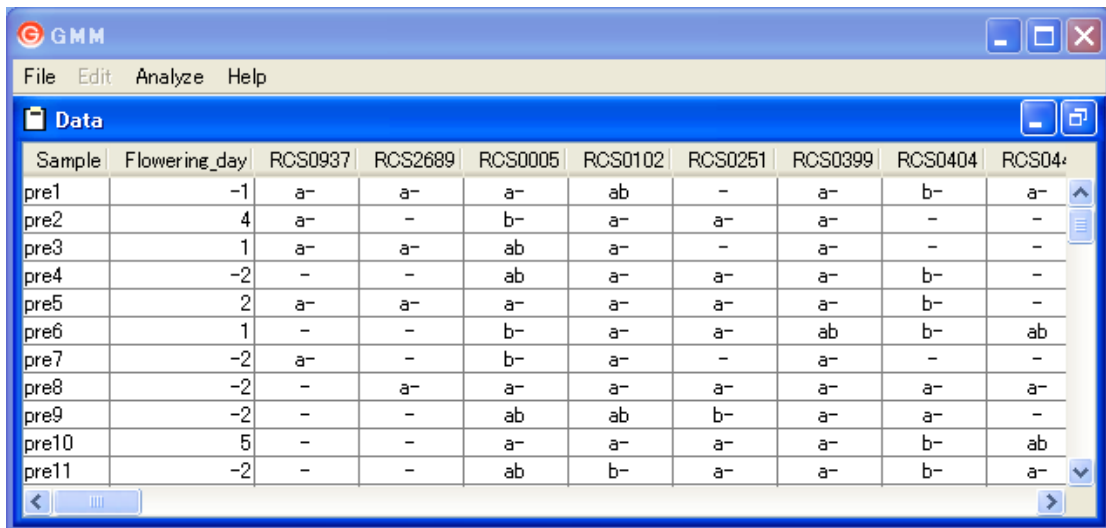
### 3. Help Menu

- |        |                         |
|--------|-------------------------|
| Sample | Open a sample data set. |
| About  | Information about GMM.  |



## 2-3. Data window

The Data window displays phenotypic and genotypic data used for the analysis. Each line indicates information about an individual sample.



The screenshot shows the GMM software interface with a 'Data' window. The window contains a table with 11 rows and 10 columns. The columns are labeled: Sample, Flowering\_day, RCS0937, RCS2689, RCS0005, RCS0102, RCS0251, RCS0399, RCS0404, and RCS0404. The rows are labeled pre1 through pre11. The data in the table is as follows:

Sample	Flowering_day	RCS0937	RCS2689	RCS0005	RCS0102	RCS0251	RCS0399	RCS0404	RCS0404
pre1	-1	a-	a-	a-	ab	-	a-	b-	a-
pre2	4	a-	-	b-	a-	a-	a-	-	-
pre3	1	a-	a-	ab	a-	-	a-	-	-
pre4	-2	-	-	ab	a-	a-	a-	b-	-
pre5	2	a-	a-	a-	a-	a-	a-	b-	-
pre6	1	-	-	b-	a-	a-	ab	b-	ab
pre7	-2	a-	-	b-	a-	-	a-	-	-
pre8	-2	-	a-	a-	a-	a-	a-	a-	a-
pre9	-2	-	-	ab	ab	b-	a-	a-	-
pre10	5	-	-	a-	a-	a-	a-	b-	ab
pre11	-2	-	-	ab	b-	a-	a-	b-	a-

First column

Sample name

Second column

Phenotypic data

Third and subsequent columns

Genotypic data

For missing data, use '\*' as a missing code. The code, '\*', is excluded from analysis.

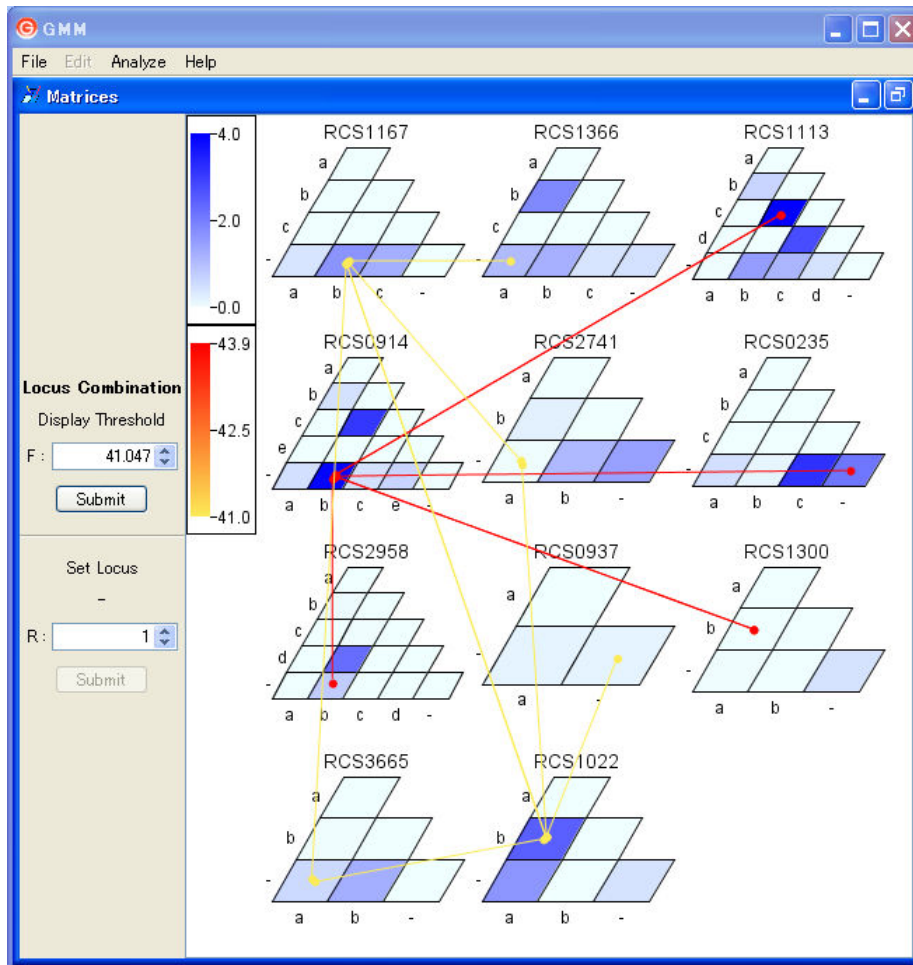
## 2-4. Result window

F	Num.(True)	Ave.(True)	Num.(False)	Ave.(False)	Length	Locus(allele)
43.94...	3	20.0	71	3.78873	3	RCS2958(b-) RCS0914(b-) RCS1300(a...
43.94...	3	20.0	71	3.78873	3	RCS1113(bc) RCS0914(b-) RCS0235(-)
43.94...	3	20.0	71	3.78873	3	RCS1113(bc) RCS0914(b-) RCS1300(a...
41.04...	3	19.6667	71	3.80282	3	RCS1366(a-) RCS1167(b-) RCS1022(a...
41.04...	3	19.6667	71	3.80282	3	RCS1167(b-) RCS3665(a-) RCS1022(a...
41.04...	3	19.6667	71	3.80282	3	RCS1167(b-) RCS2741(a-) RCS1022(a...
41.04...	3	19.6667	71	3.80282	3	RCS1167(b-) RCS1022(ab) RCS0937(-)

The Result window holds a list of analysis results. The version of the program and the analysis conditions are displayed on the upper bars.

F	F value
Num. (True)	Number of samples that correspond to the detected locus (allele).
Ave. (True)	Mean value of the samples that correspond to the detected locus (allele).
Num. (False)	Number of samples that do not correspond to the detected locus (allele).
Ave. (False)	Mean value of the samples that do not correspond to the detected locus (allele).
MSA	Between-class variance
MSW	Within-class variance
MST	Total variance
Length	Number of loci that make up the detected combination.
Locus (allele)	Names of loci and alleles.

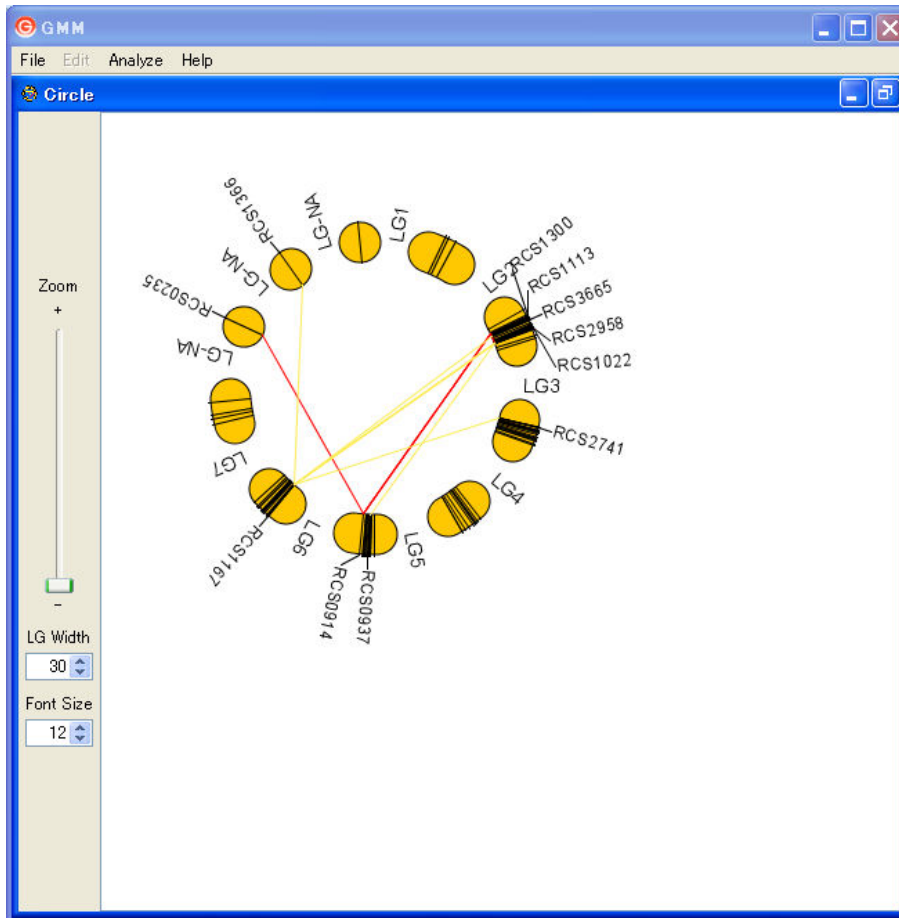
## 2-5. Matrix window



The Matrix window holds results of analyses in the form of Genetic Matrixes.

Matrix	Each matrix indicates one marker. Each cell in a matrix indicates a single QTL effect. The F value (magnitude of a single QTL effect) is represented with shades of blue.
Line	Lines between cells indicate combinations of QTLs. The F value (magnitude of QTL interactions) is represented with colors from yellow to red.
Display Threshold	Displayed lines and the cells they connect are refined based on a set threshold.
Set Locus	Displayed matrixes that interact with the selected cells are refined.

## 2-6. Circle window



The Circle window displays analysis results as a circle of linkage groups. This window is not displayed if map information is not loaded.

Linkage circle	All linkage groups are displayed on a circle, and the interacting QTLs are indicated inside of the circle.
Inside lines	The inside lines indicate relationships between interacting QTLs. The color of each line, from yellow to red, represents the magnitude of the F value (strength of the QTL interaction).
Zoom	Sets the size of the linkage circle.
LG Width	Sets the width of the linkage circle.
Font Size	Sets the font size.



## Chapter 3 Tutorial

### 3-1. Start up

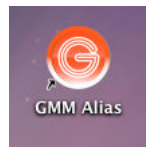
#### <Windows>

Select <all programs→GMM→GMM> on the Start Menu or double click on the GMM icon.

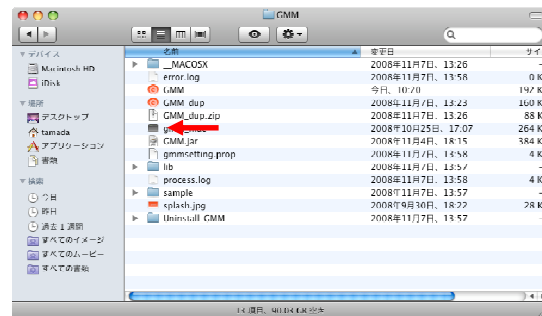


#### <Mac OS X>

Double click on the [GMM Alias] icon.

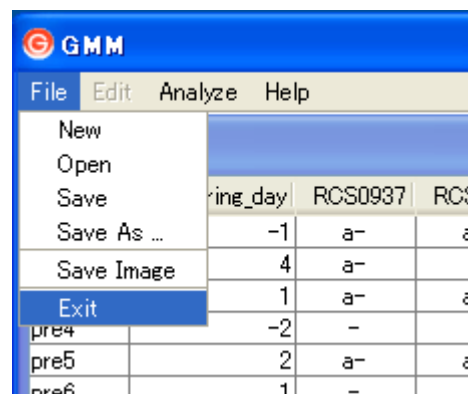


If an alias was not created at installation, start GMM from within the GMM folder.



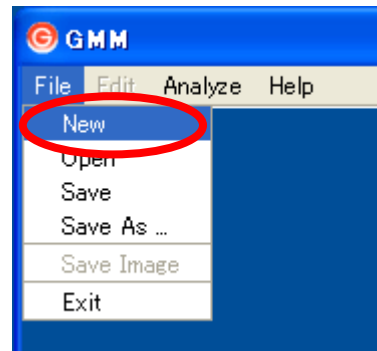
### 3-2. Exit

Select <File→Exit> on the Menu bar.

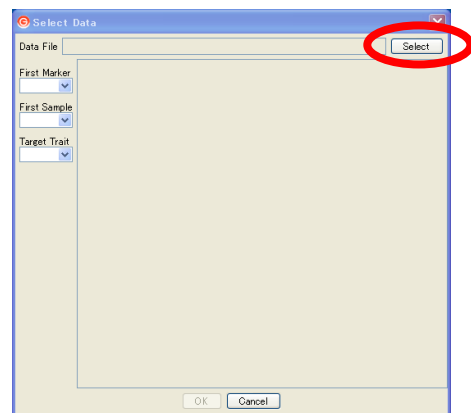


### 3-3. Data analysis

1. Select <File→New> from the Menu bar.



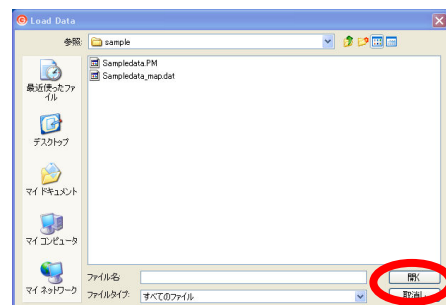
2. The screen at right is displayed. Click on the [Select] button.



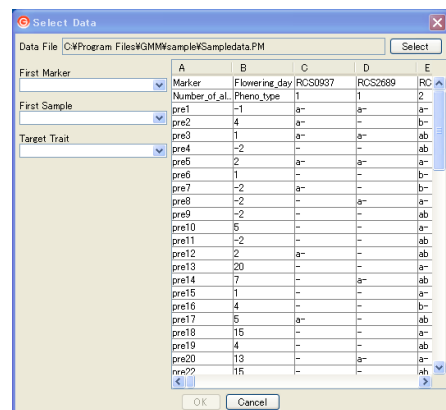
3. The Load Data dialog is displayed. Choose the data file, and then click on the [Open] button.

The data file must be saved as a tab-delimited text file. Use two characters for the genotype code and numerals for phenotypic data.

A sample data file can be found in the GMM/sample folder (Sampledata.PM).



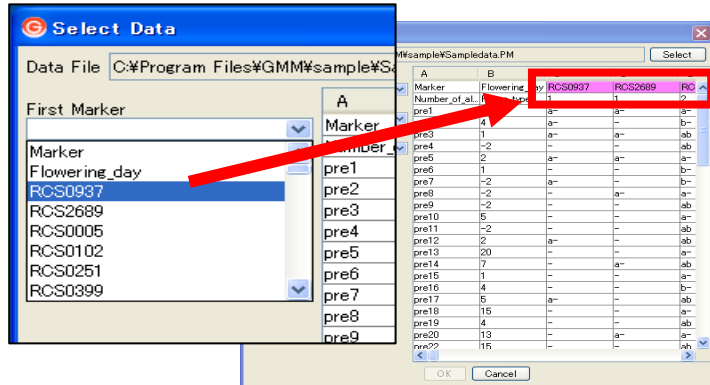
4. The chosen file is loaded and displayed in the data window.



5. Set a data set.

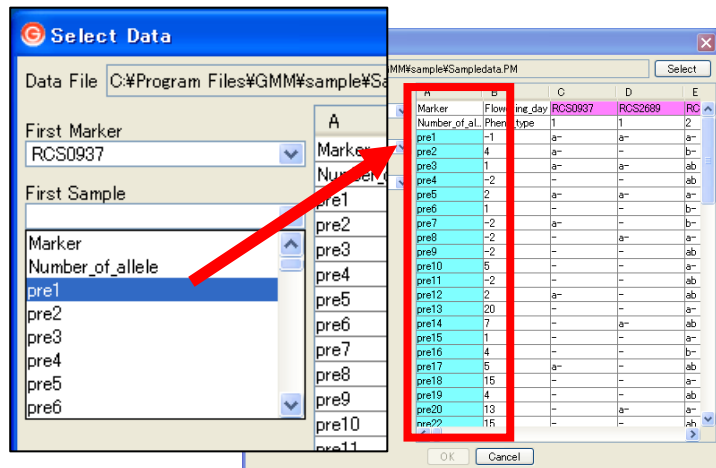
Press the uppermost marker name in the <First Marker> pulldown menu.

The column headings for the selected marker and the markers to its right are colored pink, and the data in the columns are defined as a genotypic data set.



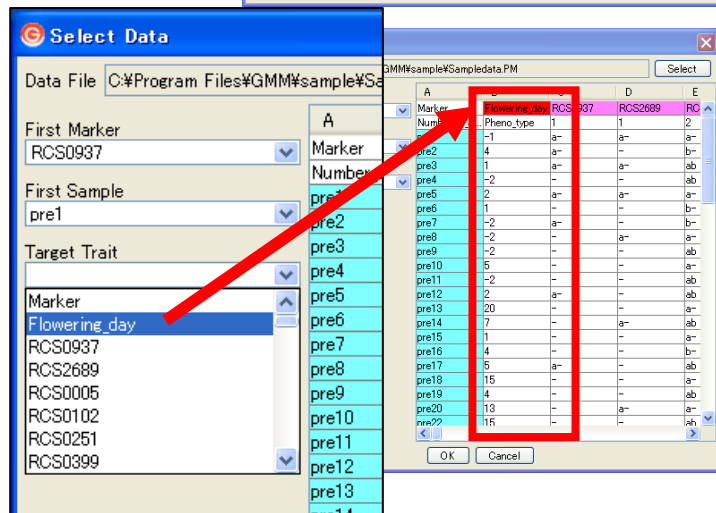
Select the uppermost sample name in the <First Sample> pulldown menu.

The column headings for the selected sample and the samples below it are colored aqua and defined as a set of sample data.



Select the phenotype data from the list in the <Target Trait> pulldown menu.

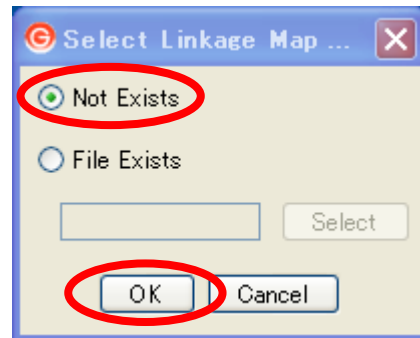
The column heading for the selected cell is colored red, and the data in the column are defined as phenotypic data.



Press the [Select] button to complete the procedure.

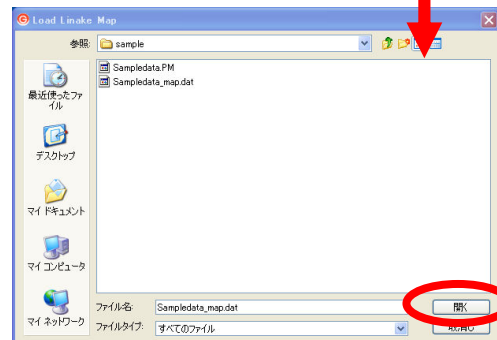
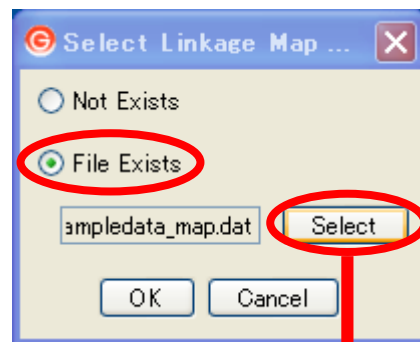
6. Loading map information.

The <Select Linkage Map Data> window is displayed. If there is no map information, select [Not Exists] and then press [OK].



If map information is available, select <File Exists>, and then press the [Select] button.

The Load Linkage Map dialog is opened. Set a map file and press the [Open] button. After selecting the map file, press the [OK] button.



The map file must be saved as a tab-delimited text file. Input data as follows:

#<Linkage group name> <total length>  
 <Marker name1> <map position>  
 <Marker name2> <map position>

Shown in the figure at right.

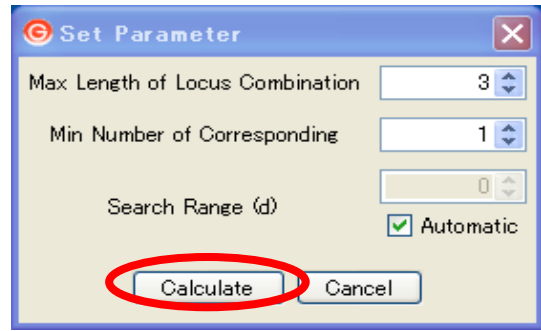
The sample data are saved in the GMM/sample folder as sampledata\_map.DAT.

```
#LG1 136.7
RCS2183 43.723
RCS0005 56.013
RCS0089 92.005
#LG2 149.7
RCS0130 10.551
RCS1708 35.664
RCS1300 39.853
RCS1113 44.200
RCS1285 47.710
#LG-NA 3
RCS0235 2.0
#LG-NA 3
RCS1366 2.0
#LG-NA 3
RCS3719 2.0
```

7. Parameter settings.

The <Set Parameter> window is displayed.

Set the following three parameters, and then press the [Calculate] button.



Max Length of Locus Combination

Maximum number of analyzed marker combinations. If “1” is selected, GMM calculates a single QTL effect. If “3” is selected, GMM calculates a maximum of three marker combinations.

Min Number of Corresponding

Minimum number of samples that meet the conditions.

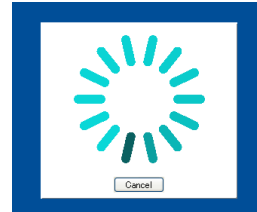
Search Range

Search range for the calculation.

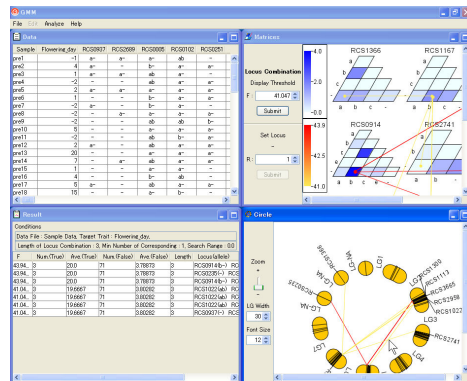
Automatic

To set the search range automatically, check [Automatic].

8. The screen shown at right is displayed during the calculation. Please wait.

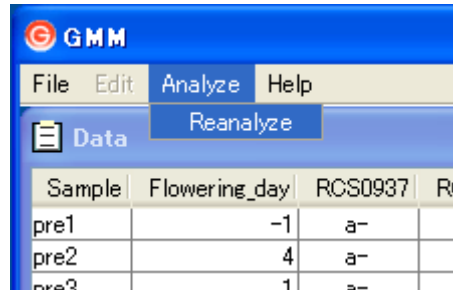


9. After the calculation, the result windows are displayed.

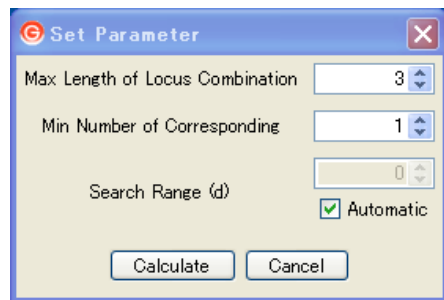


### 3-4. Data reanalysis

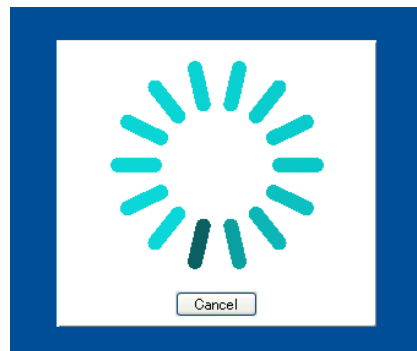
1. Select <Analyze→Reanalyze> on the Menu bar.



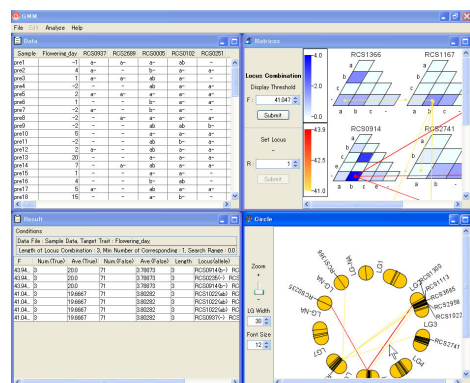
2. Set Parameters.  
Follow the instructions in “Section 3-3. Data analysis”. Then click on the [Calculate] button.



3. Please wait.



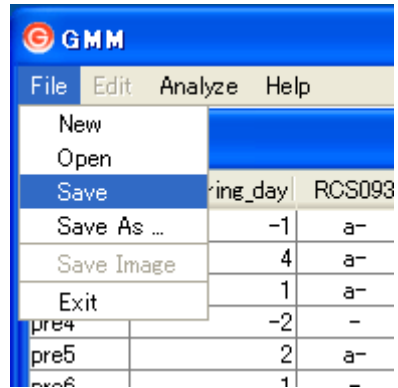
4. The Data reanalysis is complete.



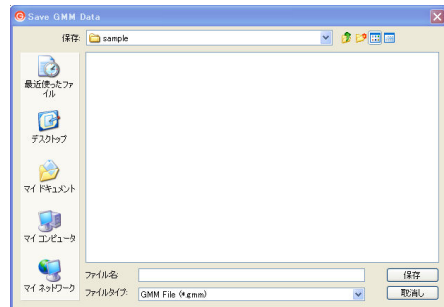
### 3-5. Save results

The analysis results can be saved as a project file (.gmm).

1. Select <File→Save> or <File→Save As> on the Menu bar.



2. Input a file name in the dialog box, and then click on the [Save] button.



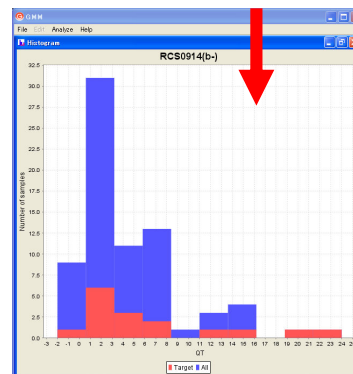
### 3-6 Distribution of phenotypic data

GMM displays the distribution of phenotypic data of the selected locus/allele.

#### Select a Data cell.

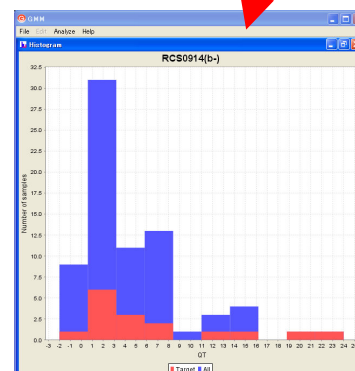
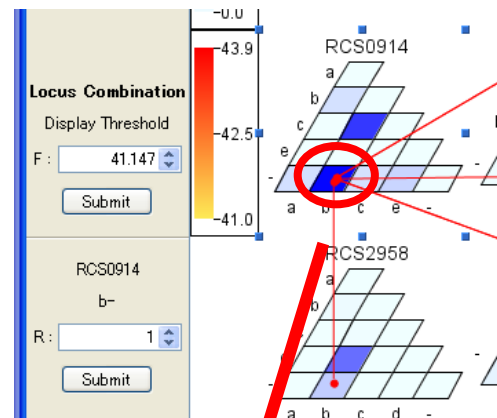
Double click on a genotypic data cell in the Data window. The distribution of phenotypic data is indicated in a new window (Red: selected locus/allele, Blue: unselected loci/alleles).

Sample	Flowering_day	RCS0907	RCS2989	RCS0005	RCS0102	RCS0251	RCS0399	RCS0404	RCS04...
pre1	-1	a-	a-	a-	ab	a-	a-	b-	a-
pre2	4	a-	-	b-	a-	a-	a-	-	-
pre3	1	a-	a-	ab	a-	-	a-	-	-
pre4	-2	-	-	ab	a-	a-	a-	b-	-
pre5	2	a-	a-	b-	a-	a-	a-	b-	-
pre6	1	-	-	b-	a-	a-	ab	b-	-
pre7	-2	a-	-	b-	-	-	a-	-	-
pre8	-2	-	a-	a-	ab	b-	a-	a-	-
pre9	-2	-	-	a-	a-	a-	a-	b-	ab
pre10	5	-	-	a-	a-	a-	a-	b-	ab
pre11	-2	-	-	ab	b-	a-	a-	b-	a-



#### Select a cell in a Matrix.

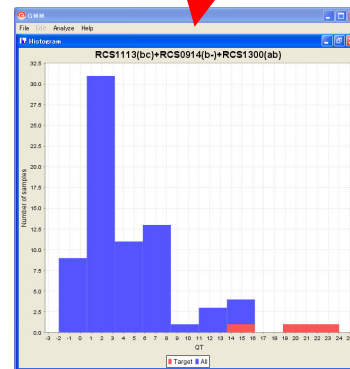
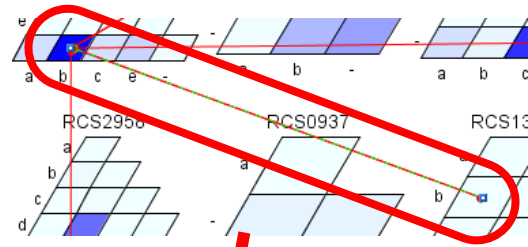
Double click on a cell in a Matrix window. The distribution of phenotypic data is indicated in a new window (Red: selected locus/allele, Blue: unselected loci/alleles).





### Select a line connecting Matrixes

Double click on a line in a Matrix window. The distribution of phenotypic data is shown in a new window (Red: locus/allele related to the selected line (combination), Blue: loci/alleles not related to the selected line).



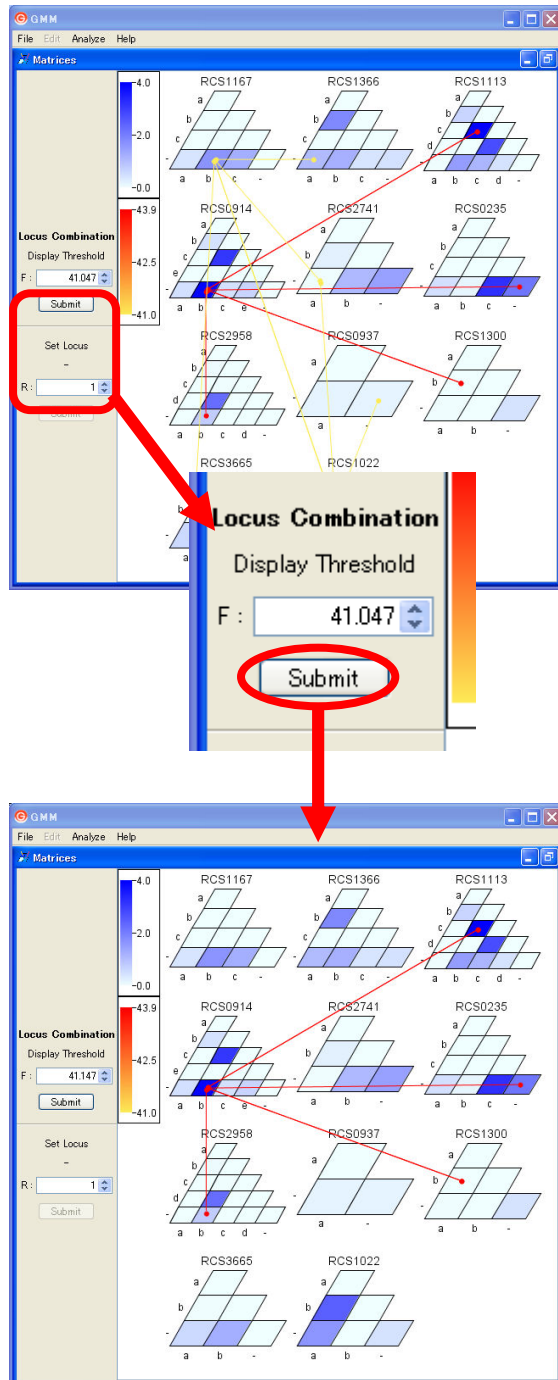
### 3-7. Refining

Once a calculation is completed, all identified loci (markers) are indicated in the Matrix window. GMM allows you to limit the display to a selected combination of identified loci in a new window by using the Refining function.

#### Line refining

Set the threshold [F], and then click on the [Submit] button.

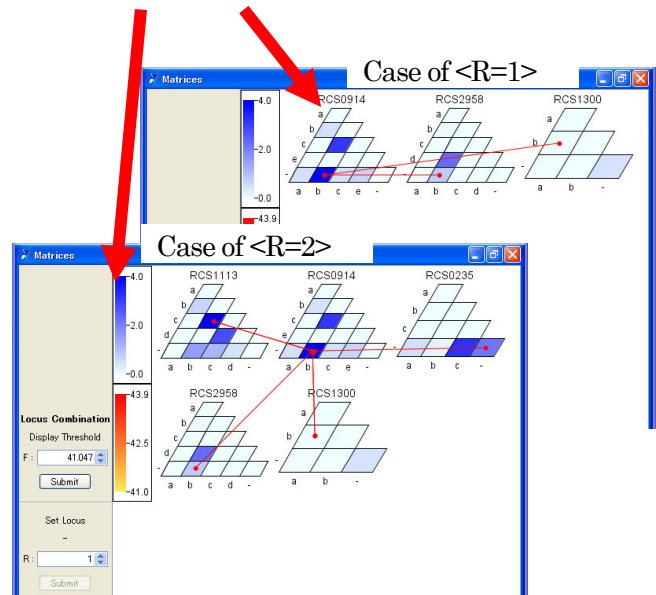
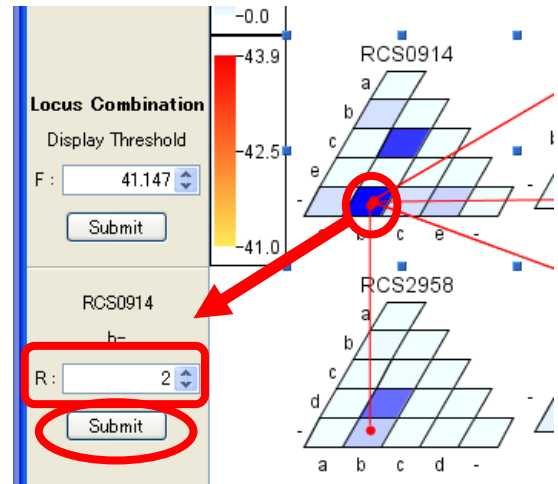
Only lines corresponding to the upper bound threshold [F] value are displayed.



## Matrix refining

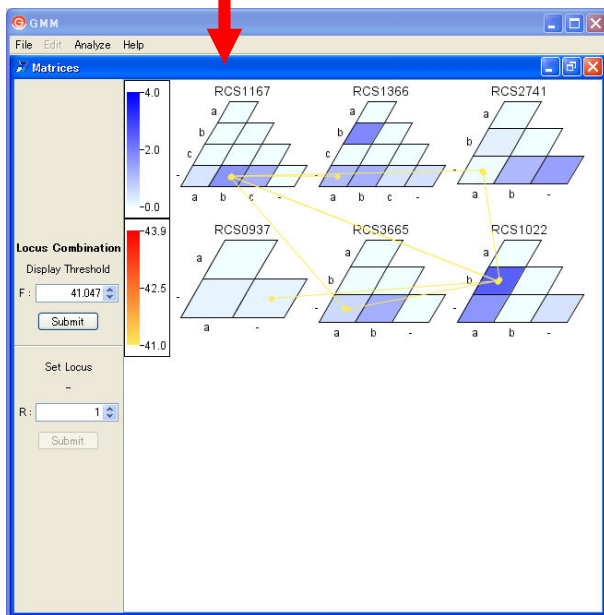
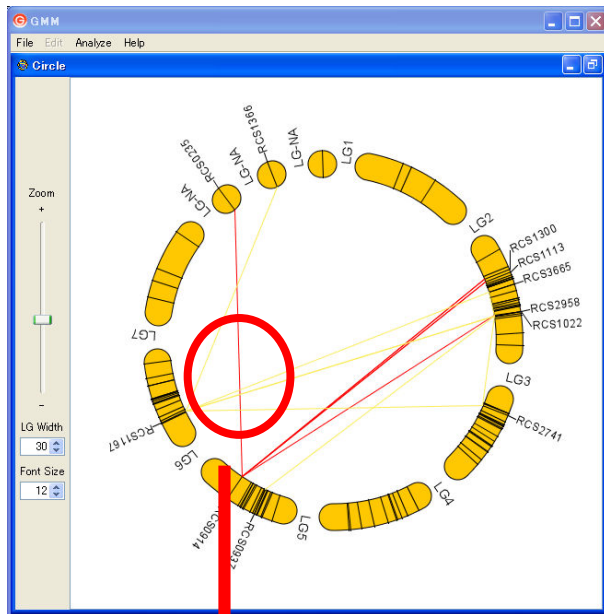
Click on a cell, and the selected Locus (allele) is indicated on the left side. Only cells generating connection lines can be selected.

R indicates the number of displayed combinations. Set <R> and click on the [Submit] button. The matrixes connected to the selected cell are indicated by lines in a new window.



### Circle refining

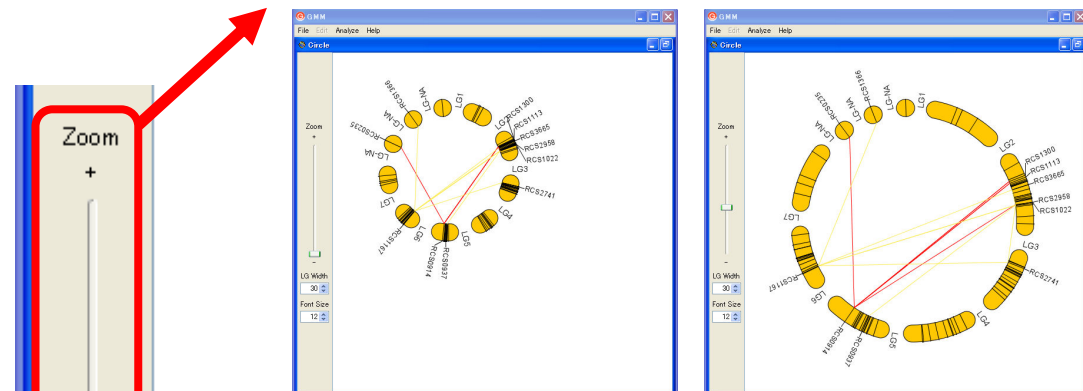
Double click an internal line in a linkage circle. The corresponding loci are indicated in a new matrix window.



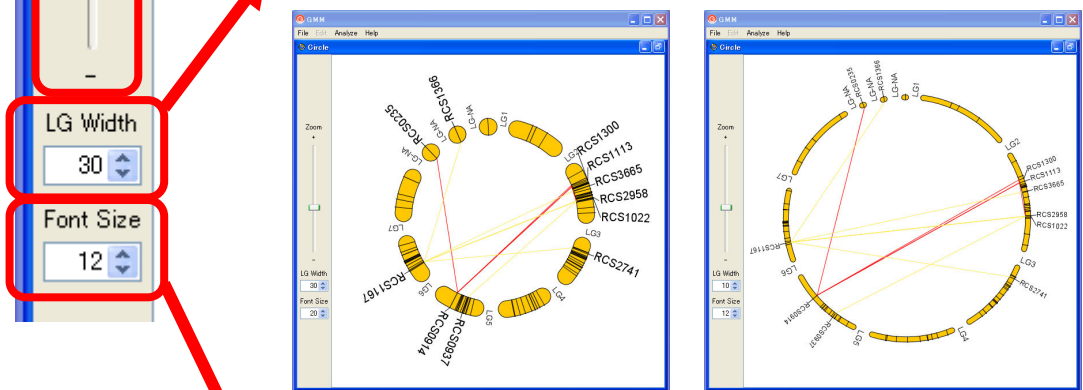
### 3-8. Change the display of a circle window

You can change the size, width and fonts of a linkage Circle.

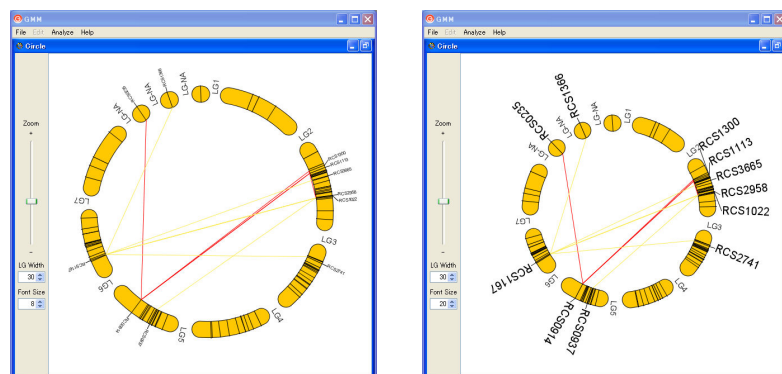
The [Zoom] slider is used for scaling the linkage circle.



[LG Width] is used for changing the width of a linkage circle.



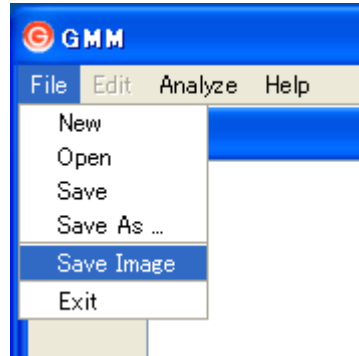
[Font Size] is used for changing the font size.



### 3-9. Save image

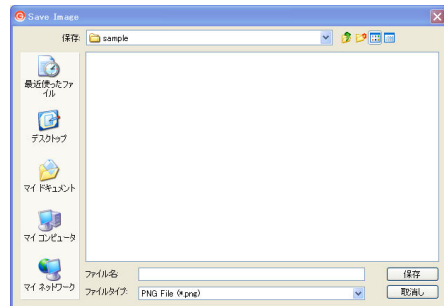
Pictures in the Matrix window and Circle window can be saved as image files.

1. Select <File→Save Image> from the Menu bar.

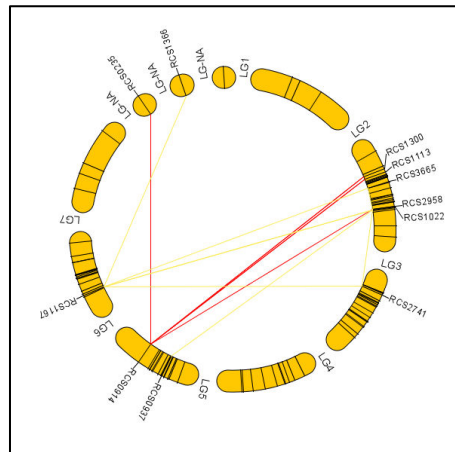


2. The File dialog is displayed.

Name the file and select the file type (.eps or .png), and then click on the [Save] button.



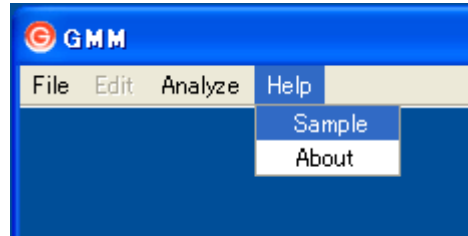
3. The image file is saved in the selected folder.



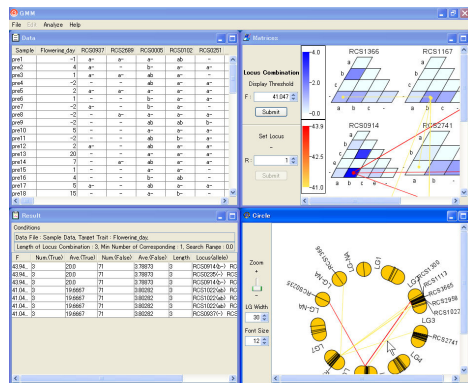
### 3-10. Display of sample data

You can explore how GMM functions by consulting the included sample data.

1. Select <Help→Sample> on the Menu bar.



2. The analyzed sample data are displayed.



### 3-11. Invoking multiple instances on Mac

Generally, invoking multiple instances is not allowed on Mac OS X, because of restrictions in the OS. To invoke multiple instances of GMM on Mac OS X, double-click on 'GMM dup' included in the GMM folder.

