GenoTypeMapper v.1.1

A quick start tutorial

Forword

We hope that this software will be useful for you and your work. In case of any questions, just visit our website www.GenoTypeMapper.org and contact us.

Sincerely,

Mathieu D.

0. Input data

Input data can be loaded in form of a GTM-specific tab delimited text file with at least nine columns (Table 1). The first two columns contain chromosome- and marker names; the third and fourth column contain physical and/or genetic positions of the markers. This information has to be specified for the usage of GTM. Column five can contain LOD-value information; column six and seven are dedicated to genotype information from the parents of a typical bi- parental population. Recurrent parents and individuals, which were used for the establishment of NILs, can be specified in the eighth and ninth column. Genotypic data of the remaining accessions can be added to the tenth and following columns. GTMs input file has a minimum of nine columns (Table 1). Column three, four and five might remain empty. However, genetic or physical positions should be specified Missing genotypic information in column six, seven, eight and nine has to be indicated with “NA”. Please note that appropriate template files are provided on www.genotypemapper.org.

Table 1: Standard input data for GTM

Chr.	**Marker**	*Genetic position*	*Physical position*	*LOD*	*A**	*B**	*C***	*x****
1A	**SNP_1**	*0.00*	*12000*	*0.3*	*A*	*T*	*A*	*A*

* Obligatory information that should be provided to the program are written in bold, additional information in italics. The different number of parents that might be used for different purposes in the analysis are also explained in Figure 1.
Note: *) parents of a bi- parental population, like DH, F_2, RILs or single parent information of NILs, **) recurrent
parent that was used to develop a near isogenic line via a three-way cross. ***) individual that was used for a crossing of the parent with the recurrent parent.

Testset_3_4_parents_no1 - Editor

Datei Bearbeiten Format Ansicht ?

Chr	Marker_ID	cM	Bp		Gitit58-E09		LDN55-box02		Uzan78	RIL55	NIL-B-2B-
1A	BS00033749_51	1.7	219507		G	A	failed	A	failed		
1A	wsnp_Ku_c1818_3557408	2.8	3072771			C	T	T	T	T	
1A	tplb0025b13_1721	2.6	3074438			G	G	G	G	G	
1A	tplb0025b13_2054	2.8	3075137			C	T	T	T	T	
1A	Kukri_c7192_1128	2.6	3080185			C	C	C	C	C	
1A	IACX2941	4.6	4242873		G	G	G	G	G		
1A	CAP12_c3074_192	4.1	4258443		A	G	G	G	G		
1A	BS00023130_51	4.1	5610497		T	G	G	G	G		
1A	Ku_c28007_1398		6123844		A	A	failed	failed	failed		
1A	Kukri_rep_c102231_265	2.6	6537879			T	T	T	T	T	
1A	wsnp_Ex_c2868_5293485	5.1	6540773			A	G	G	G	G	
1A	BS00073243_51		6619819		T	T	T	T	T		
1A	BS00056550_51	5.2	6621719		G	A	A	A	A		
1A	BS00023201_51	6.7	6918848		G	A	A	A	A		
1A	wsnp_CAP11_c710_458019		6939263			C	C	C	C	C	
1A	wsnp_Ex_c57982_59470152	6.6	7331826			A	A	A	A	A	
1A	wsnp_Ex_rep_c106111_90308719	6.6	7477864				T	T	T	T	T
1A	Excalibur_c71158_54	6.6	7600384			A	A	A	A	A	
1A	Excalibur_c82557_201	8.4	8194521			C	C	A	C	A	

Screenshot of an input file with genetic, physical position and genotypic data.

Testset_5 - Editor

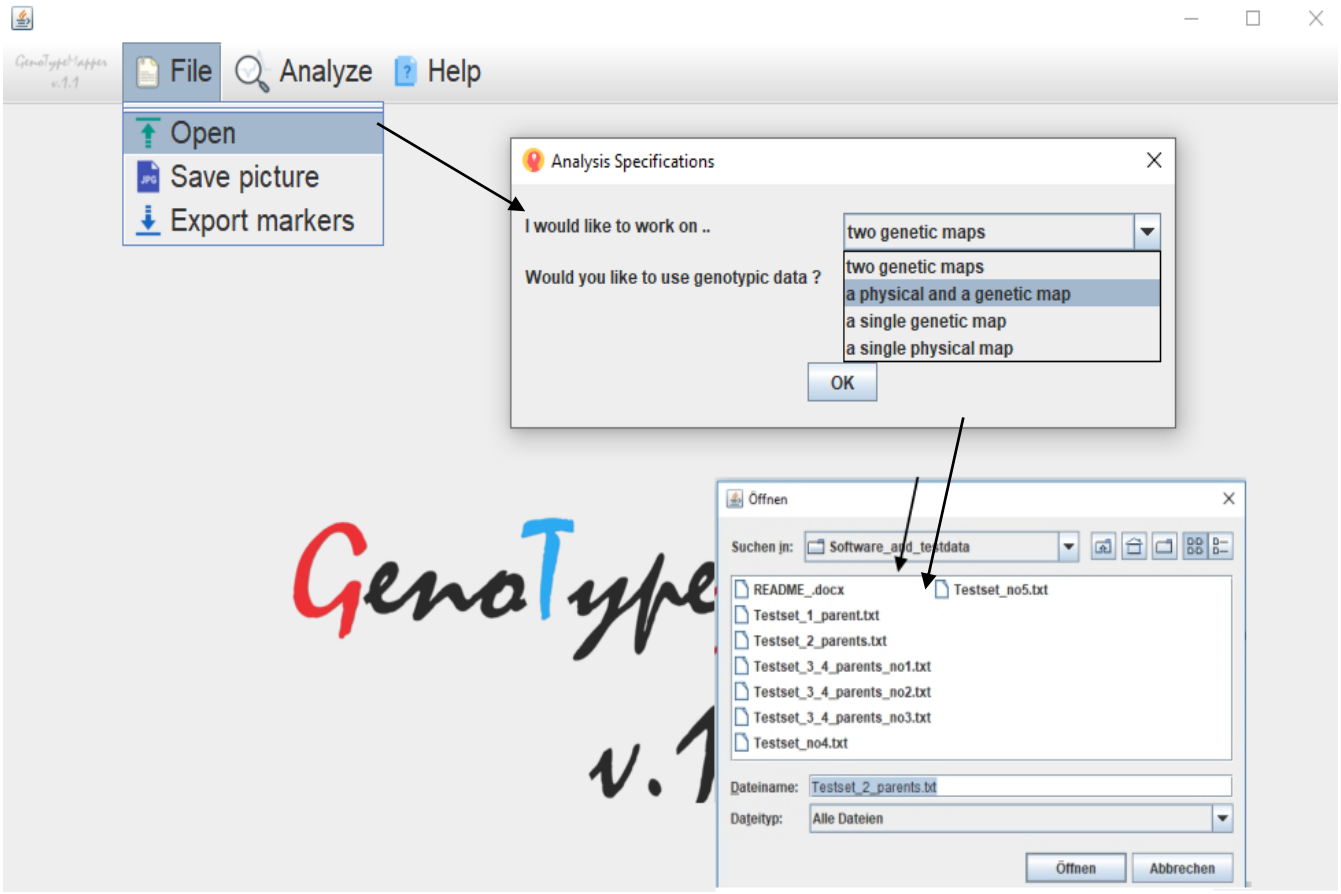
Datei Bearbeiten Format Ansicht ?

Chr	Marker_ID	cM	Bp		A	B	C	D	
1A	BS00033749_51		219507		NA	NA	NA	NA	
1A	wsnp_Ku_c1818_3557408			3072771		NA	NA	NA	NA
1A	tplb0025b13_1721			3074438		NA	NA	NA	NA
1A	tplb0025b13_2054			3075137		NA	NA	NA	NA
1A	Kukri_c7192_1128			3080185		NA	NA	NA	NA
1A	IACX2941		4242873		NA	NA	NA	NA	
1A	CAP12_c3074_192		4258443		NA	NA	NA	NA	
1A	BS00023130_51		5610497		NA	NA	NA	NA	
1A	Ku_c28007_1398		6123844		NA	NA	NA	NA	
1A	Kukri_rep_c102231_265			6537879		NA	NA	NA	NA
1A	wsnp_Ex_c2868_5293485			6540773		NA	NA	NA	NA

Example of an inputfile that harbors only physical positions and no genotypic data

1. Load data

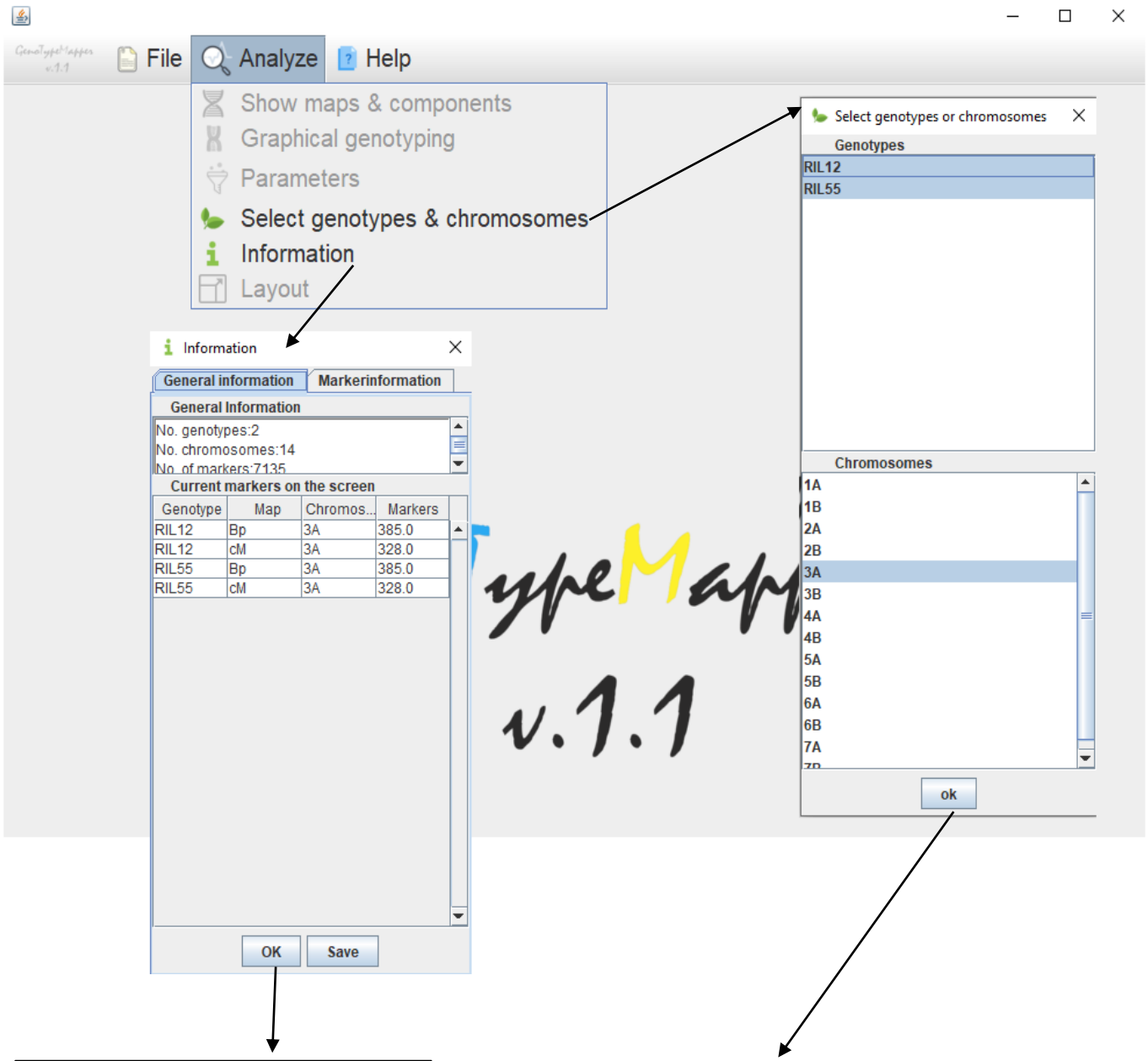
Click on "*File*" and select the item "*open*". Then choose the type of analysis that you would like to perform. Upload your input data. It should also be taken into account, that GTM offers the possibility to analyze a single genetic or physical map. Besides this, two genetic maps can be compared. Different template files are provided on www.genotypemapper.org.



Your "*analysis specifica*tions" will change the options that are enabled or disabled during your analysis.

2. Analysis

After loading the data, the "*Select genotypes and chromosomes"* and "*information"* menuItem in the "*Analyze-menue"* are enabled. Select the genotypes and chromosomes of interest and click on OK. The "*informations"* panel gives a brief overview about the genotypes/ markers that are uploaded and/ or are currently selected.



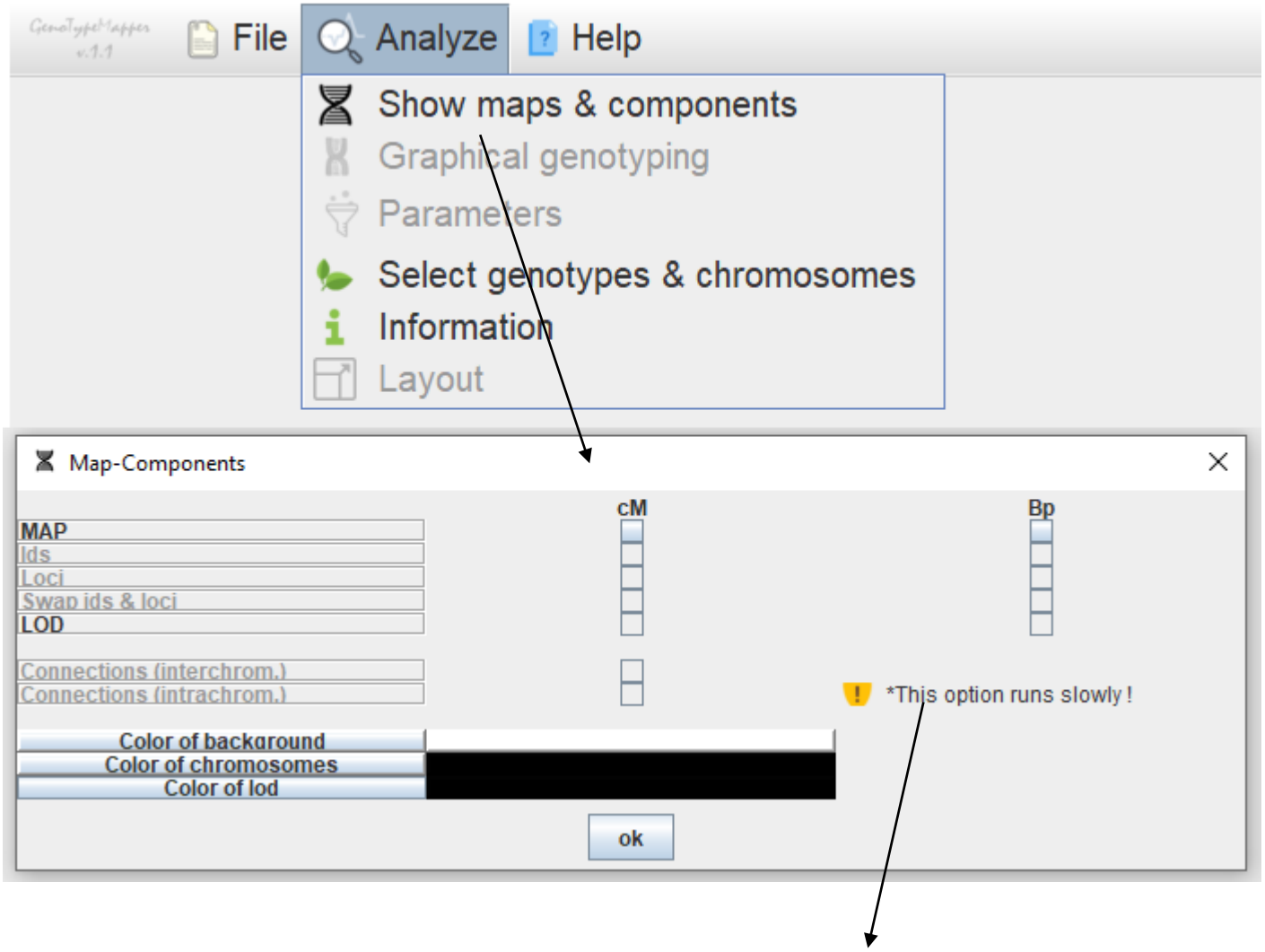
We plan to establish an information panel with a wider range of information in the future.

You can either select:

a. >1 genotypes and >1
or
b. 1 genotype and 1 chromosome.

For option a) the illustration of markers and markers name is enabled, for option b) not. More detailed information are explored in the next chapter.

After selection of genotypes and chromosomes the *" Show maps & components"* item will be enabled. Choose the map(s) that you would like to analyse. If both maps are selected, interchromosomal and intrachromosomal connections can be displayed. Besides this, the color of the background, the chromosomes and Lod-values can be modified. Please note that IDs and Loci can be displayed if a single chromosome and single genotype were selected for the analysis.



The detection of intrachromosomal connection is time- intensive. We therefore suggest to perform this step at the very end of your analysis.

The two examples on the next page illustrate, which kind of analysis can be performed with this menue panel..

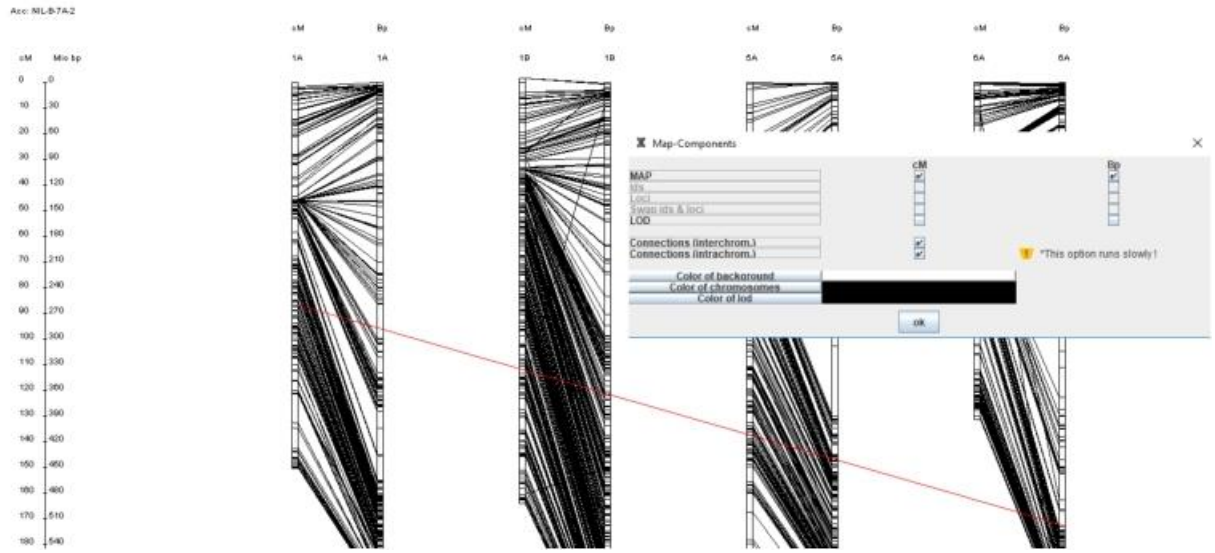


Figure 1: This figure illustrates the comparisson of a genetic and of a physical map. A single genotype and more than one chromosome were analyzed, inter- and intrachromosomal connections are shown.

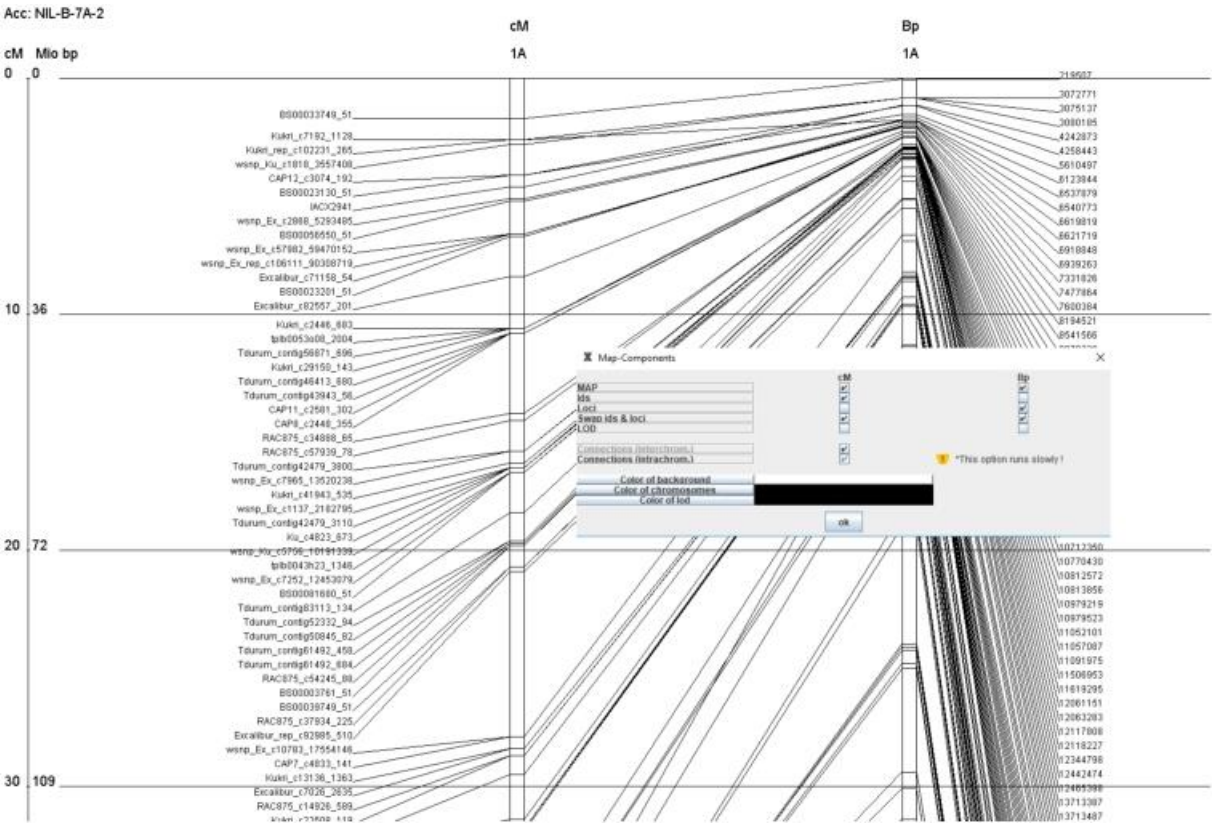
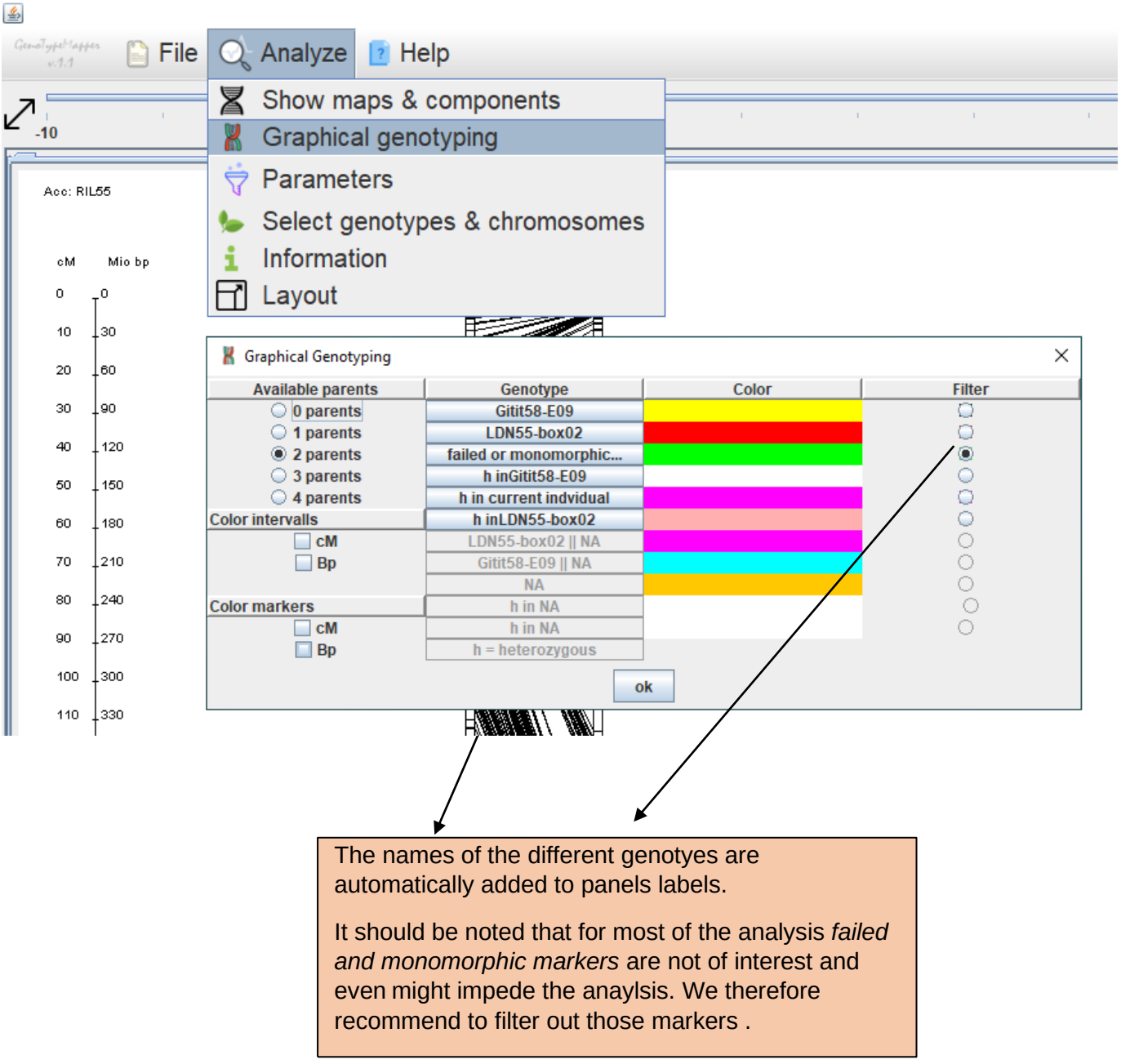


Figure 2 : This figure illustrates the comparisson of a genetic and of a physical map. A single genotype and single chromosome were analyzed, inter- and intrachromosomal connections are shown. The illustration of marker and loci names is enabled.

The “*Parameters”* menue can be used to improve your illustration (e.g. to enlarge the font size or to increase the chromosomes width). The “*Layout”* menue allows you to modify the imagesize of your illustration. We did not further explore these menues here, because they are easy to handle and self explaining.
The *“Graphical Genotyping”* item allows to color different allels of the genotypes according to different criteria. *Please read our article (link) to understand the idea and theoretical bakckground of this panel.*



The names of the different genotyes are automatically added to panels labels.

It should be noted that for most of the analysis *failed and monomorphic markers* are not of interest and even might impede the anaylsis. We therefore recommend to filter out those markers .

The two examples on the next page illustrate, which kind of analysis can be performed with the help of this panel.

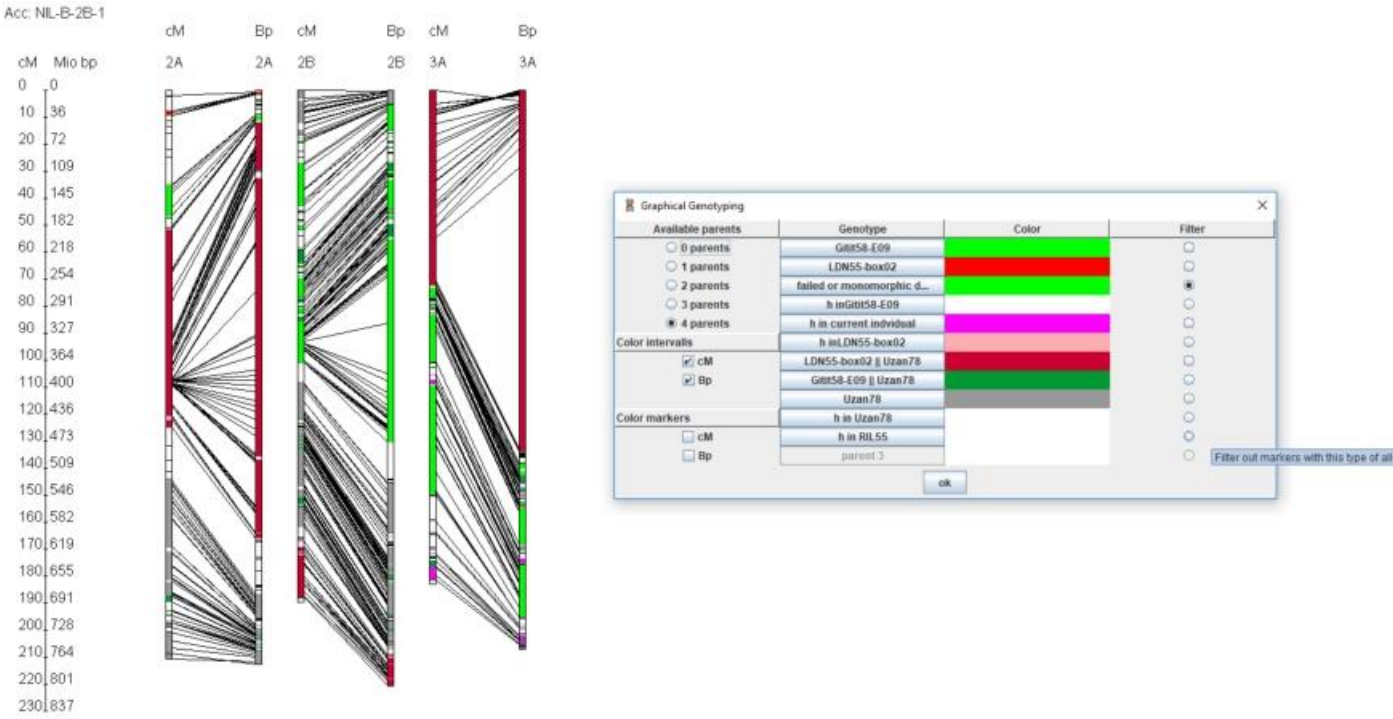


Figure 3: Comparisson of different allelic regions in a genetic and physical map of the genotype NIL- B-2B-1. Four parents were available and interval coloring was selected. As recommended previously, monomorphic markers or markers with failed genotypic data were filtered out.

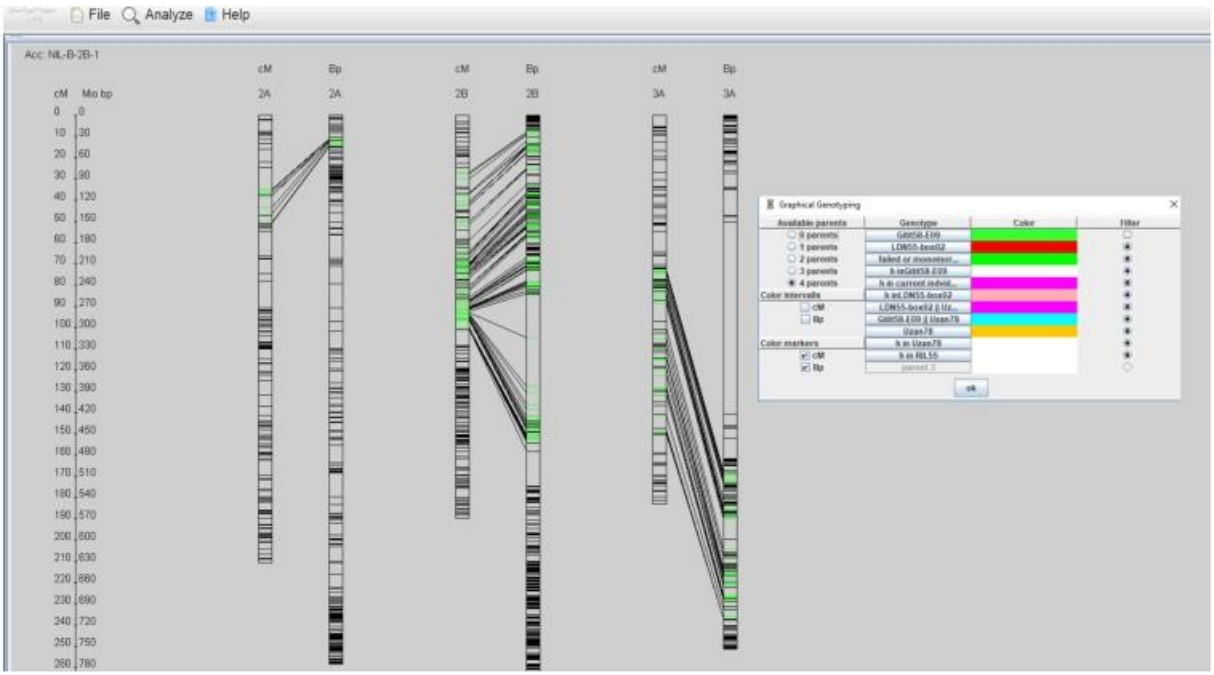


Figure 4: Comparisson of different allelic regions in a genetic and physical map of the genotype NIL- B-2B-1. Four parents were available and marker coloring was selected. Beside this, only markers, genetic regions from a specfici genotype were highlighted.