

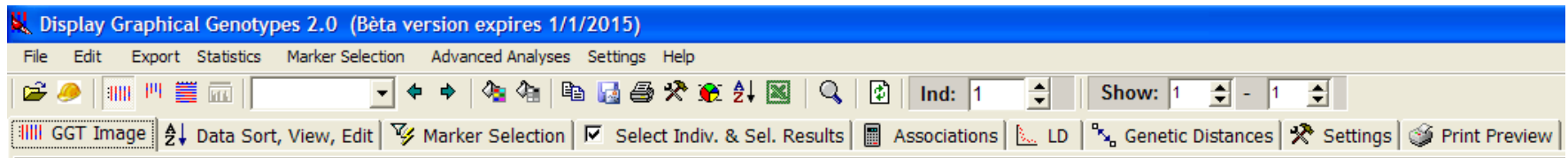
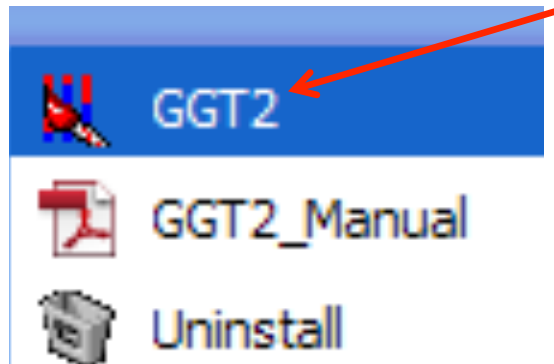
# **Estimation of LD decay using Graphical GenoTypes (GGT) 2.0 software (van Berloo 2008)**

**By**

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**Click on “GGT2” to  
start the software**



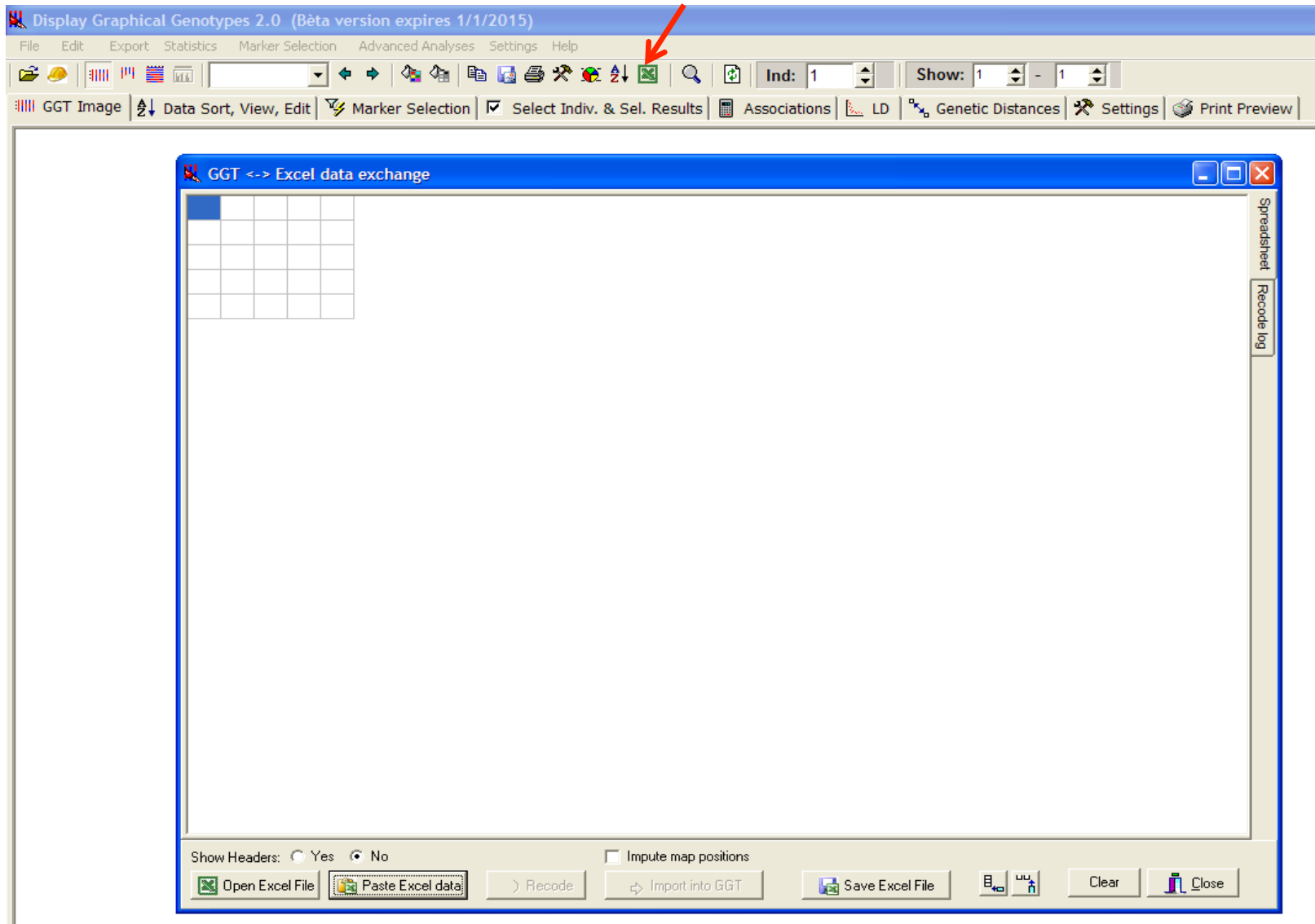
> No Data Available <

Open a file or choose "Build GGT File" from the  
"File" menu to create a GGT file from MAP & LOC data...

New! import GGT data from Excel files - see menu

New! drag and drop .ggt files here to open..

Click on “excel” icon, it will open “excel data exchange” window to enter data



# Copy data from tabsheet “Demonstration data GAS” of excel file “Demonstration data-LD-GGT”

Display Graphical Genotypes 2.0 (Beta version expires 1/1/2015)

File Edit Export Statistics Marker Selection Advanced Analyses Settings Help

GGT Image Data Sort, View, Edit Marker Selection Select Indiv. & Sel. Results Associations LD Genetic Distances Settings Print Preview

Ind: 1 Show: 1 - 0

GGT <-> Excel data exchange

alias	Dis	Out_Sd035071	Out_Sd035072	Out_Sd035073	Out_Sd035074	Out_Sd035075	Out_Sd035076	Out_Sd035077	Out_Sd035078	Out_Sd035079	Out_Sd035081	Out_Sd035084	Out_Sd035085	Out_Sd035086	Out_Sd035087	Out_Sd035088	Out_Sd035089	Out_Sd035090	Out_Sd035291	Out_Sd035292	Out_Sd035294	Out_Sd035295	Out_Sd035296	Out_Sd035297	Out_Sd035298	Out_Sd035299	Out_Sd035300	Out_Sd035302
nchrom	1.0																											
popt	Natpop																											
locus	pos																											
name=GAS																												
B32731_497	0.3	B	B	H	A	B	B	H	H	B	A	H	B	A	H	A	A	H	A	B	B	A	H	H	B	H	B	B
U3704_1129	0.7	H	H	B	A	H	B	H	B	A	H	H	H	H	A	H	H	A	A	A	B	B	A	A	H	H	H	H
U3704_1032	0.8	H	H	A	B	H	A	H	H	B	H	B	H	B	H	H	B	B	B	A	B	B	A	B	B	H	B	H
U3704_237	1.6	B	H	B	H	B	B	B	B	B	H	B	B	B	B	B	A	B	H	B	H	B	H	B	B	H	B	H
U10601_94	2.0	H	B	B	H	H	B	B	B	H	B	A	B	A	B	A	H	B	H	B	A	H	H	H	A	A	H	H

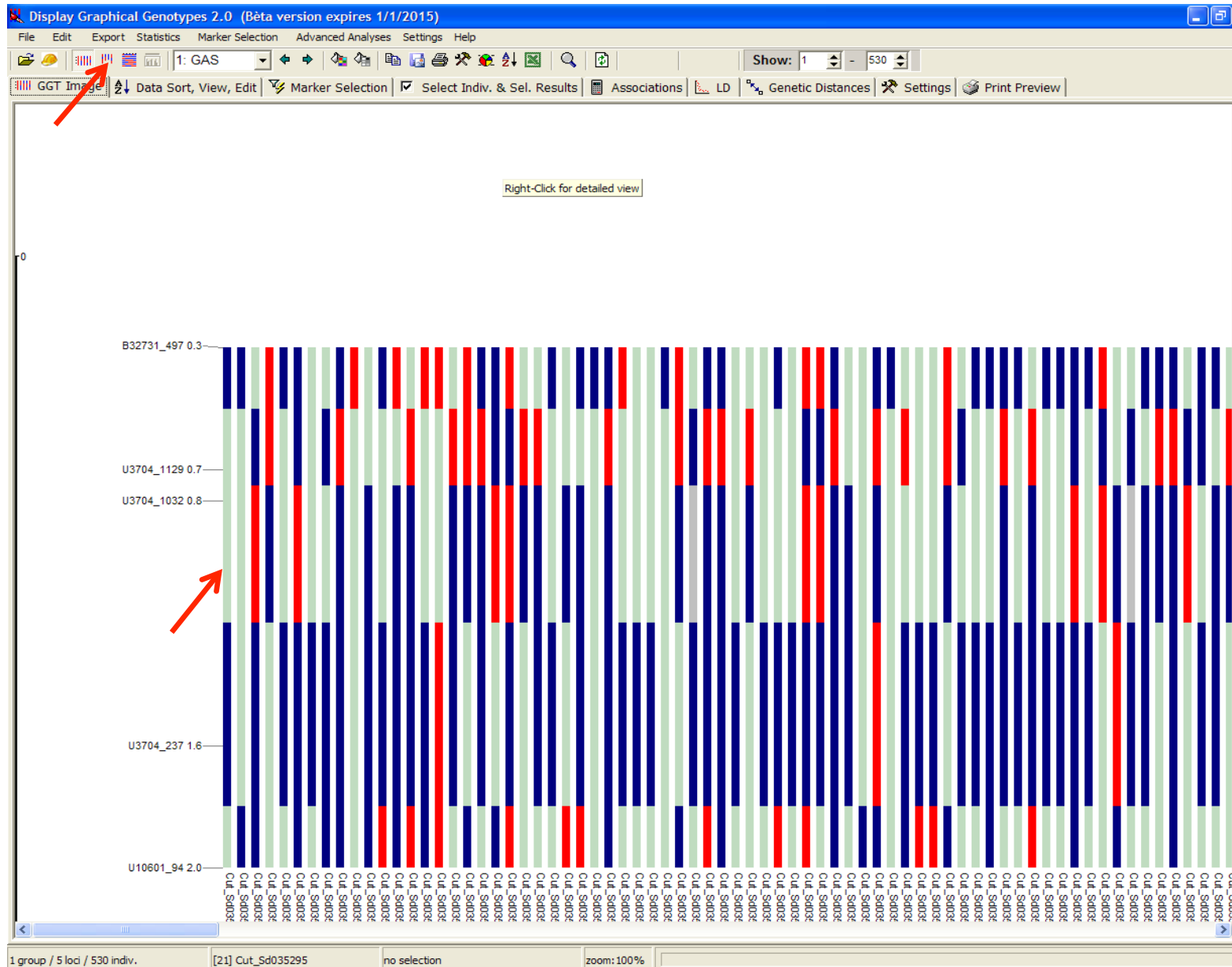
Spreadsheet Recode log Association Mapping

Show Headers: ☒ Yes ☐ No ☐ Impute map positions

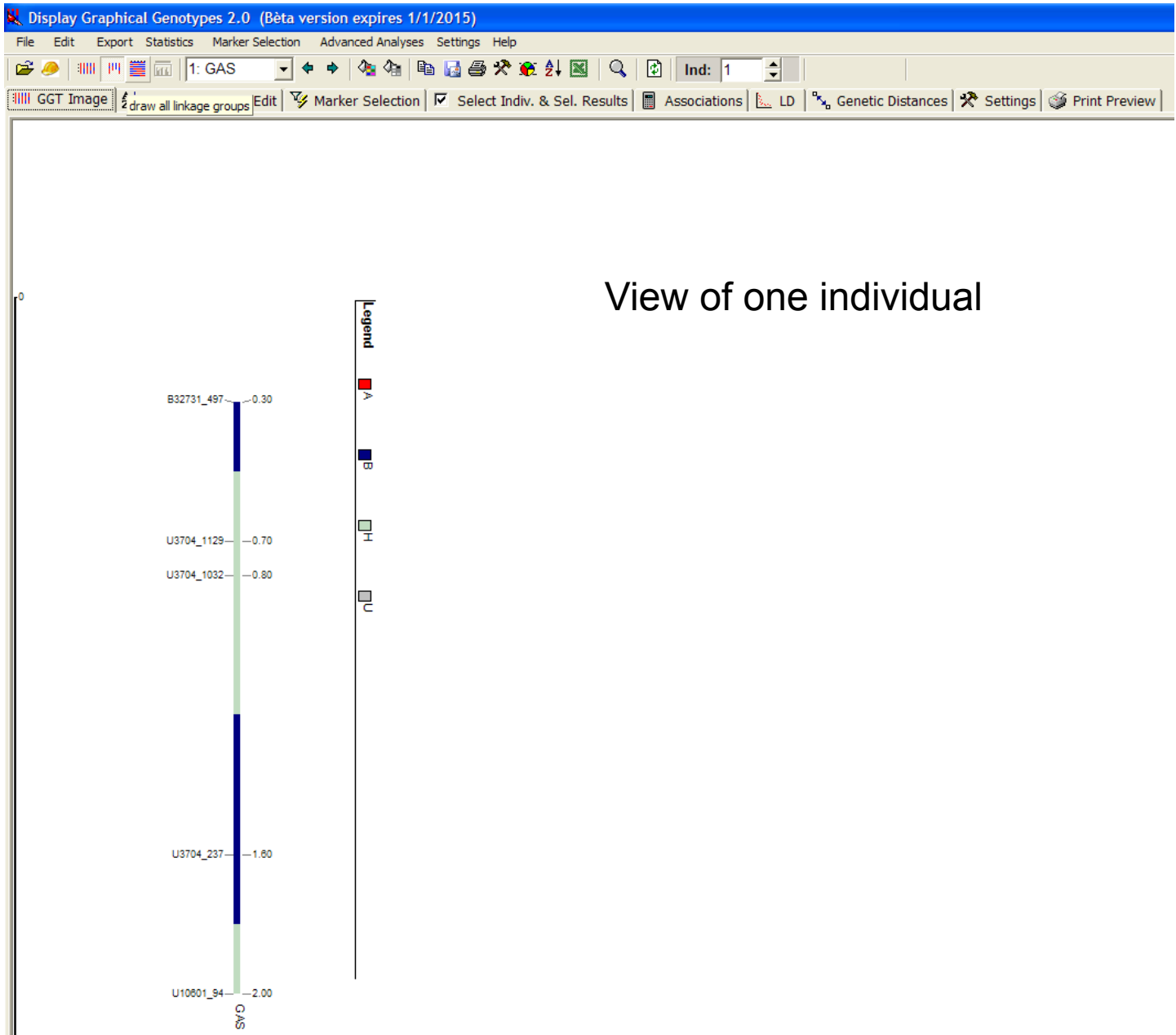
Open Excel File Paste Excel data Recode Import into GGT Save Excel File Clear Close

Click on “Yes” for “Show Headers” and then Click on “Past Excel data” to paste data into “Excel data exchange” window

Click “import into GGT” to import data pasted into GGT

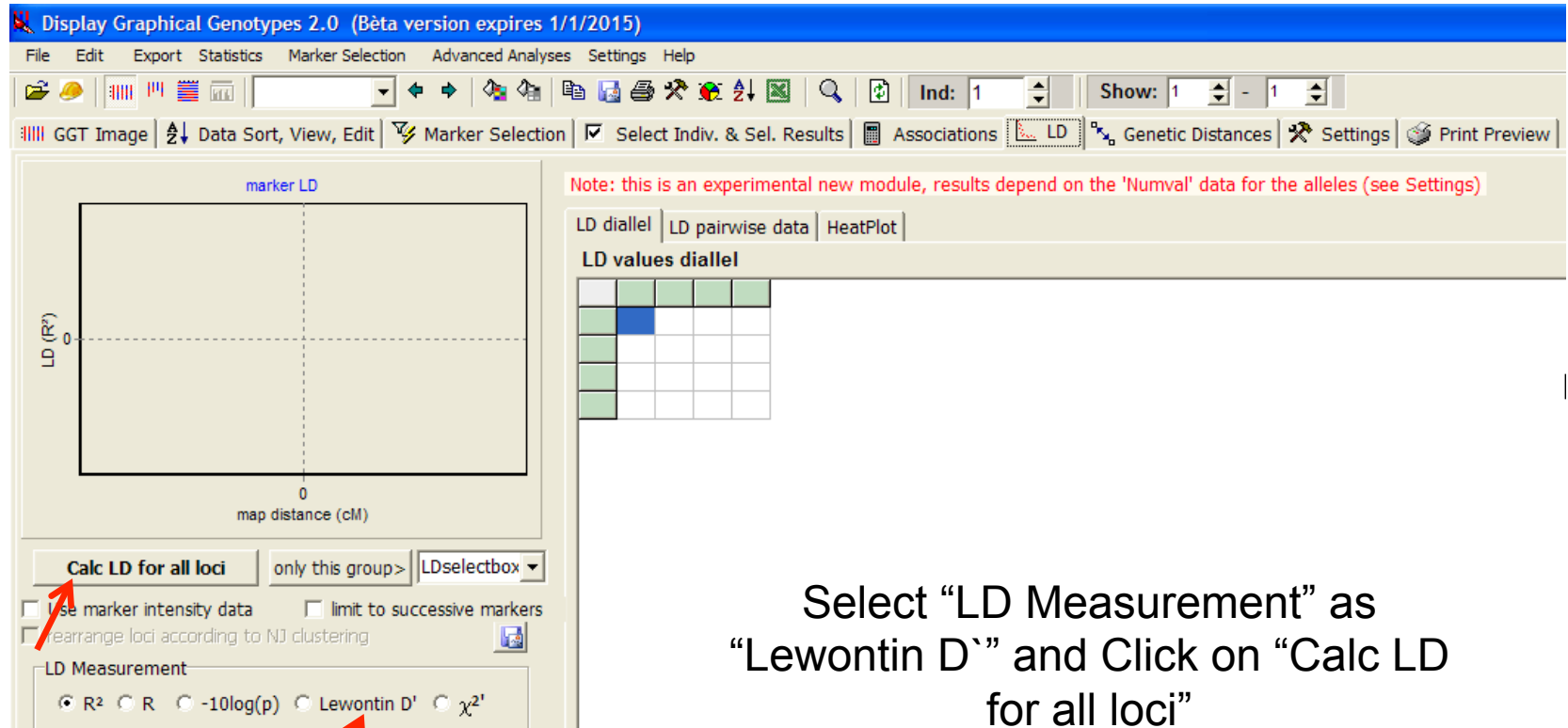
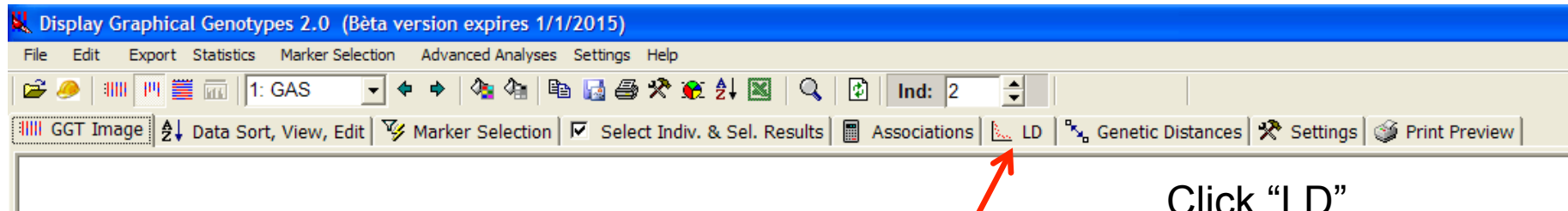


Each bar represents the genome of a single individual. Right Click individual bar or Click as shown above to see the detailed view of the genome of each individual



View of one individual

# Calculation of LD



Display Graphical Genotypes 2.0 (Bèta version expires 1/1/2015)

File Edit Export Statistics Marker Selection Advanced Analyses Settings Help

1: GAS Ind: 1

GGT Image Data Sort, View, Edit Marker Selection Select Indiv. & Sel. Results Associations LD Genetic Distances Settings Print Preview

marker LD

LD (D')

map distance (cM)

Calc LD for all loci only this group> 1: GAS

☐ Use marker intensity data ☐ limit to successive markers

☐ rearrange loci according to NJ clustering

LD Measurement

☐  $R^2$  ☐  $R$  ☐  $-10\log(p)$  ☒ Lewontin  $D'$  ☐  $\chi^2$

Note: this is an experimental new module, results depend on the 'Numval' data for the alleles (see Settings)

LD diallel LD pairwise data HeatPlot

LD values diallel

LD (D')	1>B32731_497	1>U3704_1129	1>U3704_1032	1>U3704_237	1>U10601_94
1>B32731_497					
1>U3704_1129	0.04				
1>U3704_1032	0.05	0.73			
1>U3704_237	0.07	0.11	0.09		
1>U10601_94	0.03	0.07	0.08	0.10	

Click on "LD diallel" to view LD values in diallel format



Display Graphical Genotypes 2.0 (Bêta version expires 1/1/2015)

File Edit Export Statistics Marker Selection Advanced Analyses Settings Help

1: GAS Ind: 1

GGT Image Data Sort, View, Edit Marker Selection Select Indiv. & Sel. Results Associations LD Genetic Distances Settings Print Preview

marker LD

LD (p')

map distance (cM)

Calc LD for all loci only this group> 1: GAS

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☐ rearrange loci according to NJ clustering

LD Measurement

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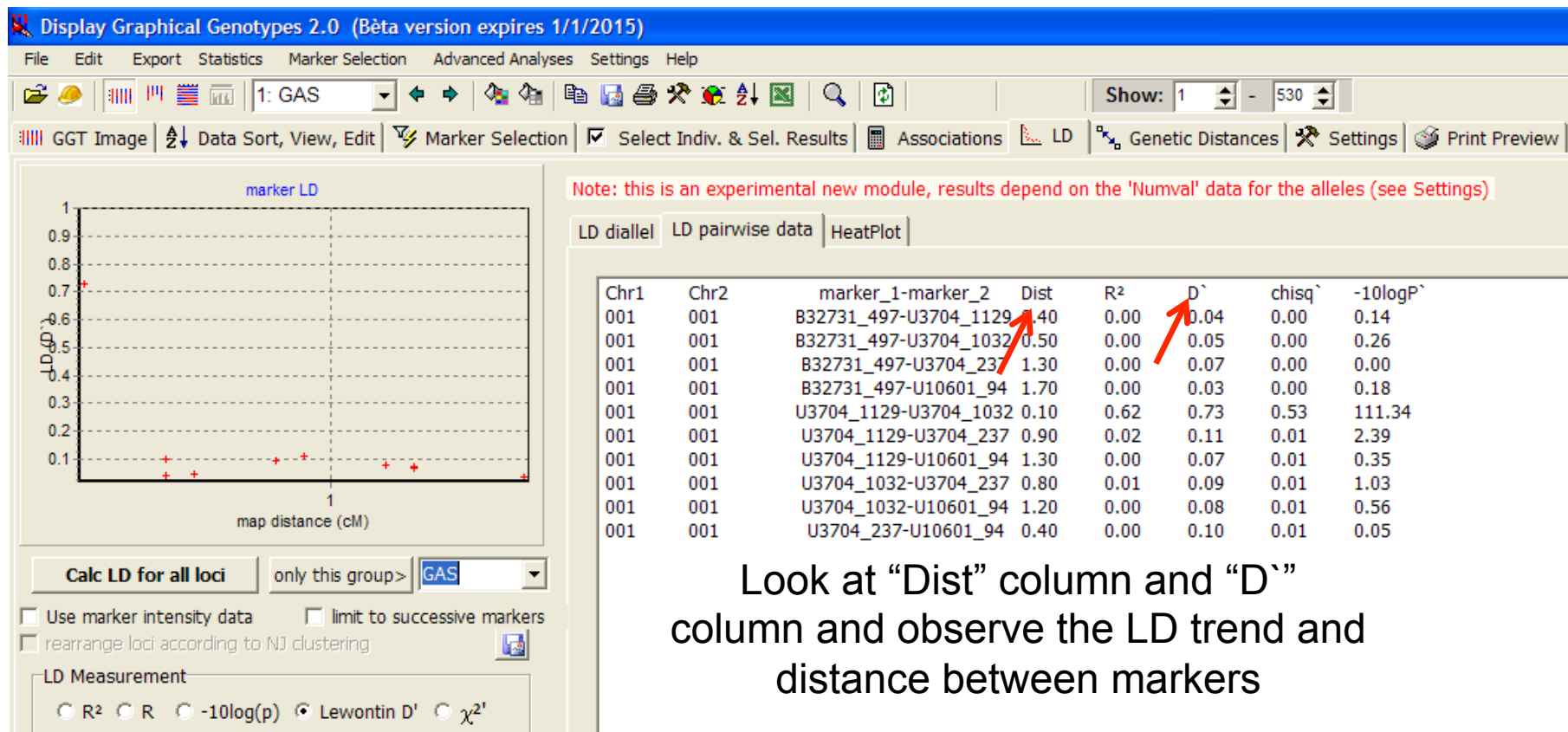
Note: this is an experimental new module, results depend on the 'Numval' data for the alleles (see Settings)

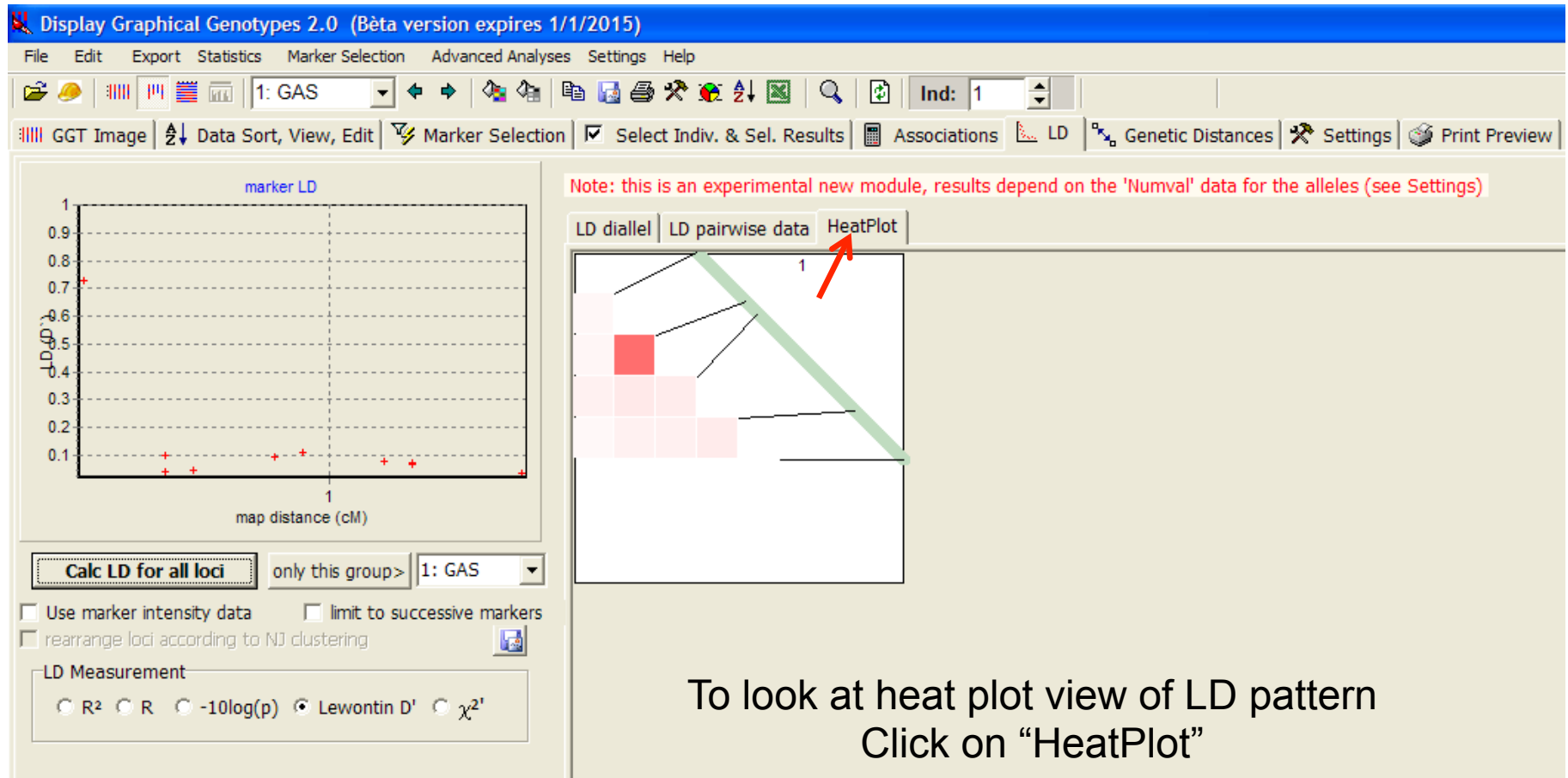
LD diallel LD pairwise data HeatPlot

LD values diallel

LD (p')	1>B32731_497	1>U3704_1129	1>U3704_1032	1>U3704_237	1>U10601_94
1>B32731_497					
1>U3704_1129	0.04				
1>U3704_1032	0.05	0.73			
1>U3704_237	0.07	0.11	0.09		
1>U10601_94	0.03	0.07	0.08	0.10	

Click on “LD pairwise data” to view pairwise distance between markers and pairwise LD values for different LD measurements

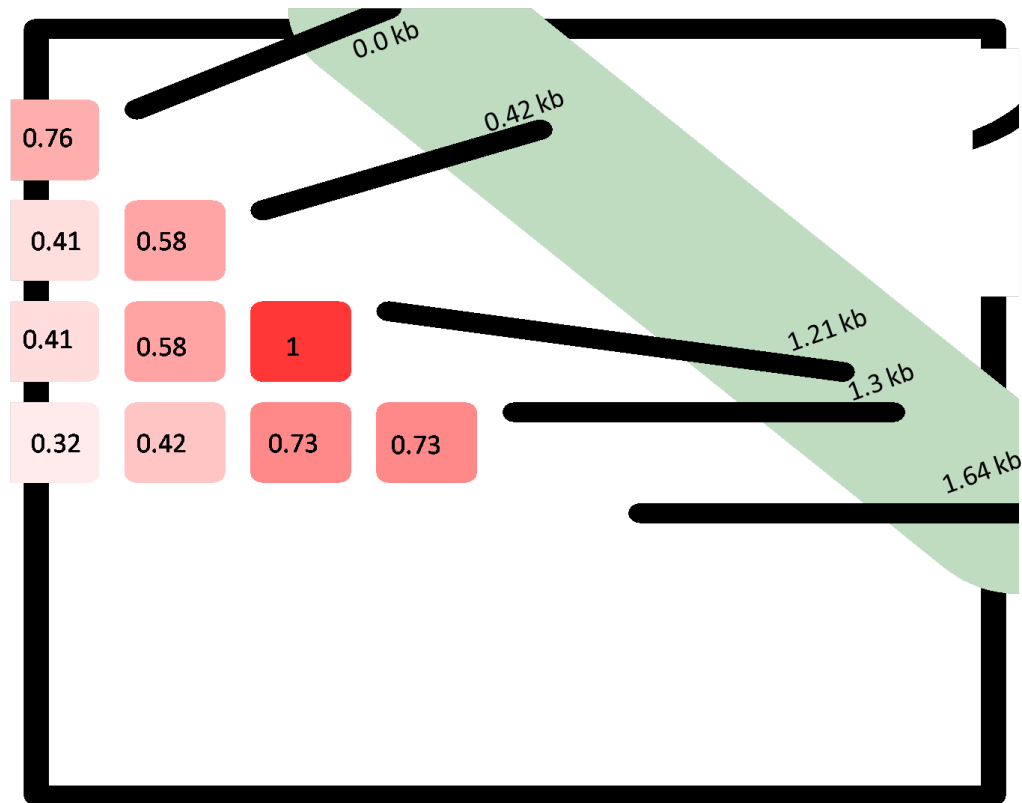




# Summary of the results

Marker_1-Marker_2	Dist	R <sup>2</sup>	D'
M1-M2	0.42	0.4	0.76
M1-M3	1.21	0.17	0.41
M1-M4	1.3	0.17	0.41
M1-M5	1.64	0.1	0.32
M2-M3	0.78	0.45	0.58
M2-M4	0.88	0.46	0.58
M2-M5	1.21	0.29	0.42
M3-M4	0.1	1	1
M3-M5	0.43	0.6	0.73
M4-M5	0.33	0.59	0.73

LD between the 5 SNPs in 1.64 kb region of a gene. The values in colored squares represent D' between SNP pairs.



**Reference:**

van Berloo R. 2008. GGT 2.0: versatile software for visualization and analysis of genetic data. *J. Hered.* 99:232–236