

## Plot genomic region with SNPs genes and LD

This app can be used to create a plot that show a genomic region of interest with the SNPs and genes in that locus combined with the GWAS results. It can be used to communicate your results in a nice way, it is not recommended for exploring the data (so first find the locus you are interested in and then use this app to plot).

The application can be found here:

[http://icci-2:9100/plot\\_ld/](http://icci-2:9100/plot_ld/)

In the first stage, the app search for all GAPIT outputs in a specified folder and will produce a table with each significant locus it finds, then in the next stage the user can choose a locus and produce the figure.

**IMPORTANT:** There are heavy calculations involve in the second stage and it can take some time to produce the output, so you need to be patient and to be careful with the size of region you choose (!).

### Part I:

Select a folder with GAPIT output, the P-value threshold, LOD threshold, minor allele frequency, and locus width.



The George S. Wise Faculty of Life Sciences  
Institute for Cereal Crops Research  
Tel Aviv University

## Plot genes associated with significant SNPs

Choose folder

Select GAPIT results folder from the server

GWAS threshold

0.001

Lod threshold

5.3

MAF

0.05

Locus width

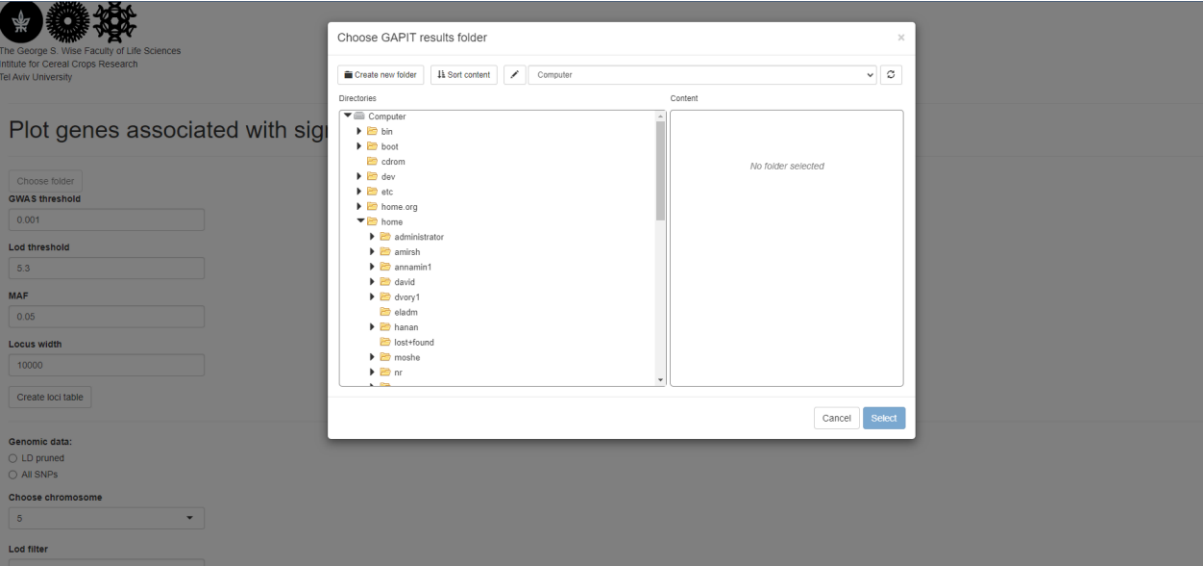
10000

Create loci table

Create the table

I recommend keeping all parameters as default at start, create the table and then change and re-create if you need.

The folder needs to be in your file system on the ICCR server (could be the GAPIT output folder):



The loci table show the position, highest LOD score, genes in locus and the model, You can sort or search the table to find the locus you are interested in.

Plot genes associated with significant SNPs

Choose folder

GWAS threshold

0.001

Lod threshold

5.3

MAF

0.05

Locus width

10000

Create loci table

Show10entries

Search:

	locusID	chrom	start	end	best_SNP_lod	n_genes_in_loci	genes_names	Model
25	145	chr5S	590255467	590260290	9.04645625220043	2	AE.LONG.r1.5SG0402240, AE.LONG.r1.5SG0402250	MLM.ME1CB_trait259
38	170	chr5S	691737743	691739110	8.60639771872736	1	AE.LONG.r1.5SG0416770	MLM.ME1CB_trait259
9	33	chr5S	438628423	438639418	8.53310163654746	1	AE.LONG.r1.5SG0385140	MLM.ME1CB_trait259
22	138	chr5S	582237275	582239083	8.31617963399511	1	AE.LONG.r1.5SG0401020	MLM.ME1CB_trait259
45	183	chr5S	754209804	754233273	8.26137024106178	3	AE.LONG.r1.5SG0425970, AE.LONG.r1.5SG0425980, AE.LONG.r1.5SG0425990	MLM.ME1CB_trait259
20	125	chr5S	581444199	581453514	7.89219695144667	3	AE.LONG.r1.5SG0400930, AE.LONG.r1.5SG0400940, AE.LONG.r1.5SG0400950	MLM.ME1CB_trait259
37	169	chr5S	680653081	680656020	7.77890915006139	1	AE.LONG.r1.5SG0415310	MLM.ME1CB_trait259
26	151	chr5S	590527503	590548854	7.69781481788311	3	AE.LONG.r1.5SG0402260, AE.LONG.r1.5SG0402270, AE.LONG.r1.5SG0402280	MLM.ME1CB_trait259
16	60	chr5S	510964348	510969407	7.50430838894768	2	AE.LONG.r1.5SG0392620, AE.LONG.r1.5SG0392630	MLM.ME1CB_trait259
39	171	chr5S	694358914	694359358	7.21802817713047	1	AE.LONG.r1.5SG0417170	MLM.ME1CB_trait259

Showing 1 to 10 of 50 entries

Genomic data:

## Part II:

When you find the locus you want to plot, select it on the table (it will be highlighted) and then choose the chromosome, the LOD parameters, the region to plot and a title (optional).

26	151	chr5S	590527603	590548854	7.69761481788311	3	AE.LONG.r1.SSG0402260, AE.LONG.r1.SSG0402270, AE.LONG.r1.SSG0402280	MLM.ME1CB_trait259
16	60	chr5S	510964348	510969407	7.50430838894768	2	AE.LONG.r1.SSG0392620, AE.LONG.r1.SSG0392630	MLM.ME1CB_trait259
39	171	chr5S	694358914	694359358	7.21802817713047	1	AE.LONG.r1.SSG0417170	MLM.ME1CB_trait259

Showing 1 to 10 of 50 entries

Previous12345Next

Genomic data:  
☐ LD pruned  
☐ All SNPs

Choose chromosome  
5

Lod filter  
0

Lod max  
17

WinUp  
500

WinDown  
500

Enter plot title

Create plotDownload plot

The amount of bp to add to the range in the table

The plot will show all SNPs and genes in range with notation for introns and exons.

Each SNP is colored according to the value of the LD between it and the most significant SNP, while the most significant SNP is marked with an asterisk.

10000

Create loci table

20	125	chr5S	581444199	581453514	7.89219695144667	3	AE.LONG.r1.SSG0400930, AE.LONG.r1.SSG0400940, AE.LONG.r1.SSG0400950	MLM.ME1CB_trait259
37	169	chr5S	680653081	680656020	7.77890915006139	1	AE.LONG.r1.SSG0415310	MLM.ME1CB_trait259
26	151	chr5S	590527603	590548854	7.69761481788311	3	AE.LONG.r1.SSG0402260, AE.LONG.r1.SSG0402270, AE.LONG.r1.SSG0402280	MLM.ME1CB_trait259
16	60	chr5S	510964348	510969407	7.50430838894768	2	AE.LONG.r1.SSG0392620, AE.LONG.r1.SSG0392630	MLM.ME1CB_trait259
39	171	chr5S	694358914	694359358	7.21802817713047	1	AE.LONG.r1.SSG0417170	MLM.ME1CB_trait259

Showing 1 to 10 of 50 entries

Genomic data:  
☐ LD pruned  
☒ All SNPs

Choose chromosome  
5

Lod filter  
0

Lod max  
17

WinUp  
500

WinDown  
500

Enter plot title  
Title

Create plotDownload plot

Lod Score

Title

510.954 Mb510.955 Mb510.956 Mb510.957 Mb510.958 Mb510.959 Mb510.97 Mb