

ISMAB
*Information System for
Marker-Assisted Backcrossing*

Version 1.0

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1. Installation and Startup

To run the application double click on the **ISMAB** product (i.e. ISMAB version 1.0.exe) icon (illustrated in Fig 1.1).

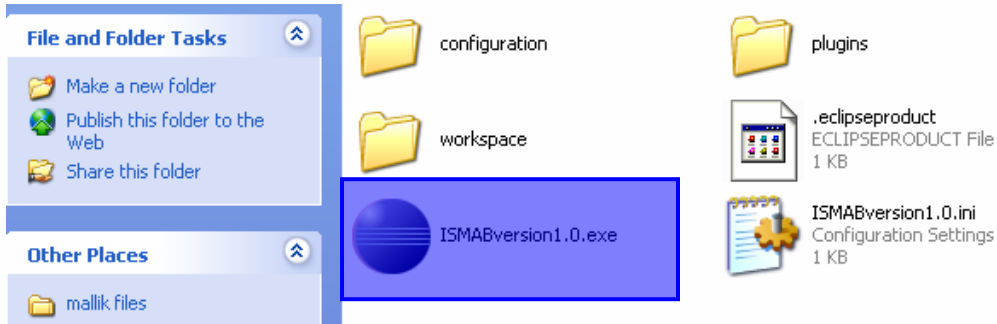


Fig 1.1 ISMAB Product Icon

It will load the application as follows.

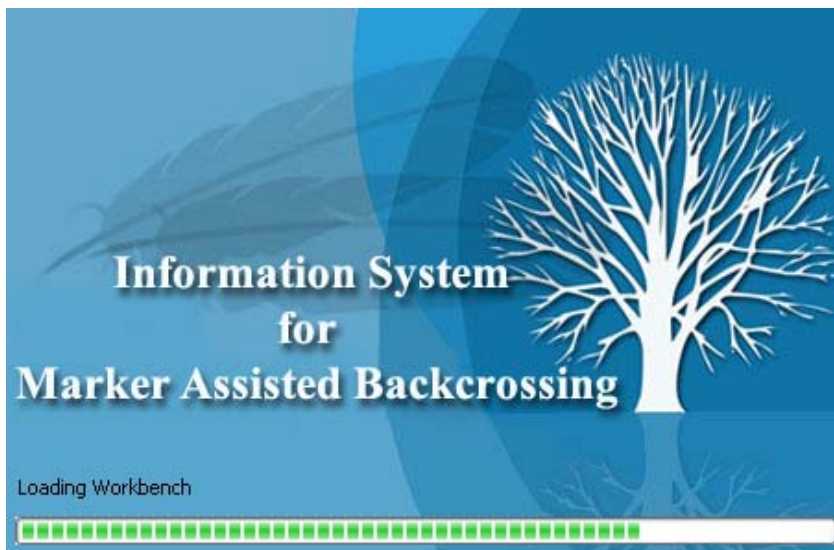


Fig 1.2 Loading the Workbench

2. The Workbench

The application opens with the ISMAB workbench, where you can create and manage your projects.

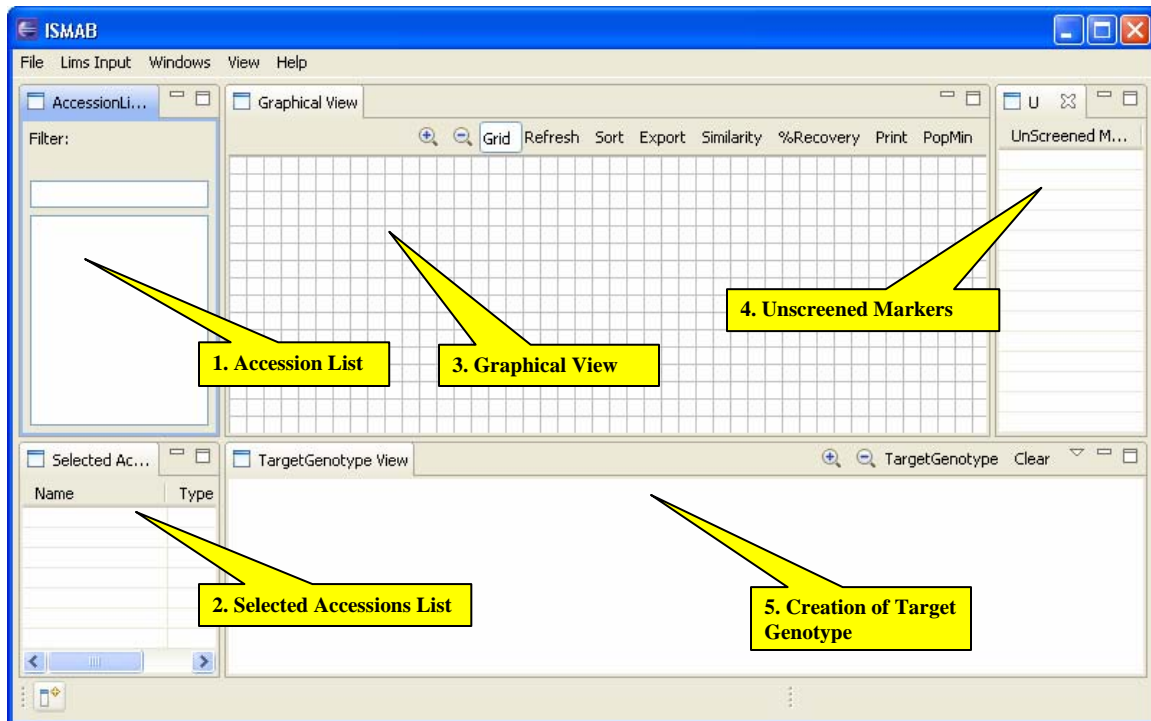



Fig 2.1 Ismab Workbench

3 Navigating Views

To navigate the views in the ISMAB workbench, click on  (i.e. show views as fast view) icon at the bottom of the workbench, clicking this will give the option to choose the category, select **Other...** category as illustrated below.

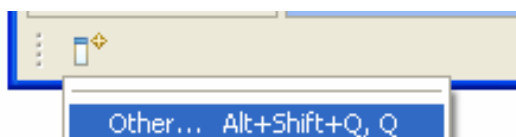
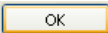


Fig 3.1 Show views as fast View

As soon as you select the **Other...** category, **Show View** dialog will opens as shown in fig 3.2. Select the appropriate view and click on .

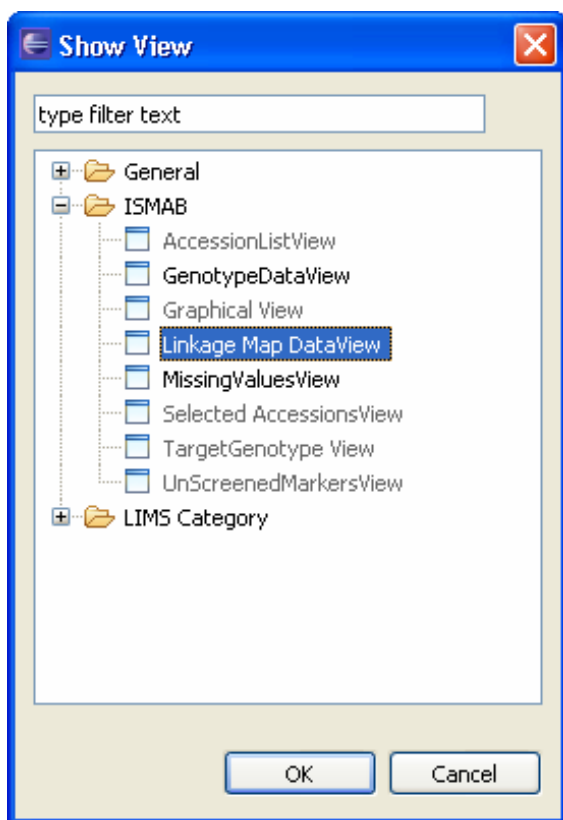


Fig 3.2 Show View Dialog in ISMAB

The Linkage Map Data View is opened in the workbench at the starting position of the workbench as shown in Fig 3.3. You can move the view to any location in the workbench by holding the view and drag to the required location as shown in Fig 3.4. and Fig 3.5

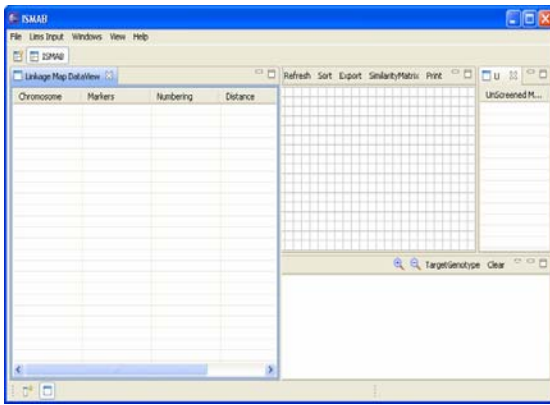


Fig 3.3 Navigating View

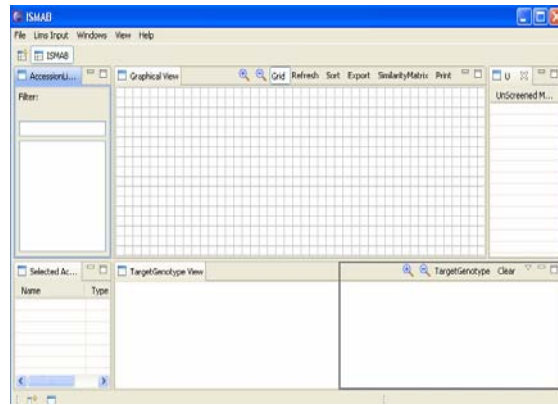


Fig 3.4 Navigating View

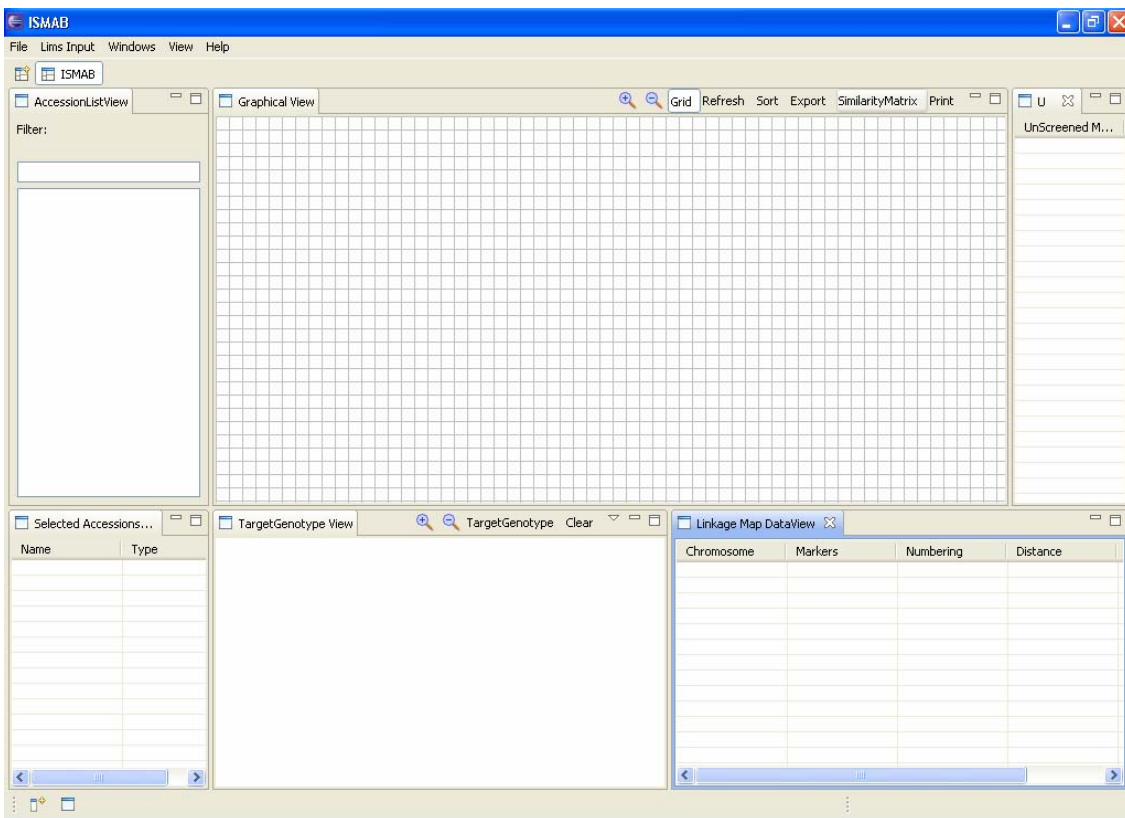


Fig 3.5 Navigating View

Follow the same steps to navigate other views in workbench.

4. Input Data Files

To start working with the application, one requires four input files which consist of 1) **Genotype data** in GCP genotyping data template, 2) **Linkage Map data** in CMTV readable file format, 3) **QTL information** from iMAS and 4) Phenotype Data.

Template of input files:

1) Prepare the **Genotype data** file with Marker data in row wise and Accession list in column wise, and save the file with ***.txt** as file type. DatasetID is an identifier of the dataset, Genotype column has the lines or accessions and the rest of the columns will contain the marker data.

DatasetID	Genotype/Marker	umc83a	umc83a	bnl6.29b	bnl6.29b
2	IS8603	191	191	110	110
2	IS8607	191	191	125	125
2	IS8608	191	191	110	110
2	IS8610	191	191	113	122

2) Arrange the data for **Linkage Map** file with Chromosome as first column, marker names in the second column, position of the marker in the respective Chromosome as the third column, distance of the marker as fourth column and the last column as cumulative distance of the Marker and Save as ***.txt** file type.

C1:Ch1 bnl5.62a	0	0	0
C1:Ch1 umc164c	1	7.4	7.4
C1:Ch1 gsr1	2	33.9	41.3
C1:Ch1 UMC11a	3	32.1	73.4
C1:Ch1 umc53c	4	10	83.4

3) Prepare the **QTL** file with Name (name of the QTL), Chromosome (name of the Chromosome), Position (at where the QTL detected), Pos-min (starting position of the QTL), Pos-max (ending position of the QTL), Trait (name of the trait), Experiment (environment name), CLEN (Chromosome length), LFM (Left Flanking Marker), PLFM(position of Left Flanking Marker) RFM (Right Flanking Marker), PRFM (position of the Right Flanking Marker), Effect, LOD and R^2 as columns and save with ***.txt** as file extension:

Name	Chromosome	Position	Pos-min	Pos-max	Trait	Experiment	CLEN	LFM	PLFM	RFM	PRFM	Effect	LOD	R ²
QTL1	Chrom1	22	20	26	FT	1	38.5	MK171	9.4	MK172	26.4	0.578	5.76	30.1
QTL2	Chrom1	5	2	14	FT	2	38.5	MK171	9.4	MK172	26.4	0.578	5.76	30.1
QTL3	Chrom1	25	24	28	BDW	1	57.3	MK830	48.5	MK186	50.2	-0.699	7	37.3

4) Arrange the data for **Phenotype data** file with trait data in row wise and Accession list in column wise, and save the file with ***.txt** as file extension.

Genotype	yield	heading
IS8603	7.232	200
IS8607	6.326	193
IS8608	6.533	197
IS8610	7.469	200.5

5) Prepare **Genotype data** file for **Advanced generation** with ***.txt** as file extension.

DatasetID	Genotype/Marker	umc83a	bnl6.29b	umc53a	UMC80b
2	Xisep0101	A	B	B	A
2	Xisep0107	A	B	B	A
2	Xisep0108	A	B	B	B
2	Xisep0114	A	B	B	A

5. Importing Data

5.1. Importing Input Files

To load the input files, go to **File** menu, select **New Project** action, will direct you to the page as shown in Fig 5.1.2.

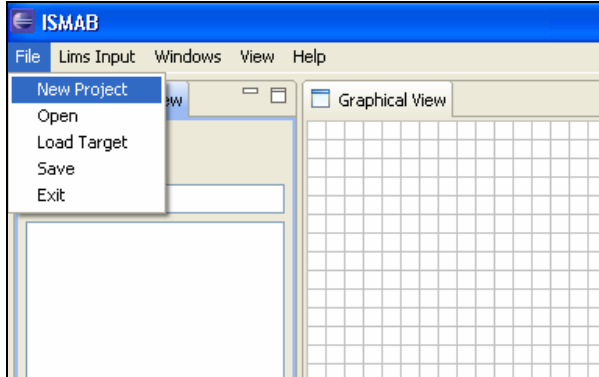


Fig 5.1.1 File menu

Browse the required files (i.e. Genotype File, Columns per markers, Linkage Map File, QTL File and Phenotype File). Genotype File, Columns per markers, Linkage Map file are mandatory.

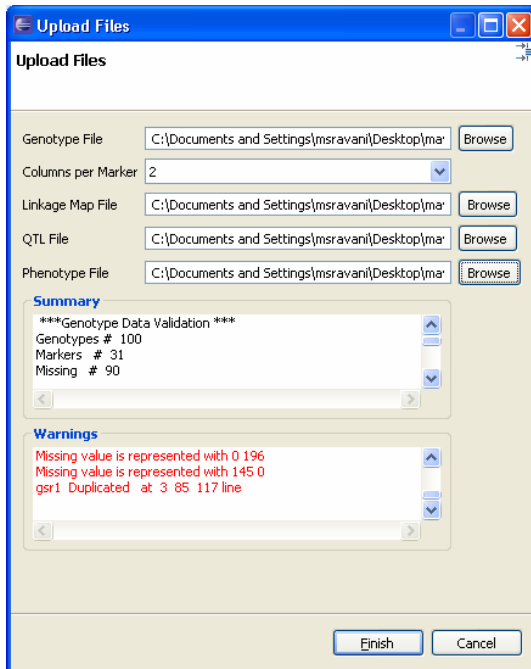


Fig 5.1.2 Upload Files wizard

Once you browse the files, the system validates the input files and prompts the validation summary with information about input data like marker type, number of genotype, markers, traits, and QTL's in the Summary dialog box. The information about missing data, duplicated markers and other relevant warnings are displayed in the Warnings log. After viewing the validation summary, click on **OK**.

Click on **Finish** button of Upload files wizard. A click on **Finish** button will load the input files into the application as shown in the Fig 5.1.3.

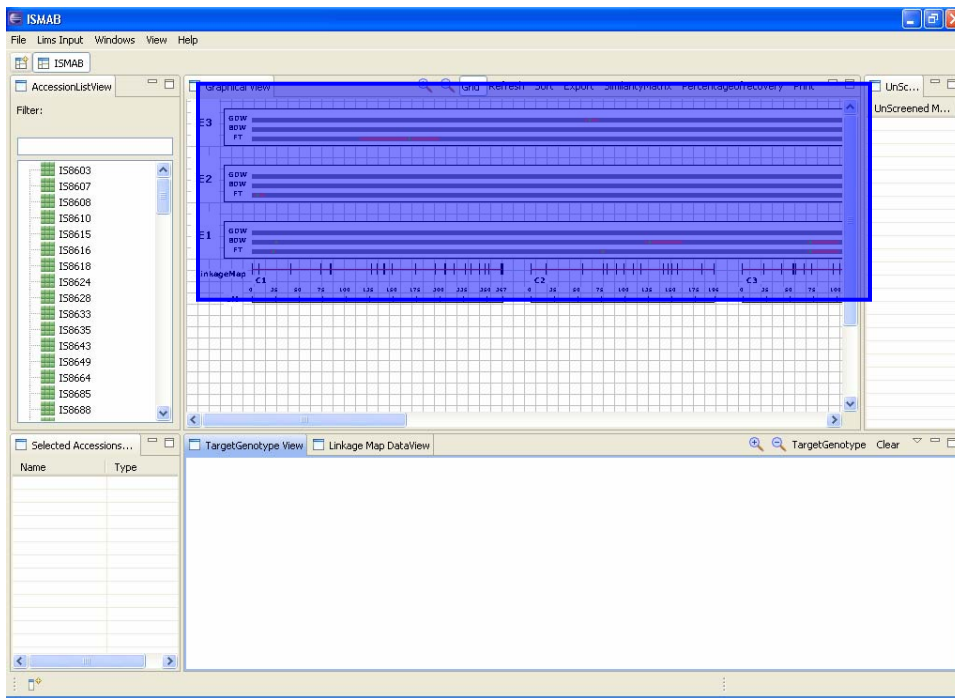


Fig 5.1.3 Ismab Workbench

The **Graphical View** is refreshed; the **QTL maps**, the **Linkage Map** and **scale** are added to the view. **E1, E2 and E3** are the QTL maps for three different environments. E1 block represents the E1 environment data, each gray bar inside the E1 block represents trait information, red colored region represents the QTL region, and green point represents the peak point. A click on QTL region will pop up a dialog box with the QTL information as shown in the Fig 5.1.4.

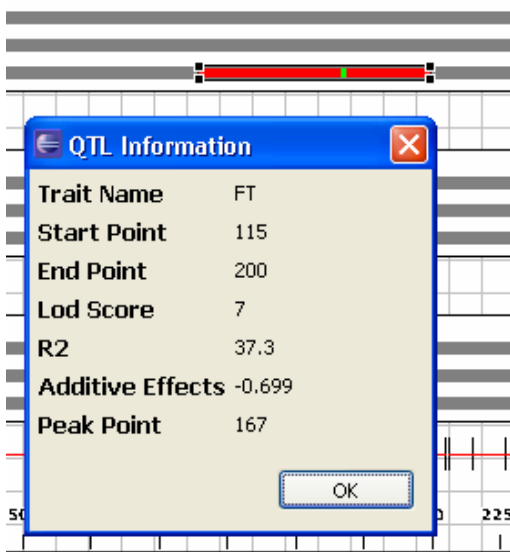


Fig 5.1.4 QTL information

Below the QTL maps, the **Linkage Map** and **Scale** are displayed. Linkage map is drawn with respect to markers and their positions on the particular chromosome as shown in Fig 5.1.5.



Fig 5.1.5 Linkage Map

From the **AccessionList View**, one can select individuals, which are likely to be probable donor or recurrent parents; selection is completely based on user's prior information. User can use **Ctrl/ Shift** Key for multiple selections; user can also edit the list by adding or removing the individual in subset.

As you select the parents from the list, the selected parents will be displayed in the **Selected Accessions View** and **Graphical View** as shown in the Fig 5.1.6.

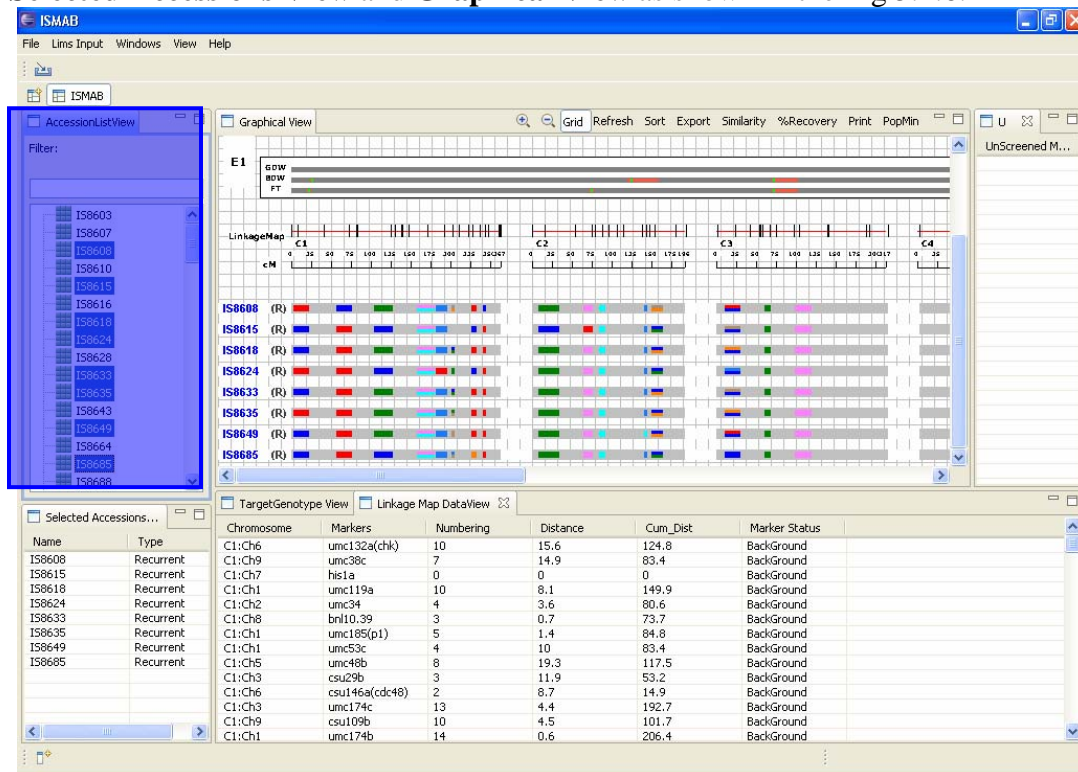


Fig 5.1.6 AccessionList View

In the **Selected Accessions View**, the type of each individual will be **Recurrent** by default. User can change the type of each individual either as **Donor** or **Recurrent** as shown in Fig 5.1.7.

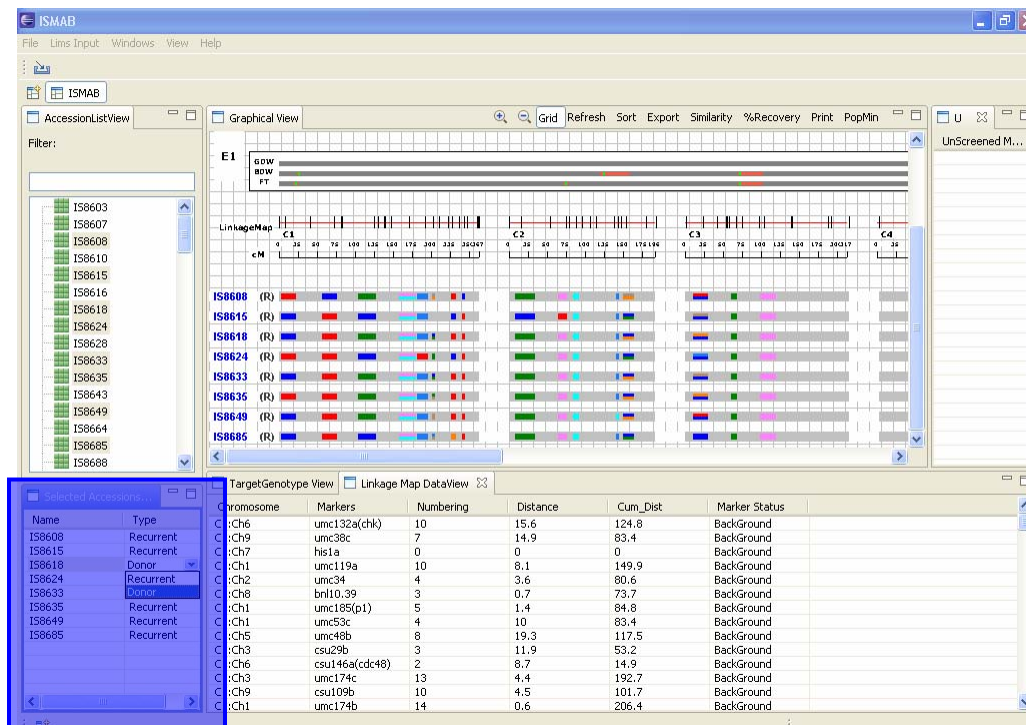


Fig 5.1.7 Selected Accessions View

Heat maps are used to display the genotype information of selected accessions and heat strips are generated for each individual per chromosome. These maps are aligned with the linkage map allowing comparison of genotype information with linkage and QTL map. Rectangles on the gray bar represent the screened marker (i.e. for which genotype data is available). The markers are colored based on the allele values. The missing values are colored in background color (i.e. light gray, the color of chromosome).

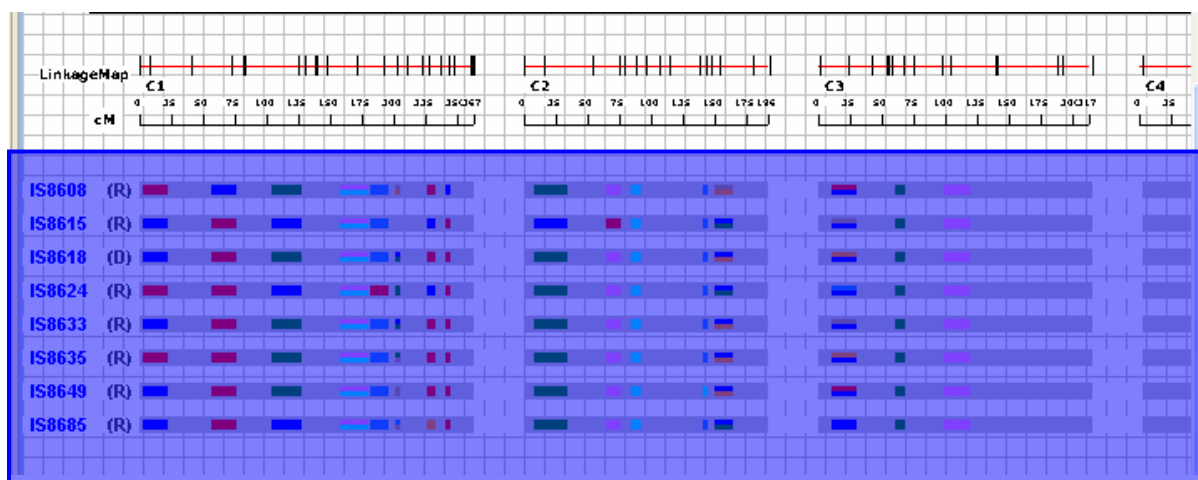
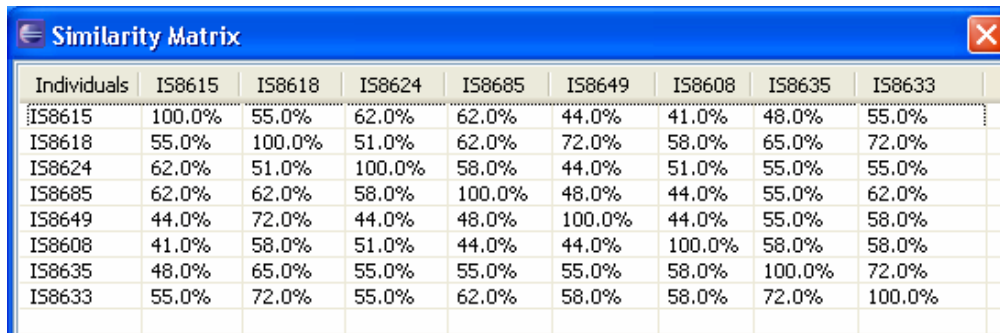


Fig 5.1.8 Heat maps in Graphical View

5.2 Tools with Graphical View

5.2.1 Similarity Matrix:

A click on **SimilarityMatrix**, will generate a similarity matrix to visualize the percentage of similarity between **selected** parents. This similarity is based on the number of shared alleles between **respective** parents.



Individuals	IS8615	IS8618	IS8624	IS8685	IS8649	IS8608	IS8635	IS8633
IS8615	100.0%	55.0%	62.0%	62.0%	44.0%	41.0%	48.0%	55.0%
IS8618	55.0%	100.0%	51.0%	62.0%	72.0%	58.0%	65.0%	72.0%
IS8624	62.0%	51.0%	100.0%	58.0%	44.0%	51.0%	55.0%	55.0%
IS8685	62.0%	62.0%	58.0%	100.0%	48.0%	44.0%	55.0%	62.0%
IS8649	44.0%	72.0%	44.0%	48.0%	100.0%	44.0%	55.0%	58.0%
IS8608	41.0%	58.0%	51.0%	44.0%	44.0%	100.0%	58.0%	58.0%
IS8635	48.0%	65.0%	55.0%	55.0%	55.0%	58.0%	100.0%	72.0%
IS8633	55.0%	72.0%	55.0%	62.0%	58.0%	58.0%	72.0%	100.0%

Fig 5.2.1 Similarity Matrix

5.2.2 Sorting:

User can **Sort** the individuals based on the frequency of alleles for the selected marker. For Sorting, select **Marker** of user's interest and click on **Sort** or right click on Graphical view and click on **Sort** as shown in Fig 5.2.2.1

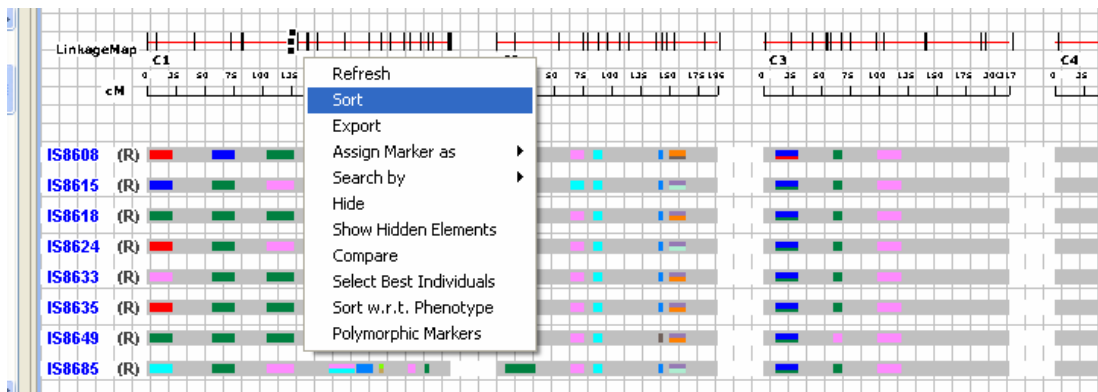


Fig 5.2.2.1 Sorting Markers

Another process for sorting is through dialog box. For this go to **Windows** then select **Sorting Markers** option.

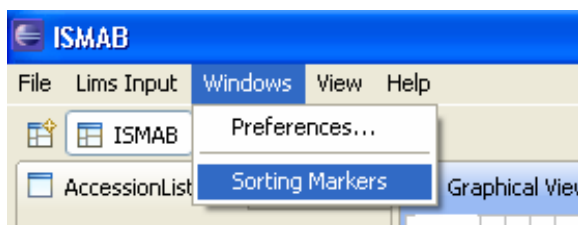
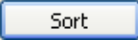


Fig 5.2.2.2 Sorting Markers window

A click on **Sorting Markers** will opens the Sorting Markers window, Select the Chromosome and the marker. Click on the 

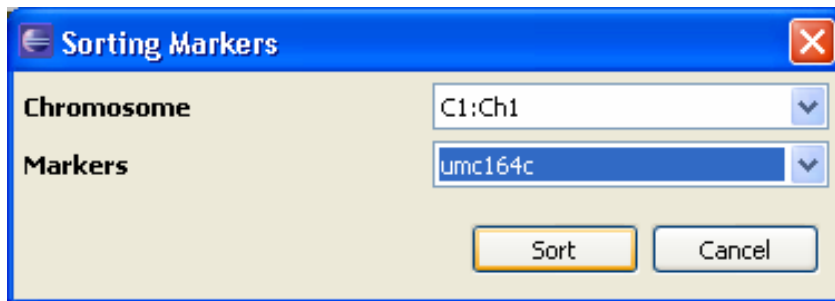


Fig 5.2.2.3 Marker Selection

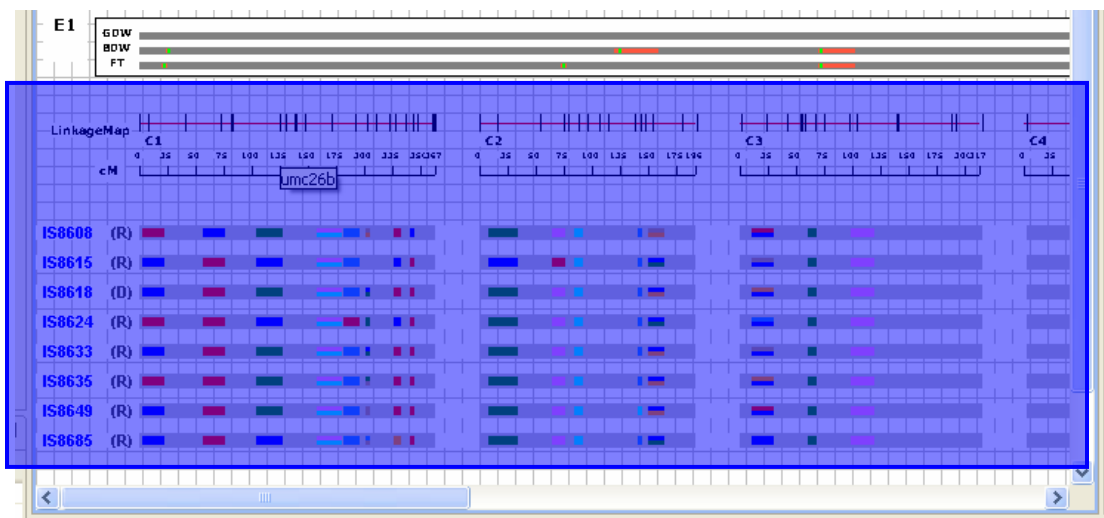


Fig 5.2.2.4 Marker Selection

Sort action will display the individuals having common alleles for selected marker at the bottom and the rare alleles at the top as shown in the Fig 5.2.3.

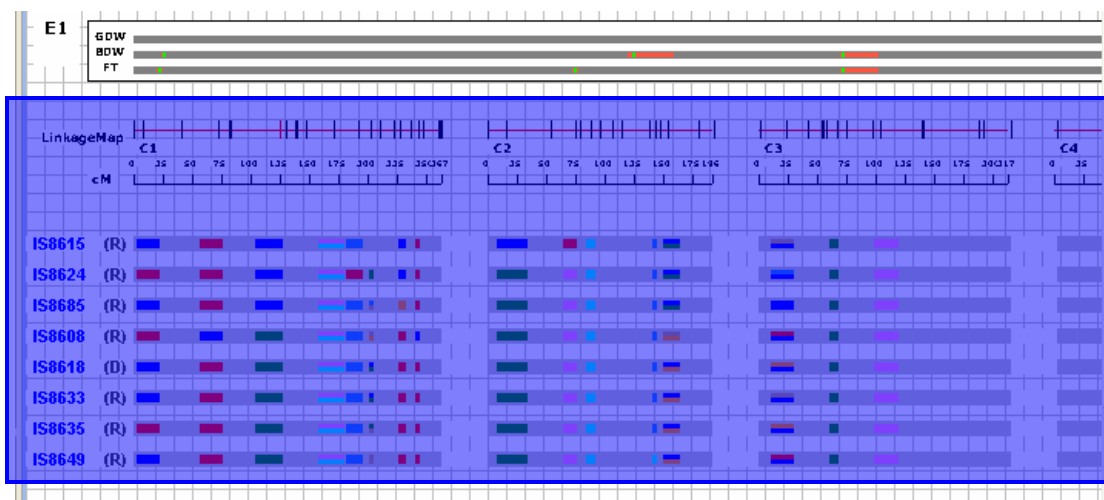


Fig 5.2.3 Order of heat maps after Sorting

5.2.3 Color Customization

We have used default color-coding; User has an option to change his selection of colors. In order to customize colors, go to **Window** menu and select **Preferences...** option.

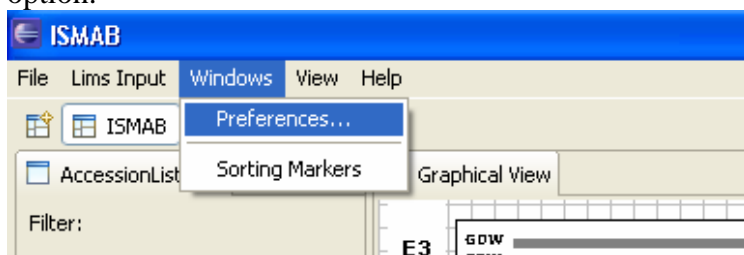


Fig 5.2.4 Window menu

A click on **Preferences...** option, will open the Preferences window with the colors for maximum number of alleles in selected data as shown in Fig 5.2.5. User can change the color of any allele. A click on allelic color will open the **color** palliate, where user can select based on their preference of colors.

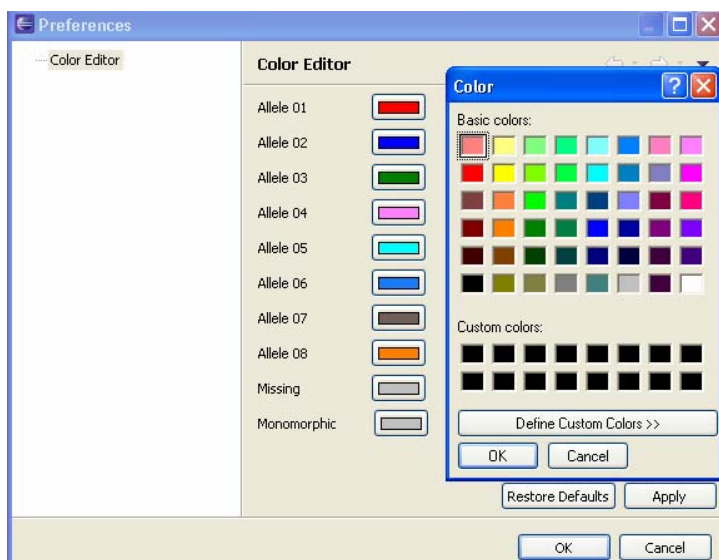
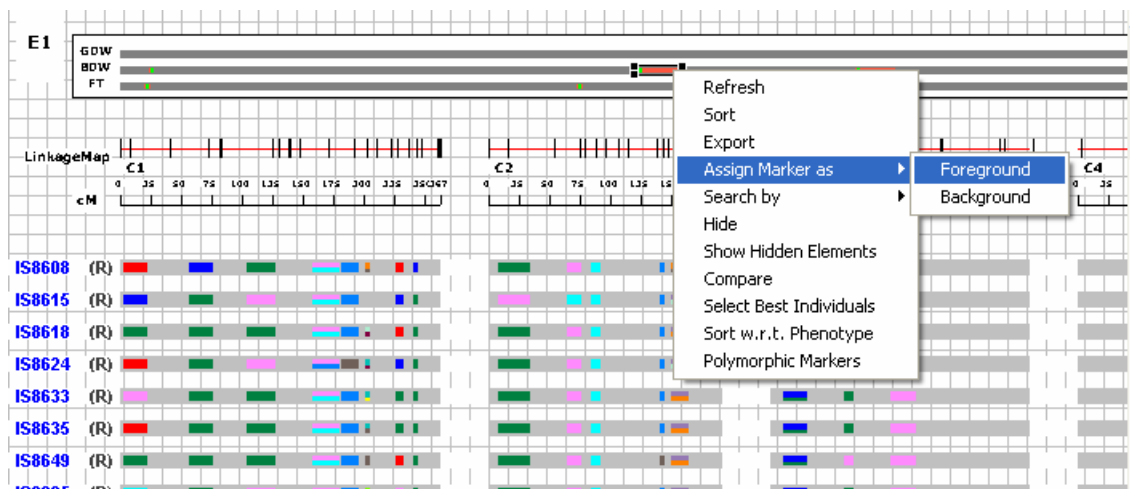


Fig 5.2.5 Color Editor Dialog

5.2.4 Foreground and Background Markers

Foreground Markers are the markers linked to QTL and coming from **donor** parent. In order to assign markers as Foreground markers, select a **QTL** on the **QTL map** or select a **portion** of **Linkage map**, right click on Graphical view and choose **Assign Markers as** and click on **Foreground**.



A click on **Foreground** markers will change the markers under the **QTL** region to Foreground by broadening the representative rectangular bars. The status of marker in the LinkageMap data view will also be changed accordingly.

Background Markers are the markers used for screening to recover the genome of the recurrent parent. In order to assign markers as Background markers, select a **QTL** on the **QTL map** or select a **portion of Linkage map**, right click on Graphical view and choose **Assign Markers as** and click on **Background**

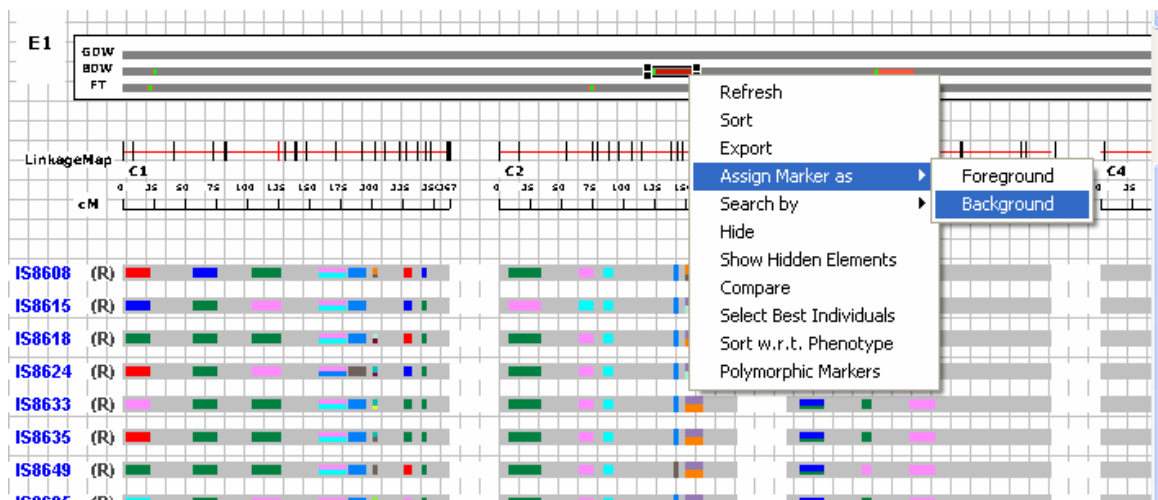


Fig 5.2.8 Assigning Markers under QTL as BackGround

A click on **Background** markers will change the markers under the **QTL** region to Background. The status of marker in LinkageMap data view has been changed to Background.

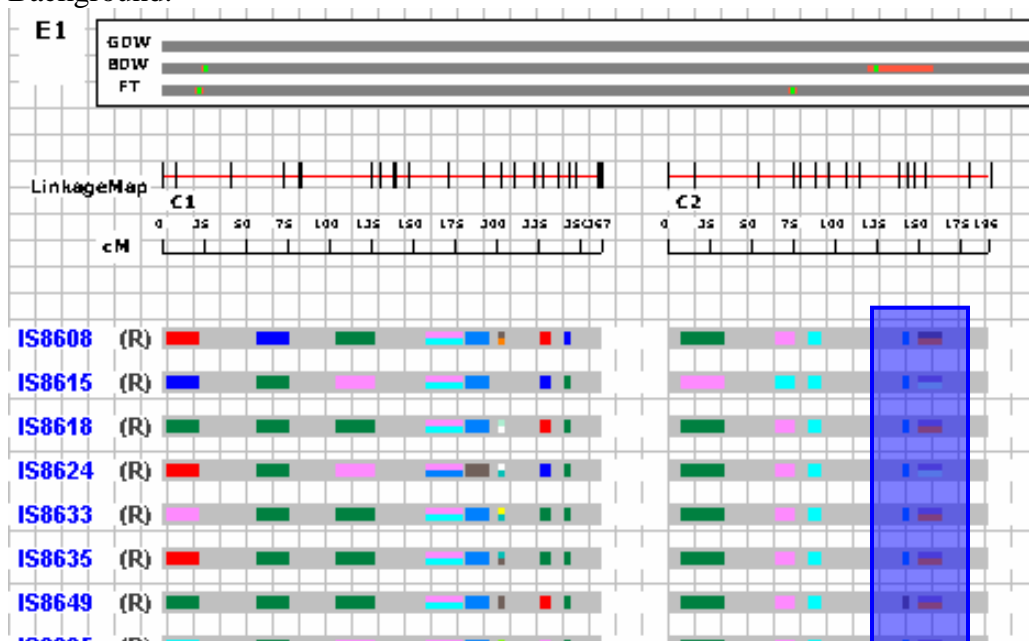


Fig 5.2.9 Markers under QTL after changing to Background

5.2.5 Export

Ismab provides a facility to export graphical view to an image file. To export the contents of graphical view to an image file, click on the **Export** button. It opens a **Save As** dialog box, where user can choose a name and export to an image file as shown in 5.2.10.

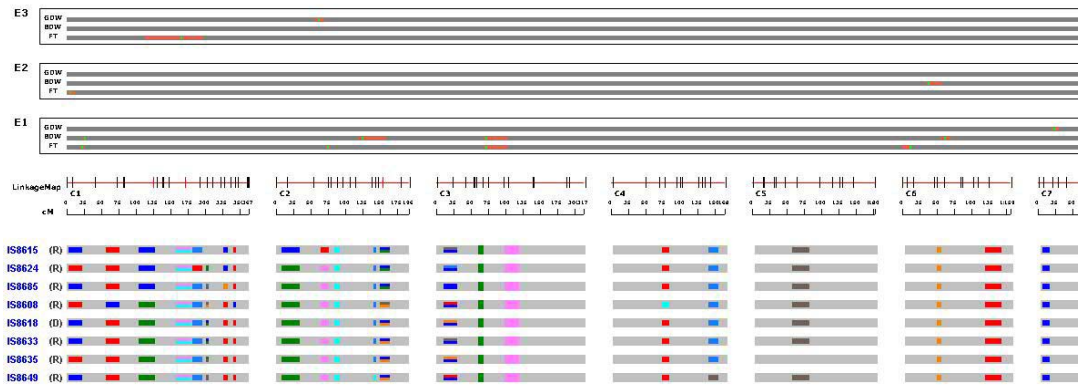


Fig 5.2.10 Graphical View

5.2.6 Print

User has a facility to print the Graphical View for further reference. To print the contents of Graphical view, click on **Print** opens a **Print** dialog, where user can choose the print option.

5.2.7 Popmin

Popmin is third party software; enables you to determine the minimum number of individuals that must be genotyped in each BC generation. After identifying trait-linked markers, you may like to introgress a target QTL from a donor parent into the Target Genotype through backcrossing. An important decision to make here is the minimum number of individuals that must be genotyped in each successive BC generation, so that at least one double homozygote for recipient type alleles at the two markers flanking the target QTL is obtained by the end of the program. To estimate the optimal sample size using PopMin within iSMAB, click on **PopMin** button. It opens Popmin dialog box, where the user has to provide the required data and Click on **OK** button.

Fig 5.2.11 POPMIN Dialog

The estimated result is printed on the terminal.

5.3 Creating Target Genotype

5.3.1 Guidelines for preparing Target Genotype are:

After analyzing the compatibility between potential **Donor** and **Recurrent**, user has to select the **Donor** and **Recurrent** heat maps from Graphical View to create a **Target Genotype** as in Fig 5.3.1.

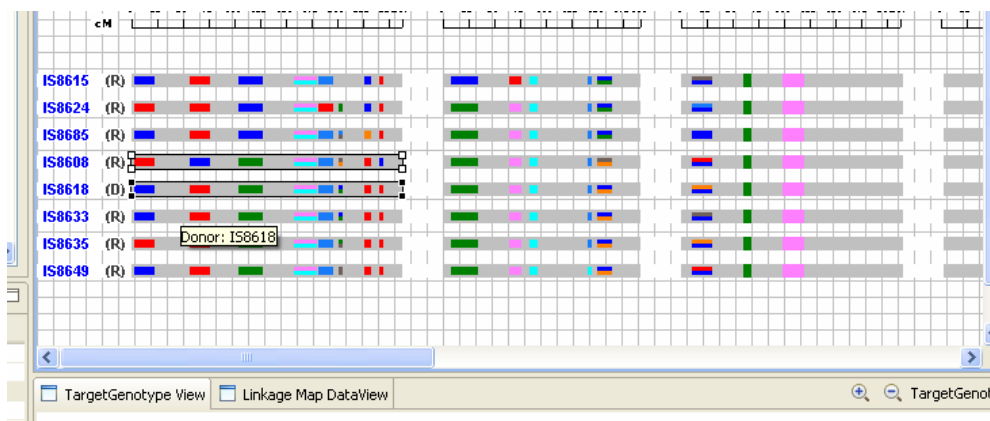


Fig 5.3.1 Selection of parents from Graphical View

After selecting the parents from Graphical View, go to **Target Genotype View** and click on **TargetGenotype**. It will display both the parents (i.e. Donor and Recurrent) along with a Target Genotype which is a copy of the Recurrent parent as shown in Fig 5.3.2. The Foreground markers of Target are replaced by Donor parent alleles automatically. **Monomorphic** Markers are the markers on Target whose allele sizes are same in both Donor and Recurrent parents. By default they will be in background color of Chromosome.

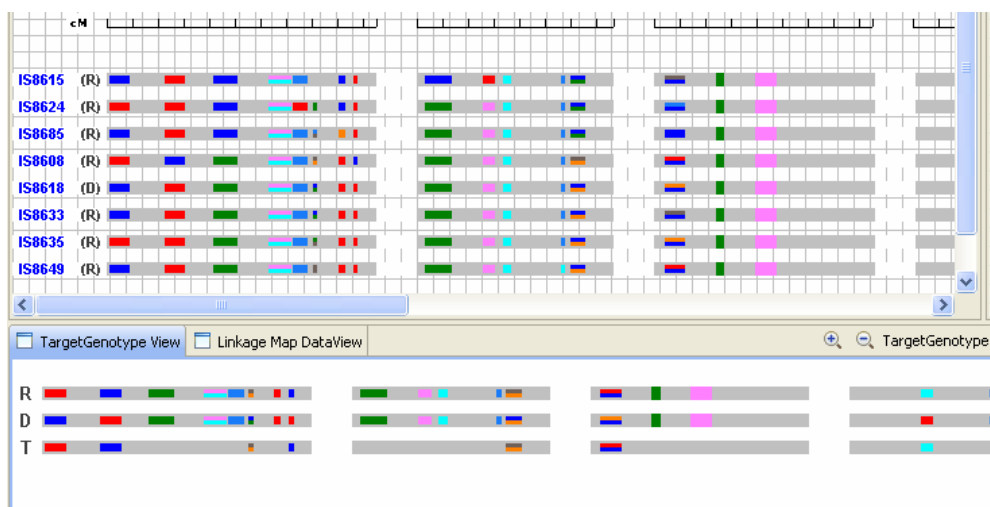


Fig 5.3.2 Creating Target Genotype

In order to prepare **Target Genotype**, drag the required portion (i.e. marker) from the Donor parent and drop on Target Genotype from left as in Fig 5.3.3. As once the marker is moved from Donor parent to Target, then the respective marker will be changed to Foreground Marker.

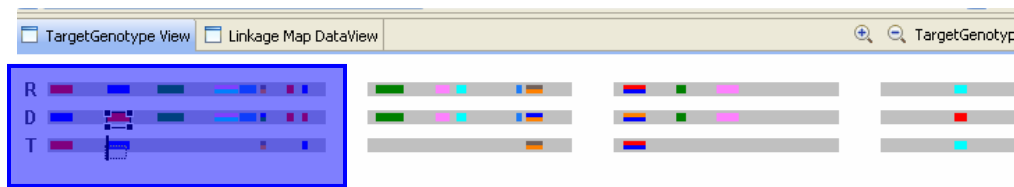



Fig 5.3.3 Creating Target Genotype

If a **Monomorphic** marker is dragged from Donor to target, then also the marker will remain as Monomorphic.

5.3.2 Save the History of Movements of Markers:

In order to save the movements of markers while preparing Target Genotype, click on drop down arrow  choose **Action** and then **History of movements** as in Fig 5.3.4.

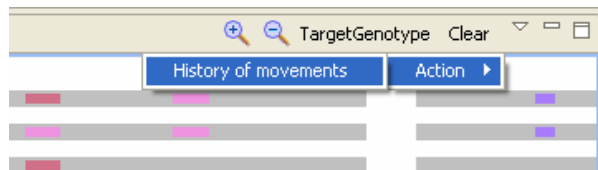


Fig 5.3.4 Action menu in Target Genotype View

A click on **History of movements** will opens a **Save As** File Dialog to save the list of moved markers into text file with *.txt file.

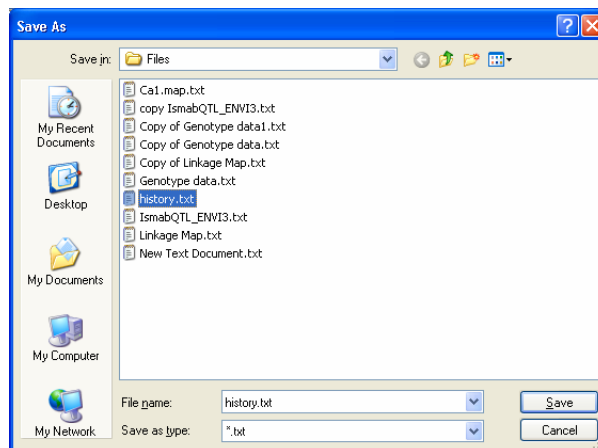


Fig 5.3.5 Save As Dialog

The moves of selected markers are stored into a text file as shown in Fig 5.3.6.

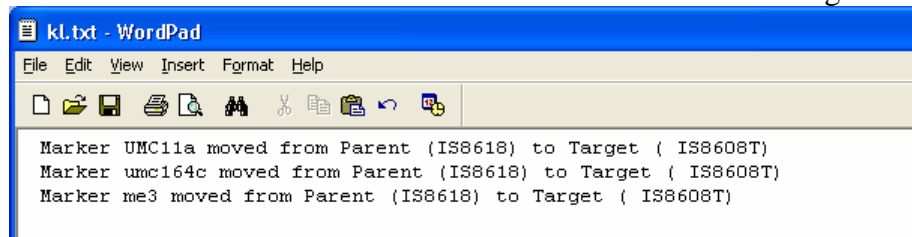


Fig 5.3.6 History of movements file

5.4 Ismap Views

5.4.1 Unscreened Markers:

Unscreened Markers are those markers which are present on the Linkage Map but do not contain any genotyping data. To identify those unscreened markers, select a portion of **linkage map** in **Graphical View** as shown in Fig 5.4.1.

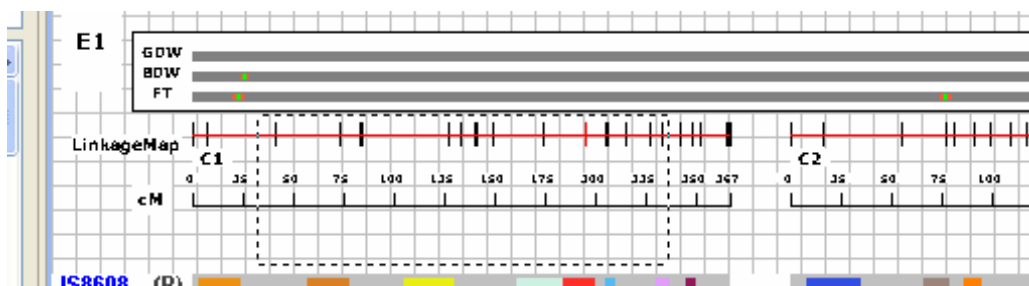


Fig 5.4.1 selecting portion of Linkage map

As you select the portion of Linkage map, the markers with out allelic data are added to the **Unscreened Markers View** as in Fig 5.4.2.

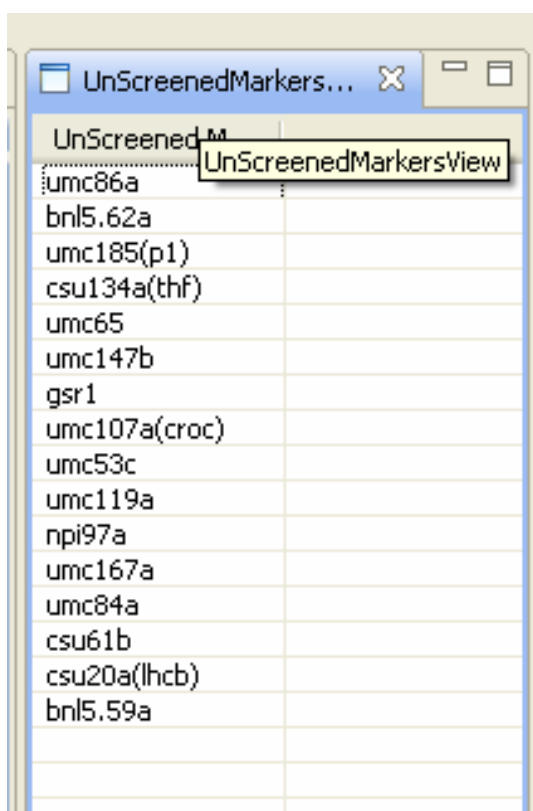


Fig 5.4.2 Unscreened Markers View

5.4.2 Missing Values View:

Missing Values View will display the list of missing values (i.e. whose allelic value is 0) for the Group of markers via Accession. In order to get missing values, click on the **View** menu and select **Missing values**.

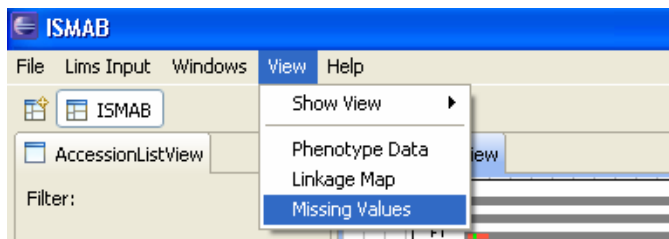
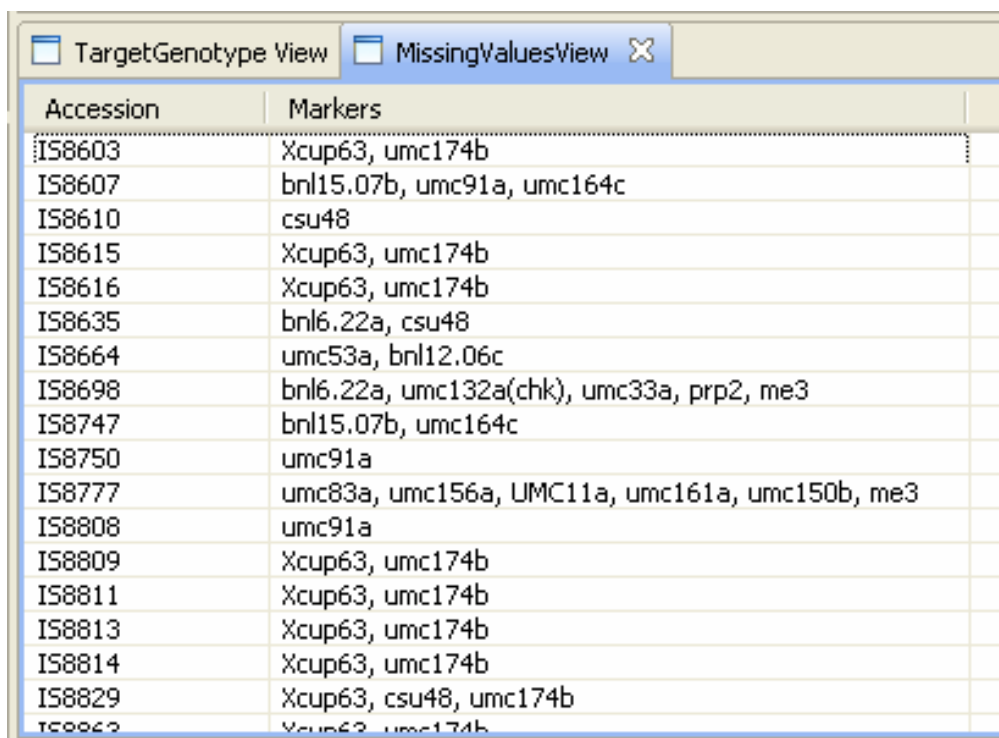


Fig 5.4.3 View menu

Selecting the Missing Values action, will add the list of **Markers** and **Accessions** whose allelic data is missing (i.e. 0) to **Missing Values View**

The screenshot shows the 'MissingValuesView' window. It has a tabbed interface with 'TargetGenotype View' and 'MissingValuesView'. The 'MissingValuesView' tab is active, displaying a table with two columns: 'Accession' and 'Markers'. The table lists various accessions and their corresponding markers.

Accession	Markers
IS8603	Xcup63, umc174b
IS8607	bnl15.07b, umc91a, umc164c
IS8610	csu48
IS8615	Xcup63, umc174b
IS8616	Xcup63, umc174b
IS8635	bnl6.22a, csu48
IS8664	umc53a, bnl12.06c
IS8698	bnl6.22a, umc132a(chk), umc33a, prp2, me3
IS8747	bnl15.07b, umc164c
IS8750	umc91a
IS8777	umc83a, umc156a, UMC11a, umc161a, umc150b, me3
IS8808	umc91a
IS8809	Xcup63, umc174b
IS8811	Xcup63, umc174b
IS8813	Xcup63, umc174b
IS8814	Xcup63, umc174b
IS8829	Xcup63, csu48, umc174b
IS8863	Xcup63, umc174b

Fig 5.4.4 Missing values view

5.4.3 Lims Markers:

Lims Markers are those markers which are involved in the Linkage Map. To identify those markers, select a portion of **Linkage map** in **Graphical View**.

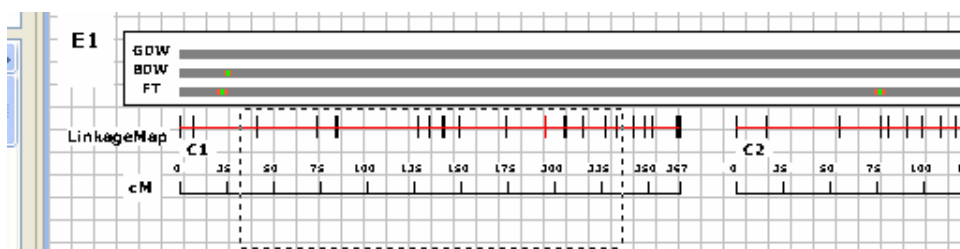


Fig 5.4.5 Selecting portion of Linkage map

From the menu bar, click on **Lims Input** menu and select **Lims Markers**.

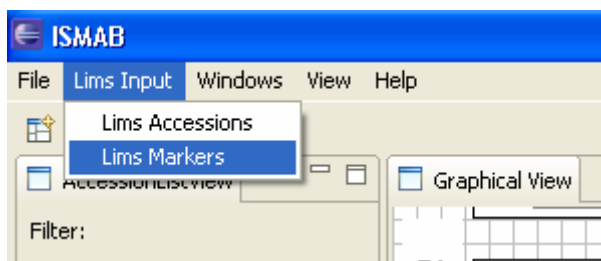


Fig 5.4.6 LIMS Input menu

A click on **Lims Markers** action, will add the Markers which are there in the selected portion of Linkage Map are added along with their status as Screened or Unscreened to **LIMS List of Markers View**.

List of Markers	Status
umc33a	Screened
umc185(p1)	UnScreened
bnl5.62a	UnScreened
csu61b	UnScreened
umc107a(croc)	UnScreened
np197a	UnScreened
umc98a	UnScreened
umc84a	UnScreened
csu134a(thf)	UnScreened
bnl5.59a	UnScreened
umc65	UnScreened
umc53c	UnScreened
umc147b	UnScreened
umc83a	Screened
umc53a	Screened
umc164c	Screened
bnl12.06c	Screened
gsr1	UnScreened
umc6a	UnScreened
umc161a	Screened
UMC11a	Screened
umc174b	Screened
prp2	Screened
umc55a	UnScreened

Fig 5.4.7 LIMS List of Markers View

User has an option to **save** this file, which can be uploaded to molecular LIMS for further Screening. User can delete any Marker, if they don't want that marker to be further Screened. To delete a particular Marker, right click on the respective row and select **Delete Selected Marker**. It will delete that particular Marker from the LIMS List of Markers.

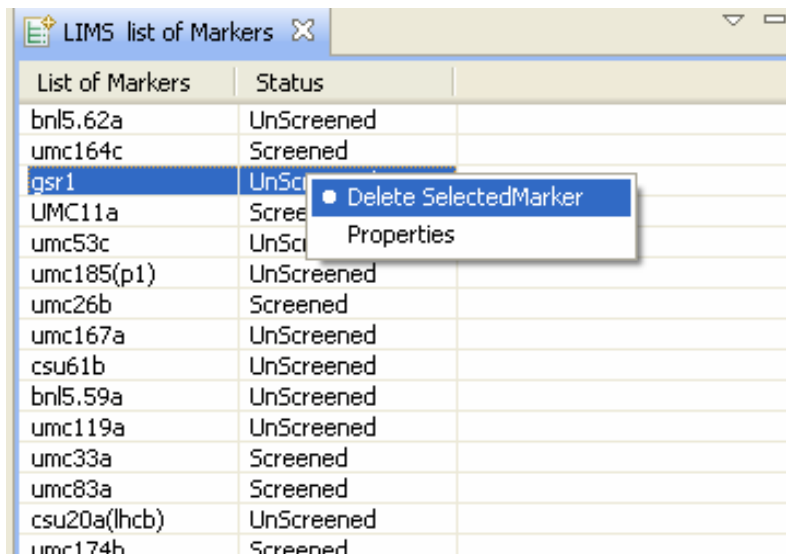
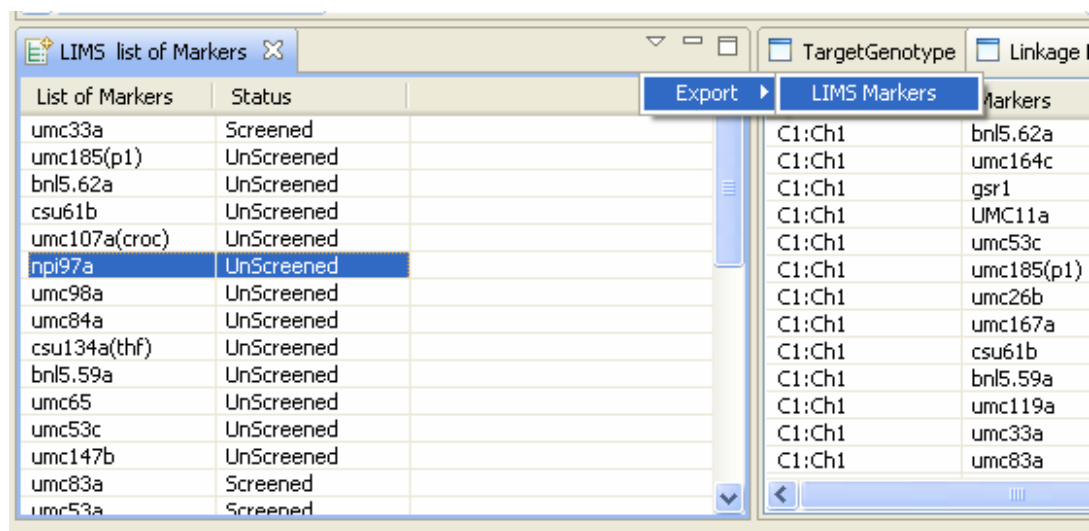


Fig 5.4.8 Deleting Selected marker

To Save the Marker information into a file click on dropdown arrow and choose **Export** and then **LIMS Markers**



5.4.9 Export to LIMS Markers

As the user chooses the LIMS Markers it open a Save as dialog, where user has to choose the file name and select **Save**, will save the list of markers as ***.CSV** file.

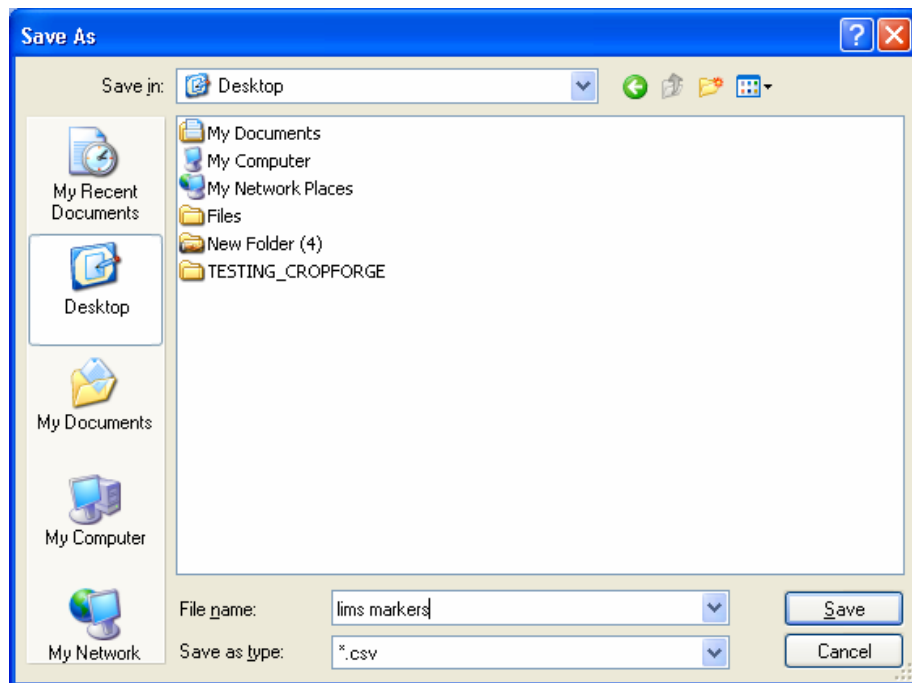
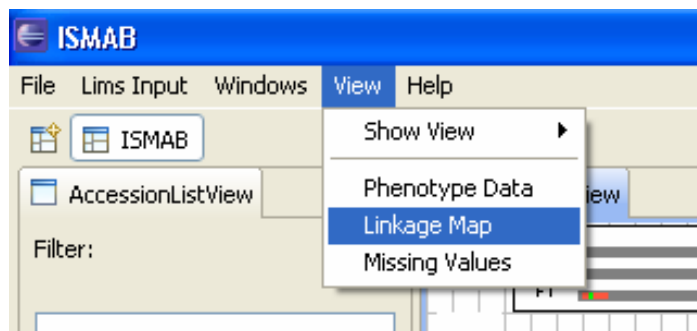


Fig 5.4.10 Save As Dialog

5.4.4 Linkage Map Data:

Linkage Map Data View consists of information of the Markers, its position, distance between Markers, its cumulative distance and marker status via Chromosomes. In order to get linkage map data, click on the **View** menu and select **Linkage Map**.



Selecting the Linkage Map action, will display the Linkage map data in the Linkage Map Data view.

Chromosome	Markers	Numbering	Distance	Cum_Dist	Marker Status
C1:Ch1	bnl5.62a	0	0	0	BackGround
C1:Ch1	umc164c	1	7.4	7.4	BackGround
C1:Ch1	gsr1	2	33.9	41.3	BackGround
C1:Ch1	UMC11a	3	32.1	73.4	BackGround
C1:Ch1	umc53c	4	10	83.4	BackGround
C1:Ch1	umc185(p1)	5	1.4	84.8	ForeGround
C1:Ch1	umc26b	6	42.7	127.5	ForeGround
C1:Ch1	umc167a	7	6	133.5	ForeGround
C1:Ch1	csu61b	8	7.4	140.9	ForeGround
C1:Ch1	bnl5.59a	9	0.9	141.8	ForeGround
C1:Ch1	umc119a	10	8.1	149.9	ForeGround
C1:Ch1	umc33a	11	24.5	174.4	ForeGround
C1:Ch1	umc83a	12	21	195.4	ForeGround
C1:Ch1	csu20a(lhcb)	13	10.4	205.8	ForeGround
C1:Ch1	umc174b	14	0.6	206.4	BackGround
C1:Ch1	umc65	15	8.6	215	BackGround
C1:Ch1	umc107a(croc)	16	12	227	BackGround
C1:Ch1	bnl6.29b	17	5.7	232.7	BackGround
C1:Ch1	umc147b	18	9	241.7	BackGround
C1:Ch1	umc161a	19	6.4	248.1	BackGround
C1:Ch1	npi97a	20	4	252.1	BackGround
C1:Ch1	csu134a(thf)	21	13.1	265.2	BackGround
C1:Ch1	umc84a	22	1.3	266.5	BackGround
C1:Ch1	umc86a	23	0.9	267.4	BackGround
C1:Ch2	npi22a	0	0	0	BackGround

Fig 5.4.11 Linkage Map Data View

5.4.5 LIMS Subset View:

From the menu bar, click on **Lims Input** menu and select **Lims Accessions**.



Fig 5.4.12 Lims Input menu

A click on **Lims Accessions** will show the **Lims subset View**, with all the selected Accessions from Accessions View. You can export the selected accessions to molecular Lims in two formats. 1) **Lims Genotype List** or 2) **Lims PCR plate**. As the user chooses the format, it open a Save As dialog, where user has to chose the file name and click on **Save**, will save the list of markers as *.xls file.

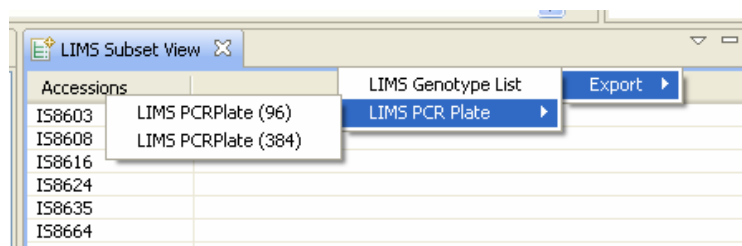
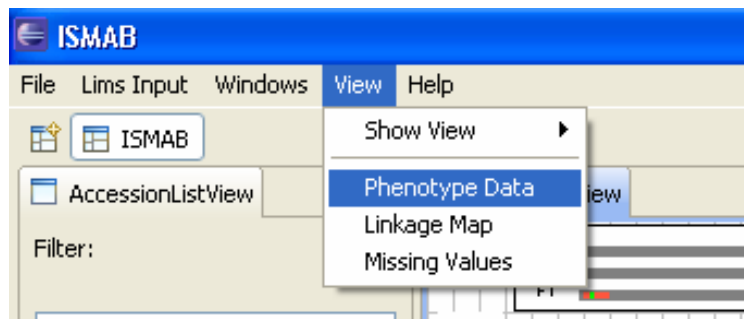


Fig 5.4.13 Lims Subset View

5.4.6 Phenotype Data View:

Phenotype Data View contains the list of Genotypes along with their trait information via Genotypes. In order to get Phenotype data, click on the **View** menu and select **Phenotype Data**.



Selecting the Phenotype Data action, will display the Trait data (can be 'n' number of traits with user's interest) in the Phenotype Data view. You can Sort the data with respect to any trait.

Genotype/Acc...	yield	heading
IS8603	7.232	200
IS8607	6.326	193
IS8608	6.533	197
IS8610	7.469	200.5
IS8615	5.997	191
IS8616	6.525	203.5
IS8618	6.564	204.5
IS8624	7.03	193.5
IS8628	8.432	203
IS8633	7.287	202.5
IS8635	7.701	194.5
IS8643	6.842	198
IS8649	5.735	192.5
IS8664	8.491	204
IS8685	6.474	197
IS8688	7.289	199
IS8698	5.984	201
IS8721	7.111	188
IS8744	8.048	200
IS8747	5.956	202
IS8749	6.046	189.5
IS8750	6.084	192
IS8751	8.435	200.5
IS8752	6.413	202
IS8756	6.089	201
IS8768	7.898	200.5
IS8772	6.781	199.5
IS8773	6.612	192
IS8774	6.391	197.5
IS8776	5.821	188.5
IS8777	6.283	201
IS8808	7.987	199

Fig 5.4.14 Phenotype Data View

5.4.7 Chromosome View

Chromosome View will display the contents as in Graphical view but limited to a particular Chromosome. In order to view Chromosome wise data, click on the **View** menu and select **Chromosome View**.

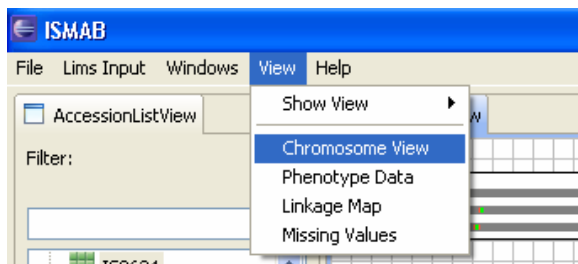
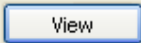


Fig 5.4.15 Chromosome View Window

A click on **Chromosome View** will opens the Chromosome View window; Select the Chromosome and Click on .

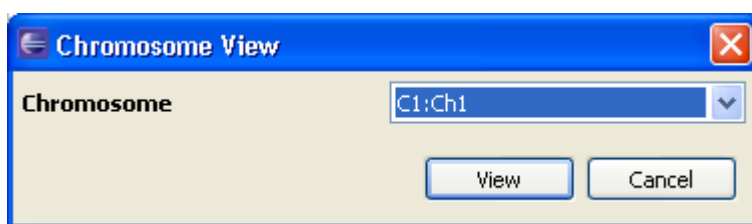



Fig 5.4.16 Chromosome selection

A click on  will refresh the Chromosome view with the selected Chromosome.

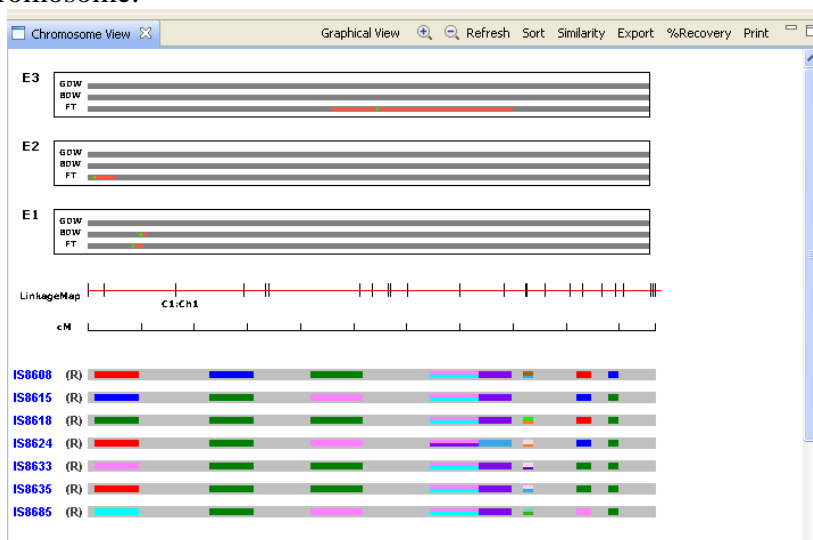



Fig 5.4.17 Chromosome wise view

All the functions in Graphical View are available in Chromosome View. To get back the Graphical view click on .

6. Saving and Loading Workbench

6.1 Save Project:

To save the whole workbench for future use, go to **File** menu choose **Save** option as in Fig 6.1.1.

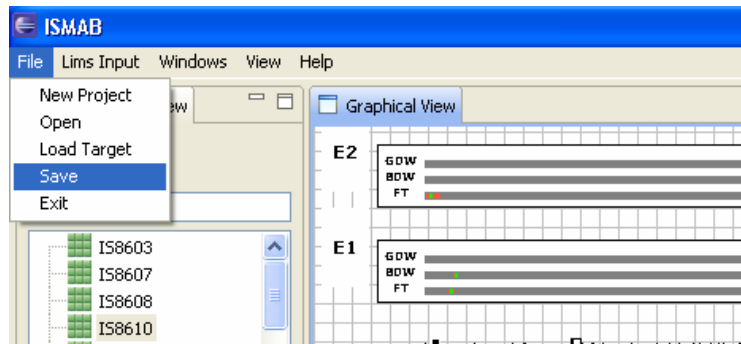


Fig 6.1.1 File menu

A click on **Save** option will display a **Save** dialog box, where the user has to provide **Project** name and **Generation** and click on button, Will prompt a message as **File created**.

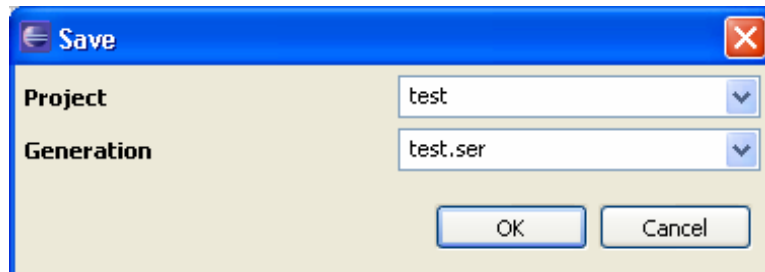


Fig 6.1.2 Save dialog

6.2 Load Project:

To load project into the workbench, go to **File** menu, choose **Load** option.

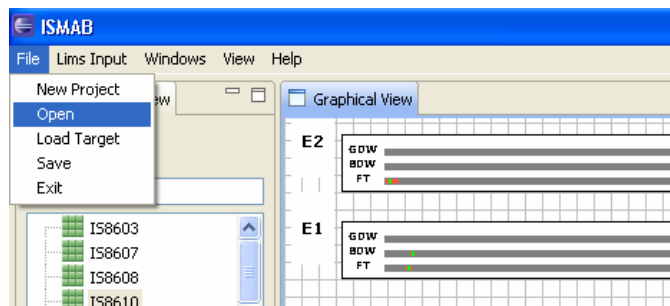
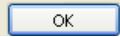


Fig 6.2.1 File menu

A click on Load button will display a **Load** dialog box, where the user has to provide **Project** name and **Generation** and click on  button, Will load the workbench with saved data.

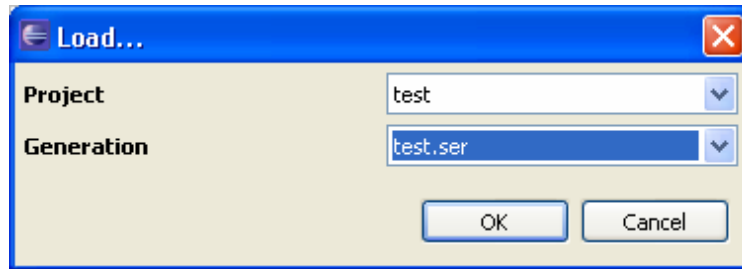


Fig 6.2.2 Load dialog

7. Advanced Generations of Ismab

7.1 Importing Advanced Generation Input files

To import **Advanced** generation input files into the Ismab workbench, go to File menu, and choose **Load Target** action, will direct you to the page as shown in fig 7.1.2.

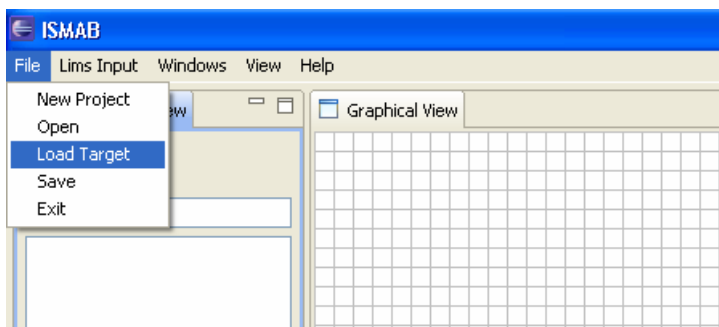


Fig 7.1.1 File menu

Browse the required files (i.e. Project name, generation name, Genotype File).

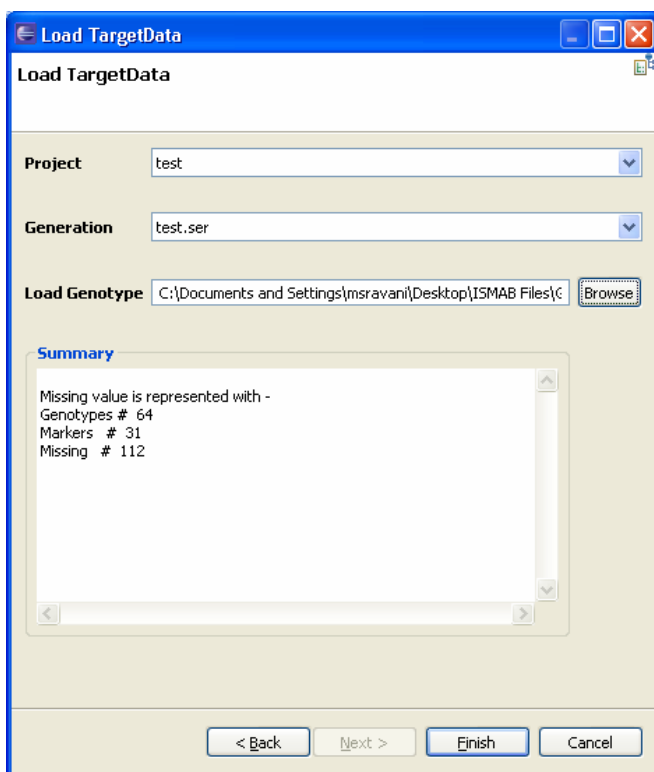


Fig 7.1.2 loading input files

Once you browse the files, click on **Finish** button. A click on **Finish** button will load the input files into the application as shown in the fig 7.1.3.

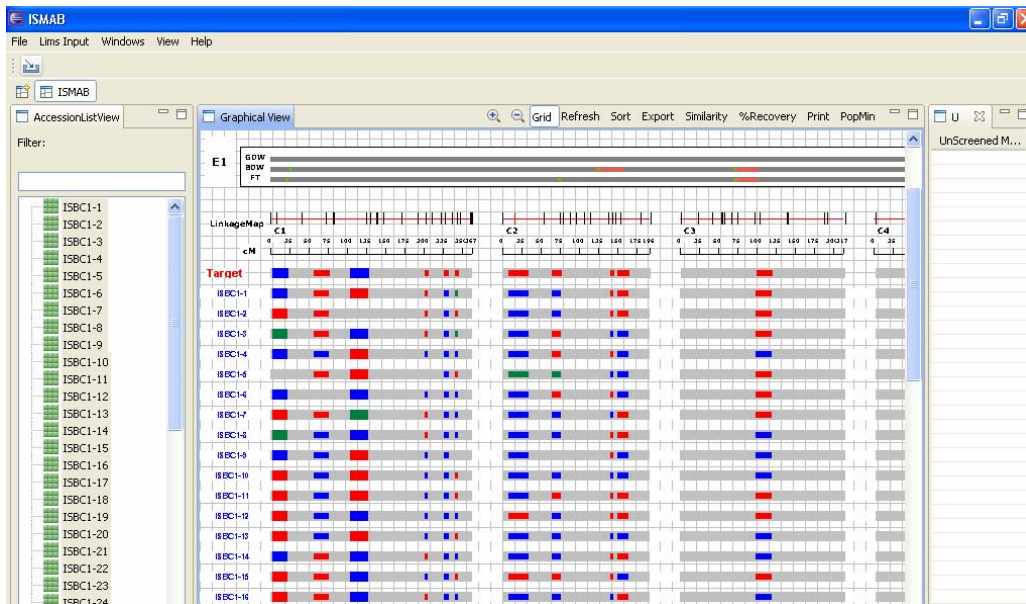


Fig 7.1.3 Ismab workbench

The **Graphical View** is loaded with QTL Map, Linkage Map, Scale, Target data from first generation and heat maps. The **heat maps** are displayed below the **Target**.

Heat maps will display the genotype information of selected accessions and have generated heat strip for each individual per chromosome. These maps are layered along with Target under the linkage map that allows comparison of genotype information with linkage and QTL map.

7.2 Tools in Graphical View for Advanced generation

7.2.1 Hide

In order to hide some of the heat maps in Graphical View, Select the appropriate heat maps. Right click on **Graphical View** and select **Hide**.

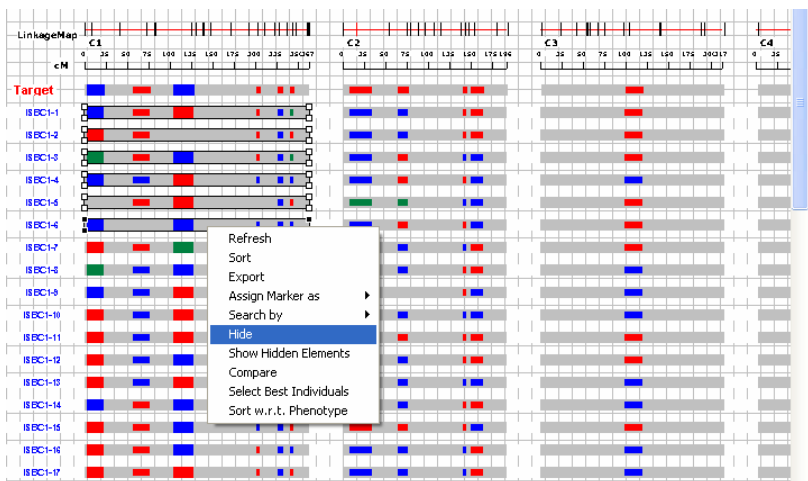


Fig 7.2.1 Hiding heat maps on Graphical View

A click on **Hide** action will hide the selected heat maps on Graphical View as shown in fig 7.2.2.

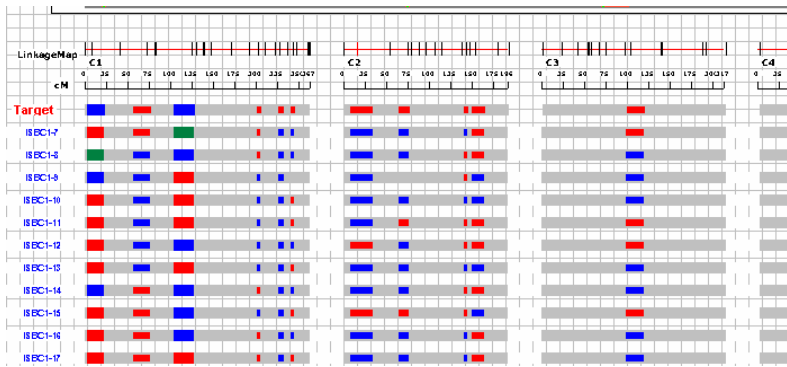


Fig 7.2.2 Graphical View with Hidden heat maps

7.2.2 Show Hidden Elements

In order to view the hidden elements, Right click on the **Graphical View** and select **Show Hidden Elements**.

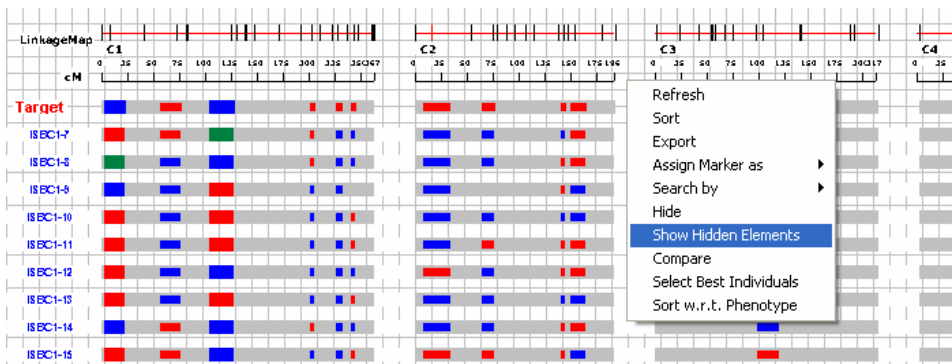


Fig 7.2.3 Un hiding heat maps on Graphical View

A click on Show Hidden Elements will opens a show Hidden Elements window as shown in the fig. 7.2.4

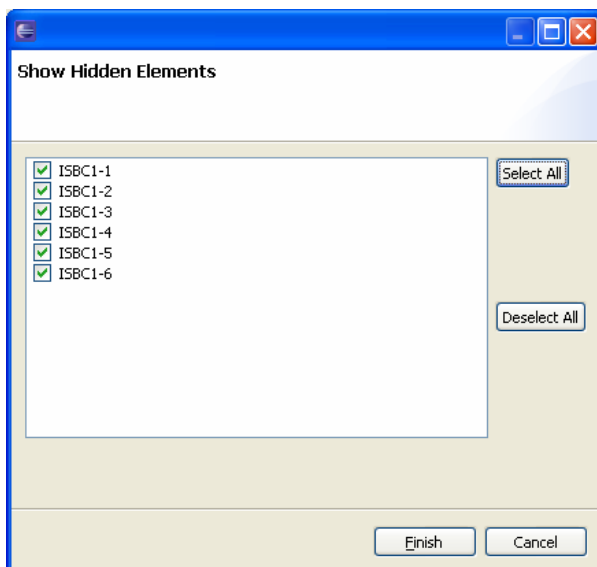


Fig 7.2.4 Show Hidden Elements window

Click on **Select All** to select all the Accessions in the window. Click on **Deselect All** to deselect all the Accessions in the window. Select the required Accessions and click on **Finish**. A click on **Finish** button will unhide the hidden Accessions on the Graphical View.

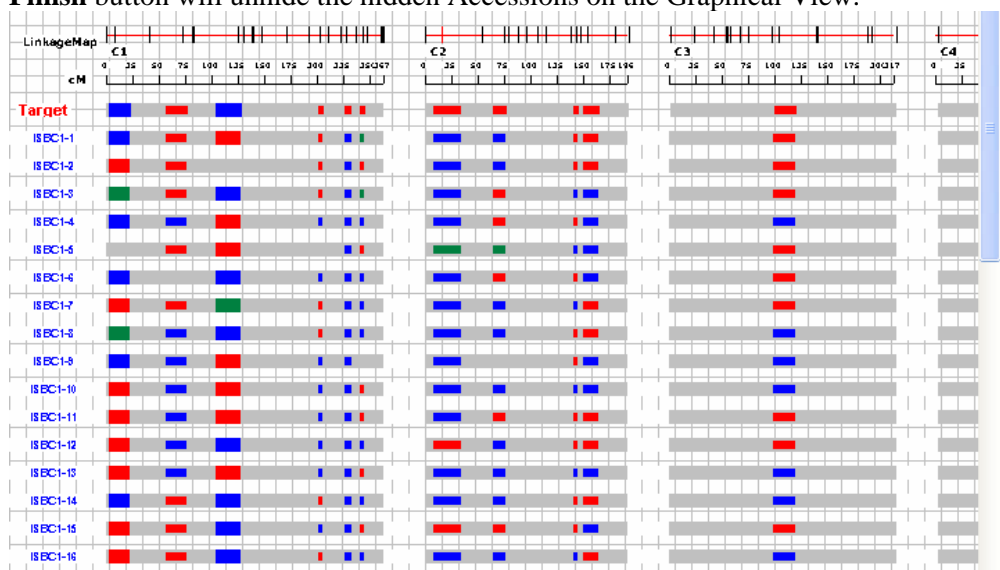


Fig 7.2.5 Graphical View with all accessions

7.2.3 Compare

To compare the heat maps on Graphical view, select the appropriate Accessions, Right click on Graphical View and select **Compare**.

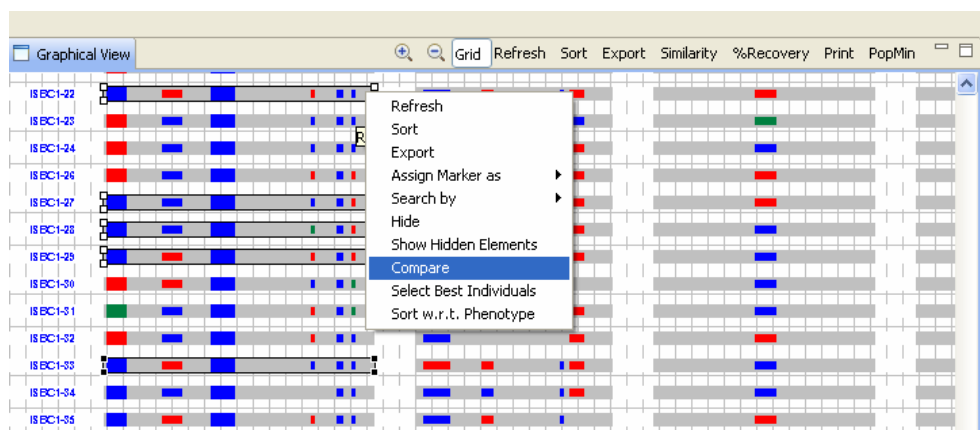


Fig 7.2.6 Comparing the selected Accessions

As the Compare action is chosen, the selected Accessions will remain on Graphical View and other Accessions are hidden.

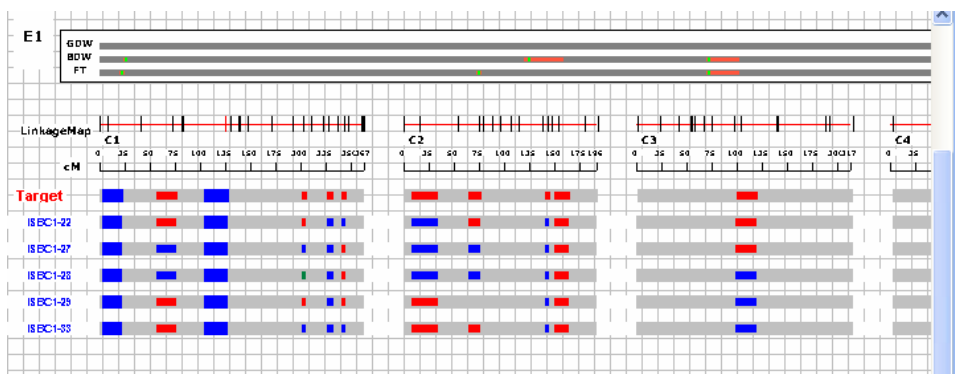


Fig 7.2.7 The selected Accessions on Graphical view

7.2.4 Percentage of Recovery

Percentage of Recovery will give you, how much the Recurrent parent genome is recovered during back crossing program. To view the Percentage of Recovery, click on

%Recovery. A click on it will display the percentage of recovery dialogue.

Percentage of Recovery			
Individuals	% Rec	% Rec mis	
ISBC1-40	25.0	44.0	0 T and 11 Geno are Missing
ISBC1-42	50.0	53.0	0 T and 1 Geno are Missing
ISBC1-41	50.0	50.0	0 T and 0 Geno are Missing
ISBC1-44	50.0	53.0	0 T and 1 Geno are Missing
ISBC1-43	31.0	33.0	0 T and 2 Geno are Missing
ISBC1-46	43.0	50.0	0 T and 2 Geno are Missing
ISBC1-45	56.0	56.0	0 T and 0 Geno are Missing
ISBC1-48	62.0	66.0	0 T and 3 Geno are Missing
ISBC1-47	25.0	25.0	0 T and 1 Geno are Missing
ISBC1-49	31.0	31.0	0 T and 0 Geno are Missing
ISBC1-12	50.0	53.0	0 T and 1 Geno are Missing
ISBC1-13	25.0	25.0	0 T and 0 Geno are Missing
ISBC1-14	50.0	50.0	0 T and 0 Geno are Missing
ISBC1-15	50.0	50.0	0 T and 0 Geno are Missing
ISBC1-16	43.0	43.0	0 T and 0 Geno are Missing
ISBC1-17	43.0	46.0	0 T and 1 Geno are Missing
ISBC1-18	43.0	46.0	0 T and 2 Geno are Missing
ISBC1-19	37.0	37.0	0 T and 0 Geno are Missing
ISBC1-6	50.0	53.0	0 T and 2 Geno are Missing
ISBC1-5	31.0	33.0	0 T and 2 Geno are Missing
ISBC1-4	18.0	18.0	0 T and 0 Geno are Missing
ISBC1-3	56.0	56.0	0 T and 1 Geno are Missing
ISBC1-2	68.0	73.0	0 T and 5 Geno are Missing

Fig 7.2.8 Percentage of Recovery dialog

7.2.5 Search by Accessions

In order to search the appropriate Accessions/ Heat Maps on the Graphical View, Right click on the **Graphical View** and select **Search by Accessions**.



Fig 7.2.9 Searching Accessions on Graphical View

A click on **Search by Accessions** will opens a Search Accessions window as shown in the fig. 7.2.10. Select the list of Accessions using Ctrl/Shift key and click on **OK**.

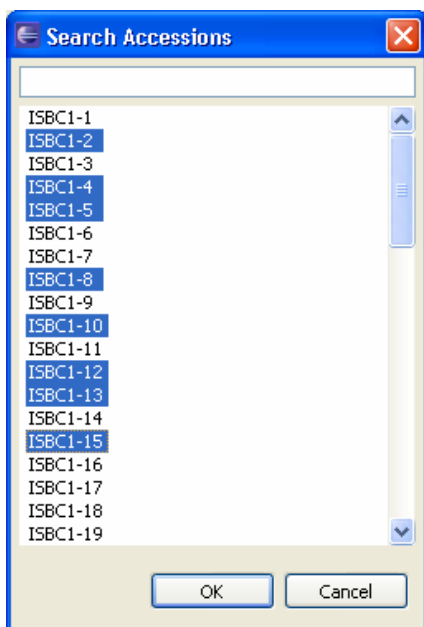


Fig 7.2.10 Searching Accessions Dialog

A click on OK button will select those accessions on the Graphical View.

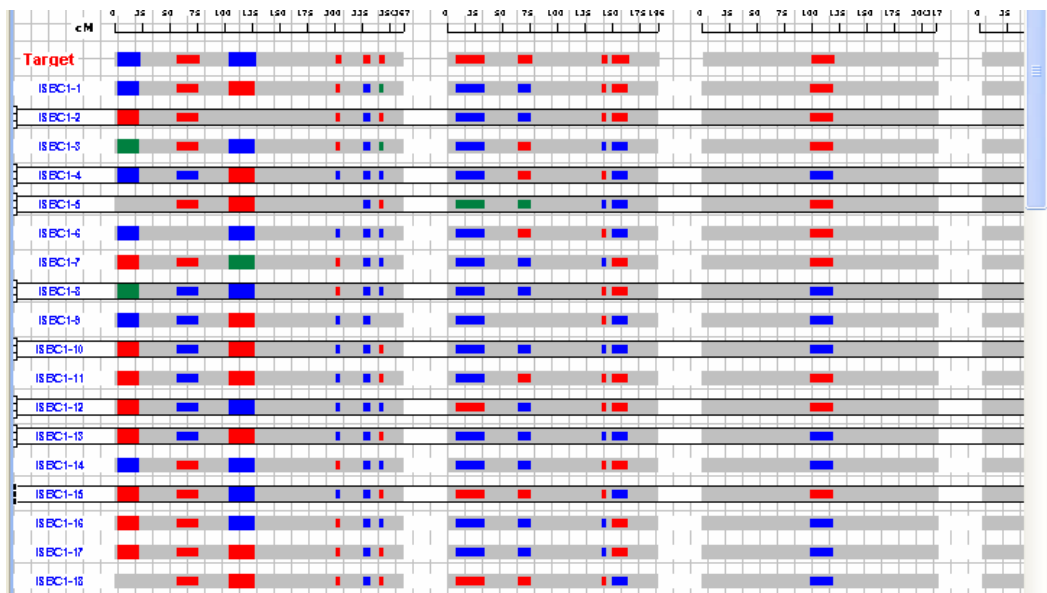


Fig 7.2.11 Highlighting the Accessions

7.2.7 Search by Markers

In order to search the appropriate Markers on the linkage map, Right click on the **Graphical View** and select **Search by Markers**.

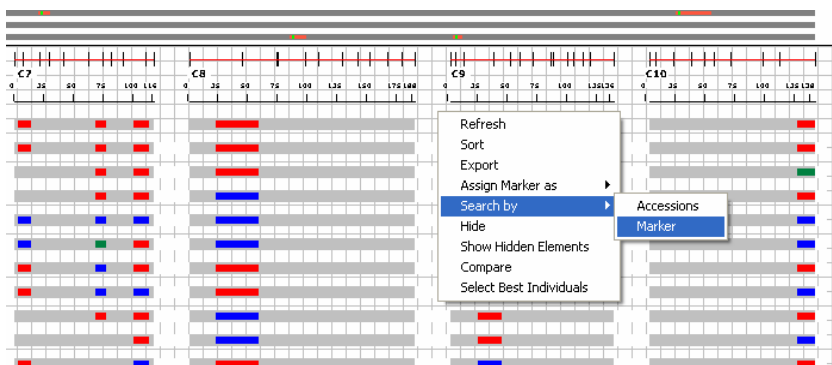


Fig 7.2.12 Searching Marker on Linkage map in Graphical View

A click on **Search by Markers** will opens a Search Markers window as shown in the fig. 7.2.10. Select the marker from the list and click on **OK**.

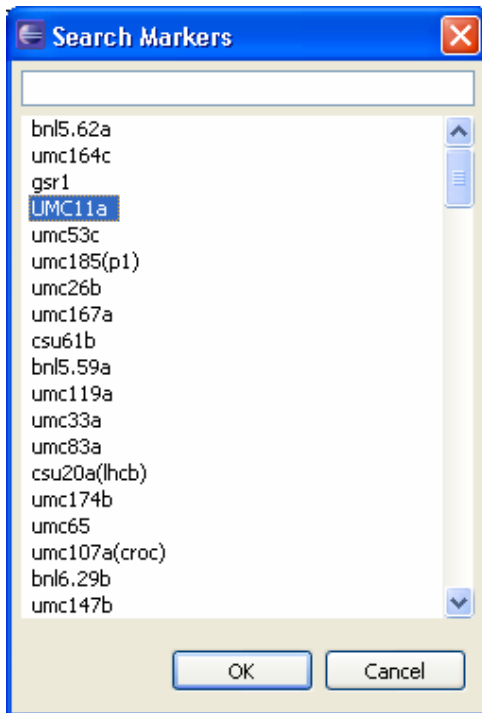


Fig 7.2.13 Search Markers Dialog

A click on OK button will select that Marker on the Linkage map as shown in the Fig 7.2.14.

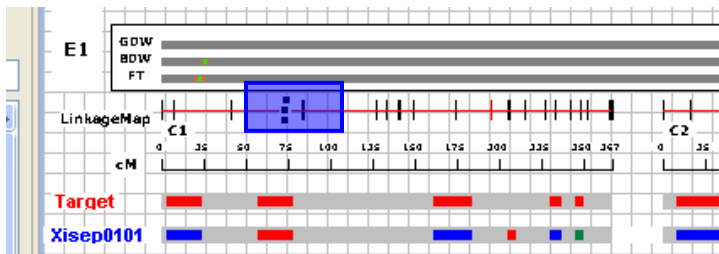


Fig 7.2.14 High lightening the Marker

7.2.7 Selection of Best Individuals

In order to select the best individuals, Right click on the **Graphical View** and click on **Select Best Individuals**.



Fig 7.2.15 Selection of Best Individuals

It will open a window with list of Foreground markers along with their count (i.e. number of appearances of target allele under that marker) as shown in the fig. 7.2.16. To include missing values select the ☒ Missing option. Select the markers of interest from the list. After selecting the foreground markers, the number of common individuals will get updated with respect to data set. By default the number of best individuals will be same as common individuals, if the count is higher, then you can choose the limited numbers and click on **Finish**.

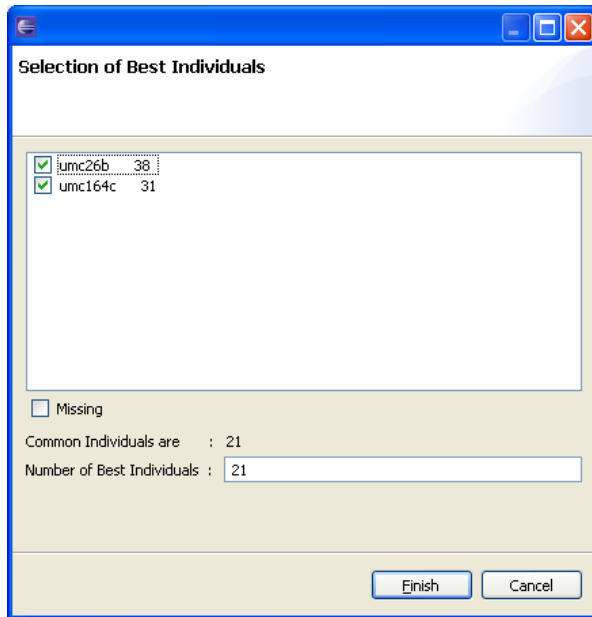


Fig 7.2.16 Selection of Best individuals

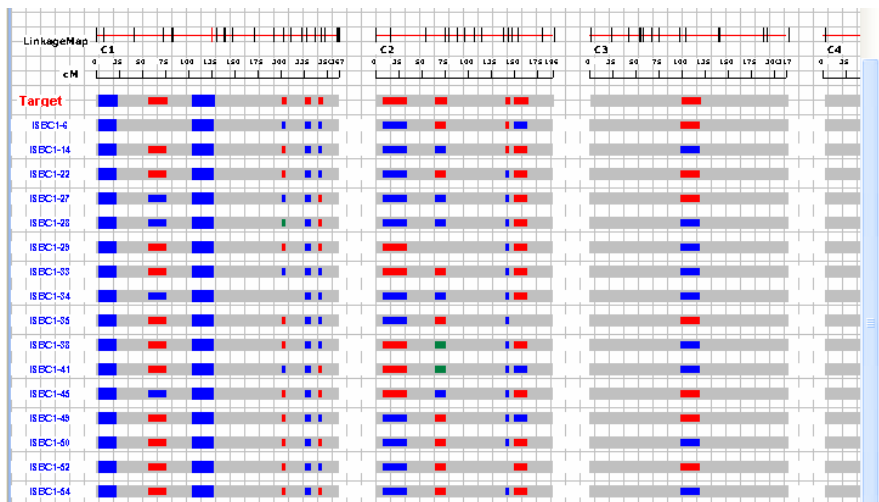


Fig 7.2.17 Selection of Best individuals

SVN Checkout from CropForge

For checkout (import) the source code use the following link
<https://svn.cropforge.org/svn/ismab>