FastMapping User Guide

Software components:

1. FastMapping executable (the software): fast_mapping.exe
2. Data file: marker file in loc format
3. Matrix file: matrix.txt

;-	A	B	C	D	H	
0	0	0	0	0	0	;-
0	0	4	3	1	2	;A
0	4	0	1	3	2	;B
0	3	1	0	1	0	;C
0	1	3	1	0	0	;D
0	2	2	0	0	0	;H

4. Parameter file: mapping_parameters.txt

matrix file = "matrix.txt"	Name of matrix file the software read
chromosomes = 12	Number of predicted groups (chromosomes)
LOD for core grouping = 16	Higher LOD for grouping (Core definer)
minimum LOD for grouping = 4	Lower LOD for grouping (Lower threshold)
missing value screening ratio = 0.4	proportion (1-0) of missing value to exclude marker
1 : 1 segregation chi_square threshold value = 1000	*Chi square test for distortion from 1:1 segregation (for BC population)
1 : 2 : 1 segregation chi_square threshold value = 50	*Chi square test for distortion from 1:2:1 segregation (for F2 population, co-dominant)
1 : 3 segregation chi_square threshold value = 50	*Chi square test for distortion from 1:3 segregation (for F2 population, dominant)
order plants = 0	on and off the individual ordering

* - The higher the number, the higher the stringency level needed to exclude a marker. Value of 1000 disables this function -.

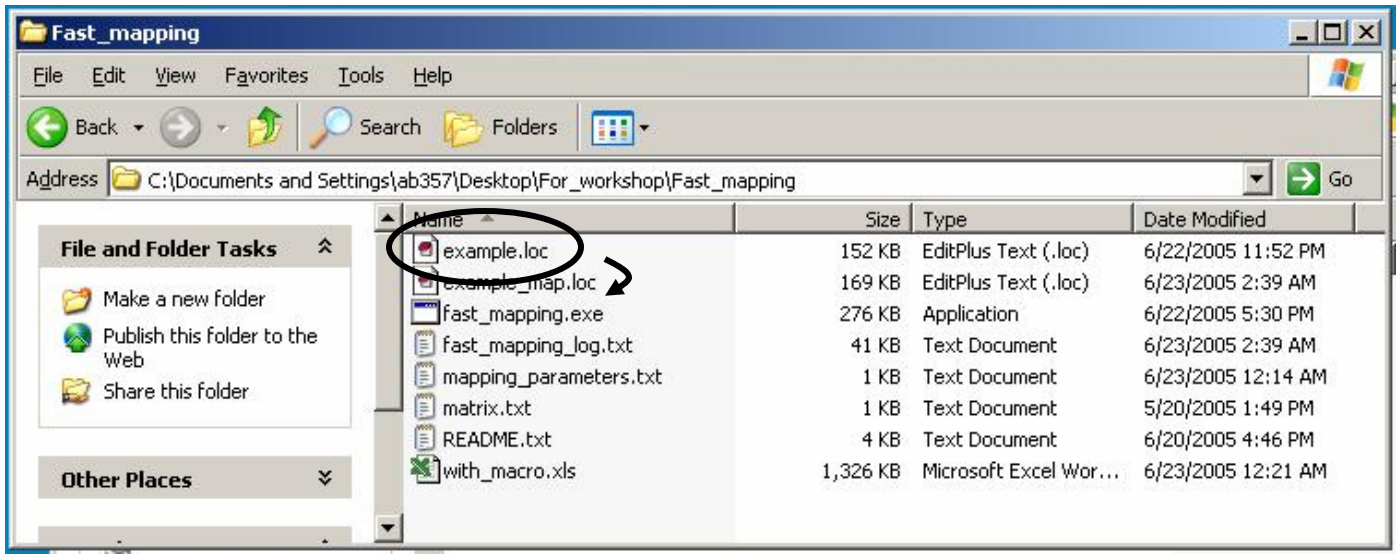
5. Color coded Excel: Excel file with macro for color coding the result file with_macro.xls

Tutorial for using the FastMapping software

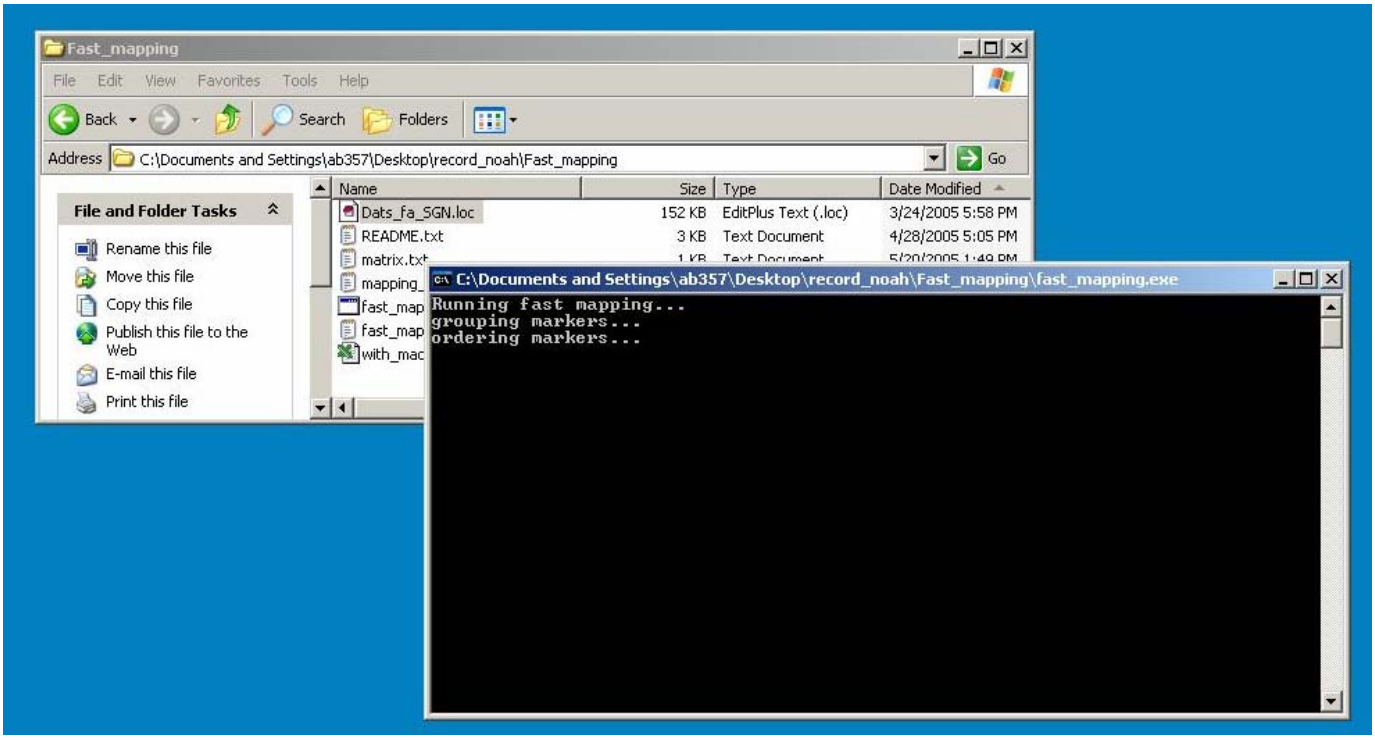
1. Set parameters in “parameter file”

matrix file = "matrix.txt"	
chromosomes = 12	Expected number of core groups
LOD for core grouping = 16	Set Higher LOD for grouping
minimum LOD for grouping = 4	Set lower LOD for grouping (lower threshold)
missing value screening ratio = 0.4	% of missing value to exclude marker
1: 1 segregation chi_square threshold value = 1000	Chi square test
1 : 2 : 1 segregation chi_square threshold value = 50	Chi square test
1 : 3 segregation chi_square threshold value = 50	Chi square test
order plants = 0	Should be 0 for disabling individuals ordering (ordering whole genome) Should be 1 for enabling individuals ordering

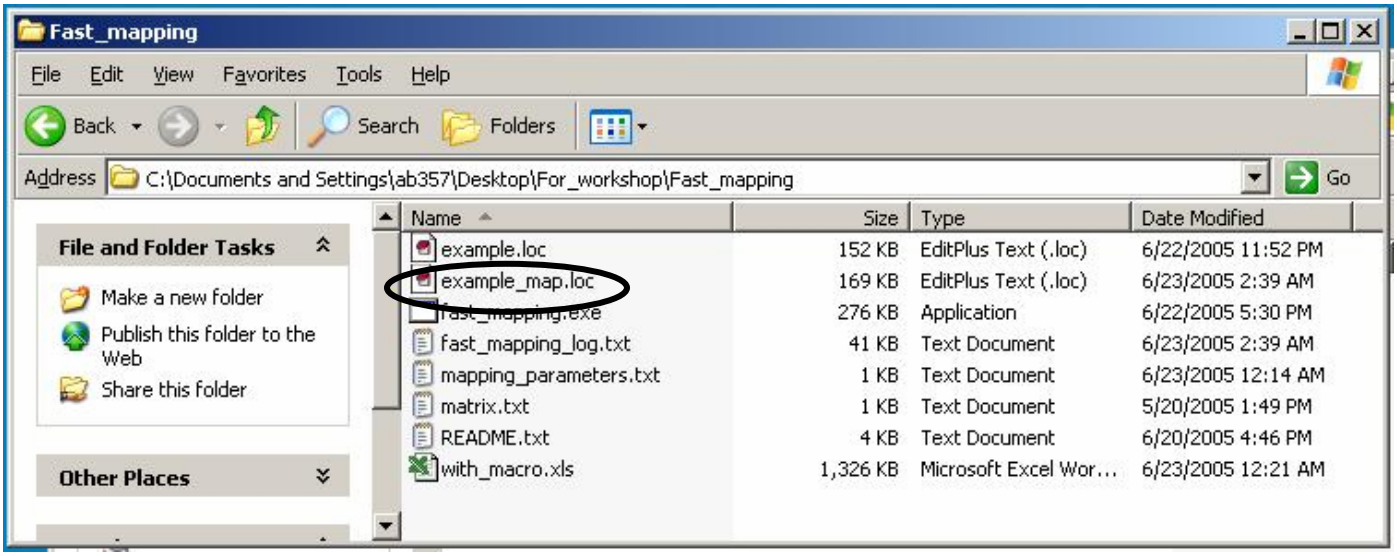
2. Drag the **loc file** onto the executable file: fast_mapping.exe



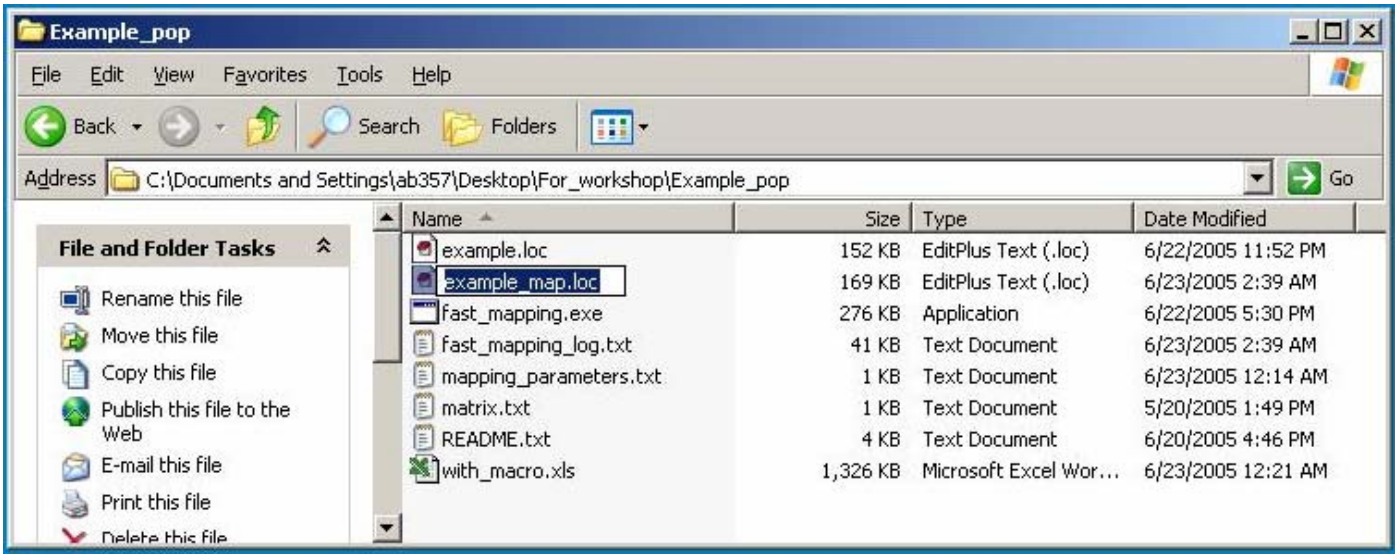
3. A black screen will appear while the program is running - Few seconds



4. A result file will be creating with a name similar to the loc file, with addition map to the name (_map.loc).

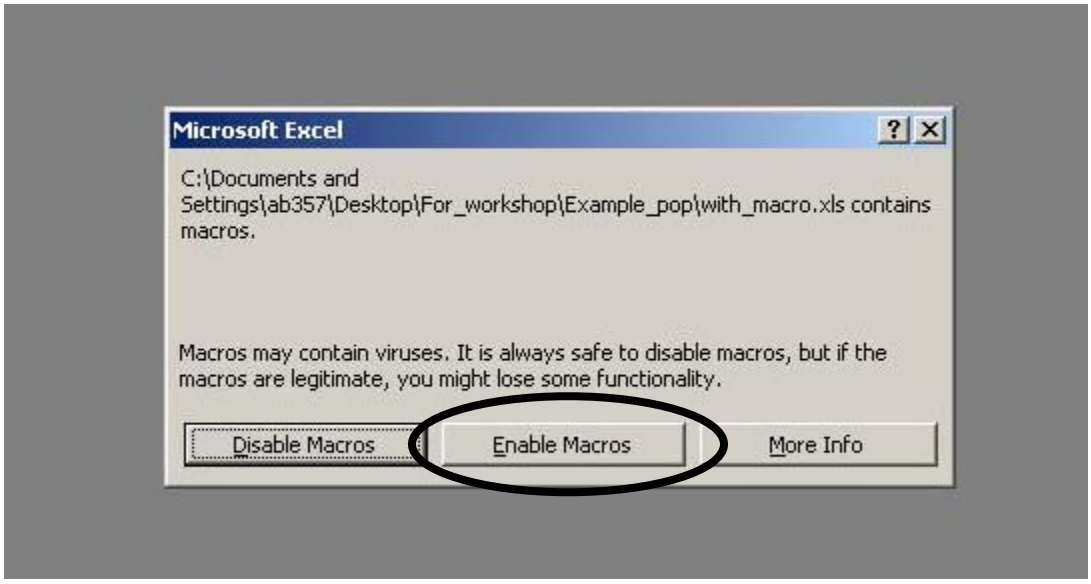


5. Copy the file name

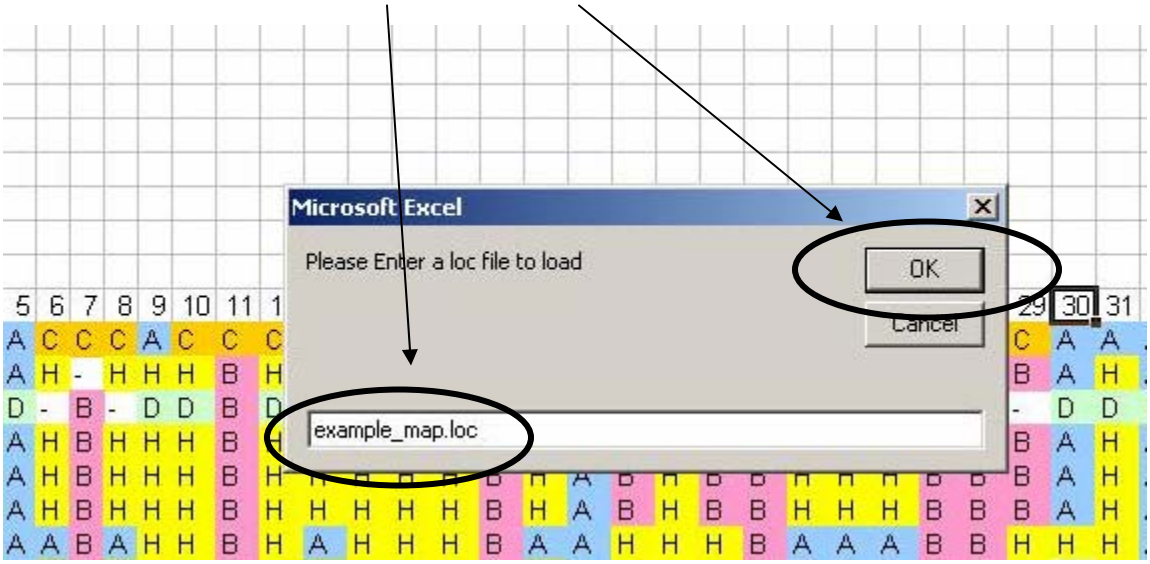


6. Open the Excel "with macro" file (the name of the file can be changed)

- A dialog box may open asking if you want to enable macros. Click the "Enable Macros" button.

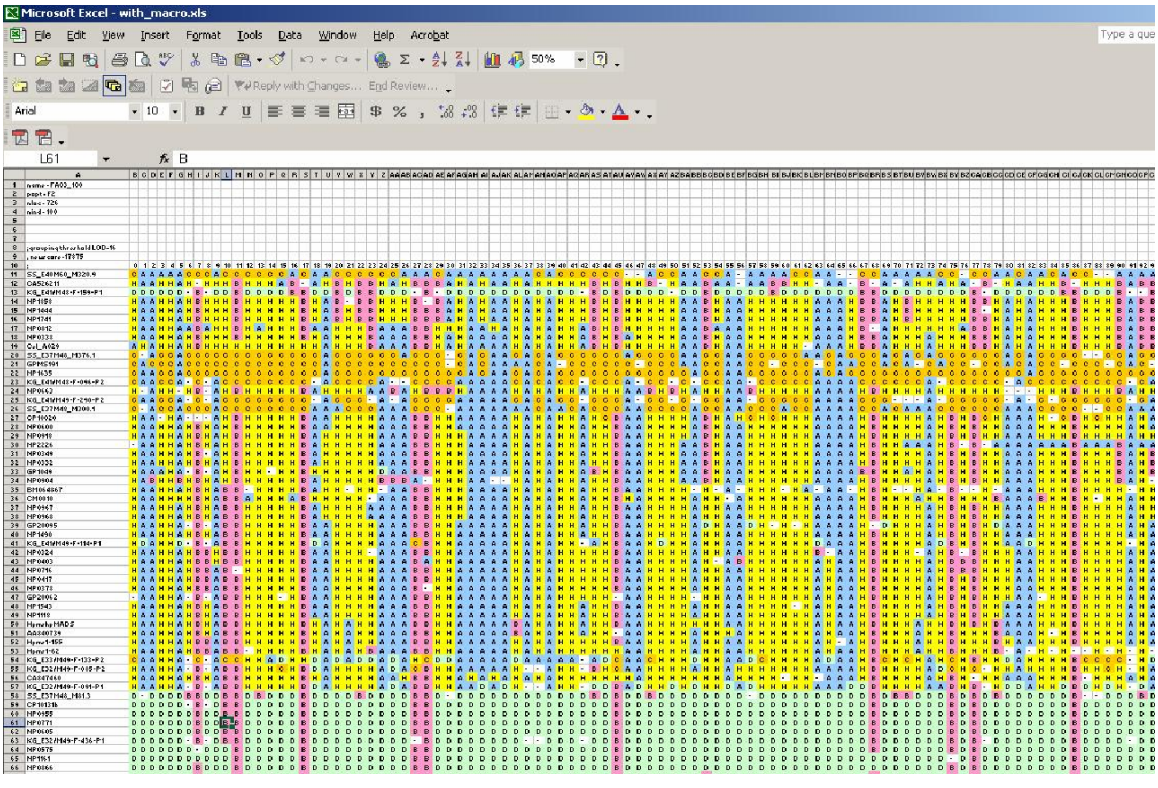


7. Load the file by running the macro
- Press "Alt F8" a dialog box will open
- Paste the result file name and click OK



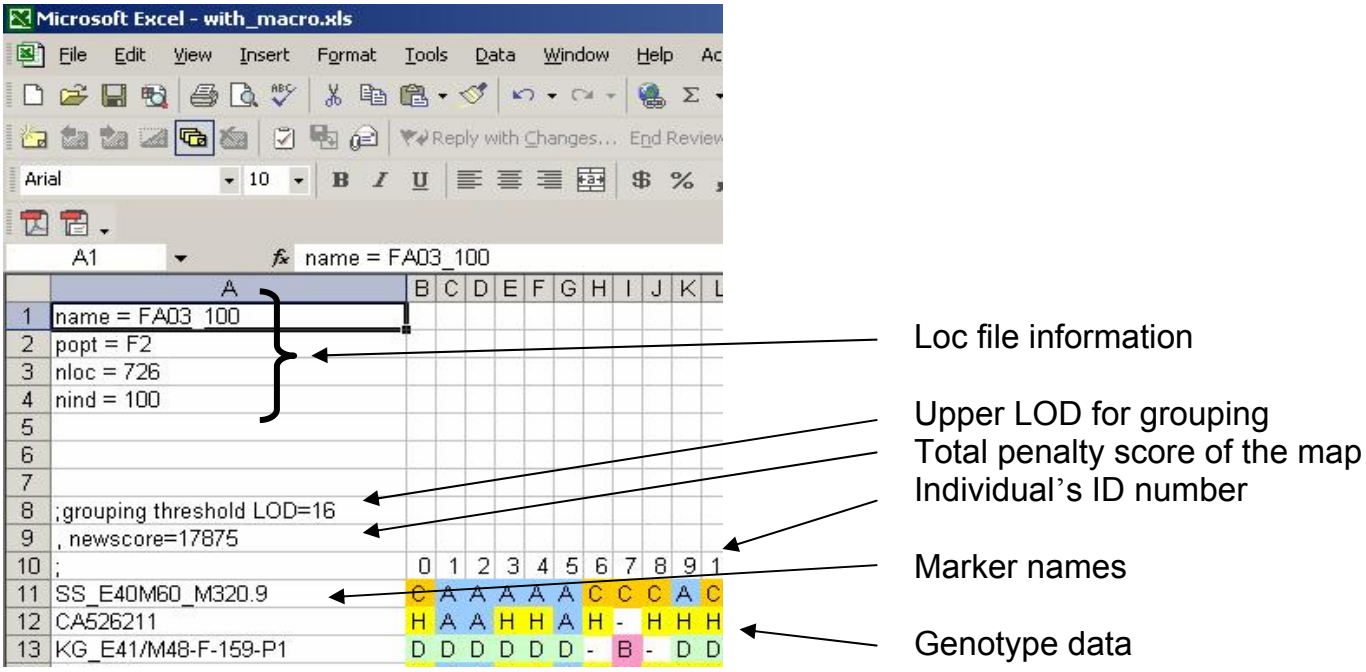
- The file will load – it can take few seconds

8. The Result file is opened in color-coded format.

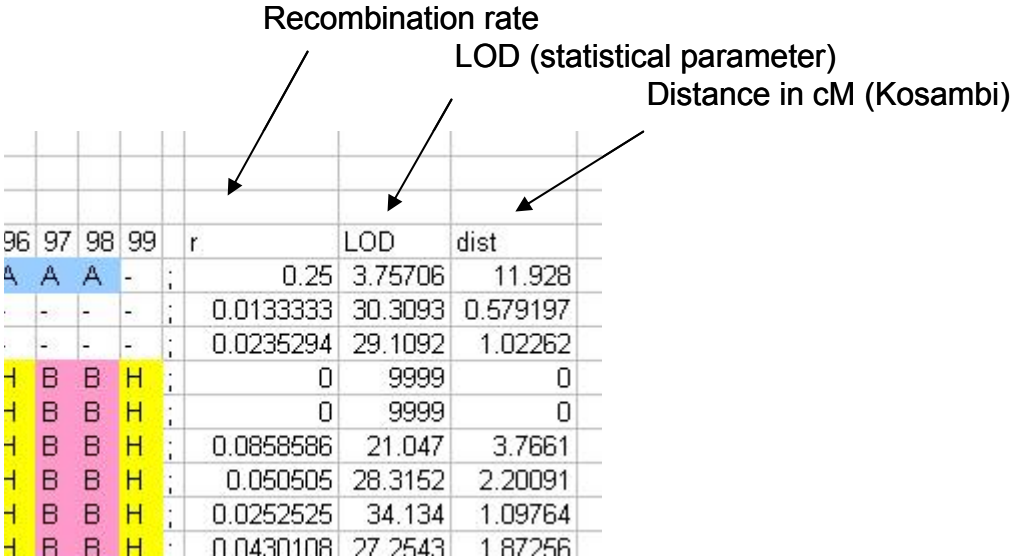


A view on the result file

1. Headers



2. Map distance information



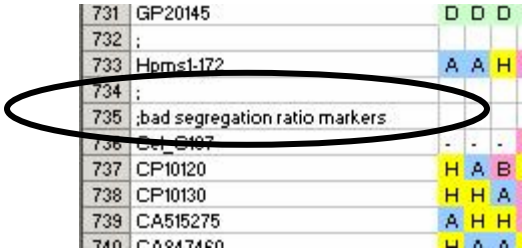
3. Gaps between linkage groups



87	Hpms1-148	D	D	D	D	B	D	D	B	B	B	D	D	-	D	D	D	D
88	NP1531	D	D	D	D	B	D	D	D	D	B	D	D	D	B	D	B	D
89	NP1009	H	H	H	H	B	H	A	H	B	B	H	H	B	H	H	B	H
90	;																	
91	SS_E36M60_M404.9	C	C	-	-	A	C	A	A	C	A	-	A	A	-	A	A	C
92	SS_E37M60_M68.0	C	A	A	A	C	C	A	A	A	C	A	A	A	A	A	C	A
93	SS_E37M54_M181.9	C	C	C	A	C	C	C	A	C	A	A	A	C	A	A	C	C
94	SS_E40M60_M117.5	C	C	C	A	C	C	A	A	A	C	A	A	C	A	A	C	A
95	SS_E37M60_M176.2	C	C	C	A	A	A	C	A	C	C	A	A	C	A	A	C	A

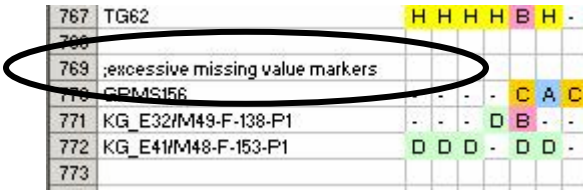
4. Excluded markers in the end of the file

- Because of distortion from mendelian segregation



731	GP20145	D	D	D
732	;			
733	Hpms1-172	A	A	H
734	;			
735	;bad segregation ratio markers			
736	Cel_C497	-	-	-
737	CP10120	H	A	B
738	CP10130	H	H	A
739	CA515275	A	H	H
740	CA847460	H	A	A

- Because of missing value

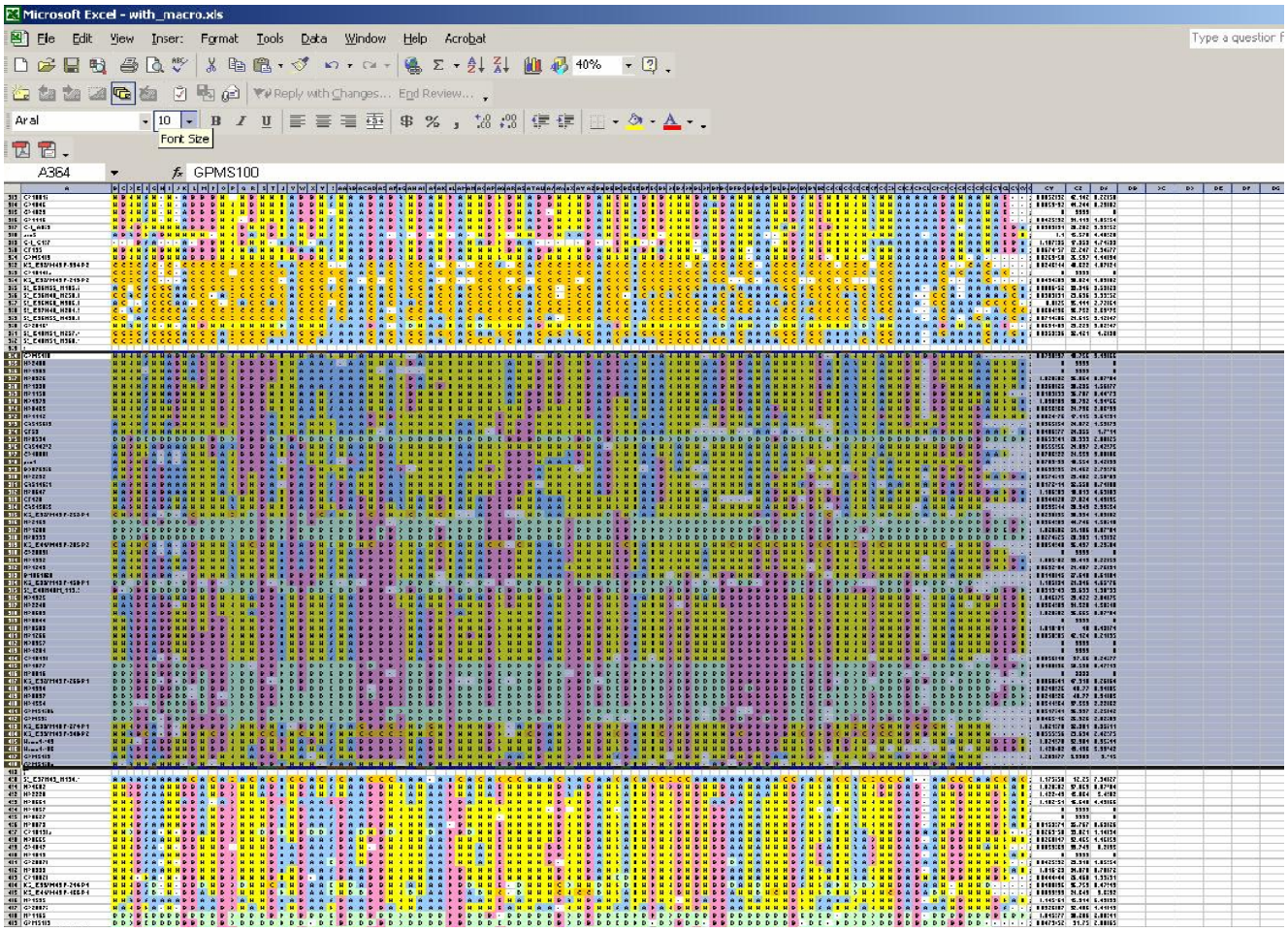


767	TG62	H	H	H	H	B	H	-
768								
769	;excessive missing value markers							
770	GPMS156	-	-	-	-	C	A	C
771	KG_E32/M49-F-138-P1	-	-	-	D	B	-	-
772	KG_E41/M48-F-153-P1	D	D	D	-	D	D	-
773								

Mapping of a single chromosome

1. Prepare a new .loc file for the desire region (With Excel)

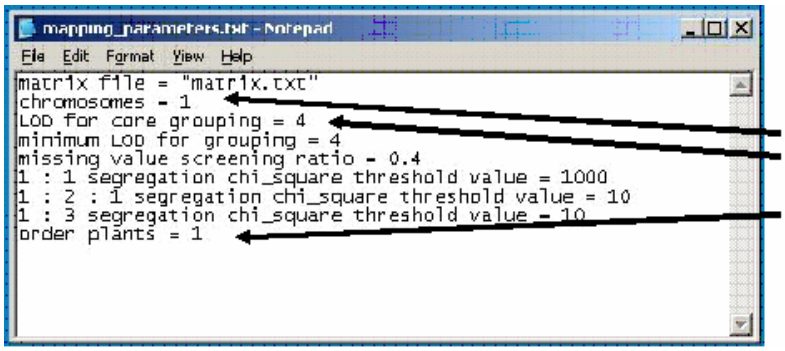
- Copy the rows from the result file of the entire population into a new Excel file



- Add the loc header to the top of the file. Make sure the number of markers (nloc) is correct

	A	B	C	D	E
1	name = FA03_100				
2	popt = F2				
3	nloc = 61				
4	nind = 100				
5					
6					

2. Change parameters in parameters file



1. Number of chromosome need to be 1
2. LOD for core grouping need to be as the minimum LOD
3. Order plant need to be 1

3. Run the mapping procedure by starting from step 2 of the "Steps in using the FastMapping software"

The result of a single chromosome mapping

- Both the markers and individuals are ordered by the FastMapping, enabling a visual review of the result

