

TASSEL

Trait Analysis by aSSociation,
Evolution and Linkage

Getting TASSEL

- www.maizegenetics.net/tassel
- Java application that runs on your computer
- launch from the website (tassel3.jnlp)
 - downloads TASSEL and library files once
 - checks for latest version after that
- download standalone
 - run without a web connection
 - increase available memory

Firefox TASSEL
www.maizegenetics.net/index.php?option=com_content&task=view&id=89&Itemid=119

Buckler Lab for Maize Genetics and Diversity

A USDA-ARS Lab with Cornell's Institute for Genomic Diversity

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Current Location

Home

TASSEL

[Tassel Version 3.0 \(Build: February 9, 2012 Requires: Java 1.6\)](#)

- [Launch TASSEL 3.0](#)
- [Launch TASSEL 3.0 \(950Mb Heap Size\)](#)
- [Launch TASSEL 3.0 \(512Mb Heap Size\)](#)

[Tassel Version 3.0 Standalone \(Build: February 9, 2012 Requires: Java 1.6\)](#)

- [TASSEL 3.0 Standalone](#)

[Tassel Version 4.0 Beta \(Build: February 9, 2012 Requires: Java 1.6\)](#)

- [Launch TASSEL 4.0](#)
- [Launch TASSEL 4.0 \(950Mb Heap Size\)](#)
- [TASSEL 4.0 Standalone](#)

[Tassel Version 2.1 \(Build: March 15, 2010\)](#)

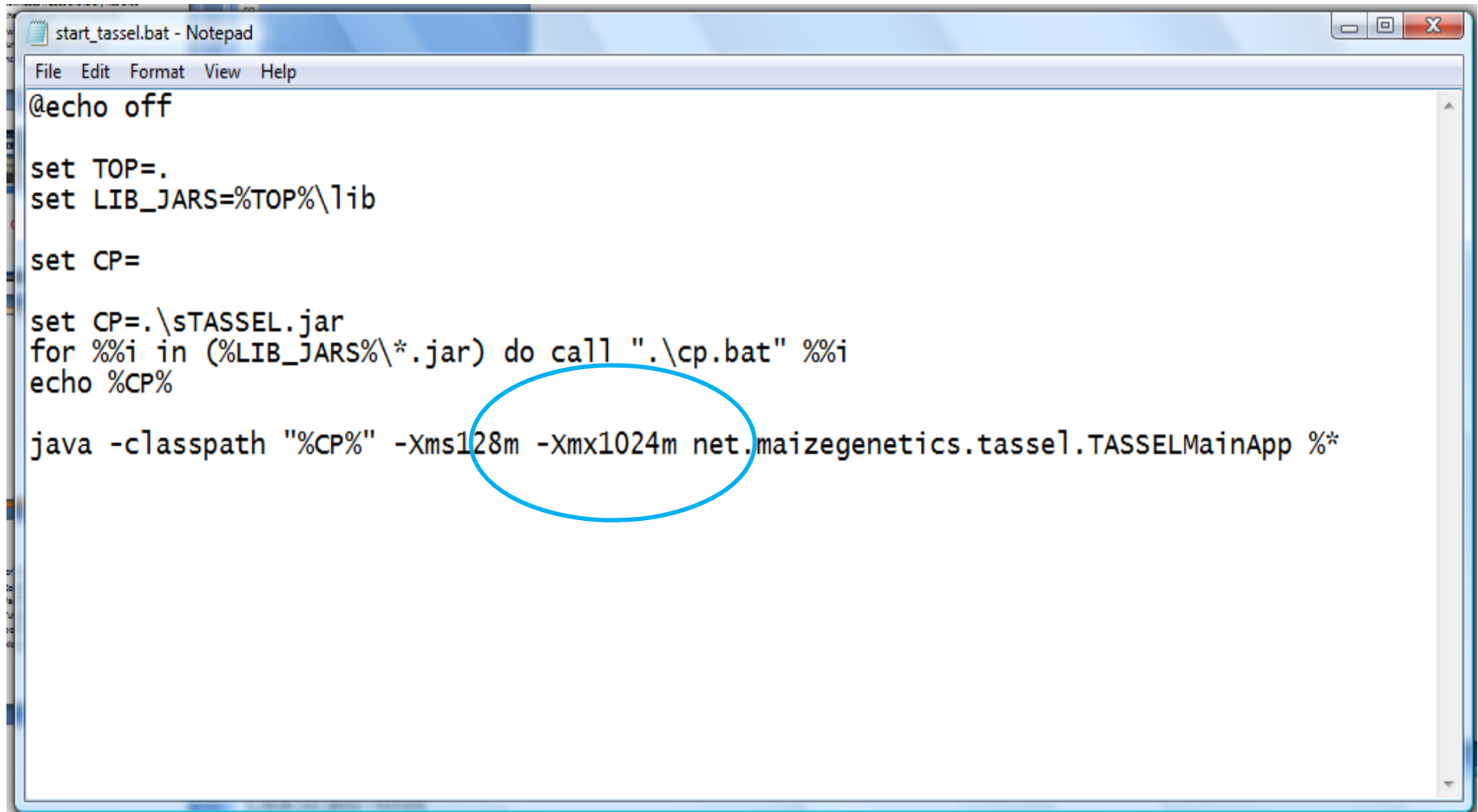
- [Launch TASSEL 2.1 \(Requires: Java 1.6\)](#)
- [Launch TASSEL 2.1 \(Requires: Java 1.5\)](#)
- [TASSEL 2.1 Standalone \(Requires: Java 1.5\)](#)

[Tassel Version 2.0.1 \(Build: April 23, 2007 Requires: Java 1.5\)](#)

- [Launch TASSEL 2.0.1](#)

[To Report Bugs or Request Features, please go to \[sourceforge\]\(#\), and click "Add new"...](#)

Edit the start_tassel.bat file in tassel3.0_standalone to increase the available memory



```
start_tassel.bat - Notepad
File Edit Format View Help
@echo off

set TOP=.
set LIB_JARS=%TOP%\lib

set CP=

set CP=.\sTASSEL.jar
for %%i in (%LIB_JARS%\*.jar) do call ".\cp.bat" %%i
echo %CP%

java -classpath "%CP%" -Xms128m -Xmx1024m net.maizegenetics.tassel.TASSELMainApp %*
```

Documentation

- User's Guide
- Tutorial
 - Part of users guide
 - Tutorial data set
- Pipeline
 - Allows TASSEL to be run from the command line

Resources

To Report Bugs or Request Features, please go to [sourceforge](#), and click "Add new"...

[Tassel Bug Tracking](#)

[Tassel Feature Requests](#)

To report problems or make feature requests

Contacts

We recommend posting questions to the discussion group

[Tassel User Group \(\[tassel@googlegroups.com\]\(mailto:tassel@googlegroups.com\) \)](#)

General Questions / Pipeline

Terry Casstevens (tmc46@cornell.edu)

Analysis Tools / MLM / GLM

Peter Bradbury (pjb39@cornell.edu)

Zhiwu Zhang (zz19@cornell.edu)

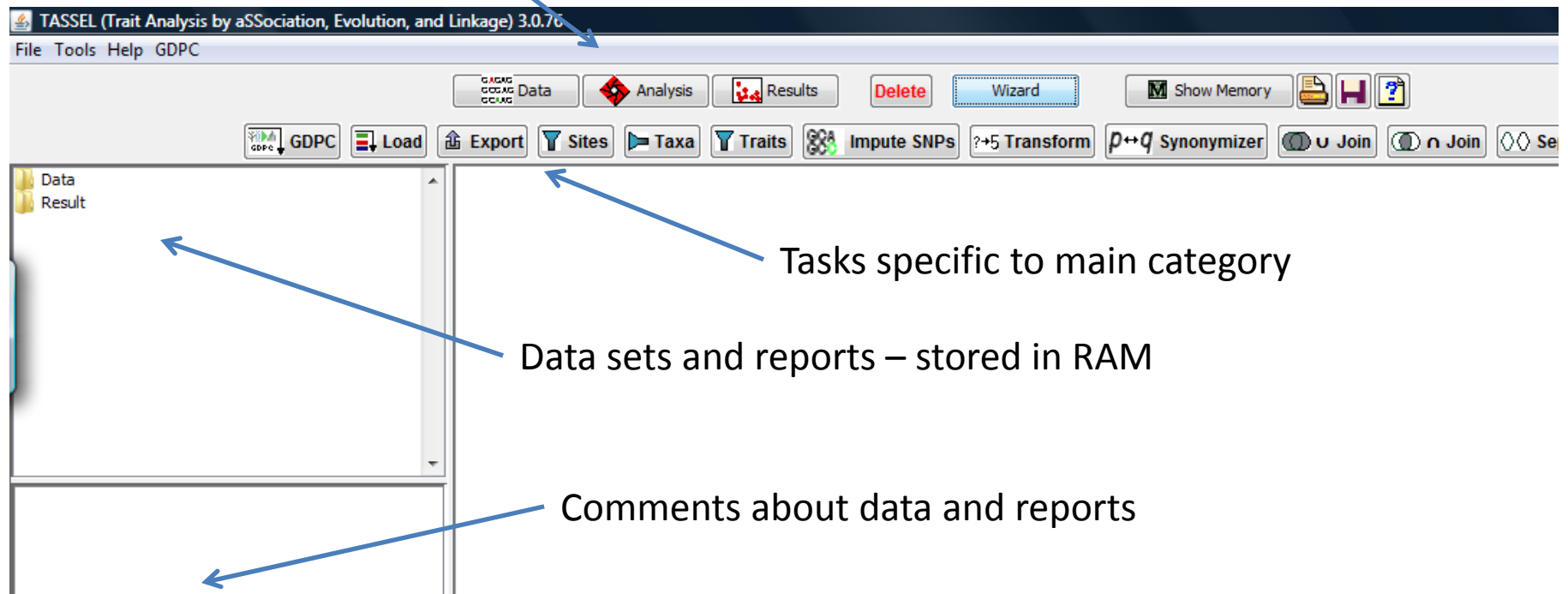
Overall Project Lead

Ed Buckler (esb33@cornell.edu)

To ask questions about TASSEL use

General Organization

Main Function Categories



Import Formats

- Hapmap
- Plink
- Flapjack
- Polymorphism
- Phylip
- Numerical Data (traits or markers)
- Square Numerical Matrix (kinship)
- Genetic Map
- Guess function

Exporting Data

The screenshot shows the TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.76 interface. The File menu is open, with 'Save Selected As...' highlighted by a blue arrow. The 'Export' button is also visible in the toolbar. An 'Export...' dialog box is overlaid on the right, titled 'Choose File Type to Export.', with 'Write BLOB (zip)' selected.

File Tools Help GDPC

- Save Data Tree
- Open Data Tree
- Save Data Tree As ...
- Open Data Tree...
- Save Selected As...
- Exit

GDPC Load Export Sites Taxa Traits

Physical Positions Site Numbers

0 352

	1214:1214	1215:1215	1216:1216	1217:1217
38-11	C	C	G	G
A272	C	C	G	G
A441-5	C	C	G	G
A554	C	C	G	G
A6	C	C	G	G
A619	C	C	G	G
A632	C	C	G	G

Number of sequences: 91
Number of sites: 2466
Data type: IUPACNucleotide

Export...

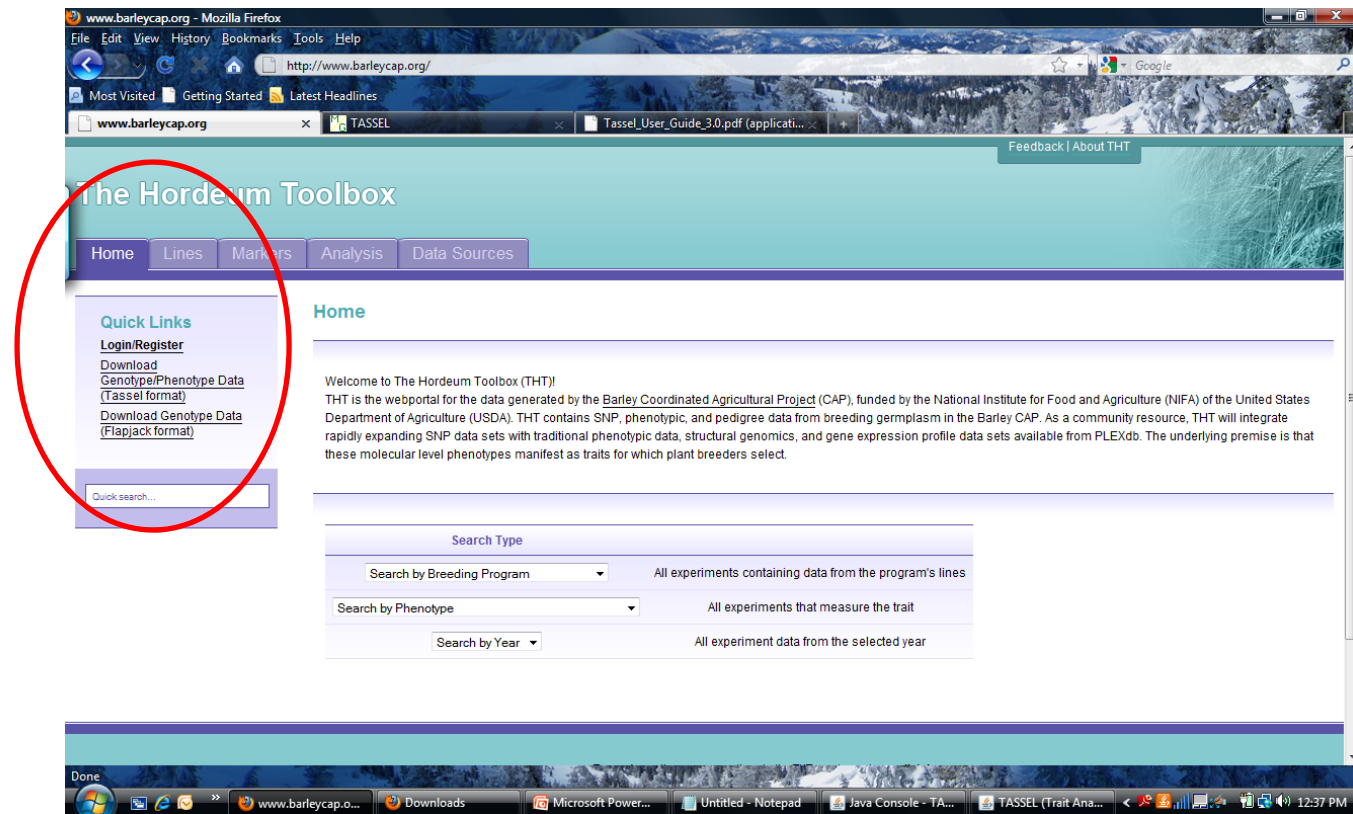
Choose File Type to Export.

- Write BLOB (zip)
- Write BLOB (gzip)
- Write Hapmap
- Write Plink
- Write Flapjack
- Write Phylip (Sequential)
- Write Phylip (Interleaved)
- Write Tab Delimited

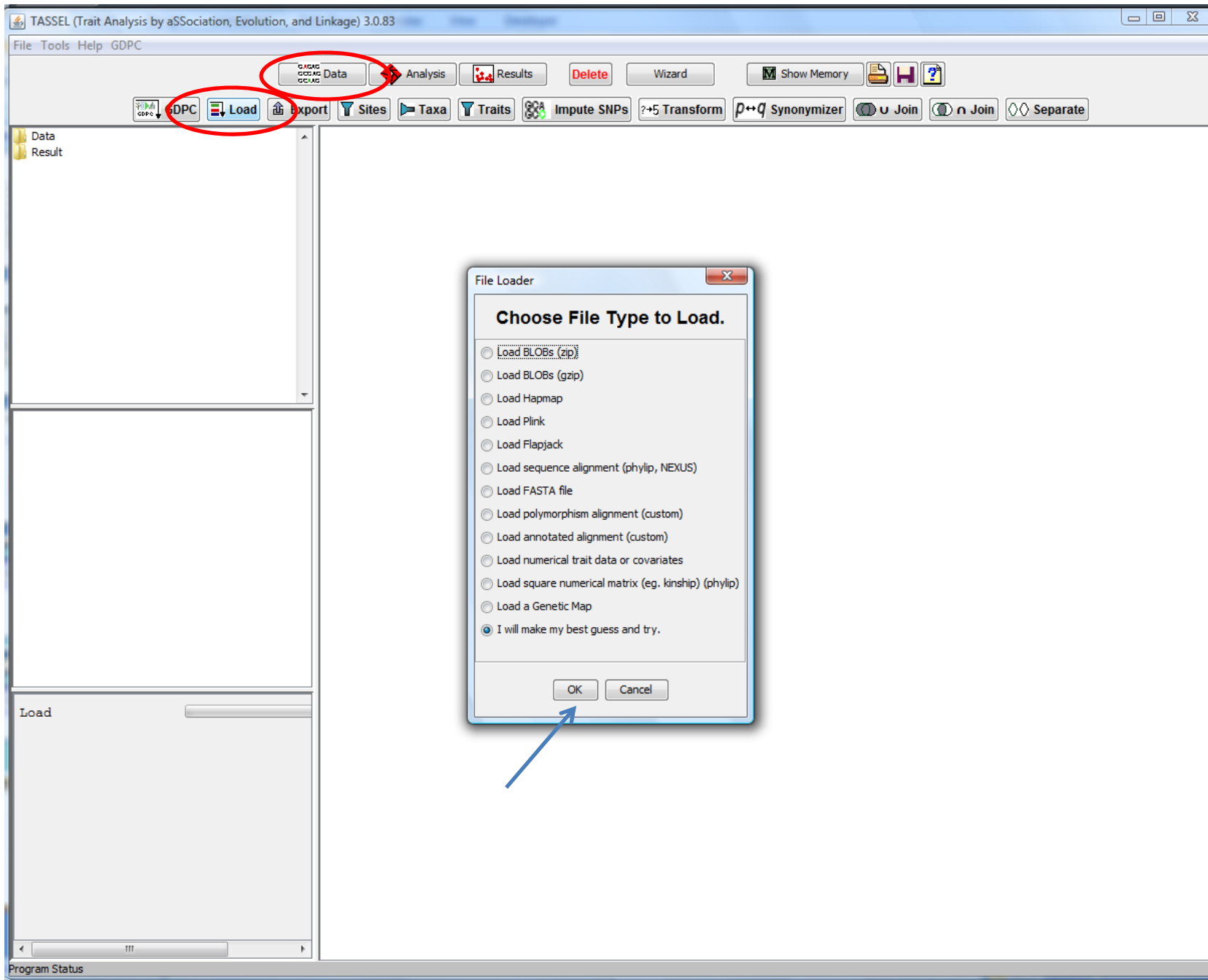
OK Cancel

Downloading Data From the Hordeum Toolbox

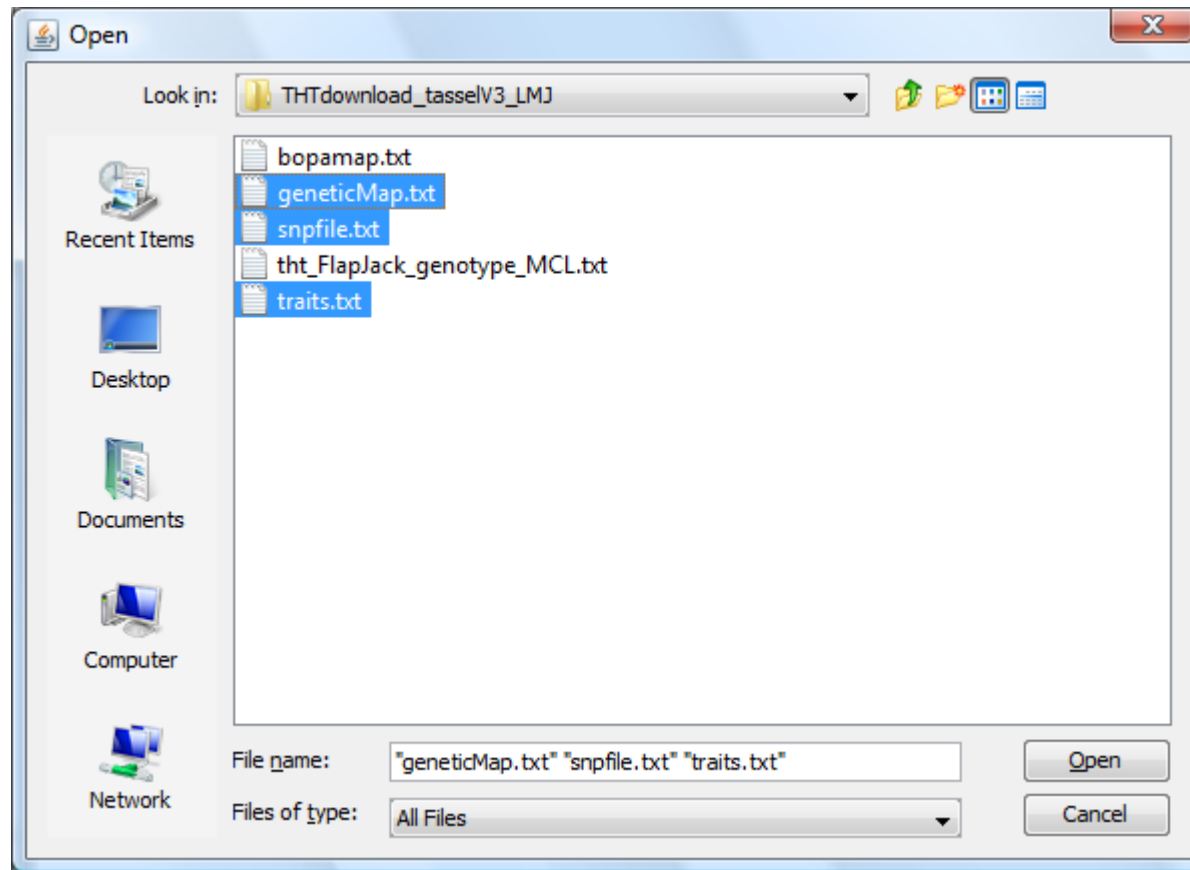
- <http://hordeumtoolbox.org/>
- now <http://triticeaetoolbox.org/>



The screenshot shows a Mozilla Firefox browser window displaying the website www.barleycap.org. The page title is "The Hordeum Toolbox". The navigation menu includes "Home", "Lines", "Markers", "Analysis", and "Data Sources". A "Quick Links" section is circled in red and contains the following links: "Login/Register", "Download Genotype/Phenotype Data (Tassel format)", and "Download Genotype Data (Flapjack format)". Below the navigation menu, there is a "Home" section with a welcome message and a search interface. The search interface has a "Search Type" dropdown menu with three options: "Search by Breeding Program" (All experiments containing data from the program's lines), "Search by Phenotype" (All experiments that measure the trait), and "Search by Year" (All experiment data from the selected year). The browser's taskbar at the bottom shows several open applications, including "www.barleycap.o...", "Downloads", "Microsoft Power...", "Untitled - Notepad", "Java Console - TA...", and "TASSEL (Trait Ana...". The system clock in the bottom right corner shows "12:37 PM".



I will make my best guess and try



Load Flapjack

Load Flapjack

Genotype File Browse...

Map File Browse...

Heterozygotes are separated by a character (eg, A/T rather than AT)

Markers are nucleotides (ie, A, C, G, or T)

Heterozygote separator character

Missing data character

Map Type

Physical

Genetic

Import Cancel

Flapjack
import
options

Genetic
positions
multiplied by
1000

Running Linkage Disequilibrium Analysis

SEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
ols Help GDPC

Data Analysis Results Delete Wizard Show Memory

Diversity Link. Diseq. Cladogram Kinship GLM MLM GS

Physical Positions Site Numbers Locus Site Name Alleles (Enter physical position)

0 20075 40150 60225 80300 100375

	0:0	1:0	2:0	3:750	4:770	5:770	6:950	7:1510	8:1510	9:1510	10:3750	11:3750	12:3750	13:4510	14:6030	15:6030	16:8290	17:8770	18:10670	19:10670	20:10670	21:11420	22:11420	23:13050	24:15400	25:17260	26:17260	27:17260	
ND20448	A:A	A:A	B:B	A:A	...	A:A	...	A:A	...	A:A	...	B:B	...	A:A	...	A:A	...	A:A	...	B:B	...	B:B	B:B	A:A	B:B	A:A	...	A:A	...
ND24843	B:B	A:A	B:B	B:B	...	A:A	...	A:A	B:B	B:B	...	B:B	...	B:B	B:B	B:B	...	A:A	...	B:B	...	B:B	B:B	B:B	B:B	A:A	...	B:B	...
ND24890	B:B	A:A	B:B	B:B	...	A:A	...	A:A	B:B	B:B	...	B:B	...	B:B	B:B	B:B	...	A:A	...	B:B	...	B:B	B:B	A:A	B:B	A:A	...	A:A	B:
ND24906	B:B	A:A	B:B	A:A	...	A:A	...	A:A	...	A:A	...	B:B	...	A:A	...	A:A	...	A:A	...	B:B	...	B:B	B:B	A:A	B:B	A:A	...	A:A	...
ND24978	A:A	A:A	B:B	A:A	...	A:A	...	A:A	...	A:A	...	B:B	...	A:A	...	A:A	...	A:A	...	B:B	...	B:B	B:B	A:A	B:B	A:A	...	A:A	...
ND25025	A:A	A:A	B:B	A:A	...	A:A	...	A:A	...	A:A	...	B:B	...	A:A	...	A:A	...	A:A	...	B:B	...	B:B	B:B	A:A	B:B	A:A	...	A:A	...

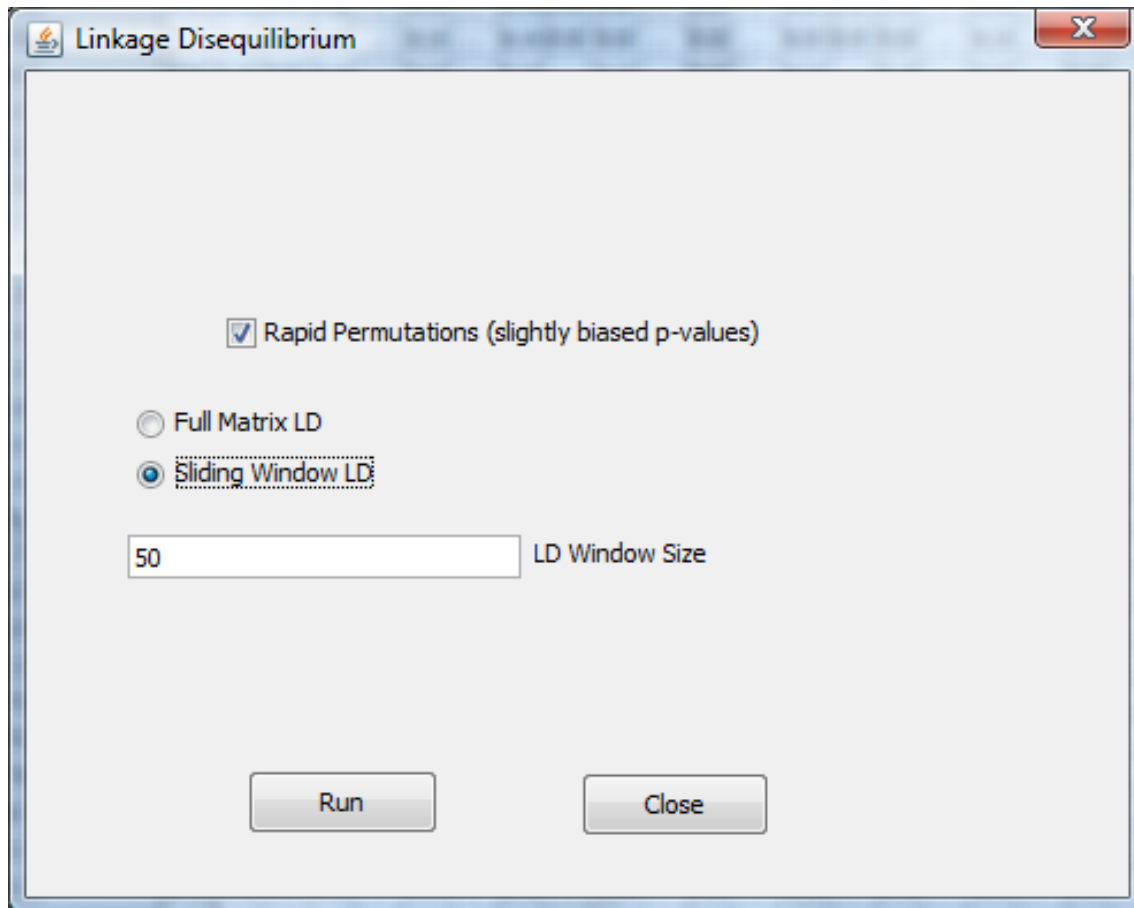
Sequence

- snpfile
- tht_FlapJack_genotype_MCL
- tht_FlapJack_genotype_MCL_align0
- tht_FlapJack_genotype_MCL_align1
- tht_FlapJack_genotype_MCL_align2
- tht_FlapJack_genotype_MCL_align3
- tht_FlapJack_genotype_MCL_align4
- tht_FlapJack_genotype_MCL_align5
- tht_FlapJack_genotype_MCL_align6
- tht_FlapJack_genotype_MCL_align7

Polymorphisms

Numerical

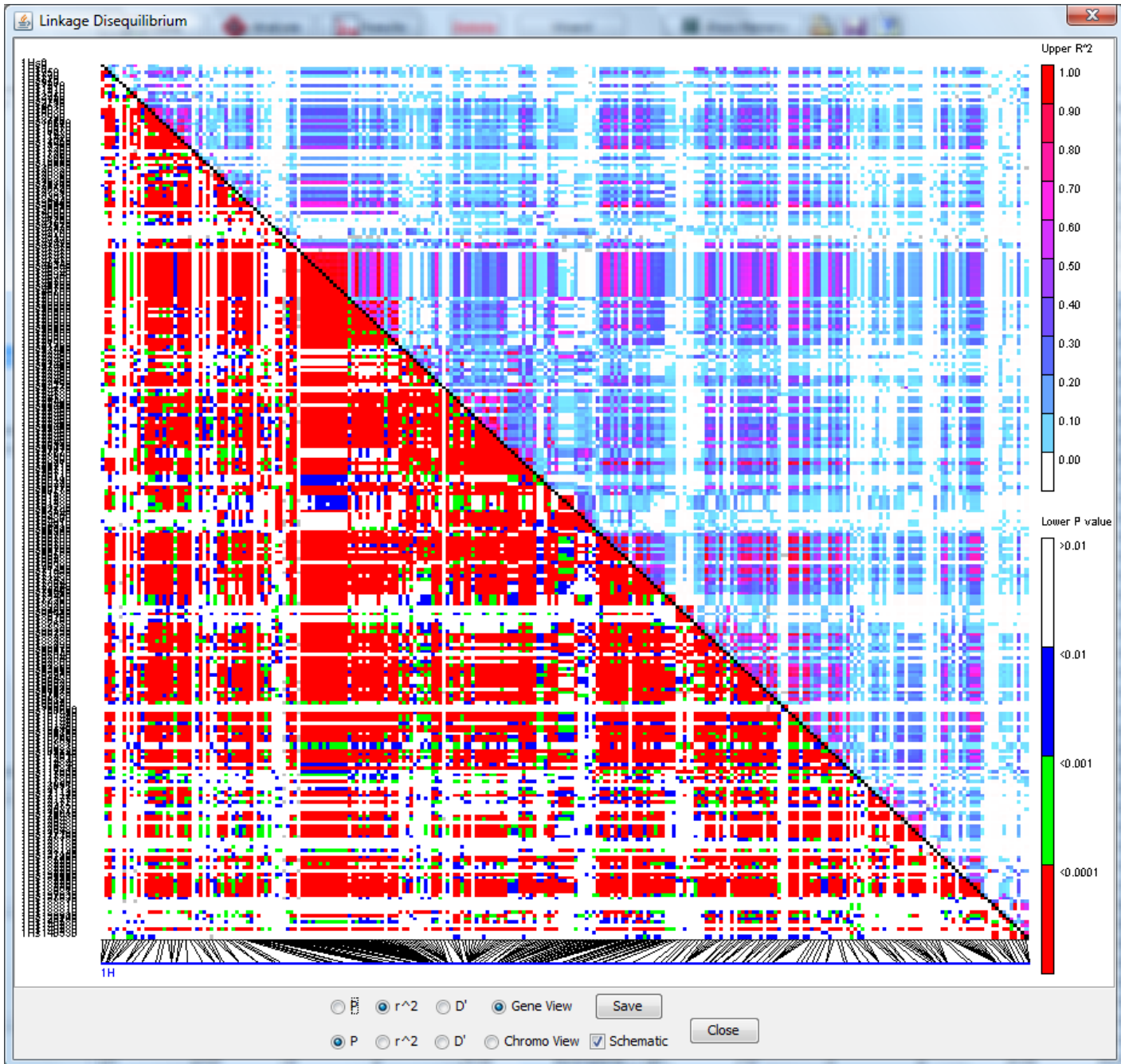
- geneticMap
- traits

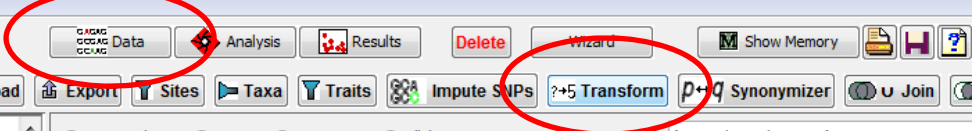


Display an LD Plot

The screenshot shows the TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83 software interface. The title bar reads "TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83". The menu bar includes "File", "Tools", and "Help", with "GDPC" selected. The toolbar contains buttons for "Data", "Analysis", "Results", "Delete", "Wizard", "Show Memory", and a help icon. Below the toolbar, there are view options: "Table", "Tree Plot", "2D Plot", "LD Plot", "Chart", "QQ Plot", and "Manhattan Plot". The "Results" button in the toolbar and the "LD Plot" button in the view options are both circled in red. On the left, a tree view shows a project structure with "LD:tht_FlapJack_genotype_MCL_align0" selected. The main window displays a table with the following columns: Locus1, Position1, Site1, NumberOf..., States1, Frequency1, Locus2, Position2, and Site2.

Locus1	Position1	Site1	NumberOf...	States1	Frequency1	Locus2	Position2	Site2
1H	0	1	2	A:66	NotImpleme...	1H	0	0
1H	0	2	2	B:65	NotImpleme...	1H	0	0
1H	0	2	2	B:65	NotImpleme...	1H	0	1
1H	750	3	2	A:66	NotImpleme...	1H	0	0
1H	750	3	2	A:66	NotImpleme...	1H	0	1
1H	750	3	2	A:66	NotImpleme...	1H	0	2
1H	770	4	2	A:66	NotImpleme...	1H	0	0
1H	770	4	2	A:66	NotImpleme...	1H	0	1
1H	770	4	2	A:66	NotImpleme...	1H	0	2
1H	770	4	2	A:66	NotImpleme...	1H	750	3
1H	770	5	2	A:66	NotImpleme...	1H	0	0
1H	770	5	2	A:66	NotImpleme...	1H	0	1
1H	770	5	2	A:66	NotImpleme...	1H	0	2
1H	770	5	2	A:66	NotImpleme...	1H	750	3





Data

- Sequence
 - snpfile
 - tht_FlapJack_genotype_MCL
 - tht_FlapJack_genotype_MCL_align0
 - tht_FlapJack_genotype_MCL_align1
 - tht_FlapJack_genotype_MCL_align2
 - tht_FlapJack_genotype_MCL_align3
 - tht_FlapJack_genotype_MCL_align4
 - tht_FlapJack_genotype_MCL_align5
 - tht_FlapJack_genotype_MCL_align6
 - tht_FlapJack_genotype_MCL_align7
- Polymorphisms
- Numerical
 - geneticMap
 - traits

Number of sequences: 192
 Number of sites: 2320
 Data type: Text
 Loci: 1H, 2H, 3H, 4H, 5H, 6H, 7H, UNK

Site Numbers Locus Site Name Alleles (Enter physical position) Search

	0	331	662	993	1324	1655	1986	2317
	2281:0	2282:0	2283:0	2284:0	2285:0	2286:0	2287:0	2288:0
ND20448	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND24843	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND24890	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND24906	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND24978	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25025	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25030	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25033	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25148	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25151	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25152	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25153	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25160	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25161	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25163	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25165	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25172	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25205	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25208	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25220	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25768	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25782	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25786	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25805	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25824	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25825	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25826	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25832	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25835	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25839	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25840	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25843	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25882	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25908	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25911	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25917	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25949	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25966	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25967	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25969	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25970	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25975	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25976	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25977	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A
ND25979	B:B	B:A	B:A	B:A	B:A	B:A	B:A	B:A

Numerical Genotype

Collapse Non Major Alleles

Separate Alleles

Create Dataset Close

Steps for running PCA analysis

Buttons: Data, Analysis, Results, Delete, Wizard, Show Memory, Print, Help

Buttons: GPC, Load, Export, Sites, Taxa, Traits, Impute SNPs, **Transform**, Synonymizer, Join, Separate

- tht_FlapJack_genotype_MCL_align4
- tht_FlapJack_genotype_MCL_align5
- tht_FlapJack_genotype_MCL_align6
- tht_FlapJack_genotype_MCL_align7
- Polymorphisms
 - Numerical
 - geneticMap
 - traits
 - tht_FlapJack_genotype_MCL_Collasped
- Matrix
- Tree
- Fusions
- Synonymizer
- Result
 - Diversity
 - SNP Assays

Taxa	S0	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11
ND20448	0	0	0	0	0	0	0	0	0	0	0	0
ND24843	1	0	0	1	0	0	0	0	1	1	0	0
ND24890	1	0	0	1	0	0	0	0	1	1	0	0
ND24906	1	0	0	0	0	0	0	0	0	0	0	0
ND24978	0	0	0	0	0	0	0	0	0	0	0	0
ND25025	0	0	0	0	0	0	0	0	0	0	0	0
ND25030	0	0	0	0	0	0	0	0	0	0	0	0

Table Title: Phenotypes
Number of columns: 2321
Number of rows: 192
Number of elements: 445632

Dialog Box: Percent Missing Data

Column	Percent Missing Data
S0.null	0.52
S1.null	0.00
S2.null	0.00
S3.null	0.00
S4.null	0.00
S5.null	0.00
S6.null	6.77
S7.null	0.00
S8.null	0.00
S9.null	13.02
S10.null	0.00
S11.null	0.00
S12.null	1.04
S13.null	0.00
S14.null	0.00
S15.null	0.00
S16.null	0.00
S17.null	0.00
S18.null	0.00
S19.null	18.23
S20.null	0.00
S21.null	0.00
S22.null	0.00
S23.null	0.00
S24.null	0.52

Options: **Manhattan Distance**, Euclid Distance, Unweighted Average, Weighted Average

Number of Neighbors (K): 5
Min. Freq. of Row Data: 0.80

Buttons: Create Dataset, Close

Table

Table

LD Plot

LD Plot

LD Plot

LD Plot

Impute SNPs

Impute SNPs

ND25967	1	0	0	1	0	0	0	0	1	1	0	0
ND25969	1	0	0	1	0	0	0	0	1	1	0	0
ND25970	0	0	0	0	0	0	0	0	0	0	0	0
ND25975	0	0	0	0	0	0	0	0	0	0	0	0
ND25976	0	0	0	0	0	0	0	0	0	0	0	0
ND25977	1	0	0	1	0	0	0	0	1	1	0	0
ND25979	0	0	0	0	0	0	0	0	0	0	0	0
ND25982	0	0	0	0	0	0	0	0	0	0	0	0
ND25986	0	0	0	0	0	0	0	0	0	0	0	0
ND25988	0	0	0	0	0	0	0	0	0	0	0	0
ND25989	0	0	0	0	0	0	0	0	0	0	0	0
ND25996	0	0	0	0	0	0	0	0	0	0	0	0
ND25998	0	0	0	0	0	0	0	0	0	0	0	0
ND25999	0	0	0	0	0	0	0	0	0	0	0	0

- tht_FlapJack_genotype_MCL_align4
- tht_FlapJack_genotype_MCL_align5
- tht_FlapJack_genotype_MCL_align6
- tht_FlapJack_genotype_MCL_align7
- Polymorphisms
- Numerical
- geneticMap
- traits
- tht_FlapJack_genotype_MCL_Collasped
- tht_FlapJack_genotype_MCL_Collasped_2320_impute
- Matrix
- Tree
- Fusions
- Synonymizer
- ult
- Diversity

Table Title: Phenotypes
 Number of columns: 2321
 Number of rows: 192
 Number of elements: 445632

Imputed Phenotypic Values.
 Taxa with insufficient data: 0
 K = 50.8% cutoff):

Table

Table

LD Plot

LD Plot

LD Plot

LD Plot

Impute SNPs

Impute SNPs

Taxa	S0	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11
ND20448	0	0	0	0	0	0	0	0	0	0	0	0
ND24843	1	0	0	1	0	0	0	0	1	1	0	0
ND24890	1	0	0	1	0	0	0	0	1	1	0	0
ND24906	1	0	0	0	0	0	0	0	0	0	0	0
ND24978	0	0	0	0	0	0	0	0	0	0	0	0
ND25025	0	0	0	0	0	0	0	0	0	0	0	0
ND25030	0	0	0	0	0	0	0	0	0	0	0	0
ND25967	1	0	0	1	0	0	0	0	1	1	0	0
ND25969	1	0	0	1	0	0	0	0	1	1	0	0
ND25970	0	0	0	0	0	0	0	0	0	0	0	0
ND25975	0	0	0	0	0	0	0	0	0	0	0	0
ND25976	0	0	0	0	0	0	0	0	0	0	0	0
ND25977	1	0	0	1	0	0	0	0	1	1	0	0
ND25979	0	0	0	0	0	0	0	0	0	0	0	0
ND25982	0	0	0	0	0	0	0	0	0	0	0	0
ND25986	0	0	0	0	0	0	0	0	0	0	0	0
ND25988	0	0	0	0	0	0	0	0	0	0	0	0
ND25989	0	0	0	0	0	0	0	0	0	0	0	0
ND25996	0	0	0	0	0	0	0	0	0	0	0	0
ND25998	0	0	0	0	0	0	0	0	0	0	0	0
ND25999	0	0	0	0	0	0	0	0	0	0	0	0

Column Percent Missing Data

Column	Percent Missing Data
S0.null	0.00
S1.null	0.00
S2.null	0.00
S3.null	0.00
S4.null	0.00
S5.null	0.00
S6.null	0.00
S7.null	0.00
S8.null	0.00
S9.null	0.00
S10.null	0.00
S11.null	0.00
S12.null	0.00
S13.null	0.00
S14.null	0.00
S15.null	0.00
S16.null	0.00
S17.null	0.00
S18.null	0.00
S19.null	0.00
S20.null	0.00
S21.null	0.00
S22.null	0.00
S23.null	0.00
S24.null	0.00

Method

Correlation

Covariance

Output

Eigenvalue \geq 0

Var Prop % \geq 0.00043

Components = 10

Create Dataset Close

Data Analysis Results Delete Wizard Show Memory Save Print Help

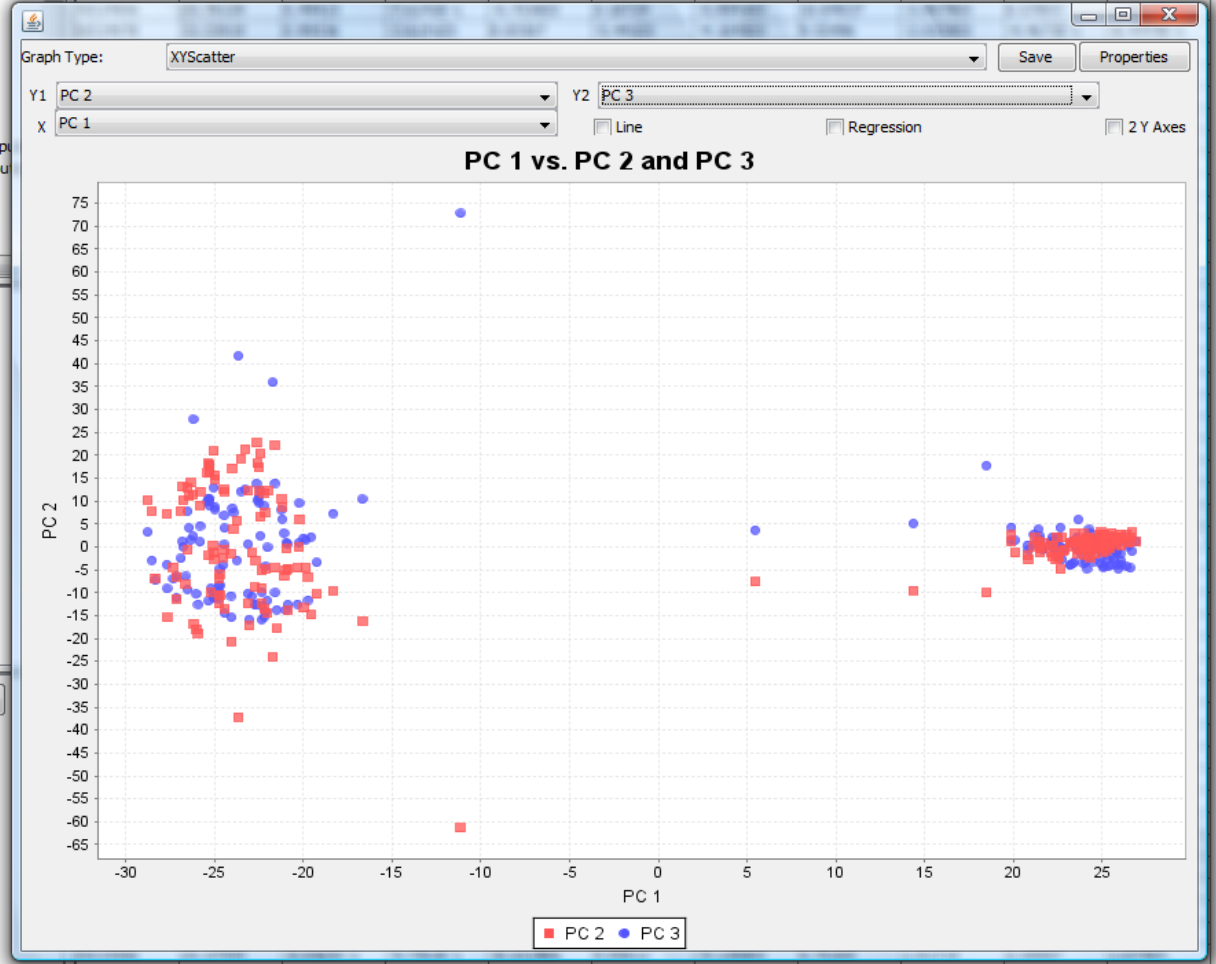
Table Tree Plot 2D Plot 3D Plot Chart QQ Plot Manhattan Plot

- tht_FlapJack_genotype_MCL_align4
- tht_FlapJack_genotype_MCL_align5
- tht_FlapJack_genotype_MCL_align6
- tht_FlapJack_genotype_MCL_align7
- Polymorphisms
- Numerical
 - geneticMap
 - traits
 - tht_FlapJack_genotype_MCL_Collasped
 - tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 - PC for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 - Eigenvectors for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 - Eigenvalues for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- Matrix
- Tree
- Fusions

Taxa	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9	PC 10
ND20448	23.95023	-5.7598E-1	1.609	-1.2456E1	5.49369	-5.7305E0	16.85857	-1.0623E1	9.41313	-5.1953E0
ND24843	23.85674	1.41352	-1.6796E0	4.31692	-4.7826E0	-2.1335E0	4.97187	0.18303	-4.2194E0	0.8734
ND24890	24.24628	2.3442E-2	3.78237	-8.2773E-1	-1.9448E0	-2.6866E0	2.22697	-1.3492E0	0.57101	-1.1231E0

Table Title: Phenotypes
 Number of columns: 11
 Number of rows: 192
 Number of elements: 2112
 Converted Column:

Procedure(s) applied:
 PCA Eigenvalues:



ND25988	23.61846	1.21791	-2.3808E-1	-5.2486E0	5.66293	-3.3975E0	2.68041	0.54295	2.15408	0.85715
ND25989	25.08941	1.02229	0.31821	-4.1679E0	4.14753	-3.0421E0	3.34315	1.54124	-1.4881E-1	0.94931
ND25996	23.55505	0.78353	-4.0614E-1	-3.8546E0	5.10696	-2.3283E0	3.57334	0.70312	-1.8565E-1	1.10169
ND25998	25.01045	-1.0733E0	1.06648	-1.1201E1	8.59548	-6.0455E0	6.95372	1.65485	0.8792	2.71499
ND25999	24.61013	-1.5628E0	1.72157	-1.1879E1	9.33142	-6.6098E0	7.64341	2.70156	1.92341	2.87924
ND26009	24.85966	-2.9434E-1	1.23014	-9.9189E0	7.26954	-3.099E0	3.22198	1.67386	6.3787	2.27229

- tht_FlapJack_genotype_MCL_align4
- tht_FlapJack_genotype_MCL_align5
- tht_FlapJack_genotype_MCL_align6
- tht_FlapJack_genotype_MCL_align7
- Polymorphisms
- Numerical
 - geneticMap
 - traits
- tht_FlapJack_genotype_MCL_Collasped
- tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- PC for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- Eigenvectors for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- Eigenvalues for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- Matrix
- Tree
- Fusions

PC	Eigenvalues	Individual ...	Cumulative...
1	568.22	0.24492	0.24492
2	104.38	0.044991	0.28991
3	93.529	0.040314	0.33023
4	78.340	0.033767	0.36399
5	72.459	0.031232	0.39523
6	57.201	0.024655	0.41988
7	56.116	0.024188	0.44407
8	51.417	0.022163	0.46623
9	49.775	0.021455	0.48769
10	47.299	0.020388	0.50807
11	43.608	0.018797	0.52687
12	36.626	0.015787	0.54266

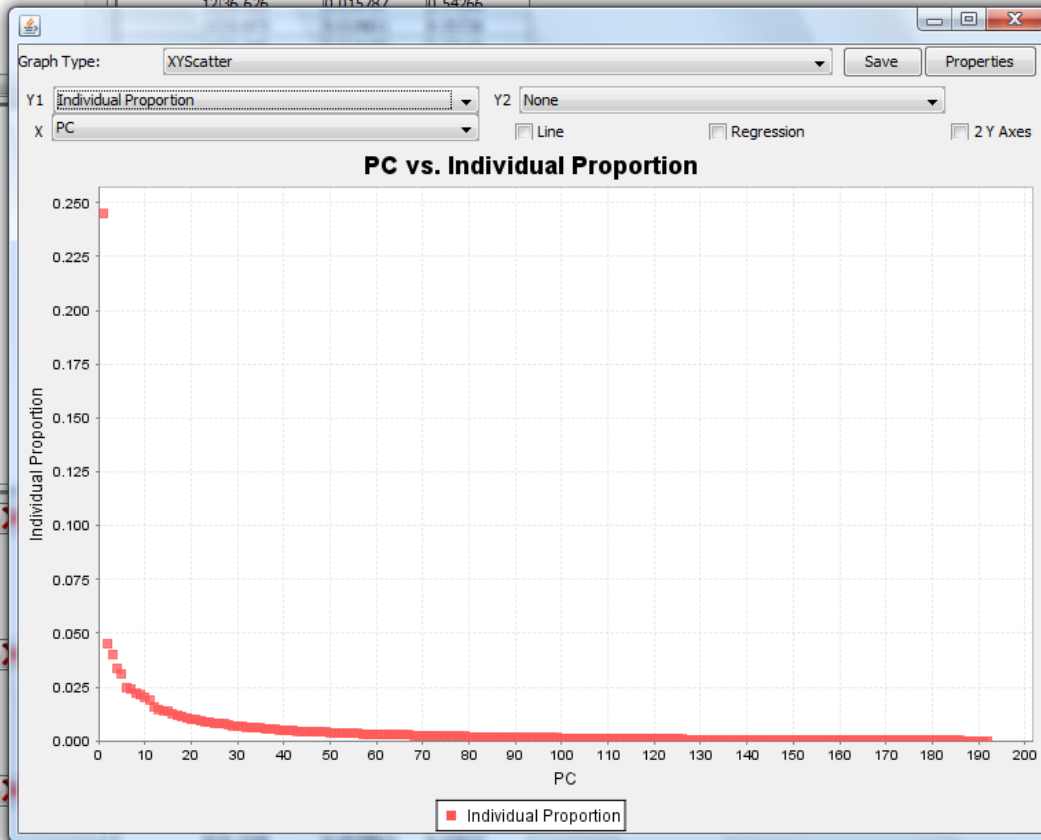
Table Title: Prop of Variance
 Number of columns: 4
 Number of rows: 192
 Number of elements: 768
 Converted Column:

Procedure(s) applied:
 PCA Eigenvalues:

Chart

LD Plot

Chart



51	9.0793	0.0039135	0.83015
52	8.7594	0.0037756	0.83392
53	8.5531	0.0036867	0.83761

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
 File Tools Help G_DPC

Data Analysis Results Delete Wizard Show Memory

Table Tree Plot 2D Plot LD Plot Chart QQ Plot Manhattan Plot

- tht_FlapJack_genotype_MCL_align5
- tht_FlapJack_genotype_MCL_align6
- tht_FlapJack_genotype_MCL_align7
- Polymorphisms
 - Numerical
 - geneticMap
 - traits
 - tht_FlapJack_genotype_MCL_Collasped
 - tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 - PC for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 - Eigenvectors for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 - Eigenvalues for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- Matrix
- Tree
- Fusions
- Synonymizer

Table Title: Phenotypes
 Number of columns: 58
 Number of rows: 96
 Number of elements: 5568

Taxa	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	p
ND20448	5.0572E3	NaN	NaN	4.8151E3	NaN	NaN	3.6907E3	NaN	NaN	NaN	10
HARRINGTON	4.0511E3	4.1534E3	3.8951E3	4.5138E3	4.3847E3	3.6476E3	4.5192E3	4.5084E3	4.6322E3	4.7505E3	89
BARONESSE	5.5952E3	5.2616E3	5.0195E3	5.0841E3	4.2932E3	4.8312E3	4.417E3	5.2616E3	5.3961E3	4.8474E3	86
ROBUST	4.6107E3	5.9664E3	4.8259E3	4.7075E3	4.6322E3	4.6967E3	3.1419E3	3.2119E3	3.5293E3	3.8951E3	10
ND24843	NaN	4.9604E3	NaN	NaN	4.1372E3	NaN	NaN	3.4862E3	NaN	4.9227E3	10
ND24890	NaN	5.3047E3	NaN	NaN	4.7774E3	NaN	NaN	3.879E3	NaN	5.154E3	10
ND24906	NaN	5.7028E3	NaN	NaN	4.6806E3	NaN	NaN	4.035E3	NaN	4.616E3	10
ND24978	NaN	5.7512E3	NaN	NaN	5.2401E3	NaN	NaN	4.0458E3	NaN	4.7828E3	10
ND25025	NaN	6.2247E3	NaN	NaN	5.0357E3	NaN	NaN	4.7667E3	NaN	4.6645E3	10
ND25030	NaN	5.8696E3	NaN	NaN	4.7882E3	NaN	NaN	4.3847E3	NaN	4.6645E3	10
ND25033	NaN	6.2785E3	NaN	NaN	5.2025E3	NaN	NaN	4.1211E3	NaN	4.4923E3	10
ND25148	NaN	5.0195E3	NaN	NaN	5.0733E3	NaN	NaN	4.0189E3	NaN	5.3531E3	10
ND25151	NaN	5.5037E3	NaN	NaN	4.729E3	NaN	NaN	4.6053E3	NaN	4.1426E3	10
ND25152	NaN	5.7243E3	NaN	NaN	4.4331E3	NaN	NaN	3.7391E3	NaN	4.7613E3	10
ND25153	NaN	5.6006E3	NaN	NaN	4.5461E3	NaN	NaN	4.0189E3	NaN	4.4224E3	10
ND25160	NaN	6.1816E3	NaN	NaN	4.9657E3	NaN	NaN	4.2394E3	NaN	5.068E3	10
ND25161	NaN	5.2885E3	NaN	NaN	4.885E3	NaN	NaN	4.0727E3	NaN	3.7875E3	10
ND25163	NaN	5.9288E3	NaN	NaN	4.6806E3	NaN	NaN	4.148E3	NaN	4.4654E3	10
ND25165	NaN	5.6598E3	NaN	NaN	4.5676E3	NaN	NaN	4.4439E3	NaN	4.2556E3	10
ND25172	NaN	5.7136E3	NaN	NaN	4.5676E3	NaN	NaN	4.1157E3	NaN	4.1265E3	10
ND25205	NaN	6.1224E3	NaN	NaN	4.8689E3	NaN	NaN	3.809E3	NaN	4.8528E3	10
ND25208	NaN	5.4338E3	NaN	NaN	5.2778E3	NaN	NaN	4.3955E3	NaN	4.7774E3	10
ND25220	NaN	5.9718E3	NaN	NaN	5.4015E3	NaN	NaN	4.1856E3	NaN	4.6322E3	10
ND25768	NaN	NaN	5.0518E3	NaN	NaN	5.2455E3	NaN	NaN	4.1426E3	NaN	10
ND25786	NaN	NaN	5.224E3	NaN	NaN	4.5461E3	NaN	NaN	3.9274E3	NaN	10
ND25805	NaN	NaN	5.0949E3	NaN	NaN	5.1702E3	NaN	NaN	4.035E3	NaN	10
ND25824	NaN	NaN	6.0686E3	NaN	NaN	4.9926E3	NaN	NaN	4.4977E3	NaN	10
ND25825	NaN	NaN	5.2724E3	NaN	NaN	5.0464E3	NaN	NaN	4.3632E3	NaN	10
ND25826	NaN	NaN	5.8534E3	NaN	NaN	5.1756E3	NaN	NaN	4.6591E3	NaN	10
3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	10
3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	10
3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	10
3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	10
3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	10
3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	10
3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	10
3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	10
3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	10
ND25967	NaN	NaN	4.8743E3	NaN	NaN	4.616E3	NaN	NaN	4.2663E3	NaN	10
ND25969	NaN	NaN	4.9442E3	NaN	NaN	4.5084E3	NaN	NaN	3.3195E3	NaN	10
ND25970	NaN	NaN	5.4392E3	NaN	NaN	5.2885E3	NaN	NaN	3.6961E3	NaN	10
ND25975	NaN	NaN	5.4015E3	NaN	NaN	4.8528E3	NaN	NaN	4.4493E3	NaN	10
ND25977	NaN	NaN	4.5084E3	NaN	NaN	4.4977E3	NaN	NaN	3.7768E3	NaN	10
ND25979	NaN	NaN	4.4493E3	NaN	NaN	4.9173E3	NaN	NaN	3.7337E3	NaN	10
ND25982	NaN	NaN	4.6107E3	NaN	NaN	4.3363E3	NaN	NaN	3.54E3	NaN	10
ND25986	NaN	NaN	5.2509E3	NaN	NaN	5.1164E3	NaN	NaN	3.9866E3	NaN	10
ND25988	NaN	NaN	5.2509E3	NaN	NaN	4.3363E3	NaN	NaN	3.0451E3	NaN	10
ND25989	NaN	NaN	4.8474E3	NaN	NaN	4.8797E3	NaN	NaN	3.8359E3	NaN	10
ND25996	NaN	NaN	5.6867E3	NaN	NaN	4.9442E3	NaN	NaN	4.2986E3	NaN	10
ND25998	NaN	NaN	4.955E3	NaN	NaN	5.6867E3	NaN	NaN	3.8736E3	NaN	10
ND25999	NaN	NaN	5.5844E3	NaN	NaN	5.4876E3	NaN	NaN	4.4654E3	NaN	10
ND26000	NaN	NaN	4.9819E3	NaN	NaN	4.4869E3	NaN	NaN	3.4324E3	NaN	10

Program Status

With multiple location data, GLM or MLM will be faster if entry means are calculated first using GLM for BLUES or other software for calculating BLUPs

- tht_FlapJack_genotype_MCL_align3
- tht_FlapJack_genotype_MCL_align4
- tht_FlapJack_genotype_MCL_align5
- tht_FlapJack_genotype_MCL_align6
- tht_FlapJack_genotype_MCL_align7
- Polymorphisms
- Numerical
 - geneticMap
 - traits
 - tht_FlapJack_genotype_MCL_Collapsed
 - tht_FlapJack_genotype_MCL_Collapsed_2320_imputed
 - PC for tht_FlapJack_genotype_MCL_Collapsed_2320_imputed
 - Eigenvectors for tht_FlapJack_genotype_MCL_Collapsed_2320_imputed
 - Eigenvalues for tht_FlapJack_genotype_MCL_Collapsed_2320_imputed
- Matrix
- Tree

Table Title: Phenotypes
 Number of columns: 58
 Number of rows: 96
 Number of elements: 5568

Sites

Traits

Taxa	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	p
ND20448	5.0572E3	NaN	NaN	4.8151E3	NaN	NaN	3.6907E3	NaN	NaN	NaN	10
HARRINGTON	4.0511E3	4.1534E3	3.8951E3	4.5138E3	4.3847E3	3.6476E3	4.5192E3	4.5084E3	4.6322E3	4.7505E3	89
BARONESSE	5.5952E3	5.2616E3	5.0195E3	5.0841E3	4.2932E3	4.8312E3	4.417E3	5.2616E3	5.3961E3	4.8474E3	80
ROBUST	4.6107E3	5.9664E3	4.8259E3	4.7075E3	4.6322E3	4.6967E3	3.1419E3	3.2119E3	3.5293E3	3.8951E3	10
	NaN	3.4862E3	NaN	4.9227E3	NaN	NaN	NaN	3.879E3	NaN	5.154E3	NaN
	NaN	4.035E3	NaN	4.616E3	NaN	NaN	NaN	4.0458E3	NaN	4.7828E3	NaN
	NaN	4.7667E3	NaN	4.6645E3	NaN	NaN	NaN	4.3847E3	NaN	4.6645E3	NaN
	NaN	4.1211E3	NaN	4.4923E3	NaN	NaN	NaN	4.0189E3	NaN	5.3531E3	NaN
	NaN	4.6053E3	NaN	4.1426E3	NaN	NaN	NaN	4.6053E3	NaN	4.1426E3	NaN
	NaN	3.7391E3	NaN	4.7613E3	NaN	NaN	NaN	4.0189E3	NaN	4.4224E3	NaN
	NaN	4.2394E3	NaN	5.068E3	NaN	NaN	NaN	4.0727E3	NaN	3.7875E3	NaN
	NaN	4.148E3	NaN	4.4654E3	NaN	NaN	NaN	4.4439E3	NaN	4.2556E3	NaN
	NaN	4.1157E3	NaN	4.1265E3	NaN	NaN	NaN	4.1157E3	NaN	4.1265E3	NaN
	NaN	3.809E3	NaN	4.8528E3	NaN	NaN	NaN	4.3955E3	NaN	4.7774E3	NaN
	NaN	4.1856E3	NaN	4.6322E3	NaN	NaN	NaN	NaN	NaN	4.1426E3	NaN
	NaN	NaN	4.1426E3	NaN	NaN	NaN	NaN	NaN	NaN	3.9274E3	NaN
	NaN	NaN	4.035E3	NaN	NaN	NaN	NaN	NaN	NaN	4.035E3	NaN
	NaN	NaN	4.4977E3	NaN	NaN	NaN	NaN	NaN	NaN	4.4977E3	NaN
	NaN	NaN	4.3632E3	NaN	NaN	NaN	NaN	NaN	NaN	4.3632E3	NaN
	NaN	NaN	4.6591E3	NaN	NaN	NaN	NaN	NaN	NaN	4.6591E3	NaN
	NaN	NaN	4.1426E3	NaN	NaN	NaN	NaN	NaN	NaN	4.1426E3	NaN
	NaN	NaN	3.7768E3	NaN	NaN	NaN	NaN	NaN	NaN	3.7768E3	NaN
	NaN	NaN	4.53E3	NaN	NaN	NaN	NaN	NaN	NaN	4.53E3	NaN
	NaN	NaN	4.6483E3	NaN	NaN	NaN	NaN	NaN	NaN	4.6483E3	NaN
	NaN	NaN	4.4815E3	NaN	NaN	NaN	NaN	NaN	NaN	4.4815E3	NaN
	NaN	NaN	4.6429E3	NaN	NaN	NaN	NaN	NaN	NaN	4.6429E3	NaN
	NaN	NaN	4.0727E3	NaN	NaN	NaN	NaN	NaN	NaN	4.0727E3	NaN
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	NaN	NaN	3.54E3	NaN	NaN	NaN	NaN	NaN	NaN	3.54E3	NaN
	NaN	NaN	3.9866E3	NaN	NaN	NaN	NaN	NaN	NaN	3.9866E3	NaN
	NaN	NaN	3.0451E3	NaN	NaN	NaN	NaN	NaN	NaN	3.0451E3	NaN
	NaN	NaN	3.8359E3	NaN	NaN	NaN	NaN	NaN	NaN	3.8359E3	NaN
	NaN	NaN	4.2986E3	NaN	NaN	NaN	NaN	NaN	NaN	4.2986E3	NaN
	NaN	NaN	3.8736E3	NaN	NaN	NaN	NaN	NaN	NaN	3.8736E3	NaN
	NaN	NaN	4.4654E3	NaN	NaN	NaN	NaN	NaN	NaN	4.4654E3	NaN
	NaN	NaN	4.4815E3	NaN	NaN	NaN	NaN	NaN	NaN	4.4815E3	NaN

Filter Traits / Modify Trait Properties

Trait	env	Type	Discrete	Include
grain_yield	Expt1_2008_Carrington	data	<input type="checkbox"/>	<input checked="" type="checkbox"/>
grain_yield	Expt2_2008_Carrington	data	<input type="checkbox"/>	<input checked="" type="checkbox"/>
grain_yield	Expt3_2008_Carrington	data	<input type="checkbox"/>	<input checked="" type="checkbox"/>
grain_yield	Expt1_2008_Fargo	data	<input type="checkbox"/>	<input checked="" type="checkbox"/>
grain_yield	Expt2_2008_Fargo	data	<input type="checkbox"/>	<input checked="" type="checkbox"/>
grain_yield	Expt3_2008_Fargo	data	<input type="checkbox"/>	<input checked="" type="checkbox"/>
grain_yield	Expt1_2008_Minot	data	<input type="checkbox"/>	<input checked="" type="checkbox"/>
grain_yield	Expt2_2008_Minot	data	<input type="checkbox"/>	<input checked="" type="checkbox"/>
grain_yield	Expt3_2008_Minot	data	<input type="checkbox"/>	<input checked="" type="checkbox"/>
grain_yield	Expt2_2008_Ray	data	<input type="checkbox"/>	<input checked="" type="checkbox"/>
plant_height	Expt1_2008_Carrington	data	<input type="checkbox"/>	<input type="checkbox"/>
plant_height	Expt2_2008_Carrington	data	<input type="checkbox"/>	<input type="checkbox"/>
plant_height	Expt3_2008_Carrington	data	<input type="checkbox"/>	<input type="checkbox"/>
plant_height	Expt1_2008_Fargo	data	<input type="checkbox"/>	<input type="checkbox"/>
plant_height	Expt2_2008_Fargo	data	<input type="checkbox"/>	<input type="checkbox"/>
plant_height	Expt3_2008_Fargo	data	<input type="checkbox"/>	<input type="checkbox"/>
plant_height	Expt1_2008_Minot	data	<input type="checkbox"/>	<input type="checkbox"/>
plant_height	Expt2_2008_Minot	data	<input type="checkbox"/>	<input type="checkbox"/>
plant_height	Expt3_2008_Minot	data	<input type="checkbox"/>	<input type="checkbox"/>
plant_height	Expt2_2008_Ray	data	<input type="checkbox"/>	<input type="checkbox"/>
heading_date	Expt1_2008_Carrington	data	<input type="checkbox"/>	<input type="checkbox"/>
heading_date	Expt2_2008_Carrington	data	<input type="checkbox"/>	<input type="checkbox"/>
heading_date	Expt3_2008_Carrington	data	<input type="checkbox"/>	<input type="checkbox"/>
heading_date	Expt1_2008_Fargo	data	<input type="checkbox"/>	<input type="checkbox"/>
heading_date	Expt2_2008_Fargo	data	<input type="checkbox"/>	<input type="checkbox"/>

- tht_FlapJack_genotype_MCL_align3
- tht_FlapJack_genotype_MCL_align4
- tht_FlapJack_genotype_MCL_align5
- tht_FlapJack_genotype_MCL_align6
- tht_FlapJack_genotype_MCL_align7
- Polymorphisms
 - Numerical
 - geneticMap
 - traits
 - tht_FlapJack_genotype_MCL_Collasped
 - tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 - PC for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 - Eigenvectors for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 - Eigenvalues for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 - Filtered_traits
 - Matrix

Taxa	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...	grain_yield...
ND20448	5.0572E3	NaN	NaN	4.8151E3	NaN	NaN	3.6907E3	NaN	NaN
HARRINGTON	4.0511E3	4.1534E3	3.8951E3	4.5138E3	4.3847E3	3.6476E3	4.5192E3	4.5084E3	4.6322E3
BARONESSE	5.5952E3	5.2616E3	5.0195E3	5.0841E3	4.2932E3	4.8312E3	4.417E3	5.2616E3	5.3961E3
ROBUST	4.6107E3	5.9664E3	4.8259E3	4.7075E3	4.6322E3	4.6967E3	3.1419E3	3.2119E3	3.5293E3
ND24843	NaN	4.9604E3	NaN	NaN	4.1372E3	NaN	NaN	3.4862E3	NaN
ND24890	NaN	5.3047E3	NaN	NaN	4.7774E3	NaN	NaN	3.879E3	NaN
ND24906	NaN	5.7028E3	NaN	NaN	4.6806E3	NaN	NaN	4.035E3	NaN
ND24978	NaN	5.7512E3	NaN	NaN	5.2401E3	NaN	NaN	4.0458E3	NaN
ND25025	NaN	6.2247E3	NaN	NaN	5.0357E3	NaN	NaN	4.7667E3	NaN
ND25030	NaN	5.8696E3	NaN	NaN	4.7882E3	NaN	NaN	4.3847E3	NaN
ND25033	NaN	6.2785E3	NaN	NaN	5.2025E3	NaN	NaN	4.1211E3	NaN
ND25148	NaN	5.0195E3	NaN	NaN	5.0733E3	NaN	NaN	4.0189E3	NaN
ND25151	NaN	5.5037E3	NaN	NaN	4.729E3	NaN	NaN	4.6053E3	NaN
ND25152	NaN	5.7243E3	NaN	NaN	4.4331E3	NaN	NaN	3.7391E3	NaN
ND25153	NaN	5.6006E3	NaN	NaN	4.5461E3	NaN	NaN	4.0189E3	NaN
ND25160	NaN	6.1816E3	NaN	NaN	4.9657E3	NaN	NaN	4.2394E3	NaN
ND25161	NaN	5.2885E3	NaN	NaN	4.885E3	NaN	NaN	4.0727E3	NaN
ND25163	NaN	5.9288E3	NaN	NaN	4.6806E3	NaN	NaN	4.148E3	NaN
ND25165	NaN	5.6598E3	NaN	NaN	4.5676E3	NaN	NaN	4.4439E3	NaN
ND25271	NaN	NaN	5.0008E3	NaN	NaN	4.9920E3	NaN	NaN	4.1426E3
ND25825	NaN	NaN	5.2724E3	NaN	NaN	5.0464E3	NaN	NaN	3.9274E3
ND25826	NaN	NaN	5.8534E3	NaN	NaN	5.1756E3	NaN	NaN	4.035E3
ND25835	NaN	NaN	5.6867E3	NaN	NaN	5.4715E3	NaN	NaN	4.4977E3
ND25839	NaN	NaN	4.7452E3	NaN	NaN	4.9442E3	NaN	NaN	4.3632E3
ND25840	NaN	NaN	6.2408E3	NaN	NaN	6.0633E3	NaN	NaN	4.6591E3
ND25843	NaN	NaN	5.875E3	NaN	NaN	5.1056E3	NaN	NaN	4.1426E3
ND25882	NaN	NaN	5.1379E3	NaN	NaN	5.4069E3	NaN	NaN	3.7768E3
ND25908	NaN	NaN	5.2885E3	NaN	NaN	3.4916E3	NaN	NaN	4.53E3
ND25917	NaN	NaN	5.1756E3	NaN	NaN	4.7882E3	NaN	NaN	4.6483E3
ND25949	NaN	NaN	4.885E3	NaN	NaN	4.616E3	NaN	NaN	4.4815E3
ND25966	NaN	NaN	4.2663E3	NaN	NaN	4.6376E3	NaN	NaN	4.6429E3
ND25967	NaN	NaN	4.8743E3	NaN	NaN	4.616E3	NaN	NaN	4.0727E3
ND25969	NaN	NaN	4.9442E3	NaN	NaN	4.5084E3	NaN	NaN	3.9328E3
ND25970	NaN	NaN	5.4392E3	NaN	NaN	5.2885E3	NaN	NaN	3.4862E3
ND25975	NaN	NaN	5.4015E3	NaN	NaN	4.8528E3	NaN	NaN	4.2663E3
ND25977	NaN	NaN	4.5084E3	NaN	NaN	4.4977E3	NaN	NaN	3.3195E3
ND25979	NaN	NaN	4.4493E3	NaN	NaN	4.9173E3	NaN	NaN	3.6961E3
ND25982	NaN	NaN	4.6107E3	NaN	NaN	4.3363E3	NaN	NaN	4.4493E3
ND25986	NaN	NaN	5.2509E3	NaN	NaN	5.1164E3	NaN	NaN	3.7768E3
ND25988	NaN	NaN	5.2509E3	NaN	NaN	4.3363E3	NaN	NaN	3.7337E3
ND25989	NaN	NaN	4.8474E3	NaN	NaN	4.8797E3	NaN	NaN	3.54E3
ND25996	NaN	NaN	5.6867E3	NaN	NaN	4.9442E3	NaN	NaN	3.9866E3
ND25998	NaN	NaN	4.955E3	NaN	NaN	5.6867E3	NaN	NaN	3.0451E3
ND25999	NaN	NaN	5.5844E3	NaN	NaN	5.4876E3	NaN	NaN	3.8359E3
ND26009	NaN	NaN	4.9819E3	NaN	NaN	4.4869E3	NaN	NaN	4.2986E3
ND26010	NaN	NaN	4.842E3	NaN	NaN	4.6698E3	NaN	NaN	3.8736E3
									4.4654E3
									3.4324E3
									3.7552E3

Calculate BLUES

The data set you have selected does not contain any marker data. Do you want to calculate BLUES (best linear unbiased estimates) of the phenotypes?

Table Title: Phenotypes
 Number of columns: 10
 Number of rows: 96
 Number of elements: 960

Sites

GLM

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83

File Tools Help GDPC

GDPC
 Load
 Export
 Sites
 Taxa
 Traits
 Impute SNPs
 Transform
 Synonymizer
 Join
 n Join
 Separate

Filtered_traits
 Filtered_PC for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
 Matrix
 Tree
 Fusions
 Synonymizer
 Result
 Diversity
 SNP Assays
 LD
 LD:tht_FlapJack_genotype_MCL_align0
 LD:tht_FlapJack_genotype_MCL_align0_chr1H_17260-50600
 Association
 Phenotype ANOVA from Filtered_traits
 BLUEs Filtered_traits
 Variances

Taxa	grain_yield
BARONESSE	5.0177E3
HARRINGTON	4.2562E3
ND20448	4.5531E3
ND24843	4.1119E3
ND24890	4.571E3
ND24906	4.7234E3
ND24978	4.9297E3
ND25025	5.2596E3
ND25030	4.9315E3
ND25033	5.118E3
ND25148	4.6212E3
ND25151	4.8633E3
ND25152	4.5495E3
ND25153	4.6392E3
ND25160	5.0462E3
ND25161	4.6661E3
ND25163	4.8364E3
ND25165	4.8077E3
ND25172	4.7163E3
ND25205	4.8508E3
ND25208	4.953E3
ND25220	5.1036E3
ND25768	4.8639E3
ND25786	4.6164E3
ND25805	4.8173E3
ND25824	5.2369E3
ND25825	4.9446E3
ND25826	5.28E3
ND25835	5.1509E3
ND25839	4.5393E3
ND25840	5.662E3
ND25843	5.2602E3
ND25882	5.0594E3
ND25908	4.525E3
ND25917	4.7294E3
ND25949	4.5286E3
ND25966	4.1807E3
ND25967	4.6362E3
ND25969	4.308E3
ND25970	4.8585E3
ND25975	4.9518E3
ND25977	4.3116E3
ND25979	4.4174E3
ND25982	4.2129E3
ND25986	4.8352E3
ND25988	4.2614E3
ND25989	4.5716E3
ND25996	5.0271E3
ND25998	4.889E3
ND25999	5.2298E3
ND26009	4.351E3
ND26010	4.473E3
ND26015	4.8424E3

Table Title: Phenotypes
 Number of columns: 2
 Number of rows: 93
 Number of elements: 186
 BLUEs calculated from Filtered_traits

Program Status

Join the resulting data set with marker and, optionally, population structure covariates

- Sequence
- snpfile
 - tht_FlapJack_genotype_MCL
 - tht_FlapJack_genotype_MCL_align0
 - tht_FlapJack_genotype_MCL_align1
 - tht_FlapJack_genotype_MCL_align2
 - tht_FlapJack_genotype_MCL_align3
 - tht_FlapJack_genotype_MCL_align4
 - tht_FlapJack_genotype_MCL_align5
 - tht_FlapJack_genotype_MCL_align6
 - tht_FlapJack_genotype_MCL_align7
 - BLUES_Filtered_traits + Filtered_PC for tht_FlapJack_genotype_MCL_Collapses

- Polymorphisms
- Numerical
 - geneticMap

Number of sequences: 90
 Number of sites: 2320
 Data type: Text
 Loci: 1H, 2H, 3H, 4H, 5H, 6H, 7H, UNK
 Table Title: Phenotypes and Genotypes
 Number of columns: 6
 Number of rows: 90
 Number of elements: 540
 Intersect Join

GLM

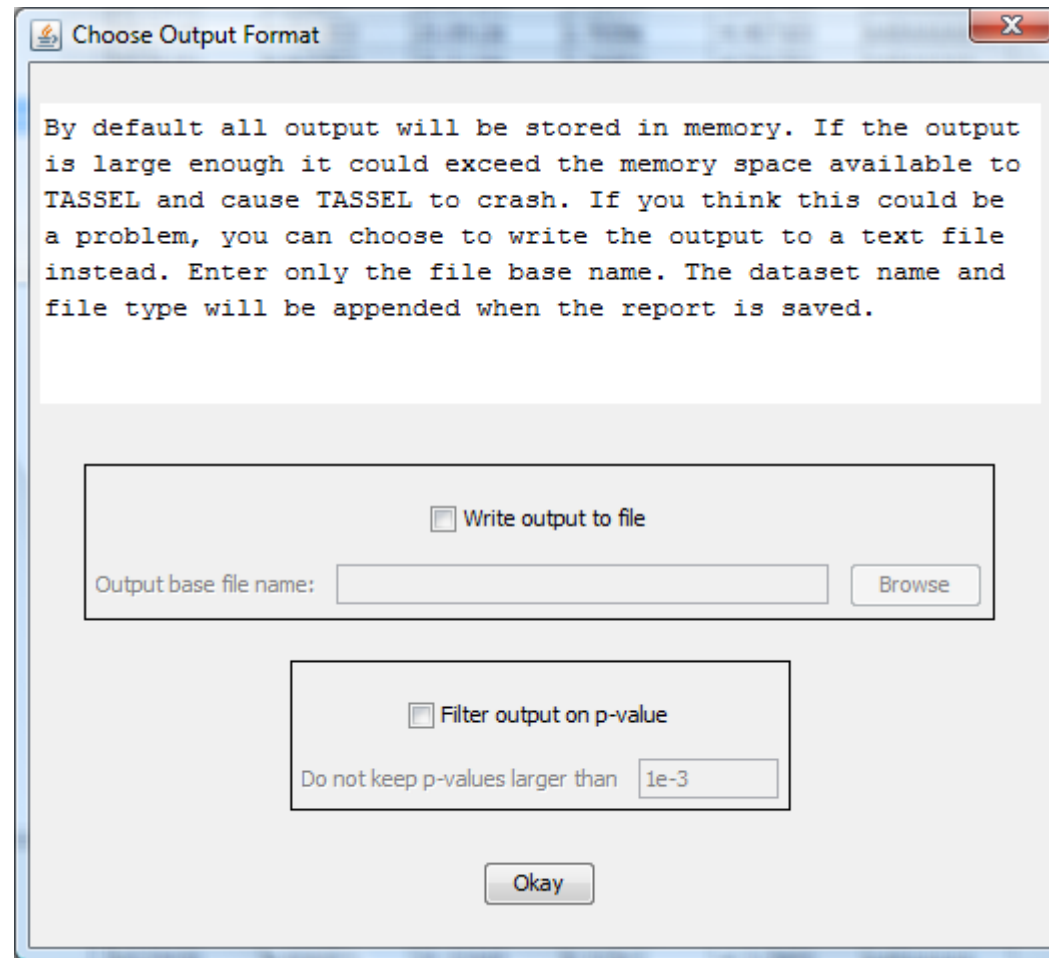
Taxa	grain_yield	PC 1	PC 2	PC 3	Haplotype
ND20448	4.5531E3	23.95023	-5.7598E-1	1.609	AABAAAAA...
ND24843	4.1119E3	23.85674	1.41352	-1.6796E0	BABAAAAAB...
ND24890	4.571E3	24.24628	2.3442E-2	3.78237	BABAAAAAB...
ND24906	4.7234E3	25.78159	0.49923	-7.6242E-1	BABAAAAA...
ND24978	4.9297E3	23.33919	0.99536	-3.6191E0	AABAAAAA...
ND25025	5.2596E3	24.15292	2.21206	-4.764E0	AABAAAAA...
ND25030	4.9315E3	25.68292	2.06961	-2.7292E0	AABAAAAA...
ND25033	5.118E3	26.67351	3.15703	-1.0104E0	AABAAAAA...
ND25148	4.6212E3	25.09126	2.70596	-4.4071E0	AABAAAAA...
ND25151	4.8633E3	25.51196	2.26901	-4.0667E0	AABAAAAA...
ND25152	4.5495E3	25.92034	1.9962	-4.7732E0	AABAAAAA...
ND25153	4.6392E3	26.56552	1.94752	-4.6219E0	AABAAAAA...
ND25160	5.0462E3	25.07346	1.89335	-4.3234E0	AABAAAAA...
ND25161	4.6661E3	24.90147	2.47547	-3.66E0	AABAAAAA...
ND25163	4.8364E3	26.07802	1.7467	-3.8583E0	AABAAAAA...
ND25165	4.8077E3	26.361	2.63197	-4.3072E0	AABAAAAA...
ND25172	4.7163E3	25.83584	1.38204	-3.9961E0	AABAAAAA...
ND25205	4.8508E3	23.43387	2.9879	-3.3992E0	AABAAAAA...
ND25208	4.953E3	26.05	2.78447	-2.9104E0	AABAAAAA...
ND25220	5.1036E3	24.95151	3.25894	-2.4413E0	AABAAAAA...
ND25768	4.8639E3	21.65103	4.9116E-2	-6.468E-1	AABAAAAA...
ND25786	4.6164E3	22.79478	-9.9531E-1	-2.6225E-1	AABAAAAA...
ND25805	4.8173E3	22.87223	-6.318E-1	-5.1623E-1	BABAAAAAB...
ND25824	5.2369E3	22.19654			
ND25825	4.9446E3	22.16704			
ND25826	5.28E3	22.49347			
ND25835	5.1509E3	23.97525			
ND25839	4.5393E3	23.97583			
ND25840	5.662E3	22.0943			
ND25843	5.2602E3	21.67394			
ND25882	5.0594E3	23.57			
ND25908	4.525E3	23.64608			
ND25917	4.7294E3	21.47679	-4.3761E-1	2.36163	AABAAAAA...
ND25949	4.5286E3	20.08553	-1.3448E0	1.37971	AABAAAAA...
ND25966	4.1807E3	24.48066	0.26432	-3.1968E0	BABAAAAAB...
ND25967	4.6362E3	24.06843	1.8913E-4	-3.3596E0	BABAAAAAB...
ND25969	4.308E3	22.53983	-1.4921E0	-2.2324E0	BABAAAAAB...
ND25970	4.8585E3	25.32585	0.11257	-4.2176E0	AABAAAAA...
ND25975	4.9518E3	25.53924	3.04817	-2.1169E0	AABAAAAA...
ND25977	4.3116E3	25.26865	0.48787	-2.6149E0	BABAAAAAB...
ND25979	4.4174E3	25.8376	1.07109	-1.2247E0	AABAAAAA...
ND25982	4.2129E3	26.4787	1.08936	0.62356	AABAAAAA...
ND25986	4.8352E3	25.37444	-8.6586E-2	-4.7402E-1	AABAAAAA...
ND25988	4.2614E3	23.61846	1.21791	-2.3808E-1	AABAAAAA...
ND25989	4.5716E3	25.08941	1.02229	0.31821	AABAAAAA...
ND25996	5.0271E3	23.55505	0.78353	-4.0614E-1	AABAAAAA...
ND25998	4.889E3	25.01045	-1.0733E0	1.06648	AABAAAAA...
ND25999	5.2298E3	24.61013	-1.5628E0	1.72157	AABAAAAA...
ND26009	4.351E3	24.85966	-2.9434E-1	1.23014	AABAAAAA...
ND26010	4.473E3	23.2853	0.11584	1.26841	AABAAAAA...
ND26015	4.8424E3	20.83769	-2.782E0	-5.6755E-1	AABAAAAA...
ND26017	4.9105E3	22.63618	-4.9141E0	4.21739	AABAAAAA...
ND26030	4.4801E3	24.31001	-2.3722E0	3.10949	BABAAAAAB...

GLM Options

Use permutation test for markers

Number of Permutations:

Option for saving output to disk for large files



- Tree
- Fusions
- Synonymizer
- Ult
- Diversity
- SNP Assays
- LD
- LD:tht_FlapJack_genotype_M
- LD:tht_FlapJack_genotype_M
- Association
- Phenotype ANOVA from Filter
- BLUEs_Filtered_traits
- GLM_marker_test_BLUEs_Filtered_traits
- GLM allele estimates for BLUEs
- Variances
- Stepwise

Table Title: Marker Test

Number of columns: 14

Number of rows: 2320

Number of elements: 32640

Tests of Marker-Phenotype Association

Data set: BLUEs_Filtered_traits

model: trait = mean +

Trait	Marker	Location	marker_F	marker_p	perm_p	markerR2	markerDF	markerMS	errorDF	errorMS	modelDF	modelMS
grain_yield	11_10259	1H	47470	0.19401	0.82402	1	4.5326E-3	2	7.6767E4	84	3.9569E5	1.27E5
grain_yield	11_10526	1H	47470	1.26701	0.2635	1	1.4478E-2	1	4.9043E5	85	3.8707E5	2.4297E5
grain_yield	11_10294	1H	47470	0.13772	0.71148	1	1.5946E-3	1	5.4016E4	85	3.9221E5	1.3387E5
grain_yield	12_10235	1H	47470	1.38844	0.24196	1	1.5844E-2	1	5.3667E5	85	3.8653E5	2.5453E5
grain_yield	12_31467	1H	47470	1.1592	0.28468	1	1.3263E-2	1	4.4926E5	85	3.8756E5	2.3268E5
grain_yield	12_30796	1H	47470	0.83909	0.43569	1	1.9309E-2	2	3.2702E5	84	3.8974E5	2.271E5
grain_yield	12_30683	1H	47470	1.1592	0.28468	1	1.3263E-2	1	4.4926E5	85	3.8756E5	2.3268E5
grain_yield	11_20855	1H	49340	1.38844	0.24196	1	1.5844E-2	1	5.3667E5	85	3.8653E5	2.5453E5
grain_yield	11_10957	1H	49340	0.87246	0.42172	1	2.029E-2	2	3.4322E5	83	3.9339E5	2.3607E5
grain_yield	11_11064	1H	49340	1.38844	0.24196	1	1.5844E-2	1	5.3667E5	85	3.8653E5	2.5453E5
grain_yield	12_11301	1H	49340	1.61372	0.20744	1	1.8366E-2	1	6.2213E5	85	3.8553E5	2.7589E5
grain_yield	11_10470	1H	49700	0.81122	0.44776	1	1.868E-2	2	3.1637E5	84	3.8999E5	2.2284E5
grain_yield	12_10159	1H	49700	1.38844	0.24196	1	1.5844E-2	1	5.3667E5	85	3.8653E5	2.5453E5
grain_yield	12_30762	1H	49700	0.85581	0.35753	1	9.8264E-3	1	3.3285E5	85	3.8893E5	2.0357E5
grain_yield	12_30438	1H	49700	1.38844	0.24196	1	1.5844E-2	1	5.3667E5	85	3.8653E5	2.5453E5
grain_yield	12_30436	1H	49700	0.85581	0.35753	1	9.8264E-3	1	3.3285E5	85	3.8893E5	2.0357E5
grain_yield	11_10438	1H	50000	1.0861E-2	0.91725	1	1.2739E-4	1	4.3099E3	84	3.9683E5	1.2456E5
grain_yield	11_11287	1H	50000	6.88705	1.0312E-2	0.979	7.467E-2	1	2.5262E6	84	3.668E5	7.5503E5
grain_yield	11_11478	1H	50000	1.25328	0.29091	1	2.8886E-2	2	4.8864E5	83	3.8989E5	2.9424E5
grain_yield	11_20660	1H	50000	6.89278	1.0281E-2	0.979	7.4727E-2	1	2.5281E6	84	3.6678E5	7.5552E5
grain_yield	12_30562	1H	50000	6.38771	1.3342E-2	0.985	6.8903E-2	1	2.334E6	85	3.6539E5	7.0386E5
grain_yield	11_20427	1H	50600	6.89278	1.0281E-2	0.979	7.4727E-2	1	2.5281E6	84	3.6678E5	7.5552E5
grain_yield	11_20698	1H	50600	6.88705	1.0312E-2	0.979	7.467E-2	1	2.5262E6	84	3.668E5	7.5503E5
grain_yield	11_21193	1H	50600	6.38771	1.3342E-2	0.985	6.8903E-2	1	2.334E6	85	3.6539E5	7.0386E5
grain_yield	11_20757	1H	50600	0.91172	0.3424	1	1.058E-2	1	3.5796E5	84	3.9262E5	2.1297E5
grain_yield	12_10300	1H	50600	6.38771	1.3342E-2	0.985	6.8903E-2	1	2.334E6	85	3.6539E5	7.0386E5
grain_yield	12_31381	1H	50600	NaN	NaN	1	0	0	NaN	86	3.8828E5	1.6048E5
grain_yield	12_31208	1H	50600	6.42464	1.3087E-2	0.984	6.9274E-2	1	2.3465E6	85	3.6524E5	7.0699E5
grain_yield	12_30404	1H	50600	6.38771	1.3342E-2	0.985	6.8903E-2	1	2.334E6	85	3.6539E5	7.0386E5
grain_yield	12_30043	1H	50600	6.38771	1.3342E-2	0.985	6.8903E-2	1	2.334E6	85	3.6539E5	7.0386E5
grain_yield	11_11484	1H	51230	4.37822	3.9383E-2	1	4.8289E-2	1	1.6357E6	85	3.736E5	5.2929E5
grain_yield	11_21357	1H	51700	0.97869	0.32533	1	1.1221E-2	1	3.801E5	85	3.8837E5	2.1539E5
grain_yield	11_20810	1H	52460	9.0568	3.4439E-3	0.941	9.4922E-2	1	3.2153E6	85	3.5502E5	9.2419E5
grain_yield	11_20912	1H	52460	NaN	NaN	1	0	0	NaN	86	3.8828E5	1.6048E5
grain_yield	11_21000	1H	52460	9.4572	2.8284E-3	0.927	9.8698E-2	1	3.3432E6	85	3.5351E5	9.5617E5
grain_yield	11_21312	1H	52460	6.48558	1.2677E-2	0.983	6.9884E-2	1	2.3672E6	85	3.65E5	7.1216E5
grain_yield	11_10833	1H	52460	2.20914	0.11613	1	4.926E-2	2	8.343E5	84	3.7766E5	4.3001E5
grain_yield	12_11169	1H	52460	8.90513	3.712E-3	0.943	9.3483E-2	1	3.1666E6	85	3.5559E5	9.1201E5
grain_yield	12_31272	1H	52460	4.37822	3.9383E-2	1	4.8289E-2	1	1.6357E6	85	3.736E5	5.2929E5
grain_yield	12_31134	1H	52460	3.6754E-2	0.84842	1	4.2607E-4	1	1.4432E4	85	3.9267E5	1.2397E5
grain_yield	12_30592	1H	52460	0.9297	0.33768	1	1.0665E-2	1	3.6127E5	85	3.8859E5	2.1068E5
grain_yield	12_30350	1H	52460	9.0568	3.4439E-3	0.941	9.4922E-2	1	3.2153E6	85	3.5502E5	9.2419E5
grain_yield	12_30522	1H	53220	1.2841E-2	0.91004	1	1.4891E-4	1	5.0439E3	85	3.9279E5	1.2162E5
grain_yield	11_11359	1H	54730	10.4057	1.7841E-3	0.898	0.10752	1	3.642E6	85	3.5E5	1.0309E6
grain_yield	11_21217	1H	54730	3.6754E-2	0.84842	1	4.2607E-4	1	1.4432E4	85	3.9267E5	1.2397E5
grain_yield	12_30786	1H	54730	0.2833	0.59593	1	3.2747E-3	1	1.1092E5	85	3.9154E5	1.4809E5
grain_yield	12_30672	1H	54730	0.2833	0.59593	1	3.2747E-3	1	1.1092E5	85	3.9154E5	1.4809E5
grain_yield	11_10075	1H	55490	6.88192	1.0339E-2	0.979	7.4618E-2	1	2.5245E6	84	3.6683E5	7.546E5
grain_yield	11_10520	1H	55490	0.2833	0.59593	1	3.2747E-3	1	1.1092E5	85	3.9154E5	1.4809E5
grain_yield	11_20798	1H	55490	0.17152	0.6798	1	1.9852E-3	1	6.7246E4	85	3.9205E5	1.3717E5
grain_yield	11_10293	1H	55490	5.5156E-2	0.81489	1	6.3926E-4	1	2.1654E4	85	3.9259E5	1.2578E5
grain_yield	11_21361	1H	55490	0.2833	0.59593	1	3.2747E-3	1	1.1092E5	85	3.9154E5	1.4809E5
grain_yield	11_10933	1H	55490	0.2515	0.61733	1	2.9415E-3	1	9.9518E4	84	3.9569E5	1.4836E5

Data

- Sequence
 - snpfile
 - tht_FlapJack_genotype_MCL
 - tht_FlapJack_genotype_MCL_align0
 - tht_FlapJack_genotype_MCL_align1
 - tht_FlapJack_genotype_MCL_align2
 - tht_FlapJack_genotype_MCL_align3
 - tht_FlapJack_genotype_MCL_align4
 - tht_FlapJack_genotype_MCL_align5
 - tht_FlapJack_genotype_MCL_align6
 - tht_FlapJack_genotype_MCL_align7
 - BLUES_Filtered_traits + Filtered_PC for tht_FlapJack_genotype_MCL_Collapsed_2
- Polymorphisms
- Numerical
 - geneticMap

Number of sequences: 192
 Number of sites: 2320
 Data type: Text
 Loci: 1H, 2H, 3H, 4H, 5H, 6H, 7H, UNK

Kinship

Site Numbers
 Locus
 Site Name
 Alleles

	0	386	772	1158	1544	1930	2316
	2289: 0	2290: 0	2291: 0	2292: 0	2293: 0	2294: 0	2295: 0
ND20448	...	B:B	...	B:B	B:B	...	B:B
ND24843	...	B:B	...	B:B	B:B	...	B:B
ND24890	...	B:B	...	B:B	B:B	...	B:B
ND24906	...	B:B	...	B:B	B:B	...	B:B
ND24978	...	B:B	...	B:B	B:B	...	A:A
ND25025	...	B:B	...	B:B	B:B	...	A:A
ND25030	...	B:B	...	B:B	B:B	...	B:B
ND25033	...	B:B	...	B:B	B:B	...	B:B
ND25148	...	B:B	...	B:B	B:B	...	B:B
ND25151	...	B:B	...	B:B	B:B	...	A:A
ND25152	...	B:B	...	B:B	B:B	...	B:B
ND2515	...	B:B	...	B:B	B:B	...	B:B
ND2516	...	B:B	...	B:B	B:B	...	B:B
ND2516	...	B:B	...	B:B	B:B	...	B:B
ND2516	...	B:B	...	B:B	B:B	...	B:B
ND2516	...	B:B	...	B:B	B:B	...	B:B
ND2517	...	B:B	...	B:B	B:B	...	B:B
ND2520	...	B:B	...	B:B	B:B	...	B:B
ND2520	...	B:B	...	B:B	B:B	...	B:B
ND2522	...	B:B	...	B:B	B:B	...	B:B
ND2576	...	B:B	...	B:B	B:B	...	B:B
ND2578	...	B:B	...	B:B	B:B	...	B:B
ND2578	...	B:B	...	B:B	B:B	...	B:B
ND2580	...	B:B	...	B:B	B:B	...	B:B
ND2582	...	B:B	...	B:B	B:B	...	B:B
ND2582	...	B:B	...	B:B	B:B	...	B:B
ND2582	...	B:B	...	B:B	B:B	...	B:B
ND2583	...	B:B	...	B:B	B:B	...	B:B
ND2583	...	B:B	...	B:B	B:B	...	B:B
ND2583	...	B:B	...	B:B	B:B	...	B:B
ND2584	...	B:B	...	B:B	B:B	...	B:B
ND2584	...	B:B	...	B:B	B:B	...	B:B
ND2588	...	B:B	...	B:B	B:B	...	B:B
ND2588	...	B:B	...	B:B	B:B	...	B:B
ND2590	...	B:B	...	B:B	B:B	...	B:B
ND25911	...	B:B	...	B:B	B:B	...	B:B
ND25917	...	B:B	...	B:B	B:B	...	B:B
ND25949	...	B:B	...	B:B	B:B	...	B:B
ND25966	...	B:B	...	B:B	B:B	...	B:B
ND25967	...	B:B	...	B:B	B:B	...	B:B
ND25969	...	B:B	...	B:B	B:B	...	B:B
ND25970	...	B:B	...	B:B	B:B	...	B:B
ND25975	...	B:B	...	B:B	B:B	...	B:B
ND25976	...	B:B	...	B:B	B:B	...	B:B
ND25977	...	B:B	...	B:B	B:B	...	B:B
ND25979	...	B:B	...	B:B	B:B	...	B:B

Kinship Options

Model heterozygotes as

Related to homozygotes
 Independent allele state

Rescale results between 2 and 0

- geneticMap
- traits
- tht_FlapJack_genotype_MCL_Collasped
- tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- PC for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- Eigenvectors for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- Eigenvalues for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- Filtered_traits
- Filtered_PC for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
- Matrix
 - kin_tht_FlapJack_genotype_MCL
- Tree
- Fusions
- Synonymizer
- Result
 - Diversity

Taxa	grain_yield	PC 1	PC 2	PC 3	Haplotype
ND20448	4.5531E3	23.95023	-5.7598E-1	1.609	AABAAAAA...
ND24843	4.1119E3	23.85674	1.41352	-1.6796E0	BABAAAAAB...
ND24890	4.571E3	24.24628	2.3442E-2	3.78237	BABAAAAAB...
ND24906	4.7234E3	25.78159	0.49923	-7.6242E-1	BABAAAAA...
ND24978	4.9297E3	23.33919	0.99536	-3.6191E0	AABAAAAA...
ND25025	5.2596E3	24.15292	2.21206	-4.764E0	AABAAAAA...
ND25030	4.9315E3	25.68292	2.06961	-2.7292E0	AABAAAAA...
ND25033	5.118E3	26.67351	3.15703	-1.0104E0	AABAAAAA...
ND25148	4.6212E3	25.09126	2.70596	-4.4071E0	AABAAAAA...
ND25151	4.8633E3	25.51196	2.26901	-4.0667E0	AABAAAAA...
ND25152	4.5495E3	25.92034	1.9962	-4.7732E0	AABAAAAA...
ND25153	4.6392E3	26.56552	1.94752	-4.6219E0	AABAAAAA...
ND25160	5.0462E3	25.07346	1.89335	-4.3234E0	AABAAAAA...

Number of sequences: 90
 Number of sites: 2320
 Data type: Text
 Loci: 1H, 2H, 3H, 4H, 5H, 6H, 7H, UNK
 Table Title: Phenotypes and Genotypes
 Number of columns: 6
 Number of rows: 90
 Number of elements: 540
 Intersect Join

MLM

MLM Options

Compression Level

Optimum Level
 Custom Level:
 No Compression

Variance Component Estimation

P3D (estimate once)
 Re-estimate after each marker

ND25989	4.5716E3	25.08941	1.02229	0.31821	AABAAAAA...
ND25996	5.0271E3	23.55505	0.78353	-4.0614E-1	AABAAAAA...
ND25998	4.889E3	25.01045	-1.0733E0	1.06648	AABAAAAA...
ND25999	5.2298E3	24.61013	-1.5628E0	1.72157	AABAAAAA...
ND26009	4.351E3	24.85966	-2.9434E-1	1.23014	AABAAAAA...
ND26010	4.473E3	23.2853	0.11584	1.26841	AABAAAAA...
ND26015	4.8424E3	20.83769	-2.782E0	-5.6755E-1	AABAAAAA...
ND26017	4.9105E3	22.63618	-4.9141E0	4.21739	AABAAAAA...
ND26030	4.4801E3	24.31001	-2.3722E0	3.10949	BABAAAAAB...

Data could not be saved: java.io.FileNotFoundException: TasselDataFile.zip (Access is denied)

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.104

File Tools Help GDPC

Data Analysis Results Delete Wizard Show Memory

Table Tree Plot 2D Plot LD Plot Chart QQ Plot Manhattan Plot

Filtered_traits

- Matrix
- Tree
- Fusions
- Synonymizer
- Result
- Diversity
- SNP Assays
- LD
- Association
 - Phenotype ANOVA from Filtered_traits
 - BLUEs_Filtered_traits
 - GLM_marker_test_BLUEs_Filtered_traits + tht
 - GLM allele estimates for BLUEs_Filtered_traits
- Variances
- Stepwise

Table Title: Marker Test
 Number of columns: 13
 Number of rows: 1907
 Number of elements: 24791
 Tests of Marker-Phenotype Association
 Data set: BLUEs_Filtered_traits + tht
 model: trait = mean + marker

Trait	Marker	Locus	Locus_pos	marker_F	marker_p	markerB2	markerDF	markerMS	errorDF	errorMS	modelDF
grain_yield	12_10235	1H	47470	4.01939	4.8053E-2	4.368E-2	1	4.8186E5	88	1.1988E5	1
grain_yield	12_31467	1H	47470	3.26545	7.4171E-2	3.578E-2	1	3.9471E5	88	1.2088E5	1
grain_yield	12_30796	1H	47470	2.25233	0.11125	4.9229E-2	2	2.7154E5	87	1.2056E5	2
grain_yield	12_30683	1H	47470	3.26545	7.4171E-2	3.578E-2	1	3.9471E5	88	1.2088E5	1
grain_yield	11_20855	1H	49340	4.01939	4.8053E-2	4.368E-2	1	4.8186E5	88	1.1988E5	1
grain_yield	11_10957	1H	49340	2.29086	0.10732	5.0581E-2	2	2.7839E5	86	1.2152E5	2
grain_yield	11_11064	1H	49340	4.01939	4.8053E-2	4.368E-2	1	4.8186E5	88	1.1988E5	1
grain_yield	12_11301	1H	49340	4.37106	3.9438E-2	4.7321E-2	1	5.2203E5	88	1.1943E5	1
grain_yield	11_10470	1H	49700	2.14208	0.12356	4.6932E-2	2	2.5887E5	87	1.2085E5	2
grain_yield	12_10159	1H	49700	4.01939	4.8053E-2	4.368E-2	1	4.8186E5	88	1.1988E5	1
grain_yield	12_30762	1H	49700	2.61332	0.10955	2.884E-2	1	3.1816E5	88	1.2174E5	1
grain_yield	12_30438	1H	49700	4.01939	4.8053E-2	4.368E-2	1	4.8186E5	88	1.1988E5	1
grain_yield	12_30436	1H	49700	2.61332	0.10955	2.884E-2	1	3.1816E5	88	1.2174E5	1
grain_yield	11_10438	1H	50000	5.1106E-3	0.94317	5.8739E-5	1	646.57879	87	1.2652E5	1
grain_yield	11_11287	1H	50000	15.85312	1.4158E-4	0.15413	1	1.6967E6	87	1.0702E5	1
grain_yield	11_11478	1H	50000	3.17712	4.6643E-2	6.8803E-2	2	3.7868E5	86	1.1919E5	2
grain_yield	11_20660	1H	50000	16.26348	1.1793E-4	0.15749	1	1.7337E6	87	1.066E5	1
grain_yield	11_11111	1H	50000	1.6533E6	88	1.0657E5	1	1.6533E6	88	1.0657E5	1
grain_yield	11_11112	1H	50000	1.7337E6	87	1.066E5	1	1.7337E6	87	1.066E5	1
grain_yield	11_11113	1H	50000	1.6967E6	87	1.0702E5	1	1.6967E6	87	1.0702E5	1
grain_yield	11_11114	1H	50000	1.6533E6	88	1.0657E5	1	1.6533E6	88	1.0657E5	1
grain_yield	11_11115	1H	50000	3.2724E5	87	1.2276E5	1	3.2724E5	87	1.2276E5	1
grain_yield	11_11116	1H	50000	1.6533E6	88	1.0657E5	1	1.6533E6	88	1.0657E5	1
grain_yield	11_11117	1H	50000	0	0	0	0	NaN	89	1.2395E5	0
grain_yield	11_11118	1H	50000	1.691E6	88	1.0614E5	1	1.691E6	88	1.0614E5	1
grain_yield	11_11119	1H	50000	1.6533E6	88	1.0657E5	1	1.6533E6	88	1.0657E5	1
grain_yield	12_30043	1H	50600	15.51354	1.6365E-4	0.14987	1	1.6533E6	88	1.0657E5	1
grain_yield	11_11484	1H	51230	4.5684	3.5341E-2	4.9352E-2	1	5.4443E5	88	1.1917E5	1
grain_yield	11_21357	1H	51700	0.86448	0.35503	9.728E-3	1	1.0732E5	88	1.2414E5	1
grain_yield	11_20810	1H	52460	11.99215	8.271E-4	0.11993	1	1.323E6	88	1.1033E5	1
grain_yield	11_20912	1H	52460	NaN	NaN	0	0	NaN	89	1.2395E5	0
grain_yield	11_21000	1H	52460	11.74992	9.2741E-4	0.11779	1	1.2995E6	88	1.1059E5	1
grain_yield	11_21312	1H	52460	13.35709	4.3724E-4	0.13178	1	1.4538E6	88	1.0884E5	1
grain_yield	11_10833	1H	52460	2.48536	8.9193E-2	5.4047E-2	2	2.9811E5	87	1.1995E5	2
grain_yield	12_11169	1H	52460	12.09379	7.8841E-4	0.12082	1	1.3329E6	88	1.1021E5	1
grain_yield	12_31272	1H	52460	4.5684	3.5341E-2	4.9352E-2	1	5.4443E5	88	1.1917E5	1
grain_yield	12_31134	1H	52460	8.477E-2	0.77162	9.6237E-4	1	1.0617E4	88	1.2524E5	1
grain_yield	12_30592	1H	52460	2.40854	0.12426	2.6641E-2	1	2.9389E5	88	1.2202E5	1
grain_yield	12_30350	1H	52460	11.99215	8.271E-4	0.11993	1	1.323E6	88	1.1033E5	1
grain_yield	11_11359	1H	54730	11.22825	1.1884E-3	0.11316	1	1.2483E6	88	1.1118E5	1
grain_yield	11_21217	1H	54730	8.477E-2	0.77162	9.6237E-4	1	1.0617E4	88	1.2524E5	1
grain_yield	12_30786	1H	54730	5.0106E-2	0.8234	5.6906E-4	1	6.2777E3	88	1.2529E5	1
grain_yield	12_30672	1H	54730	5.0106E-2	0.8234	5.6906E-4	1	6.2777E3	88	1.2529E5	1
grain_yield	11_10075	1H	55490	13.98574	3.2932E-4	0.13849	1	1.5245E6	87	1.09E5	1
grain_yield	11_10520	1H	55490	5.0106E-2	0.8234	5.6906E-4	1	6.2777E3	88	1.2529E5	1
grain_yield	11_20798	1H	55490	3.1995E-2	0.85845	3.6345E-4	1	4.0094E3	88	1.2531E5	1
grain_yield	11_10293	1H	55490	7.674E-2	0.78242	8.7128E-4	1	9.6117E3	88	1.2525E5	1
grain_yield	11_21361	1H	55490	5.0106E-2	0.8234	5.6906E-4	1	6.2777E3	88	1.2529E5	1
grain_yield	11_10933	1H	55490	5.1858E-2	0.8204	5.9572E-4	1	6.5575E3	87	1.2645E5	1

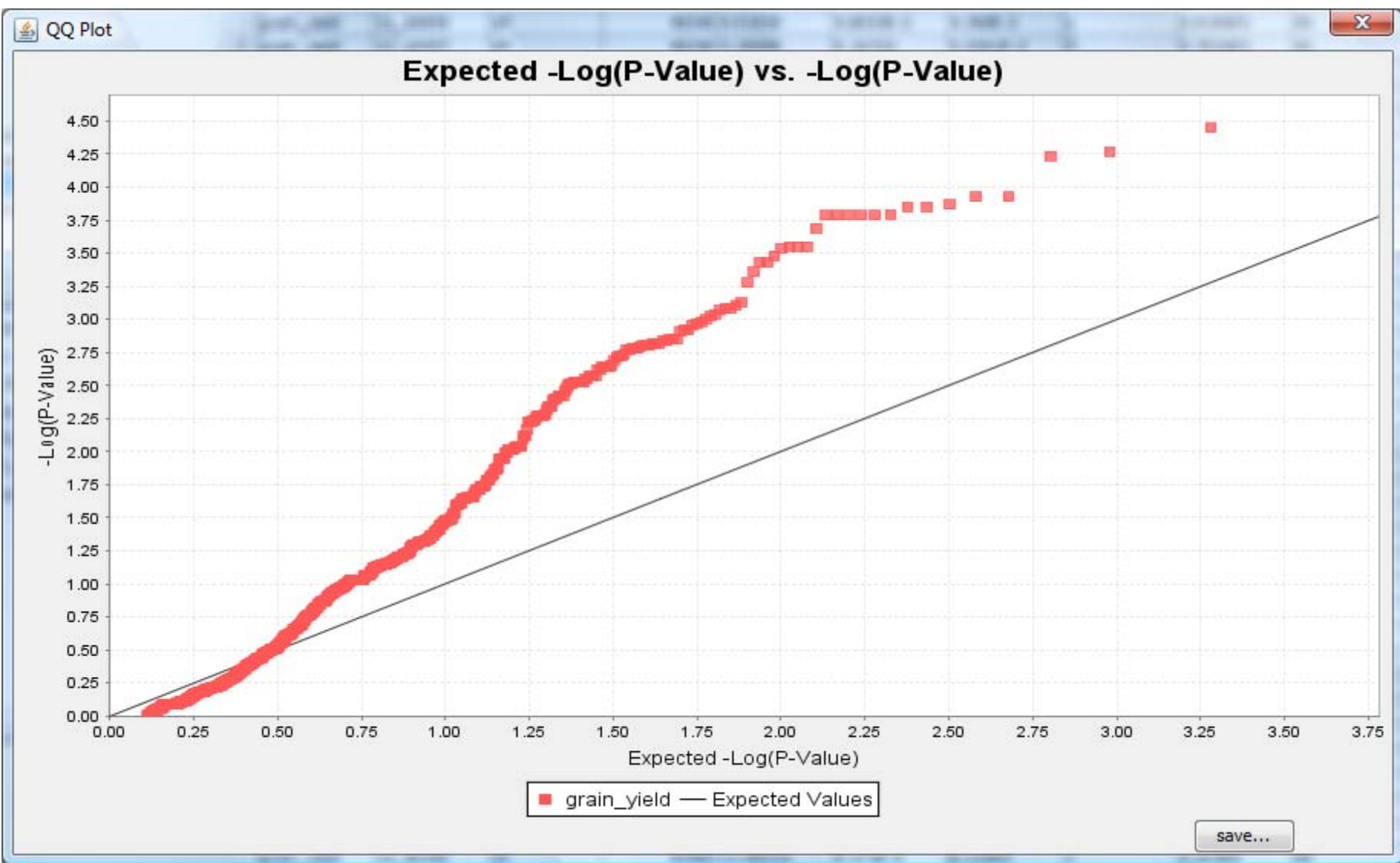
Program Status

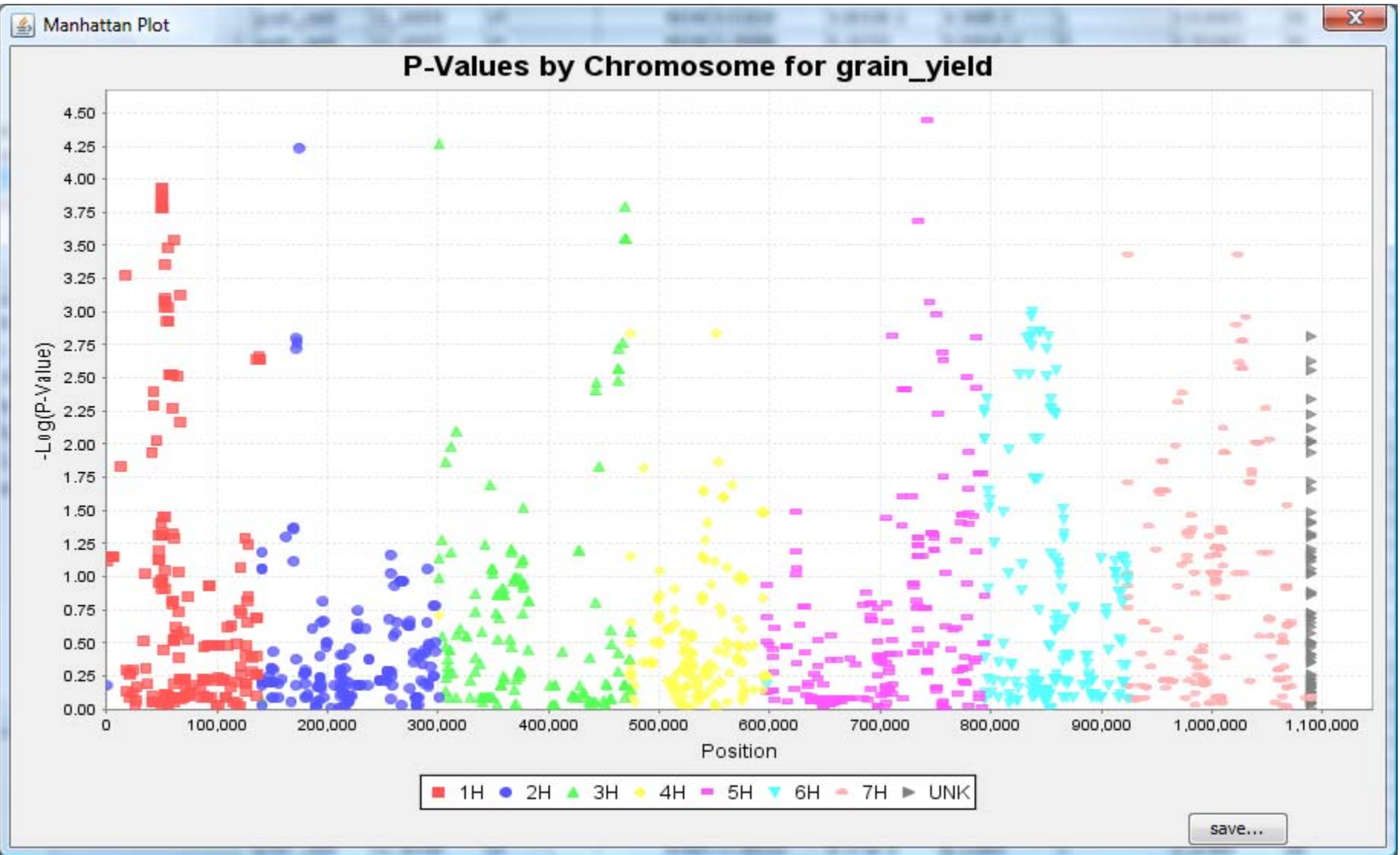
QQ Plot Options

Significant points to plot:

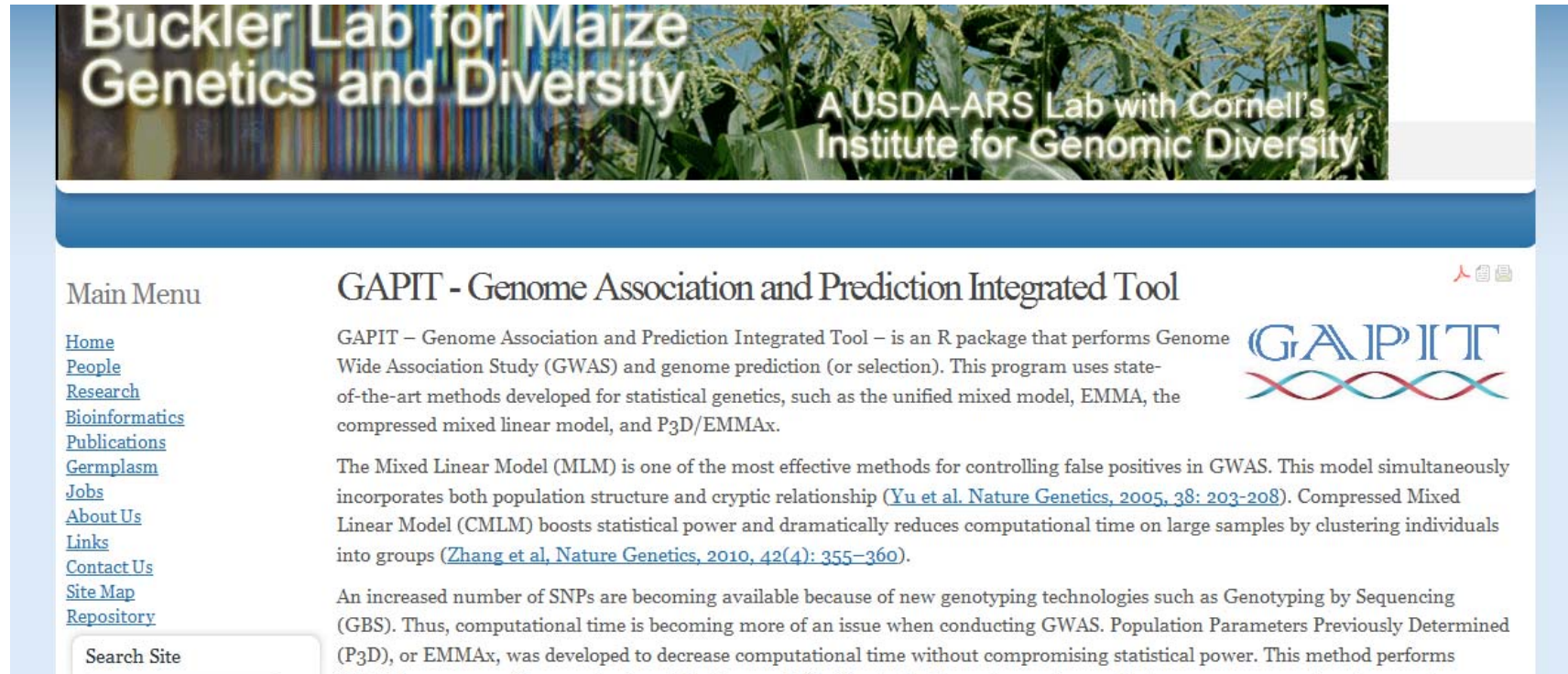
Plotting: 95 most significant out of 1907 per trait.

Okay Cancel





R Package for Association Analysis and Genomic Selection



The screenshot shows the website for the Buckler Lab for Maize Genetics and Diversity. The header features a banner with the text "Buckler Lab for Maize Genetics and Diversity" and "A USDA-ARS Lab with Cornell's Institute for Genomic Diversity" over a background image of corn plants. Below the banner is a blue navigation bar. On the left side, there is a "Main Menu" with links to Home, People, Research, Bioinformatics, Publications, Germplasm, Jobs, About Us, Links, Contact Us, Site Map, and Repository. A search box labeled "Search Site" is located below the menu. The main content area is titled "GAPIT - Genome Association and Prediction Integrated Tool" and includes a description of the R package, its capabilities, and references to scientific publications. The GAPIT logo, which consists of the letters "GAPIT" above a stylized DNA double helix, is positioned on the right side of the page.

Buckler Lab for Maize Genetics and Diversity
A USDA-ARS Lab with Cornell's Institute for Genomic Diversity

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Search Site

GAPIT - Genome Association and Prediction Integrated Tool

GAPIT – Genome Association and Prediction Integrated Tool – is an R package that performs Genome Wide Association Study (GWAS) and genome prediction (or selection). This program uses state-of-the-art methods developed for statistical genetics, such as the unified mixed model, EMMA, the compressed mixed linear model, and P₃D/EMMAx.

The Mixed Linear Model (MLM) is one of the most effective methods for controlling false positives in GWAS. This model simultaneously incorporates both population structure and cryptic relationship (Yu et al. *Nature Genetics*, 2005, 38: 203-208). Compressed Mixed Linear Model (CMLM) boosts statistical power and dramatically reduces computational time on large samples by clustering individuals into groups (Zhang et al, *Nature Genetics*, 2010, 42(4): 355–360).

An increased number of SNPs are becoming available because of new genotyping technologies such as Genotyping by Sequencing (GBS). Thus, computational time is becoming more of an issue when conducting GWAS. Population Parameters Previously Determined (P₃D), or EMMAx, was developed to decrease computational time without compromising statistical power. This method performs



visit <http://www.maizegenetics.net/gapit> or just google GAPIT