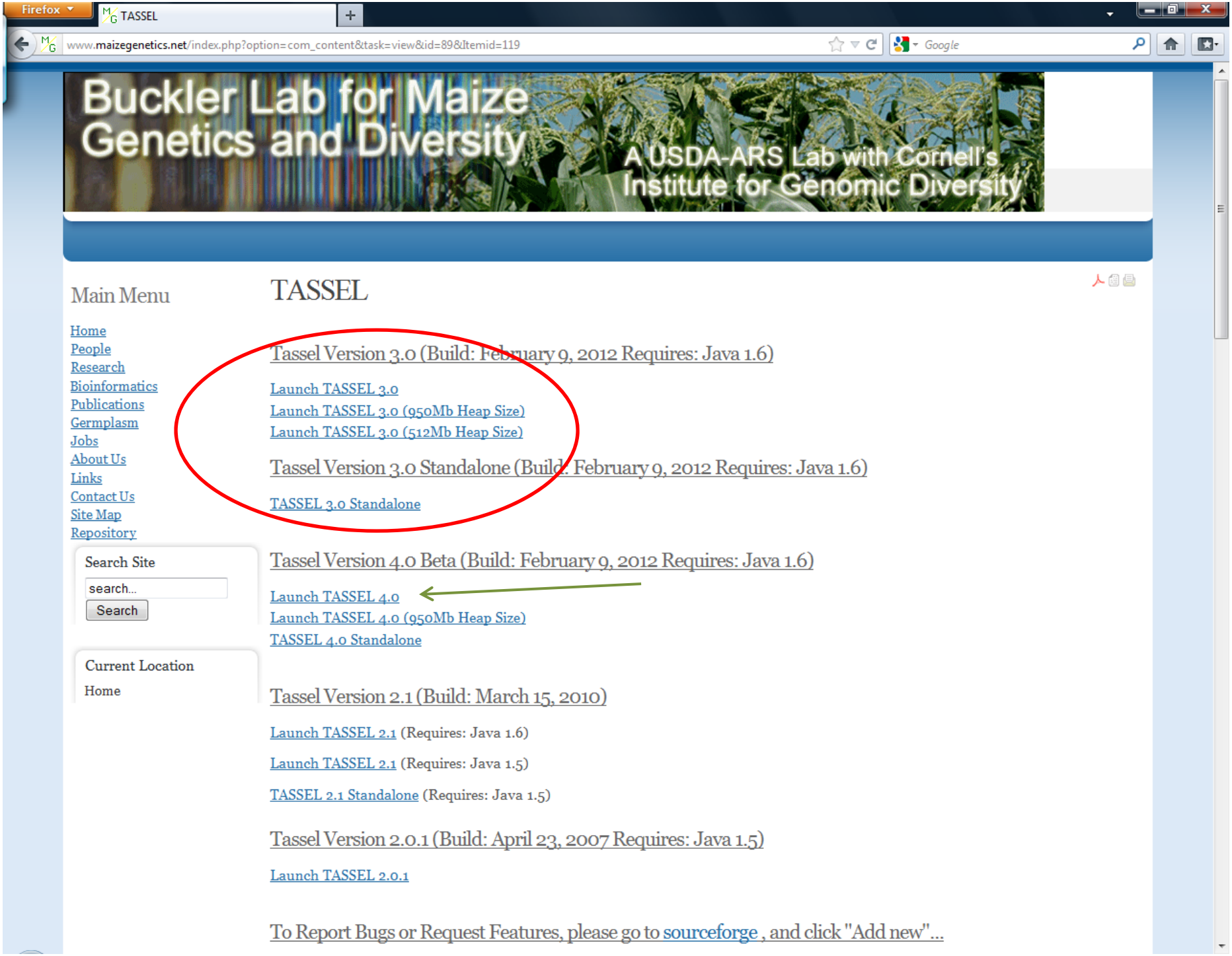
TASSEL

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
Google
Buckler Lab for Maize Genetics and Diversity
A USDA-ARS Lab with Cornell's Institute for Genomic Diversity
Main Menu
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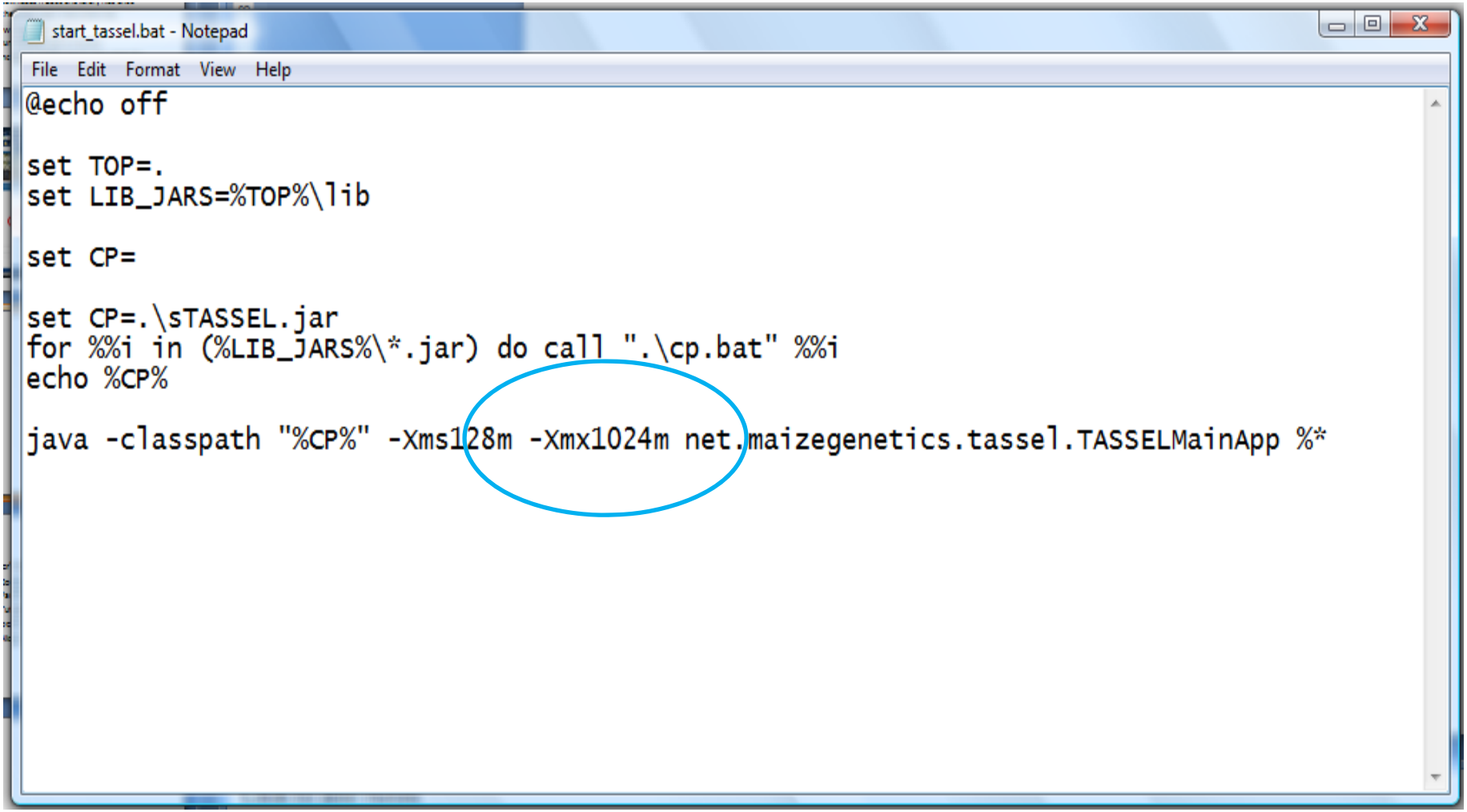
TASSEL
Tassel Version 3.0 (Build: February 9, 2012 Requires: Java 1.6)
Launch TASSEL 3.0
Launch TASSEL 3.0 (950Mb Heap Size)
Launch TASSEL 3.0 (512Mb Heap Size)
Tassel Version 3.0 Standalone (Build: February 9, 2012 Requires: Java 1.6)
TASSEL 3.0 Standalone
Tassel Version 4.0 Beta (Build: February 9, 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



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)

General Questions / Pipeline

Terry Casstevens (tmc46@cornell.edu)

Analysis Tools / MLM / GLM

Peter Bradbury (pjb39@cornell.edu)

Zhiwu Zhang (zz19@cornell.edu)

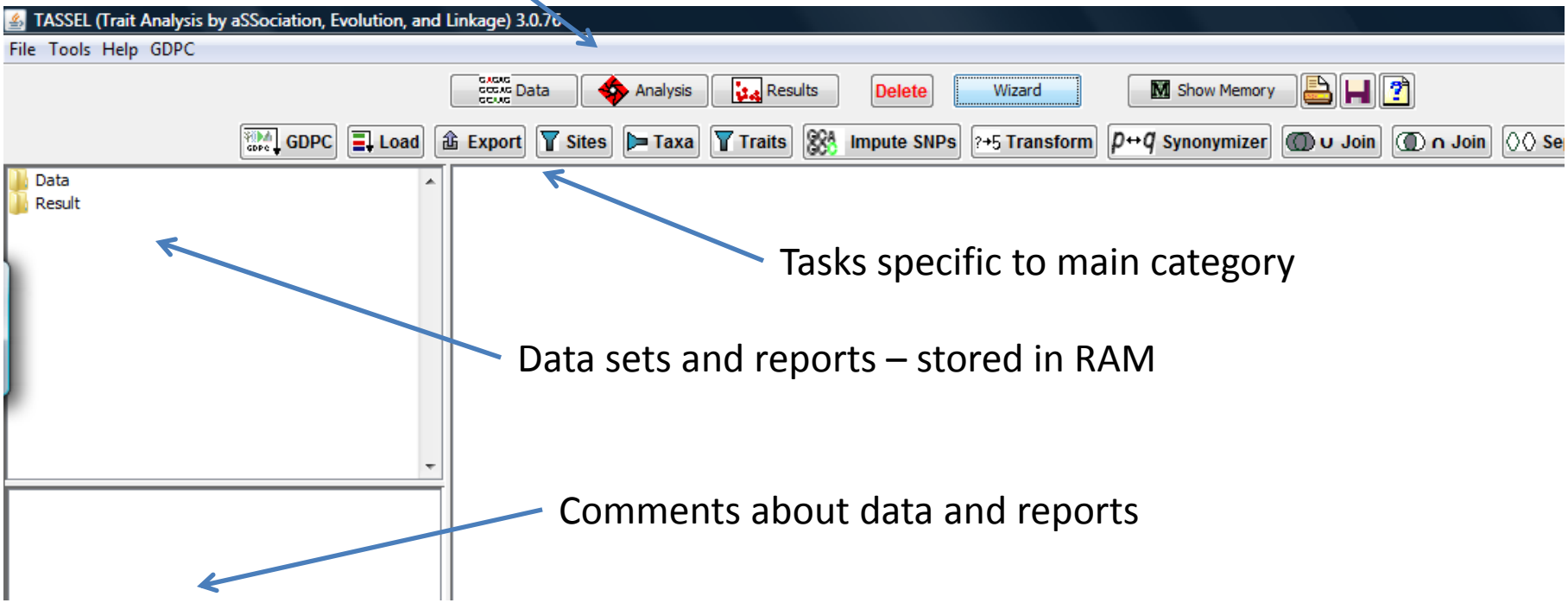
Overall Project Lead

Ed Buckler (esb33@cornell.edu)

To ask questions about TASSEL use

General Organization

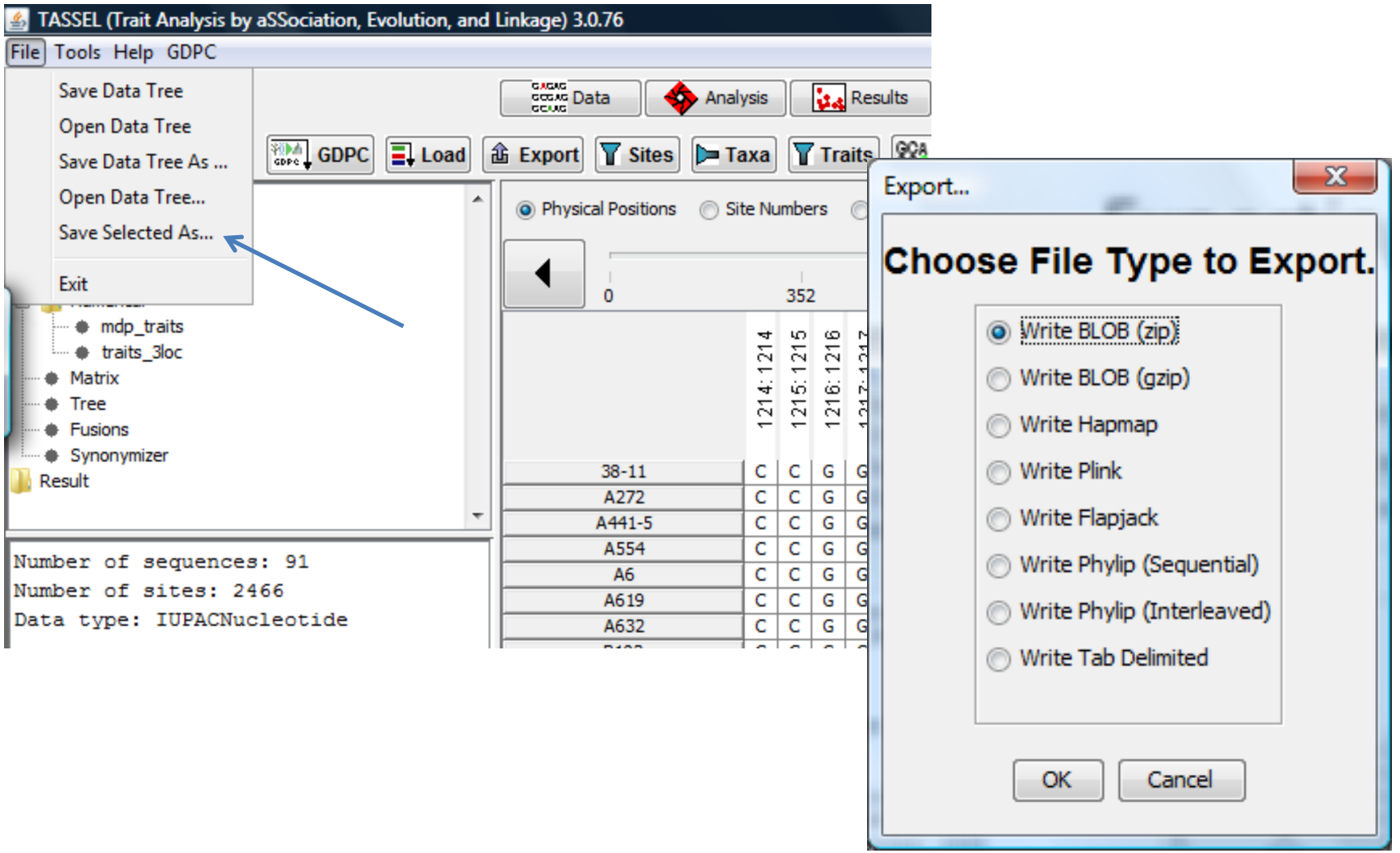
Main Function Categories



Import Formats

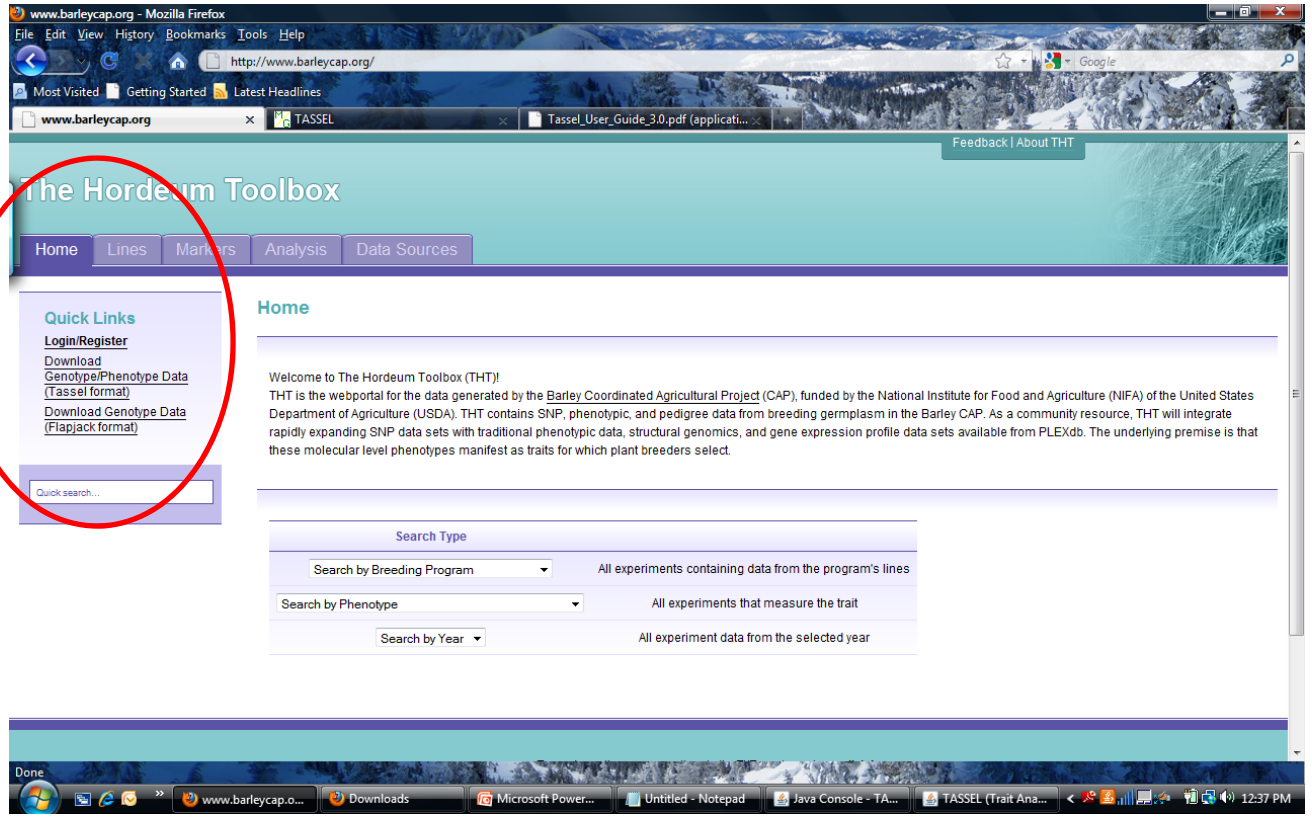
- Hapmap
- Plink
- Flapjack
- Polymorphism
- Phylip
- Numerical Data (traits or markers)
- Square Numerical Matrix (kinship)
- Genetic Map
- Guess function

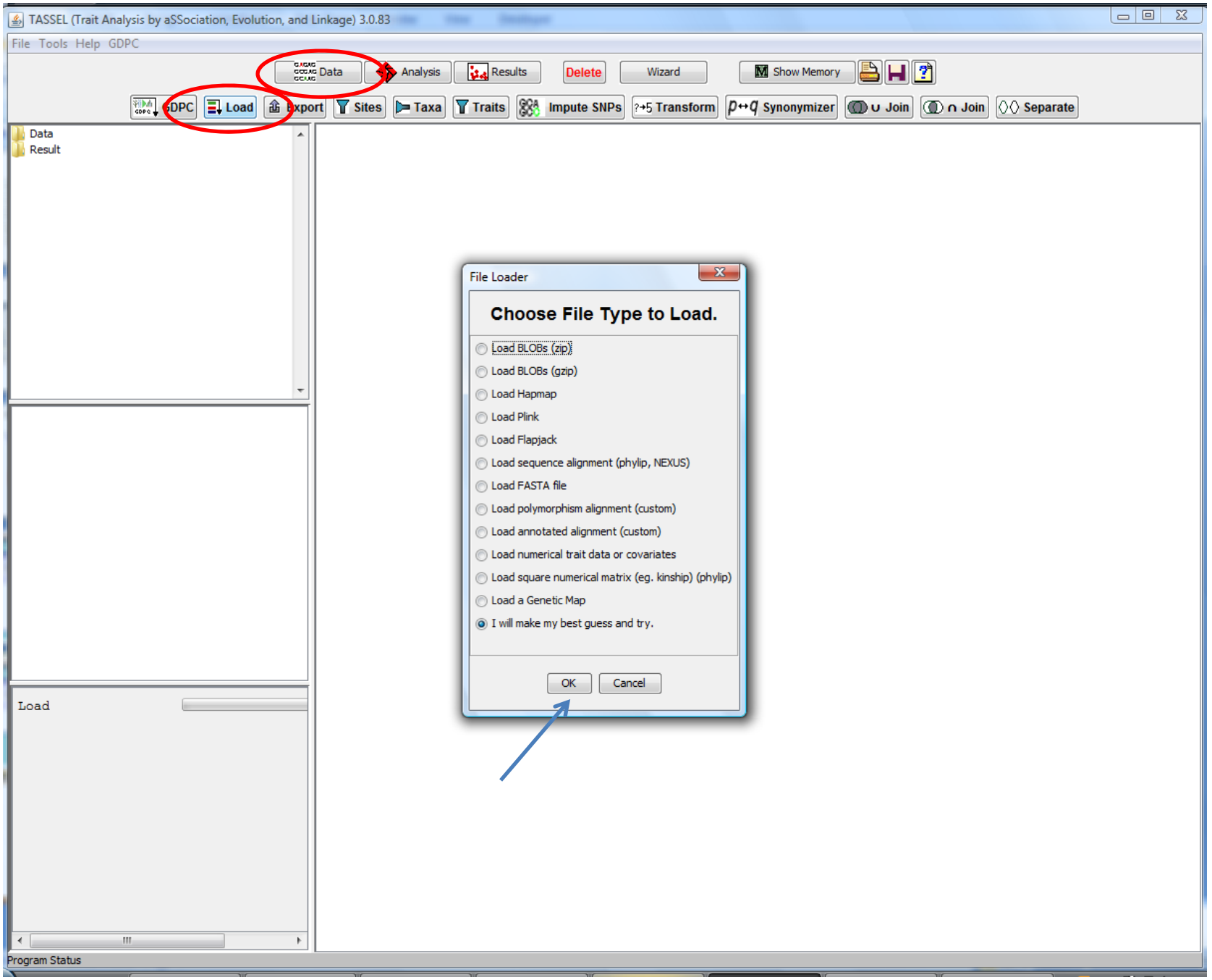
Exporting Data



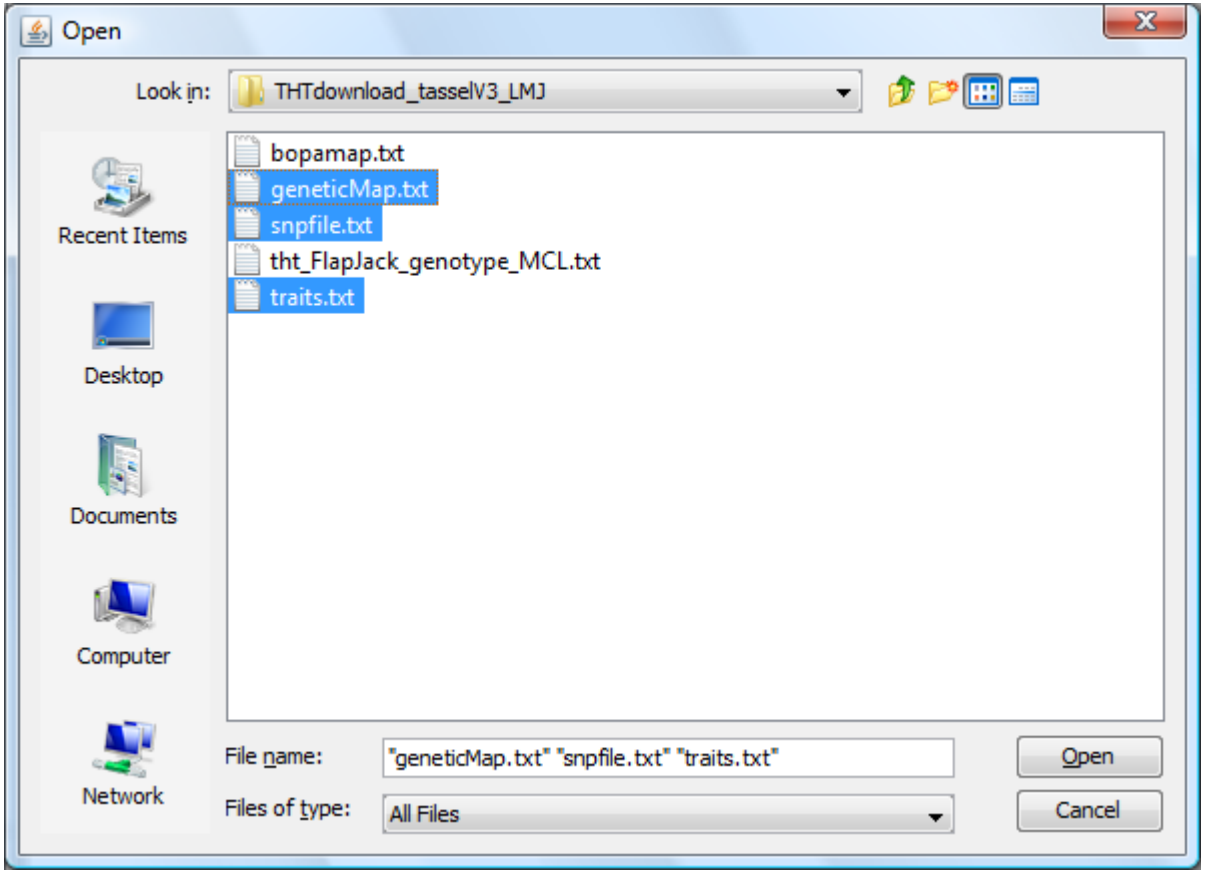
Downloading Data From the Hordeum Toolbox

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

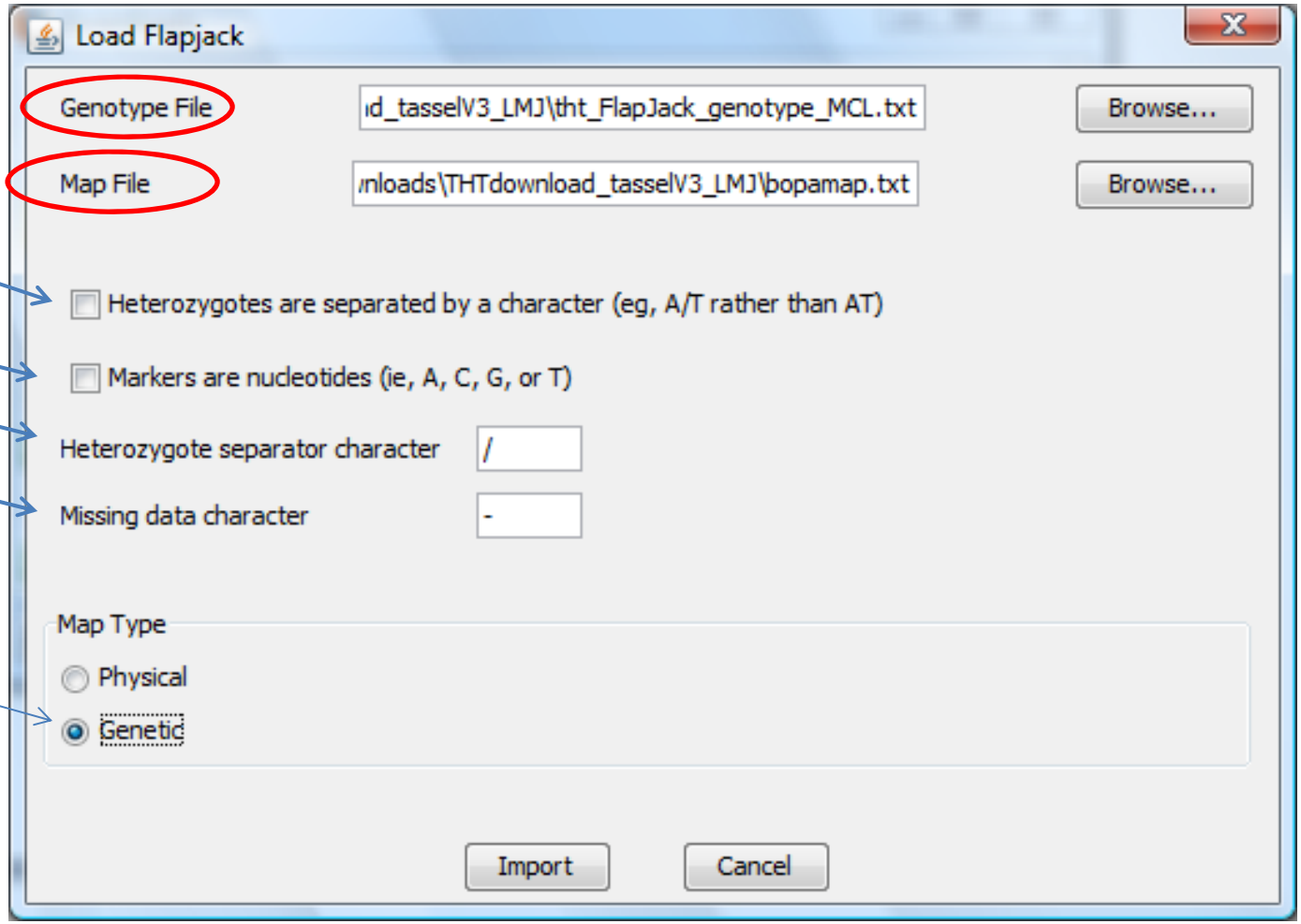



TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
File Tools Help GDPC
Data
Analysis
Results
Delete
Wizard
Show Memory
GDPC
Load
Export
Sites
Taxa
Traits
Impute SNPs
Transform
Synonymizer
Join
Join
Separate
Data
Result
Load
Program Status
File Loader
Choose File Type to Load.
Load BLOBs (zip)
Load BLOBs (gzip)
Load Hapmap
Load Plink
Load Flapjack
Load sequence alignment (phylip, NEXUS)
Load FASTA file
Load polymorphism alignment (custom)
Load annotated alignment (custom)
Load numerical trait data or covariates
Load square numerical matrix (eg. kinship) (phylip)
Load a Genetic Map
I will make my best guess and try.
OK
Cancel

I will make my best guess and try

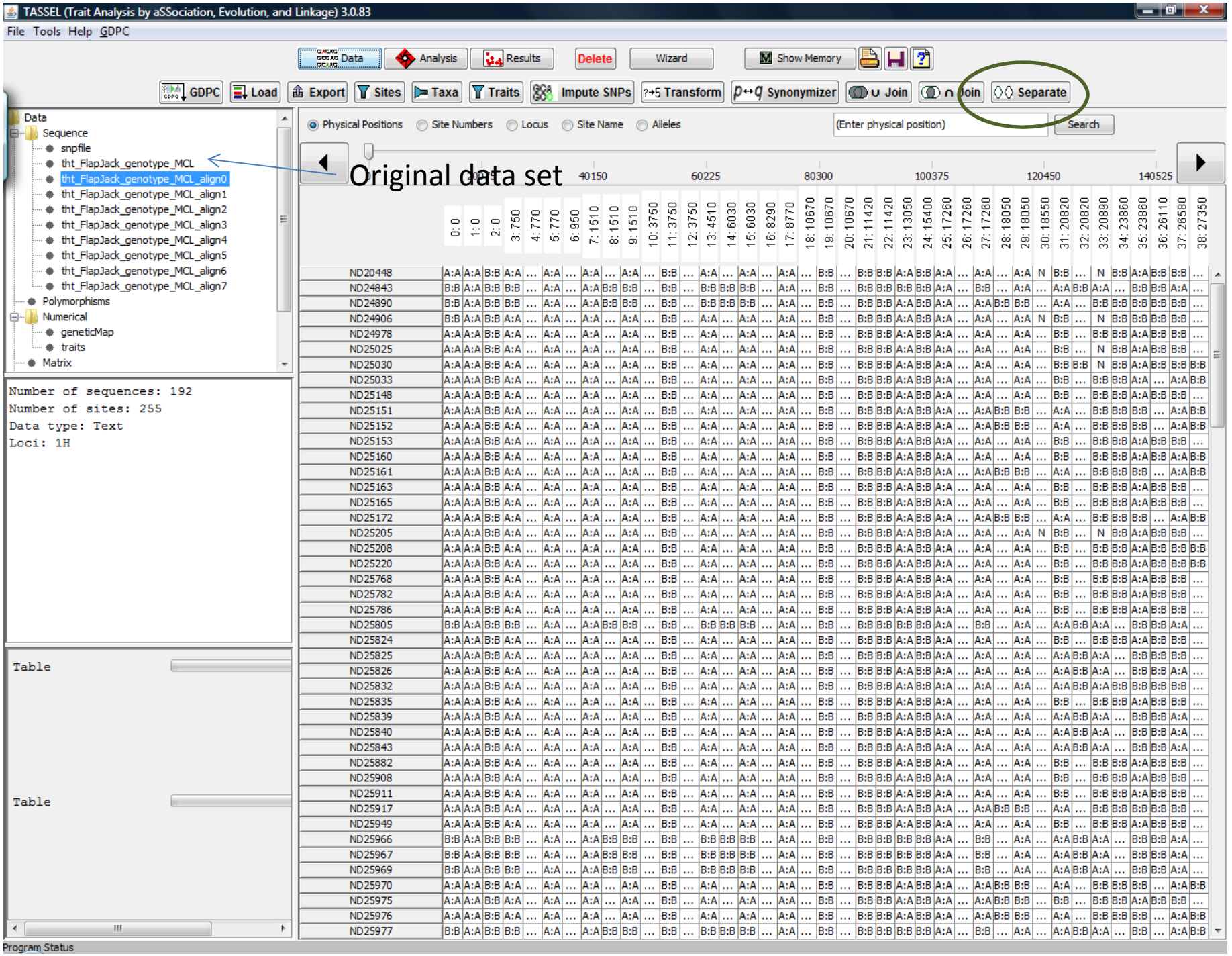


Load Flapjack



Flapjack import options

Genetic positions mutliplied by 1000


TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
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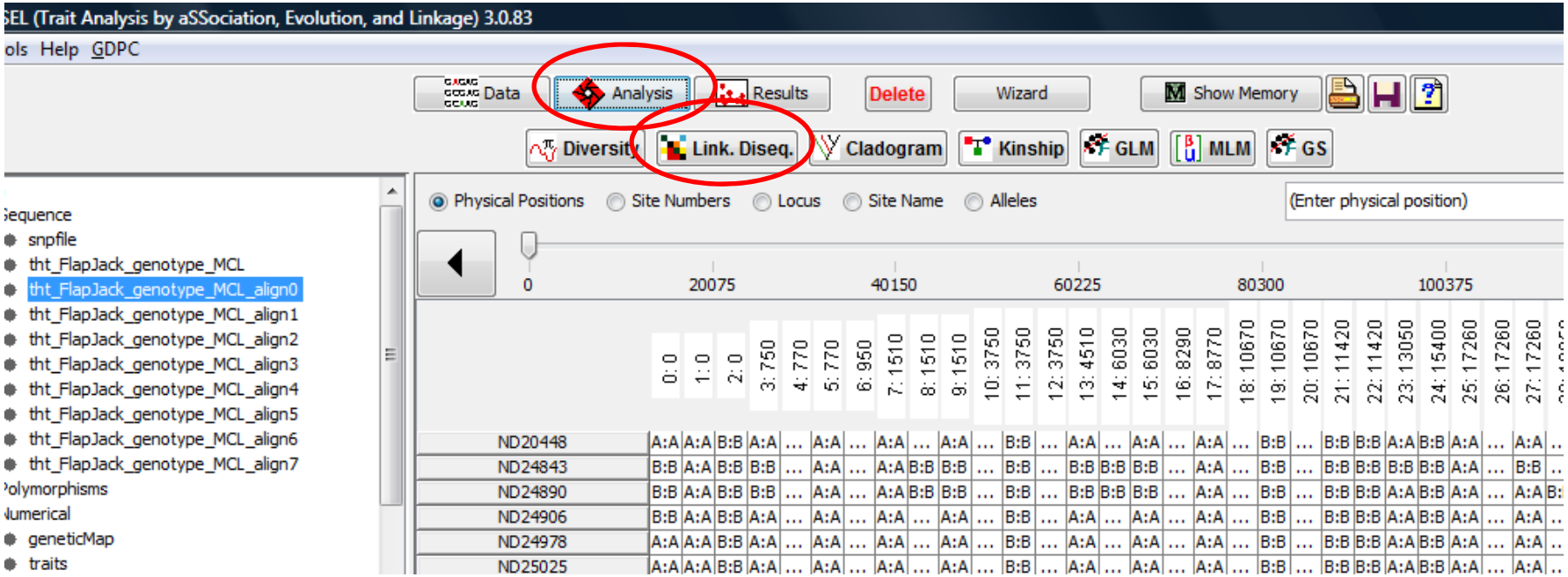
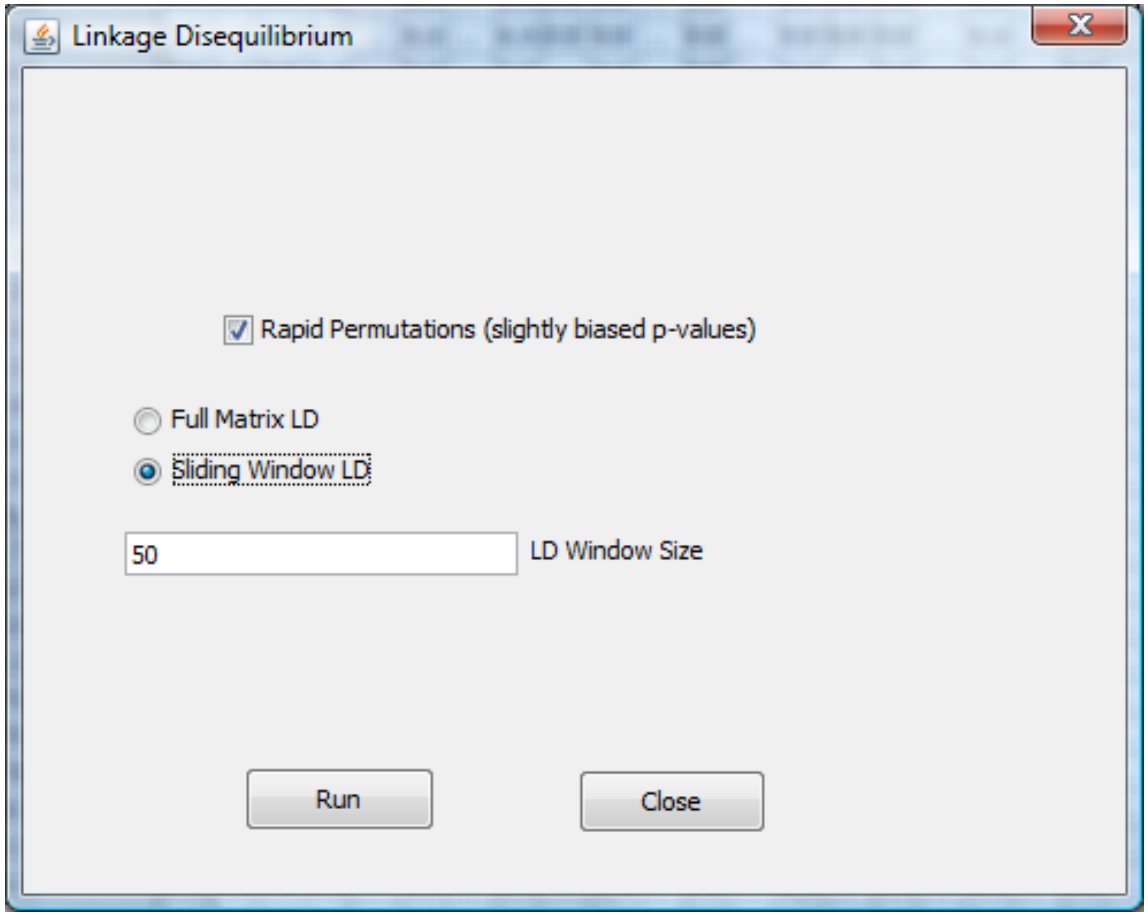
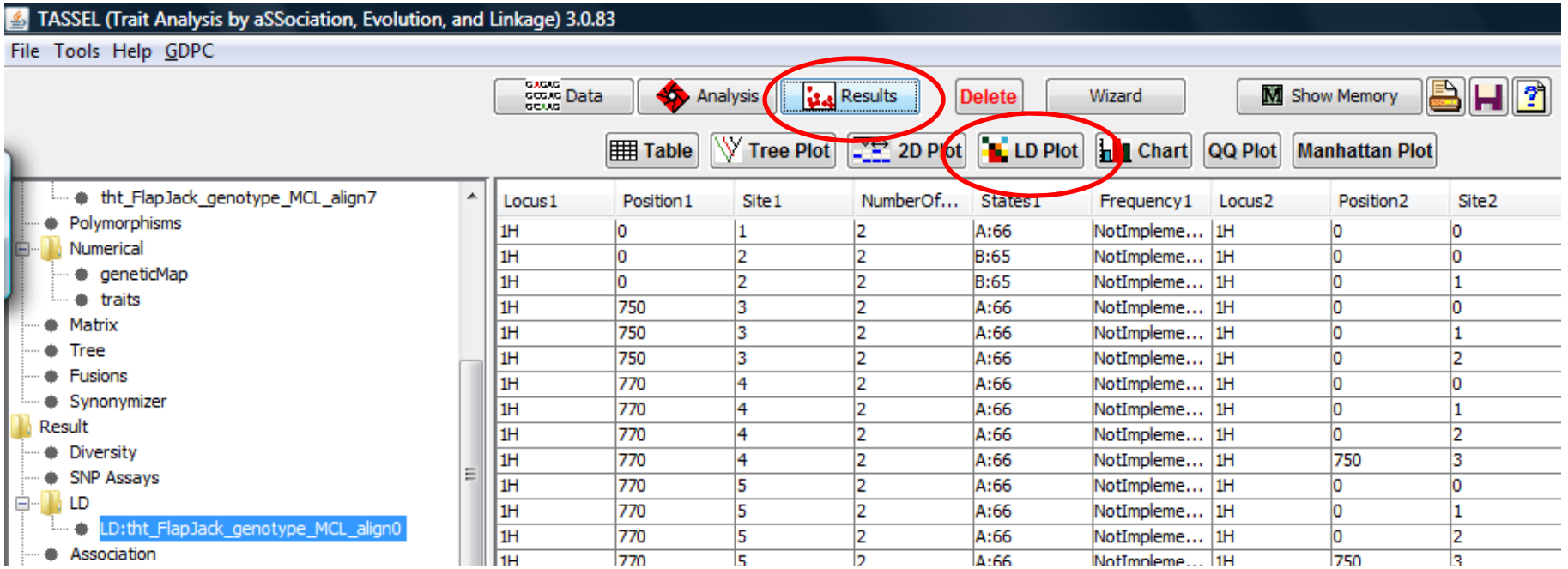
Join
Join
Separate
Data
Sequence
snpfile
tht_FlapJack_genotype_MCL
tht_FlapJack_genotype_MCL_align0
tht_FlapJack_genotype_MCL_align1
tht_FlapJack_genotype_MCL_align2
tht_FlapJack_genotype_MCL_align3
tht_FlapJack_genotype_MCL_align4
tht_FlapJack_genotype_MCL_align5
tht_FlapJack_genotype_MCL_align6
tht_FlapJack_genotype_MCL_align7
Polymorphisms
Numerical
geneticMap
traits
Matrix
Original data set
Physical Positions
Site Numbers
Locus
Site Name
Alleles
(Enter physical position)
Search
Number of sequences: 192
Number of sites: 255
Data type: Text
Loci: 1H
Table
Table
Program Status

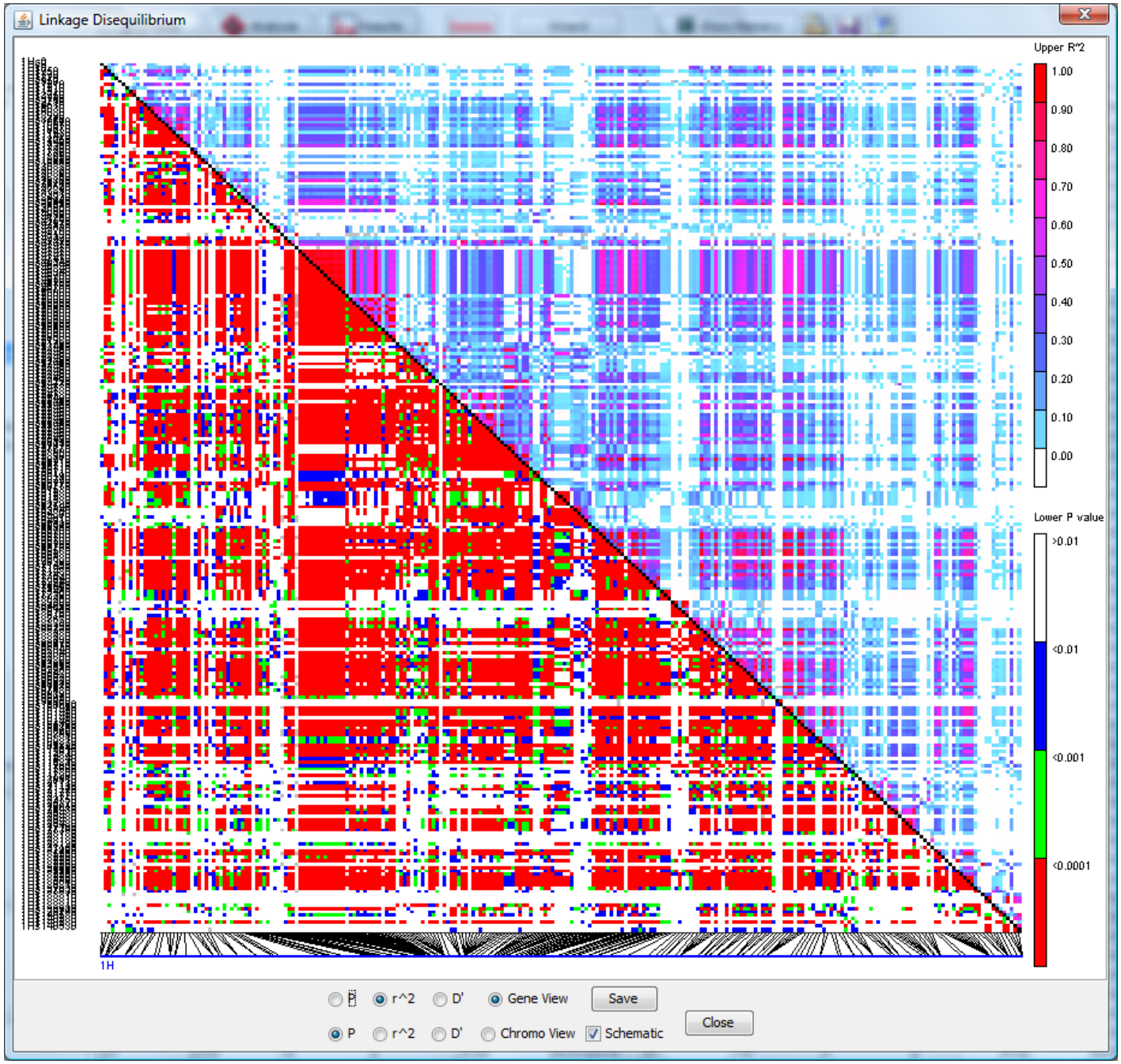
Running Linkage Disequilibrium Analysis

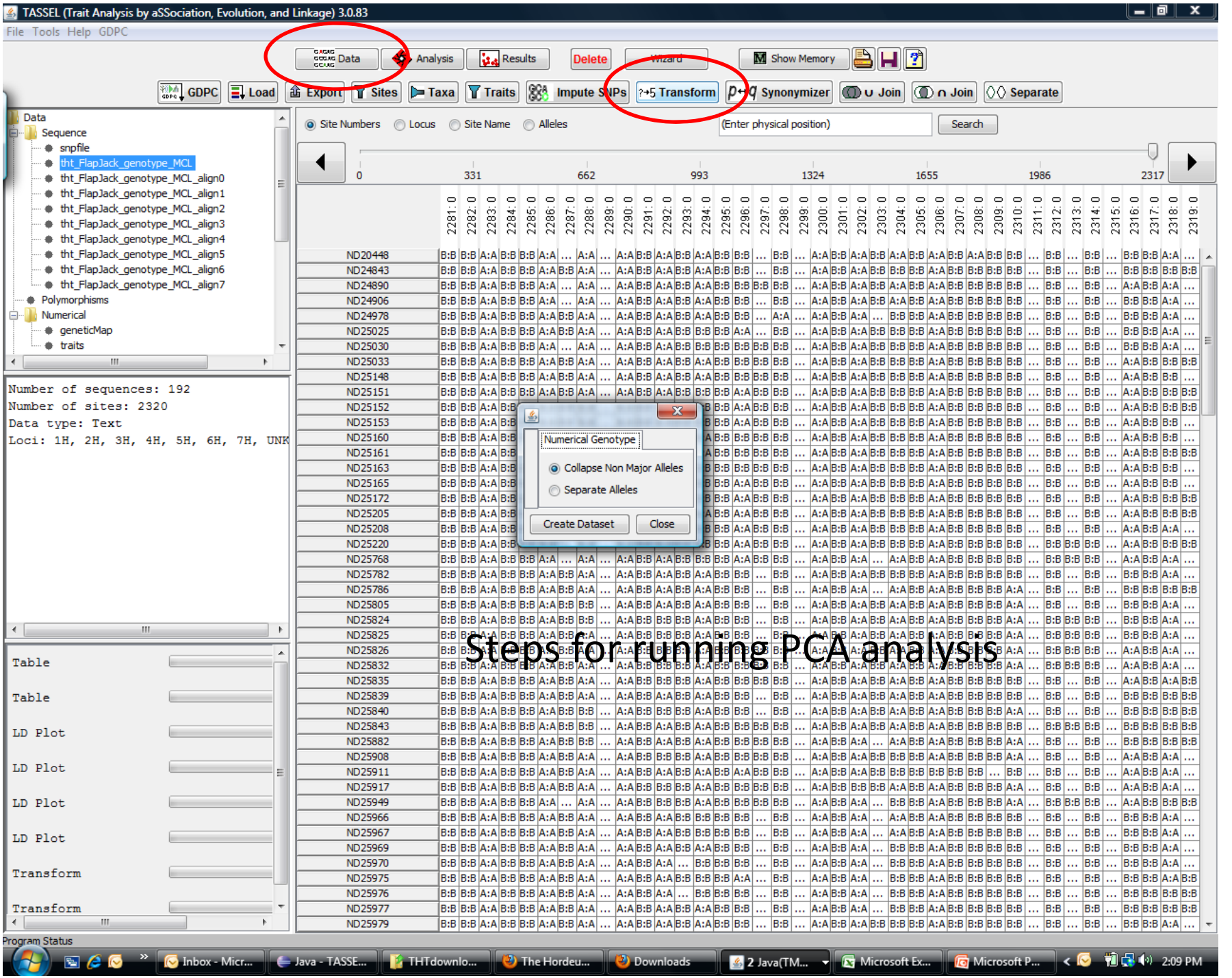



Linkage Disequilibrium
Rapid Permutations (slightly biased p-values)
Full Matrix LD
Sliding Window LD
50
LD Window Size
Run
Close

Display an LD Plot




Linkage Disequilibrium
Upper R^2
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
Lower P value
>0.01
<0.01
<0.001
<0.0001
1H
P
r^2
D'
Gene View
Save
P
r^2
D'
Chromo View
Schematic
Close


TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
File Tools Help GDPC
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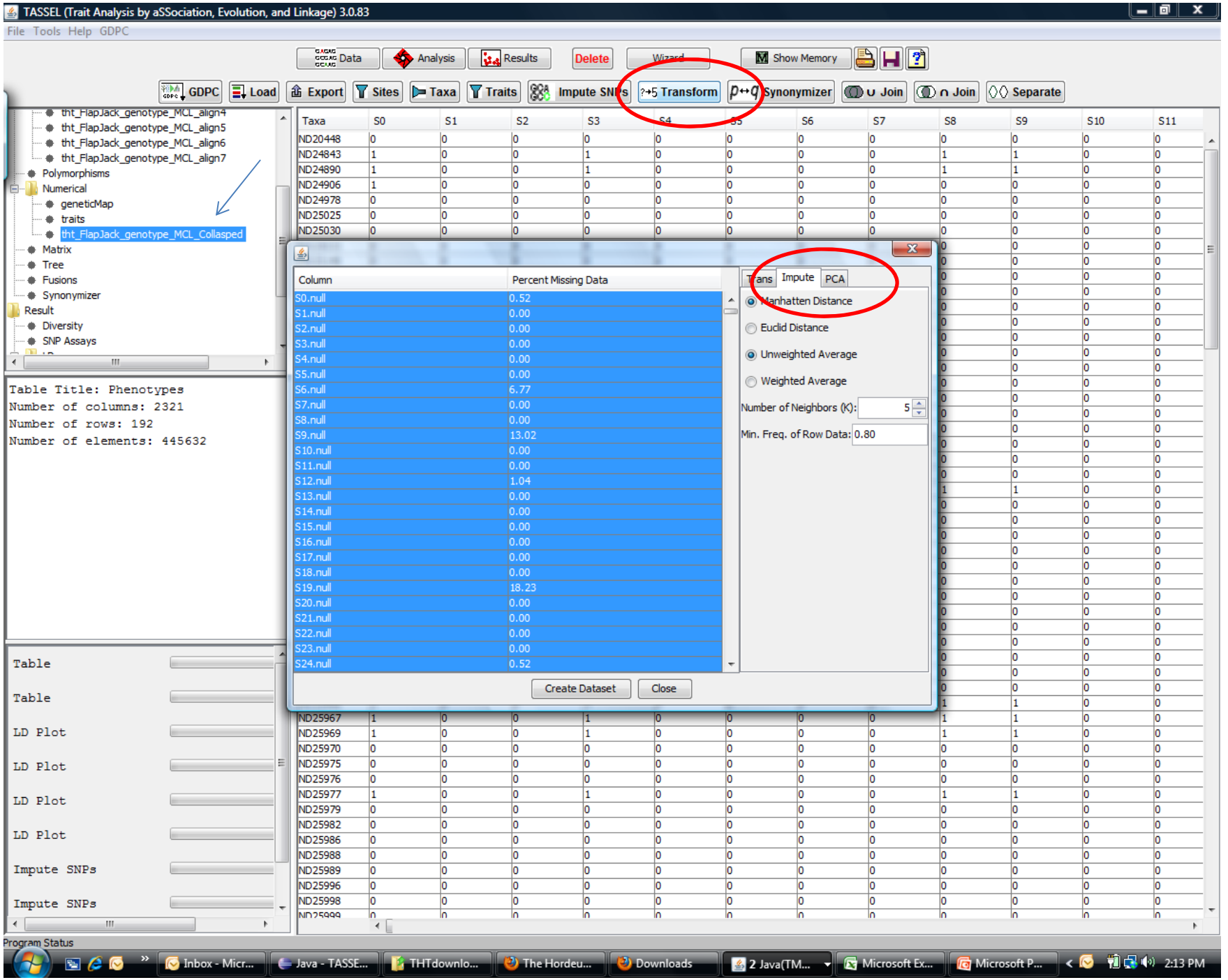
Impute SNPs
Transform
Synonymizer
Join
Join
Separate
Site Numbers
Locus
Site Name
Alleles
(Enter physical position)
Search
Data
Sequence
snpfile
tht_FlapJack_genotype_MCL
tht_FlapJack_genotype_MCL_align0
tht_FlapJack_genotype_MCL_align1
tht_FlapJack_genotype_MCL_align2
tht_FlapJack_genotype_MCL_align3
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
Numerical Genotype
Collapse Non Major Alleles
Separate Alleles
Create Dataset
Close
Table
Table
LD Plot
LD Plot
LD Plot
LD Plot
Transform
Transform
Program Status
Steps for running PCA analysis


TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
File Tools Help GDPC
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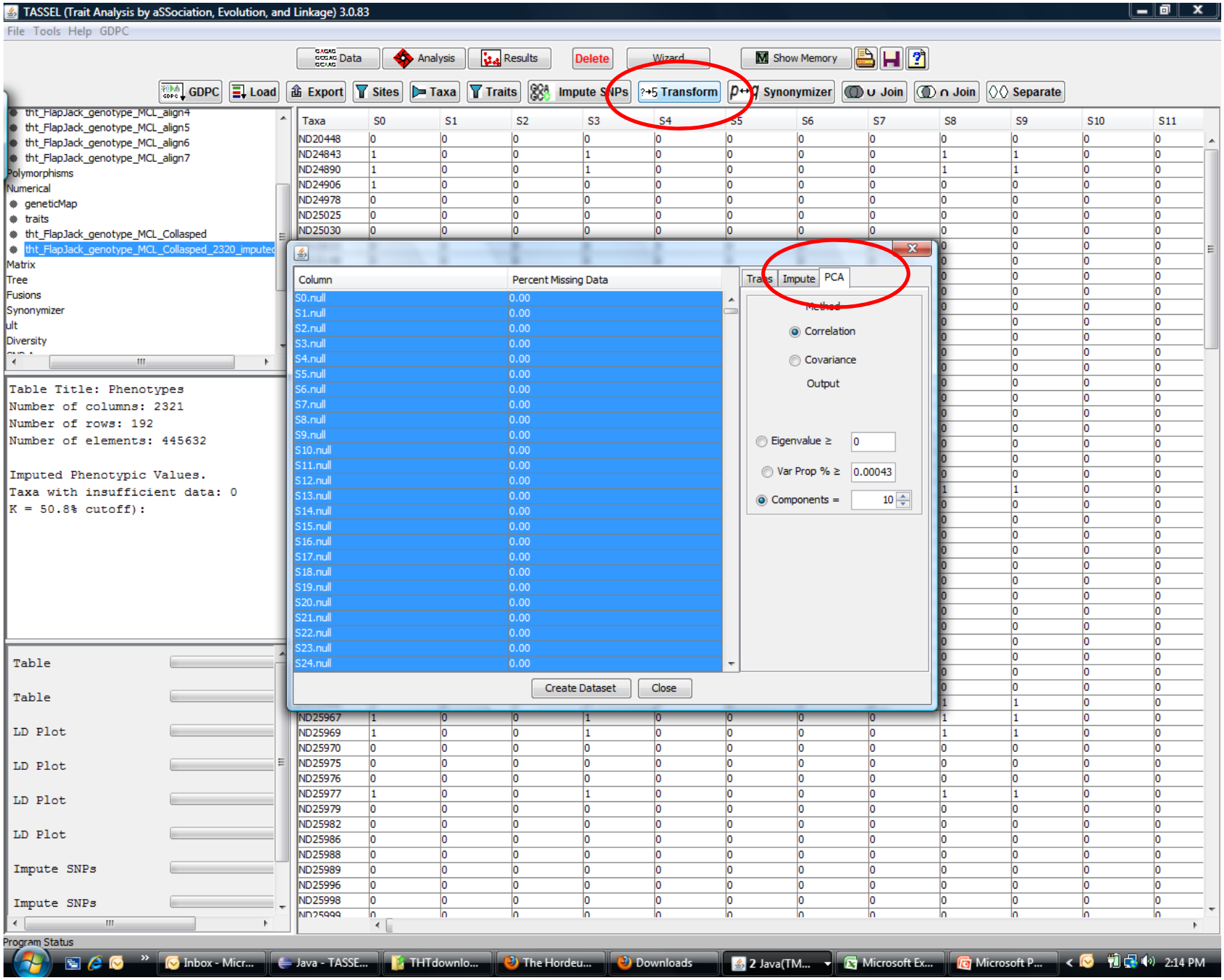
Join
Separate
tht_FlapJack_genotype_MCL_align4
tht_FlapJack_genotype_MCL_align5
tht_FlapJack_genotype_MCL_align6
tht_FlapJack_genotype_MCL_align7
Polymorphisms
Numerical
geneticMap
traits
tht_FlapJack_genotype_MCL_Collasped
Matrix
Tree
Fusions
Synonymizer
Result
Diversity
SNP Assays
Table Title: Phenotypes
Number of columns: 2321
Number of rows: 192
Number of elements: 445632
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
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
Trans
Impute
PCA
Manhatten Distance
Euclid Distance
Unweighted Average
Weighted Average
Number of Neighbors (K): 5
Min. Freq. of Row Data: 0.80
Create Dataset
Close
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
Program Status
Inbox - Micr...
Java - TASSE...
THTdownlo...
The Hordeu...
Downloads
2 Java(TM...
Microsoft Ex...
Microsoft P...
2:13 PM


TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
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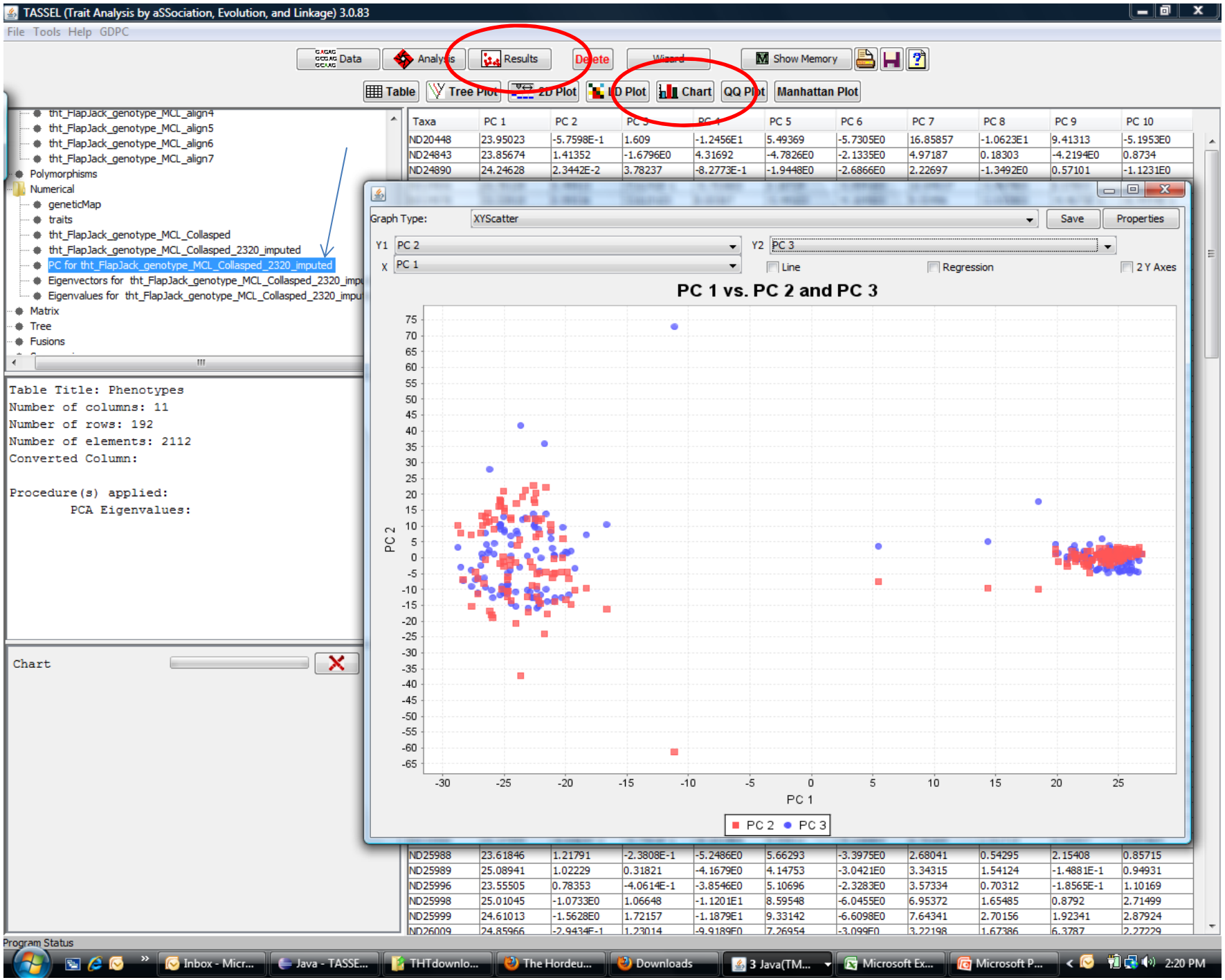
Join
Separate
tht_FlapJack_genotype_MCL_align4
tht_FlapJack_genotype_MCL_align5
tht_FlapJack_genotype_MCL_align6
tht_FlapJack_genotype_MCL_align7
Polymorphisms
Numerical
geneticMap
traits
tht_FlapJack_genotype_MCL_Collasped
tht_FlapJack_genotype_MCL_Collasped_2320_imputed
Matrix
Tree
Fusions
Synonymizer
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
Program Status
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
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
Trans
Impute
PCA
Method
Correlation
Covariance
Output
Eigenvalue ≥ 0
Var Prop % ≥ 0.00043
Components = 10
Create Dataset
Close
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
Inbox - Micr...
Java - TASSE...
THTdownlo...
The Hordeu...
Downloads
2 Java(TM...
Microsoft Ex...
Microsoft P...
2:14 PM


TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
File Tools Help GDPC
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Manhattan Plot
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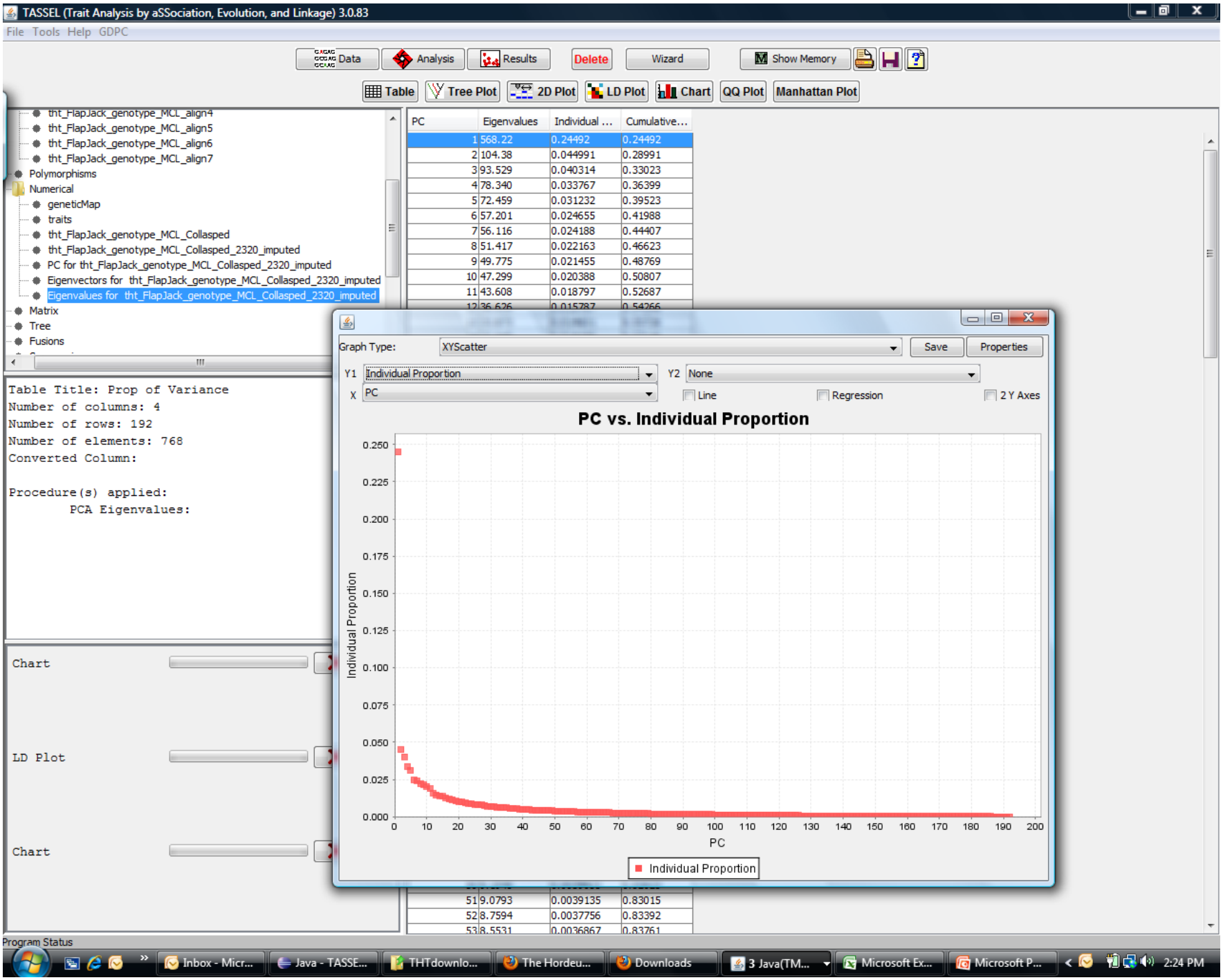
tht_FlapJack_genotype_MCL_align5
tht_FlapJack_genotype_MCL_align6
tht_FlapJack_genotype_MCL_align7
Polymorphisms
Numerical
geneticMap
traits
tht_FlapJack_genotype_MCL_Collasped
tht_FlapJack_genotype_MCL_Collasped_2320_imputed
PC for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
Eigenvectors for tht_FlapJack_genotype_MCL_Collasped_2320_imp
Eigenvalues for tht_FlapJack_genotype_MCL_Collasped_2320_imp
Matrix
Tree
Fusions
Table Title: Phenotypes
Number of columns: 11
Number of rows: 192
Number of elements: 2112
Converted Column:
Procedure(s) applied:
PCA Eigenvalues:
Chart
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
Graph Type: XYScatter
Save
Properties
Y1 PC 2
Y2 PC 3
X PC 1
Line
Regression
2 Y Axes
PC 1 vs. PC 2 and PC 3
PC 2
PC 1
PC 2 PC 3
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
Program Status
Inbox - Micr...
Java - TASSE...
THTdownlo...
The Hordeu...
Downloads
3 Java(TM...
Microsoft Ex...
Microsoft P...
2:20 PM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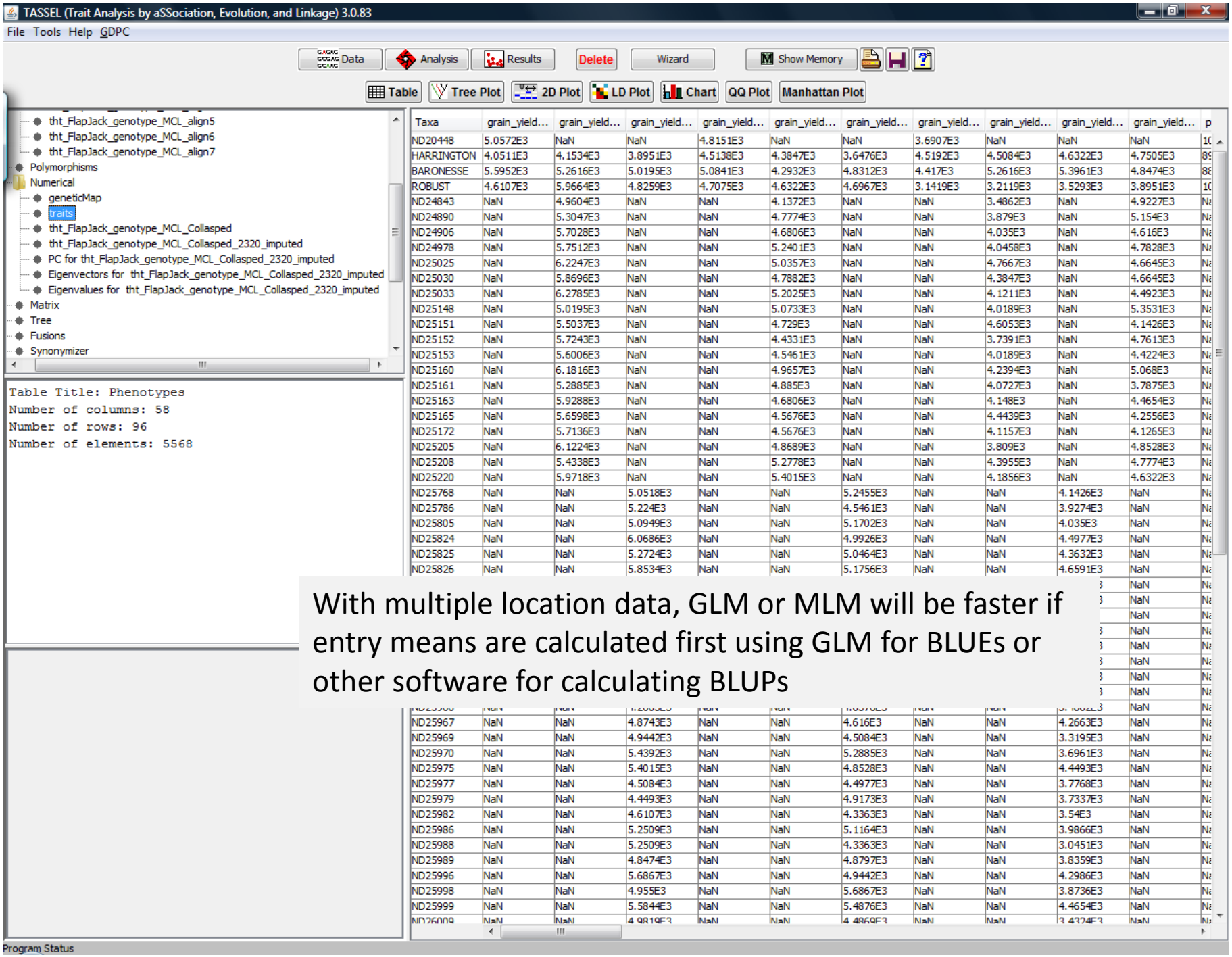
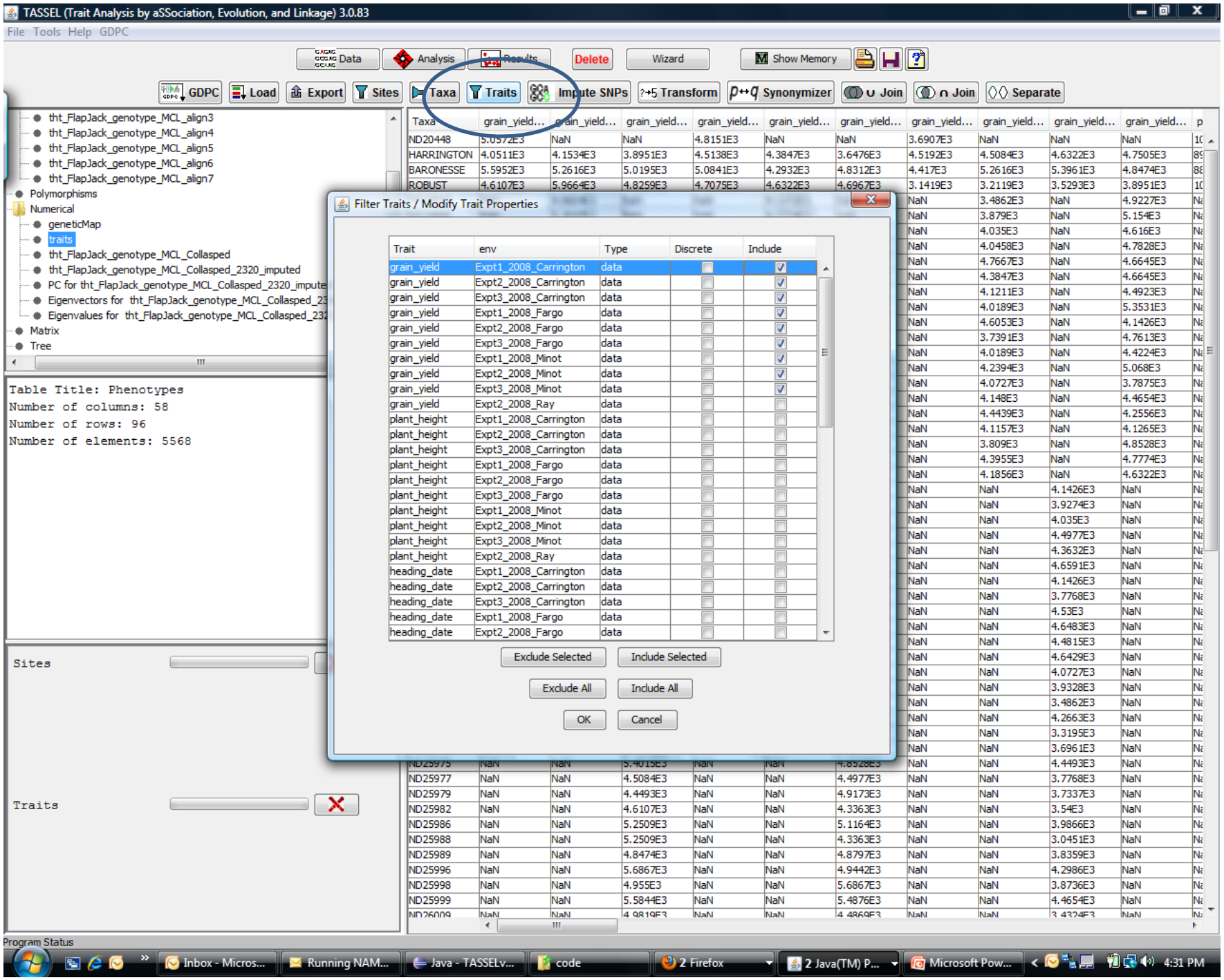
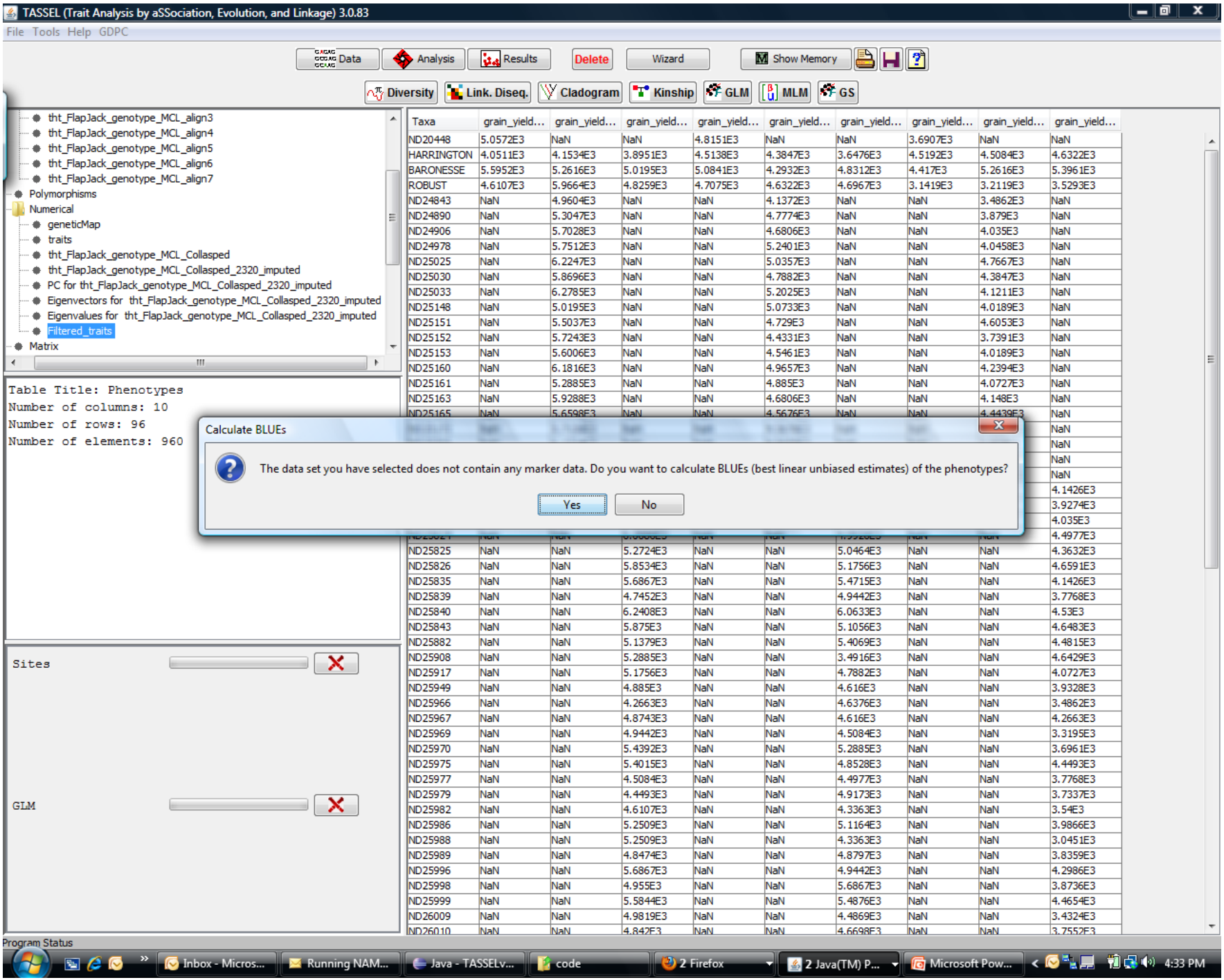
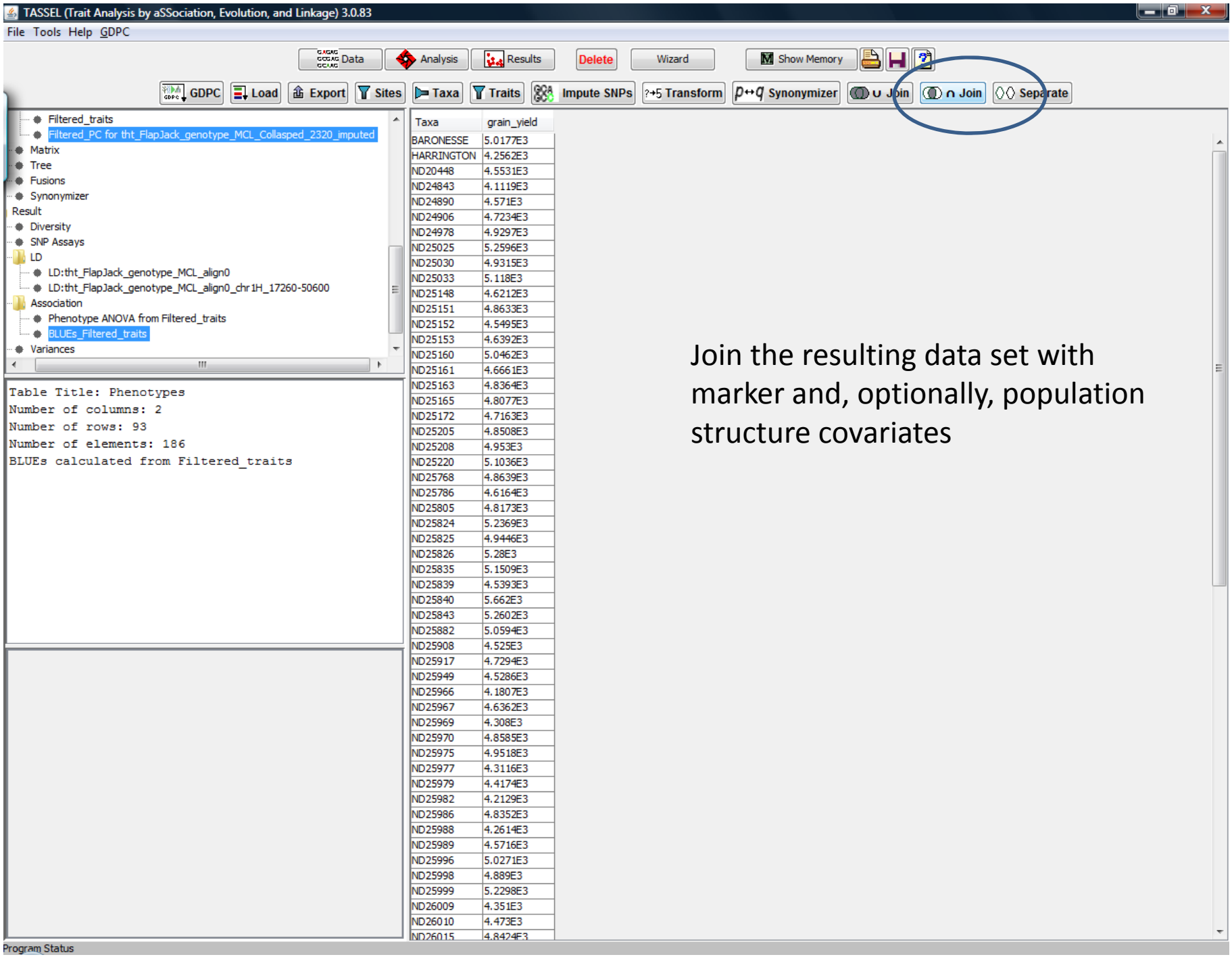
Manhattan Plot
tht_FlapJack_genotype_MCL_align4
tht_FlapJack_genotype_MCL_align5
tht_FlapJack_genotype_MCL_align6
tht_FlapJack_genotype_MCL_align7
Polymorphisms
Numerical
geneticMap
traits
tht_FlapJack_genotype_MCL_Collasped
tht_FlapJack_genotype_MCL_Collasped_2320_imputed
PC for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
Eigenvectors for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
Eigenvalues for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
Matrix
Tree
Fusions
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
51 9.0793 0.0039135 0.83015
52 8.7594 0.0037756 0.83392
53 8.5531 0.0036867 0.83761
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
Graph Type: XYScatter
Save
Properties
Y1 Individual Proportion
Y2 None
X PC
Line
Regression
2 Y Axes
PC vs. Individual Proportion
Individual Proportion
0.250
0.225
0.200
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
0 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200
PC
Individual Proportion
Program Status
Inbox - Micr...
Java - TASSE...
THTdownlo...
The Hordeu...
Downloads
3 Java(TM...
Microsoft Ex...
Microsoft P...
2:24 PM

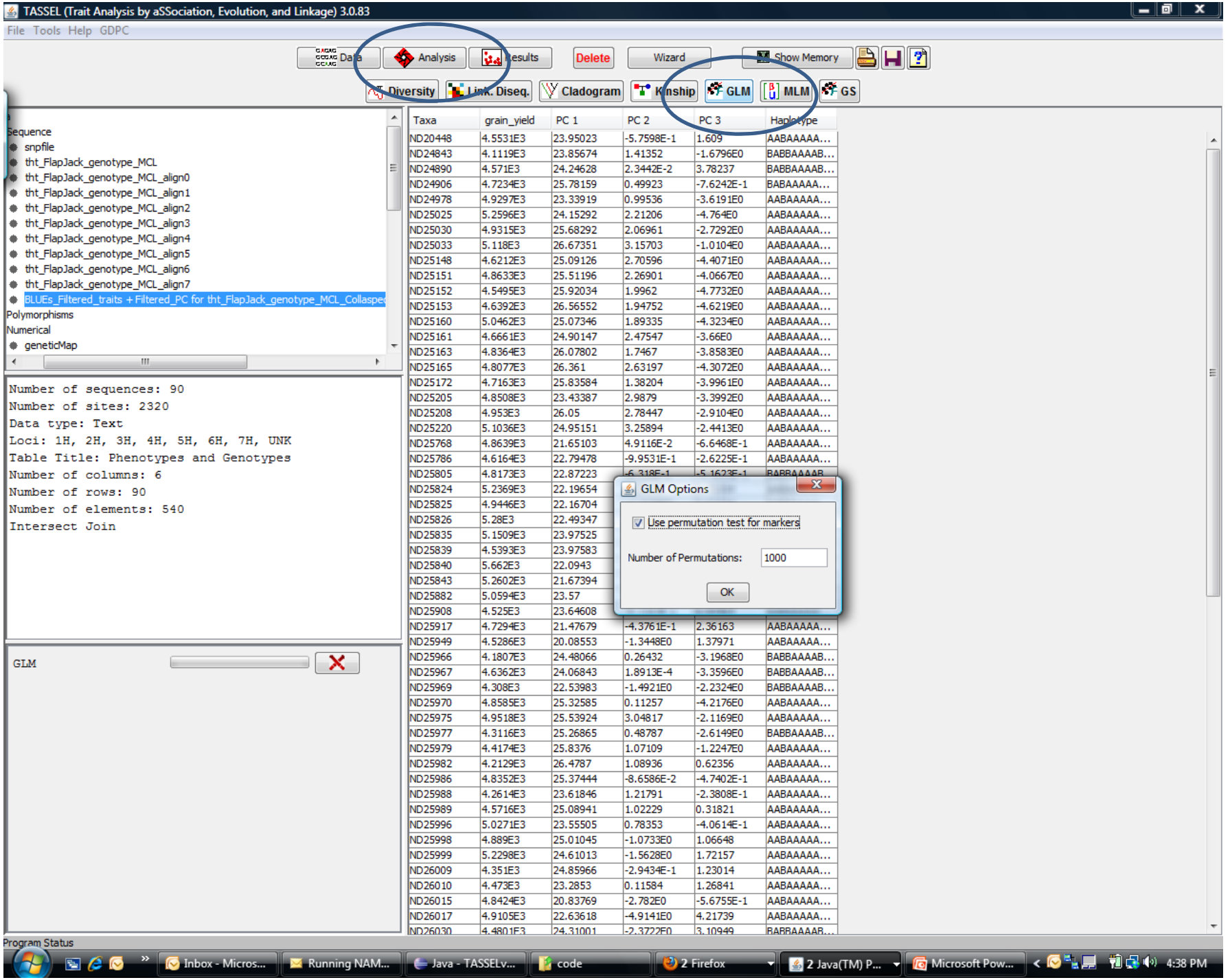

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
File Tools Help GDPC
Data
Analysis
Results
Delete
Wizard
Show Memory
Table
Tree Plot
2D Plot
LD Plot
Chart
QQ Plot
Manhattan Plot
tht_FlapJack_genotype_MCL_align5
tht_FlapJack_genotype_MCL_align6
tht_FlapJack_genotype_MCL_align7
Polymorphisms
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 88
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 Na
ND24890 NaN 5.3047E3 NaN NaN 4.7774E3 NaN NaN 3.879E3 NaN 5.154E3 Na
ND24906 NaN 5.7028E3 NaN NaN 4.6806E3 NaN NaN 4.035E3 NaN 4.616E3 Na
ND24978 NaN 5.7512E3 NaN NaN 5.2401E3 NaN NaN 4.0458E3 NaN 4.7828E3 Na
ND25025 NaN 6.2247E3 NaN NaN 5.0357E3 NaN NaN 4.7667E3 NaN 4.6645E3 Na
ND25030 NaN 5.8696E3 NaN NaN 4.7882E3 NaN NaN 4.3847E3 NaN 4.6645E3 Na
ND25033 NaN 6.2785E3 NaN NaN 5.2025E3 NaN NaN 4.1211E3 NaN 4.4923E3 Na
ND25148 NaN 5.0195E3 NaN NaN 5.0733E3 NaN NaN 4.0189E3 NaN 5.3531E3 Na
ND25151 NaN 5.5037E3 NaN NaN 4.729E3 NaN NaN 4.6053E3 NaN 4.1426E3 Na
ND25152 NaN 5.7243E3 NaN NaN 4.4331E3 NaN NaN 3.7391E3 NaN 4.7613E3 Na
ND25153 NaN 5.6006E3 NaN NaN 4.5461E3 NaN NaN 4.0189E3 NaN 4.4224E3 Na
ND25160 NaN 6.1816E3 NaN NaN 4.9657E3 NaN NaN 4.2394E3 NaN 5.068E3 Na
ND25161 NaN 5.2885E3 NaN NaN 4.885E3 NaN NaN 4.0727E3 NaN 3.7875E3 Na
ND25163 NaN 5.9288E3 NaN NaN 4.6806E3 NaN NaN 4.148E3 NaN 4.4654E3 Na
ND25165 NaN 5.6598E3 NaN NaN 4.5676E3 NaN NaN 4.4439E3 NaN 4.2556E3 Na
ND25172 NaN 5.7136E3 NaN NaN 4.5676E3 NaN NaN 4.1157E3 NaN 4.1265E3 Na
ND25205 NaN 6.1224E3 NaN NaN 4.8689E3 NaN NaN 3.809E3 NaN 4.8528E3 Na
ND25208 NaN 5.4338E3 NaN NaN 5.2778E3 NaN NaN 4.3955E3 NaN 4.7774E3 Na
ND25220 NaN 5.9718E3 NaN NaN 5.4015E3 NaN NaN 4.1856E3 NaN 4.6322E3 Na
ND25768 NaN NaN 5.0518E3 NaN NaN 5.2455E3 NaN NaN 4.1426E3 NaN Na
ND25786 NaN NaN 5.224E3 NaN NaN 4.5461E3 NaN NaN 3.9274E3 NaN Na
ND25805 NaN NaN 5.0949E3 NaN NaN 5.1702E3 NaN NaN 4.035E3 NaN Na
ND25824 NaN NaN 6.0686E3 NaN NaN 4.9926E3 NaN NaN 4.4977E3 NaN Na
ND25825 NaN NaN 5.2724E3 NaN NaN 5.0464E3 NaN NaN 4.3632E3 NaN Na
ND25826 NaN NaN 5.8534E3 NaN NaN 5.1756E3 NaN NaN 4.6591E3 NaN Na
ND25967 NaN NaN 4.8743E3 NaN NaN 4.616E3 NaN NaN 4.2663E3 NaN Na
ND25969 NaN NaN 4.9442E3 NaN NaN 4.5084E3 NaN NaN 3.3195E3 NaN Na
ND25970 NaN NaN 5.4392E3 NaN NaN 5.2885E3 NaN NaN 3.6961E3 NaN Na
ND25975 NaN NaN 5.4015E3 NaN NaN 4.8528E3 NaN NaN 4.4493E3 NaN Na
ND25977 NaN NaN 4.5084E3 NaN NaN 4.4977E3 NaN NaN 3.7768E3 NaN Na
ND25979 NaN NaN 4.4493E3 NaN NaN 4.9173E3 NaN NaN 3.7337E3 NaN Na
ND25982 NaN NaN 4.6107E3 NaN NaN 4.3363E3 NaN NaN 3.54E3 NaN Na
ND25986 NaN NaN 5.2509E3 NaN NaN 5.1164E3 NaN NaN 3.9866E3 NaN Na
ND25988 NaN NaN 5.2509E3 NaN NaN 4.3363E3 NaN NaN 3.0451E3 NaN Na
ND25989 NaN NaN 4.8474E3 NaN NaN 4.8797E3 NaN NaN 3.8359E3 NaN Na
ND25996 NaN NaN 5.6867E3 NaN NaN 4.9442E3 NaN NaN 4.2986E3 NaN Na
ND25998 NaN NaN 4.955E3 NaN NaN 5.6867E3 NaN NaN 3.8736E3 NaN Na
ND25999 NaN NaN 5.5844E3 NaN NaN 5.4876E3 NaN NaN 4.4654E3 NaN Na
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
Program Status


TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
File Tools Help GDPC
Data
Analysis
Results
Delete
Wizard
Show Memory
GDPC
Load
Export
Sites
Taxa
Traits
Impute SNPs
?→5 Transform
p↔q Synonymizer
∪ Join
∩ Join
Separate
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_impute
Eigenvectors for tht_FlapJack_genotype_MCL_Collasped_23
Eigenvalues for tht_FlapJack_genotype_MCL_Collasped_232
Matrix
Tree
Table Title: Phenotypes
Number of columns: 58
Number of rows: 96
Number of elements: 5568
Sites
Traits
Filter Traits / Modify Trait Properties
Trait
env
Type
Discrete
Include
grain_yield Expt1_2008_Carrington data
grain_yield Expt2_2008_Carrington data
grain_yield Expt3_2008_Carrington data
grain_yield Expt1_2008_Fargo data
grain_yield Expt2_2008_Fargo data
grain_yield Expt3_2008_Fargo data
grain_yield Expt1_2008_Minot data
grain_yield Expt2_2008_Minot data
grain_yield Expt3_2008_Minot data
grain_yield Expt2_2008_Ray data
plant_height Expt1_2008_Carrington data
plant_height Expt2_2008_Carrington data
plant_height Expt3_2008_Carrington data
plant_height Expt1_2008_Fargo data
plant_height Expt2_2008_Fargo data
plant_height Expt3_2008_Fargo data
plant_height Expt1_2008_Minot data
plant_height Expt2_2008_Minot data
plant_height Expt3_2008_Minot data
plant_height Expt2_2008_Ray data
heading_date Expt1_2008_Carrington data
heading_date Expt2_2008_Carrington data
heading_date Expt3_2008_Carrington data
heading_date Expt1_2008_Fargo data
heading_date Expt2_2008_Fargo data
Exclude Selected
Include Selected
Exclude All
Include All
OK
Cancel
Taxa grain_yield... p
ND20448 5.0572E3 NaN NaN 4.8151E3 NaN NaN 3.6907E3 NaN NaN NaN
HARRINGTON 4.0511E3 4.1534E3 3.8951E3 4.5138E3 4.3847E3 3.6476E3 4.5192E3 4.5084E3 4.6322E3 4.7505E3
BARONESSE 5.5952E3 5.2616E3 5.0195E3 5.0841E3 4.2932E3 4.8312E3 4.417E3 5.2616E3 5.3961E3 4.8474E3
ROBUST 4.6107E3 5.9664E3 4.8259E3 4.7075E3 4.6322E3 4.6967E3 3.1419E3 3.2119E3 3.5293E3 3.8951E3
ND25977 NaN NaN 4.5084E3 NaN NaN 4.4977E3 NaN NaN 3.7768E3 NaN
ND25979 NaN NaN 4.4493E3 NaN NaN 4.9173E3 NaN NaN 3.7337E3 NaN
ND25982 NaN NaN 4.6107E3 NaN NaN 4.3363E3 NaN NaN 3.54E3 NaN
ND25986 NaN NaN 5.2509E3 NaN NaN 5.1164E3 NaN NaN 3.9866E3 NaN
ND25988 NaN NaN 5.2509E3 NaN NaN 4.3363E3 NaN NaN 3.0451E3 NaN
ND25989 NaN NaN 4.8474E3 NaN NaN 4.8797E3 NaN NaN 3.8359E3 NaN
ND25996 NaN NaN 5.6867E3 NaN NaN 4.9442E3 NaN NaN 4.2986E3 NaN
ND25998 NaN NaN 4.955E3 NaN NaN 5.6867E3 NaN NaN 3.8736E3 NaN
ND25999 NaN NaN 5.5844E3 NaN NaN 5.4876E3 NaN NaN 4.4654E3 NaN
Program Status
Inbox - Micros...
Running NAM...
Java - TASSELv...
code
2 Firefox
2 Java(TM) P...
Microsoft Pow...
4:31 PM

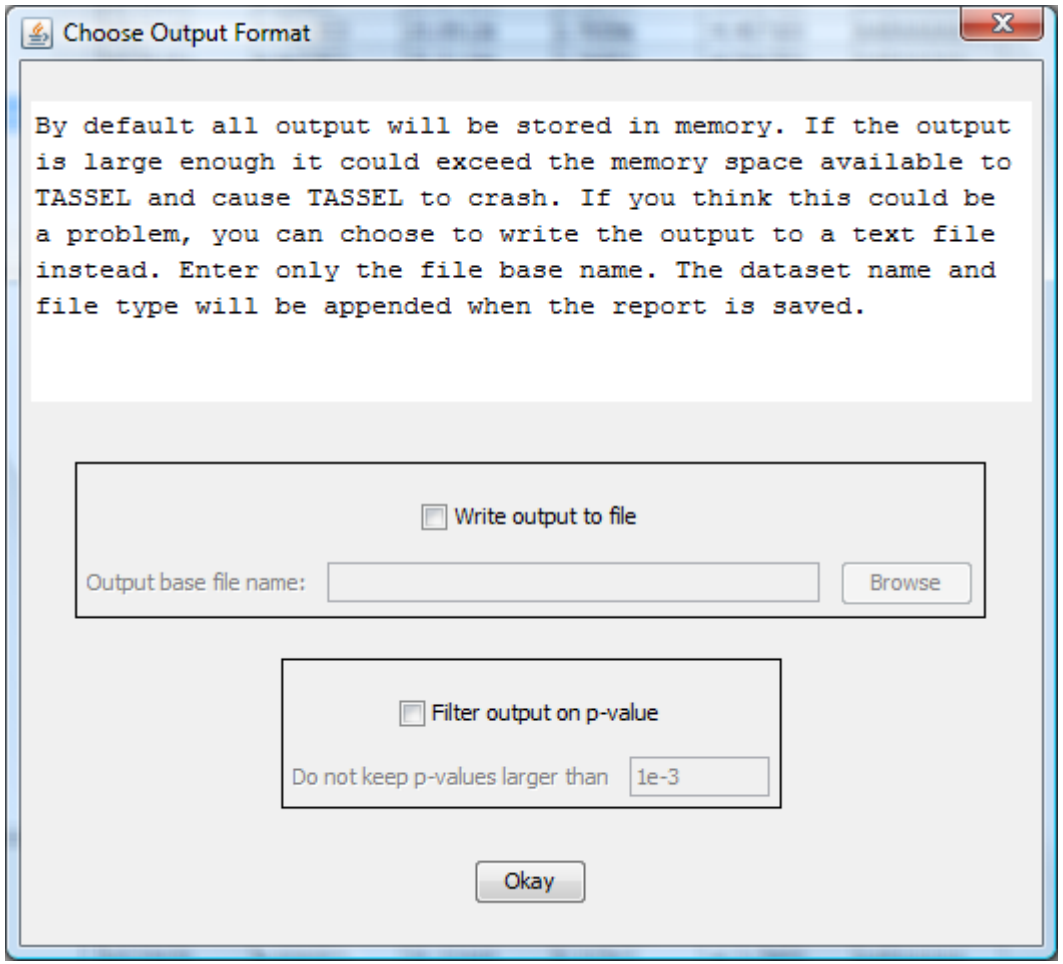

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
File Tools Help GDPC
Data
Analysis
Results
Delete
Wizard
Show Memory
Diversity
Link. Diseq.
Cladogram
Kinship
GLM
MLM
GS
tht_FlapJack_genotype_MCL_align3
tht_FlapJack_genotype_MCL_align4
tht_FlapJack_genotype_MCL_align5
tht_FlapJack_genotype_MCL_align6
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
Table Title: Phenotypes
Number of columns: 10
Number of rows: 96
Number of elements: 960
Sites
GLM
Program Status
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?
Yes
No
Taxa
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
ND25825 NaN NaN 5.2724E3 NaN NaN 5.0464E3 NaN NaN 4.3632E3
ND25826 NaN NaN 5.8534E3 NaN NaN 5.1756E3 NaN NaN 4.6591E3
ND25835 NaN NaN 5.6867E3 NaN NaN 5.4715E3 NaN NaN 4.1426E3
ND25839 NaN NaN 4.7452E3 NaN NaN 4.9442E3 NaN NaN 3.7768E3
ND25840 NaN NaN 6.2408E3 NaN NaN 6.0633E3 NaN NaN 4.53E3
ND25843 NaN NaN 5.875E3 NaN NaN 5.1056E3 NaN NaN 4.6483E3
ND25882 NaN NaN 5.1379E3 NaN NaN 5.4069E3 NaN NaN 4.4815E3
ND25908 NaN NaN 5.2885E3 NaN NaN 3.4916E3 NaN NaN 4.6429E3
ND25917 NaN NaN 5.1756E3 NaN NaN 4.7882E3 NaN NaN 4.0727E3
ND25949 NaN NaN 4.885E3 NaN NaN 4.616E3 NaN NaN 3.9328E3
ND25966 NaN NaN 4.2663E3 NaN NaN 4.6376E3 NaN NaN 3.4862E3
ND25967 NaN NaN 4.8743E3 NaN NaN 4.616E3 NaN NaN 4.2663E3
ND25969 NaN NaN 4.9442E3 NaN NaN 4.5084E3 NaN NaN 3.3195E3
ND25970 NaN NaN 5.4392E3 NaN NaN 5.2885E3 NaN NaN 3.6961E3
ND25975 NaN NaN 5.4015E3 NaN NaN 4.8528E3 NaN NaN 4.4493E3
ND25977 NaN NaN 4.5084E3 NaN NaN 4.4977E3 NaN NaN 3.7768E3
ND25979 NaN NaN 4.4493E3 NaN NaN 4.9173E3 NaN NaN 3.7337E3
ND25982 NaN NaN 4.6107E3 NaN NaN 4.3363E3 NaN NaN 3.54E3
ND25986 NaN NaN 5.2509E3 NaN NaN 5.1164E3 NaN NaN 3.9866E3
ND25988 NaN NaN 5.2509E3 NaN NaN 4.3363E3 NaN NaN 3.0451E3
ND25989 NaN NaN 4.8474E3 NaN NaN 4.8797E3 NaN NaN 3.8359E3
ND25996 NaN NaN 5.6867E3 NaN NaN 4.9442E3 NaN NaN 4.2986E3
ND25998 NaN NaN 4.955E3 NaN NaN 5.6867E3 NaN NaN 3.8736E3
ND25999 NaN NaN 5.5844E3 NaN NaN 5.4876E3 NaN NaN 4.4654E3
ND26009 NaN NaN 4.9819E3 NaN NaN 4.4869E3 NaN NaN 3.4324E3
Inbox - Micros...
Running NAM...
Java - TASSELv...
code
2 Firefox
2 Java(TM) P...
Microsoft Pow...
4:33 PM

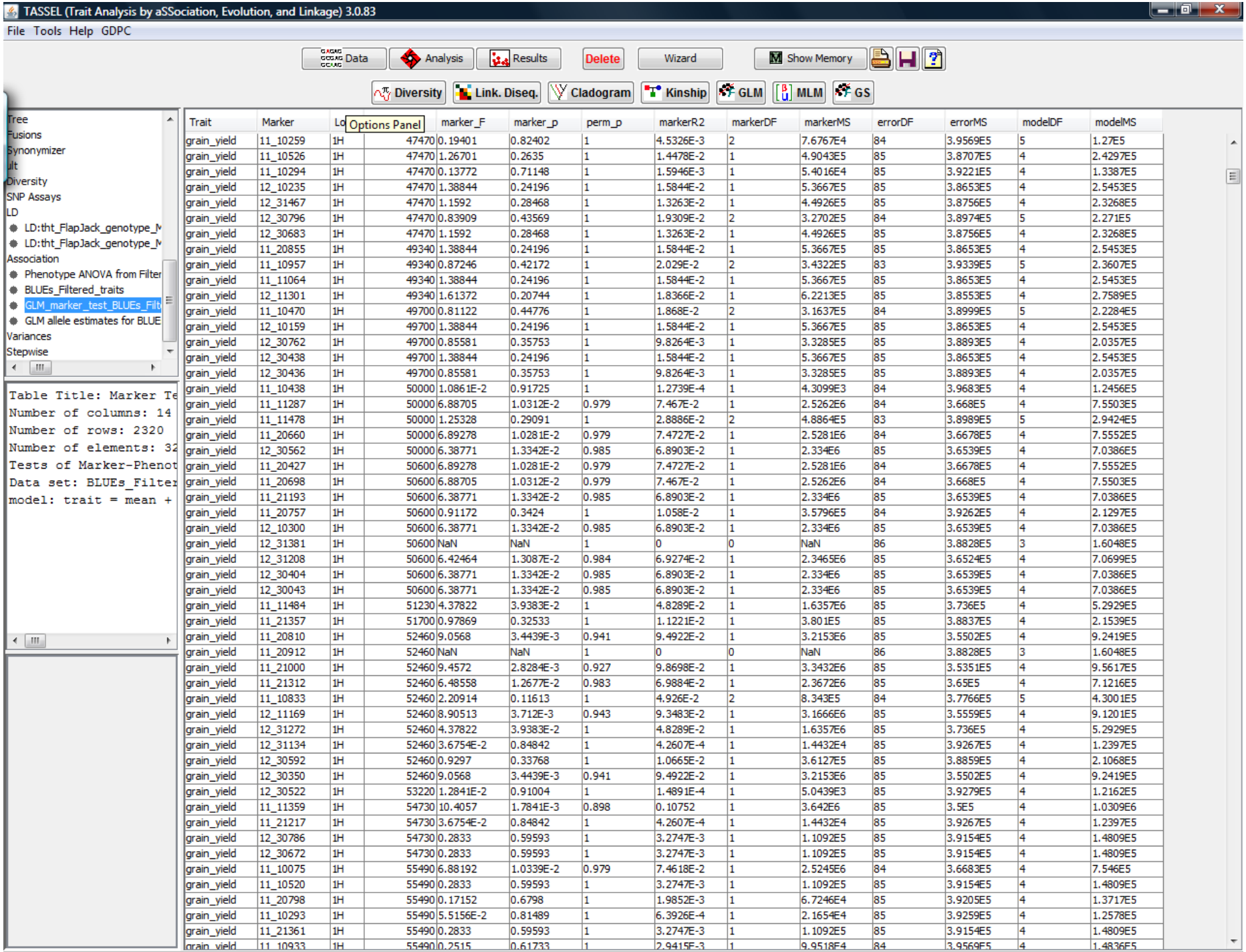


Join the resulting data set with marker and, optionally, population structure covariates


TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
File Tools Help GDPC
Data
Analysis
Results
Delete
Wizard
Show Memory
Diversity
Link. Diseq.
Cladogram
Kinship
GLM
MLM
GS
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_Collapse
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 BABBAAAAB...
ND24890 4.571E3 24.24628 2.3442E-2 3.78237 BABBAAAAB...
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 -6.6468E-1 AABAAAAA...
ND25786 4.6164E3 22.79478 -9.9531E-1 -2.6225E-1 AABAAAAA...
ND25805 4.8173E3 22.87223
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 BABBAAAAB...
ND25967 4.6362E3 24.06843 1.8913E-4 -3.3596E0 BABBAAAAB...
ND25969 4.308E3 22.53983 -1.4921E0 -2.2324E0 BABBAAAAB...
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 BABBAAAAB...
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 BABBAAAAB...
GLM Options
Use permutation test for markers
Number of Permutations: 1000
OK
Program Status
Inbox - Micros...
Running NAM...
Java - TASSELv...
code
2 Firefox
2 Java(TM) P...
Microsoft Pow...
4:38 PM

Option for saving output to disk for large files





Trait	Marker	Lo		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	5	1.27E5
grain_yield	11_10526	1H	47470	1.26701	0.2635	1	1.4478E-2	1	4.9043E5	85	3.8707E5	4	2.4297E5
grain_yield	11_10294	1H	47470	0.13772	0.71148	1	1.5946E-3	1	5.4016E4	85	3.9221E5	4	1.3387E5
grain_yield	12_10235	1H	47470	1.38844	0.24196	1	1.5844E-2	1	5.3667E5	85	3.8653E5	4	2.5453E5
grain_yield	12_31467	1H	47470	1.1592	0.28468	1	1.3263E-2	1	4.4926E5	85	3.8756E5	4	2.3268E5
grain_yield	12_30796	1H	47470	0.83909	0.43569	1	1.9309E-2	2	3.2702E5	84	3.8974E5	5	2.271E5
grain_yield	12_30683	1H	47470	1.1592	0.28468	1	1.3263E-2	1	4.4926E5	85	3.8756E5	4	2.3268E5
grain_yield	11_20855	1H	49340	1.38844	0.24196	1	1.5844E-2	1	5.3667E5	85	3.8653E5	4	2.5453E5
grain_yield	11_10957	1H	49340	0.87246	0.42172	1	2.029E-2	2	3.4322E5	83	3.9339E5	5	2.3607E5
grain_yield	11_11064	1H	49340	1.38844	0.24196	1	1.5844E-2	1	5.3667E5	85	3.8653E5	4	2.5453E5
grain_yield	12_11301	1H	49340	1.61372	0.20744	1	1.8366E-2	1	6.2213E5	85	3.8553E5	4	2.7589E5
grain_yield	11_10470	1H	49700	0.81122	0.44776	1	1.868E-2	2	3.1637E5	84	3.8999E5	5	2.2284E5
grain_yield	12_10159	1H	49700	1.38844	0.24196	1	1.5844E-2	1	5.3667E5	85	3.8653E5	4	2.5453E5
grain_yield	12_30762	1H	49700	0.85581	0.35753	1	9.8264E-3	1	3.3285E5	85	3.8893E5	4	2.0357E5
grain_yield	12_30438	1H	49700	1.38844	0.24196	1	1.5844E-2	1	5.3667E5	85	3.8653E5	4	2.5453E5
grain_yield	12_30436	1H	49700	0.85581	0.35753	1	9.8264E-3	1	3.3285E5	85	3.8893E5	4	2.0357E5
grain_yield	11_10438	1H	50000	1.0861E-2	0.91725	1	1.2739E-4	1	4.3099E3	84	3.9683E5	4	1.2456E5
grain_yield	11_11287	1H	50000	6.88705	1.0312E-2	0.979	7.467E-2	1	2.5262E6	84	3.668E5	4	7.5503E5
grain_yield	11_11478	1H	50000	1.25328	0.29091	1	2.8886E-2	2	4.8864E5	83	3.8989E5	5	2.9424E5
grain_yield	11_20660	1H	50000	6.89278	1.0281E-2	0.979	7.4727E-2	1	2.5281E6	84	3.6678E5	4	7.5552E5
grain_yield	12_30562	1H	50000	6.38771	1.3342E-2	0.985	6.8903E-2	1	2.334E6	85	3.6539E5	4	7.0386E5
grain_yield	11_20427	1H	50600	6.89278	1.0281E-2	0.979	7.4727E-2	1	2.5281E6	84	3.6678E5	4	7.5552E5
grain_yield	11_20698	1H	50600	6.88705	1.0312E-2	0.979	7.467E-2	1	2.5262E6	84	3.668E5	4	7.5503E5
grain_yield	11_21193	1H	50600	6.38771	1.3342E-2	0.985	6.8903E-2	1	2.334E6	85	3.6539E5	4	7.0386E5
grain_yield	11_20757	1H	50600	0.91172	0.3424	1	1.058E-2	1	3.5796E5	84	3.9262E5	4	2.1297E5
grain_yield	12_10300	1H	50600	6.38771	1.3342E-2	0.985	6.8903E-2	1	2.334E6	85	3.6539E5	4	7.0386E5
grain_yield	12_31381	1H	50600	NaN	NaN	1	0	0	NaN	86	3.8828E5	3	1.6048E5
grain_yield	12_31208	1H	50600	6.42464	1.3087E-2	0.984	6.9274E-2	1	2.3465E6	85	3.6524E5	4	7.0699E5
grain_yield	12_30404	1H	50600	6.38771	1.3342E-2	0.985	6.8903E-2	1	2.334E6	85	3.6539E5	4	7.0386E5
grain_yield	12_30043	1H	50600	6.38771	1.3342E-2	0.985	6.8903E-2	1	2.334E6	85	3.6539E5	4	7.0386E5
grain_yield	11_11484	1H	51230	4.37822	3.9383E-2	1	4.8289E-2	1	1.6357E6	85	3.736E5	4	5.2929E5
grain_yield	11_21357	1H	51700	0.97869	0.32533	1	1.1221E-2	1	3.801E5	85	3.8837E5	4	2.1539E5
grain_yield	11_20810	1H	52460	9.0568	3.4439E-3	0.941	9.4922E-2	1	3.2153E6	85	3.5502E5	4	9.2419E5
grain_yield	11_20912	1H	52460	NaN	NaN	1	0	0	NaN	86	3.8828E5	3	1.6048E5
grain_yield	11_21000	1H	52460	9.4572	2.8284E-3	0.927	9.8698E-2	1	3.3432E6	85	3.5351E5	4	9.5617E5
grain_yield	11_21312	1H	52460	6.48558	1.2677E-2	0.983	6.9884E-2	1	2.3672E6	85	3.65E5	4	7.1216E5
grain_yield	11_10833	1H	52460	2.20914	0.11613	1	4.926E-2	2	8.343E5	84	3.7766E5	5	4.3001E5
grain_yield	12_11169	1H	52460	8.90513	3.712E-3	0.943	9.3483E-2	1	3.1666E6	85	3.5559E5	4	9.1201E5
grain_yield	12_31272	1H	52460	4.37822	3.9383E-2	1	4.8289E-2	1	1.6357E6	85	3.736E5	4	5.2929E5
grain_yield	12_31134	1H	52460	3.6754E-2	0.84842	1	4.2607E-4	1	1.4432E4	85	3.9267E5	4	1.2397E5
grain_yield	12_30592	1H	52460	0.9297	0.33768	1	1.0665E-2	1	3.6127E5	85	3.8859E5	4	2.1068E5
grain_yield	12_30350	1H	52460	9.0568	3.4439E-3	0.941	9.4922E-2	1	3.2153E6	85	3.5502E5	4	9.2419E5
grain_yield	12_30522	1H	53220	1.2841E-2	0.91004	1	1.4891E-4	1	5.0439E3	85	3.9279E5	4	1.2162E5
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grain_yield	11_21217	1H	54730	3.6754E-2	0.84842	1	4.2607E-4	1	1.4432E4	85	3.9267E5	4	1.2397E5
grain_yield	12_30786	1H	54730	0.2833	0.59593	1	3.2747E-3	1	1.1092E5	85	3.9154E5	4	1.4809E5
grain_yield	12_30672	1H	54730	0.2833	0.59593	1	3.2747E-3	1	1.1092E5	85	3.9154E5	4	1.4809E5
grain_yield	11_10075	1H	55490	6.88192	1.0339E-2	0.979	7.4618E-2	1	2.5245E6	84	3.6683E5	4	7.546E5
grain_yield	11_10520	1H	55490	0.2833	0.59593	1	3.2747E-3	1	1.1092E5	85	3.9154E5	4	1.4809E5
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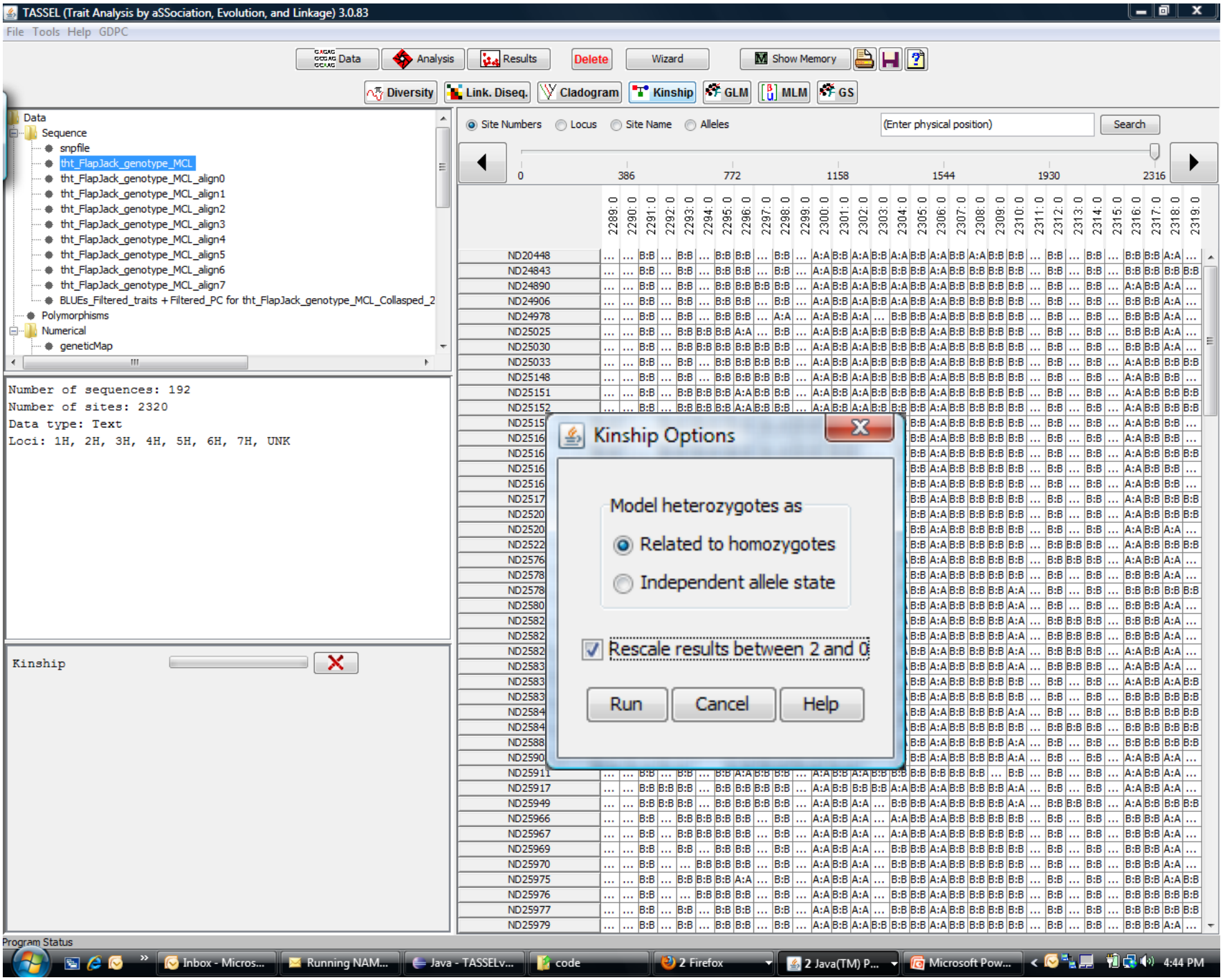
grain_yield	11_21361	1H	55490	0.2833	0.59593	1	3.2747E-3	1	1.1092E5	85	3.9154E5	4	1.4809E5
grain_yield	11_10933	1H	55490	0.2515	0.61733	1	2.9415E-3	1	9.9518E4	84	3.9569E5	4	1.4836E5


TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
File Tools Help GDPC
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Results
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Wizard
Show Memory
Diversity
Link. Diseq.
Cladogram
Kinship
GLM
MLM
GS
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Sequence
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Kinship Options
Model heterozygotes as
Related to homozygotes
Independent allele state
Rescale results between 2 and 0
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Cancel
Help
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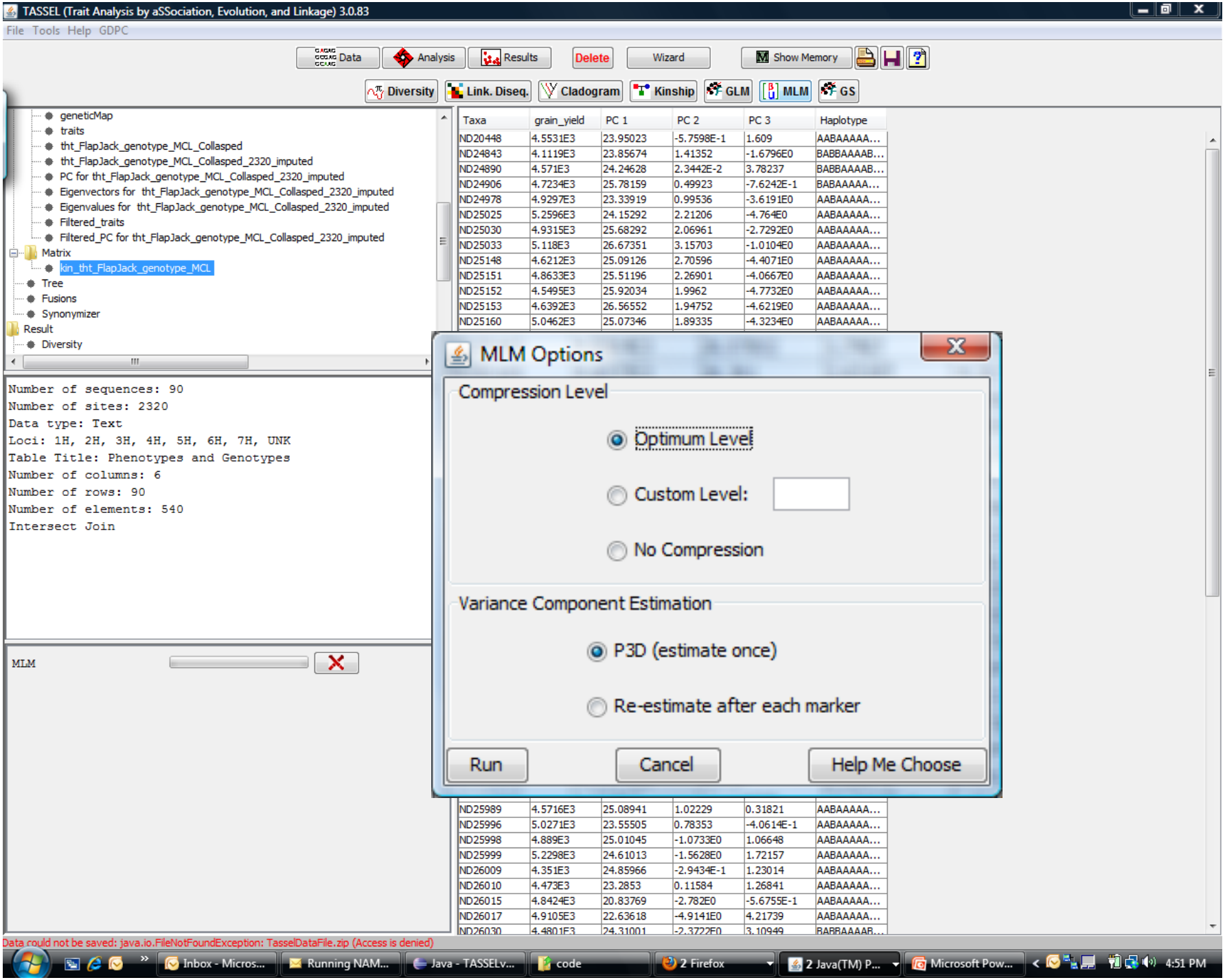
TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 3.0.83
File Tools Help GDPC
Data
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Link. Diseq.
Cladogram
Kinship
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Filtered_PC for tht_FlapJack_genotype_MCL_Collasped_2320_imputed
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Fusions
Synonymizer
Result
Diversity
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Optimum Level
Custom Level:
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Variance Component Estimation
P3D (estimate once)
Re-estimate after each marker
Run
Cancel
Help Me Choose
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Running NAM...
Java - TASSELv...
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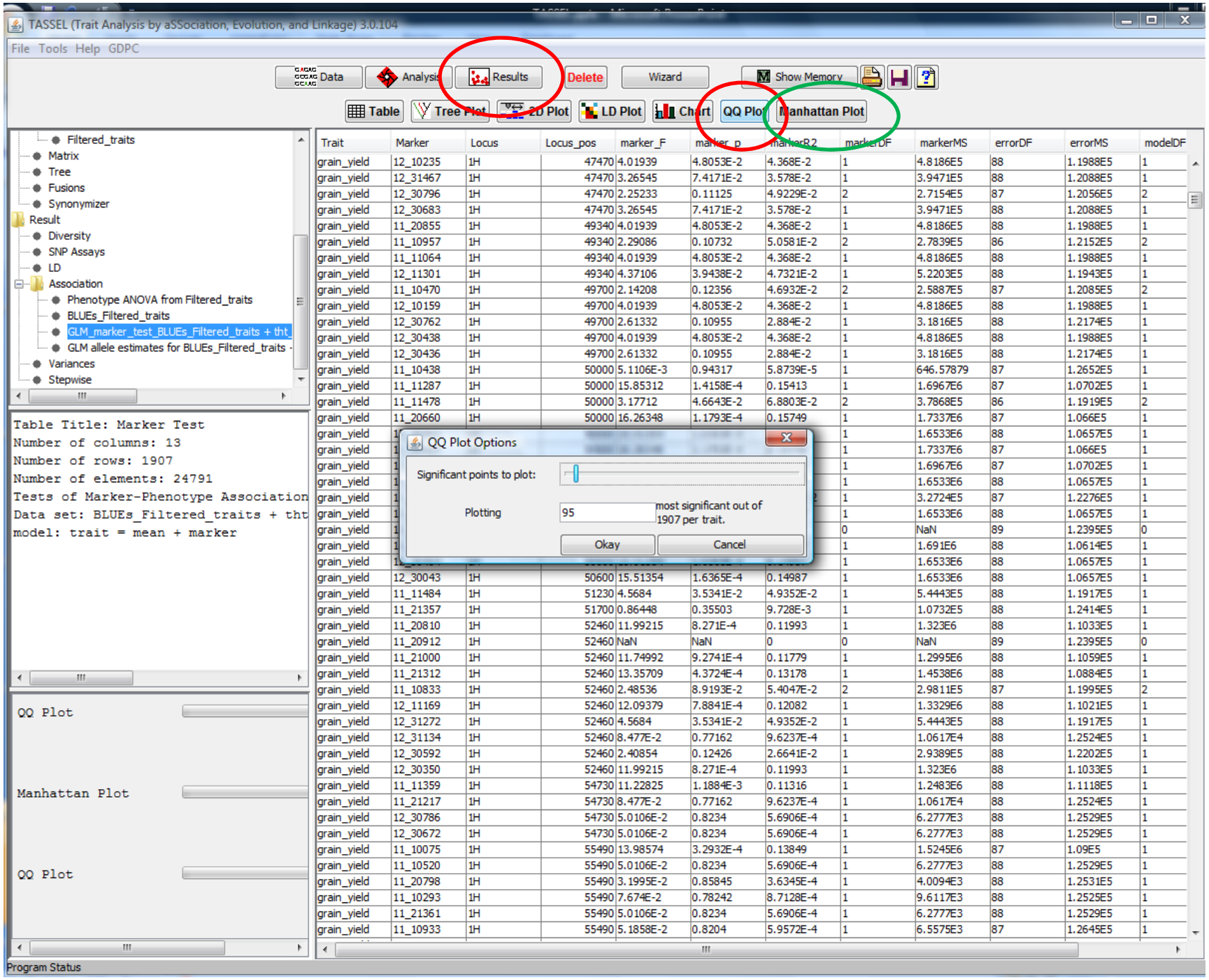

Trait	Marker	Locus	Locus_pos	marker_F	marker_p	markerR2	markerDF	markerMS	errorDF	errorMS	modelDF
grain_yield	12_10235	1H	47470	4.01939	4.8053E-2	4.368E-2	1	4.8186E5	88	1.1988E5	1
grain_yield	12_31467	1H	47470	3.26545	7.4171E-2	3.578E-2	1	3.9471E5	88	1.2088E5	1
grain_yield	12_30796	1H	47470	2.25233	0.11125	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
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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
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grain_yield	1						1	1.7337E6	87	1.066E5	1
grain_yield	1						1	1.6967E6	87	1.0702E5	1
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grain_yield	1						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
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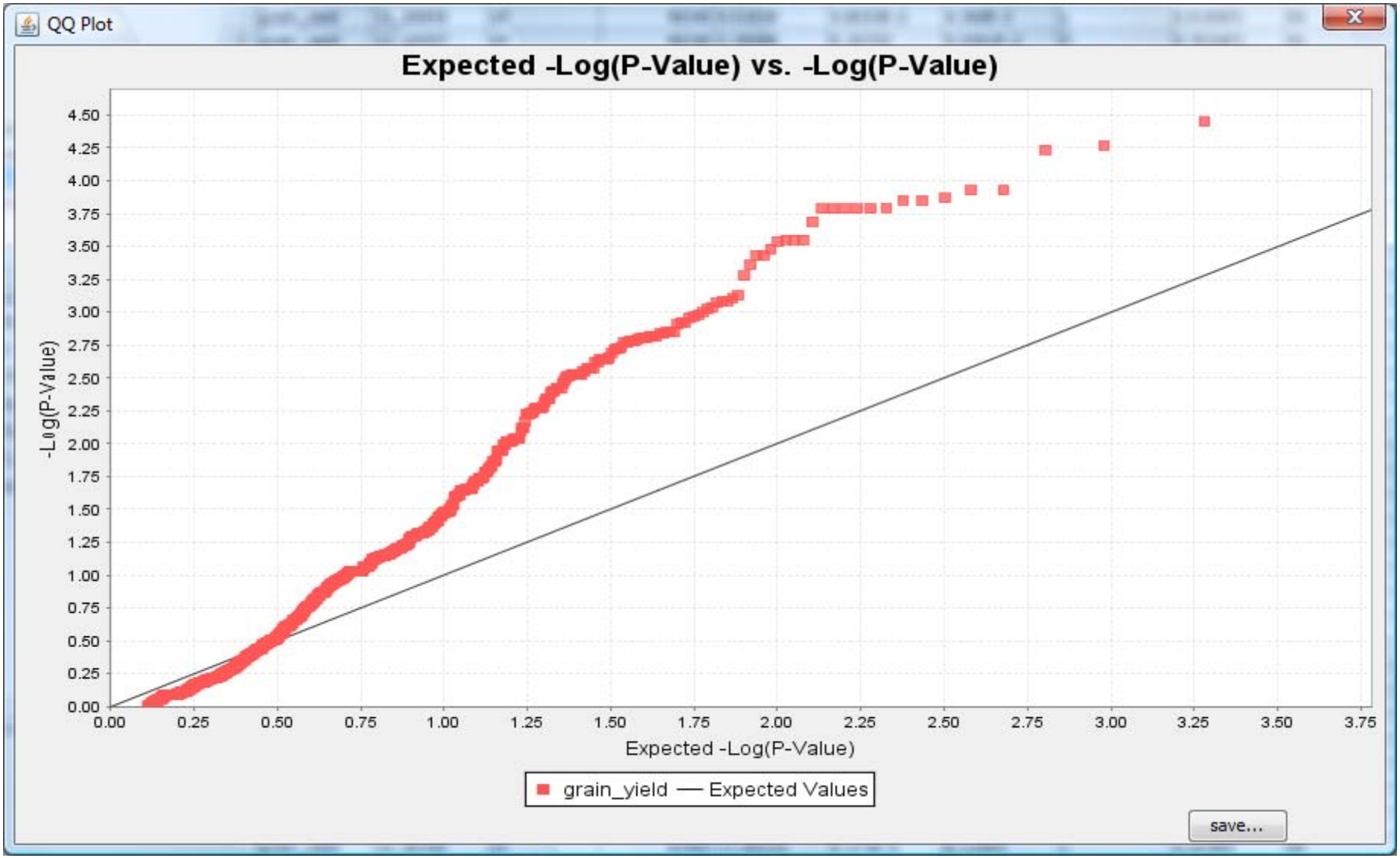
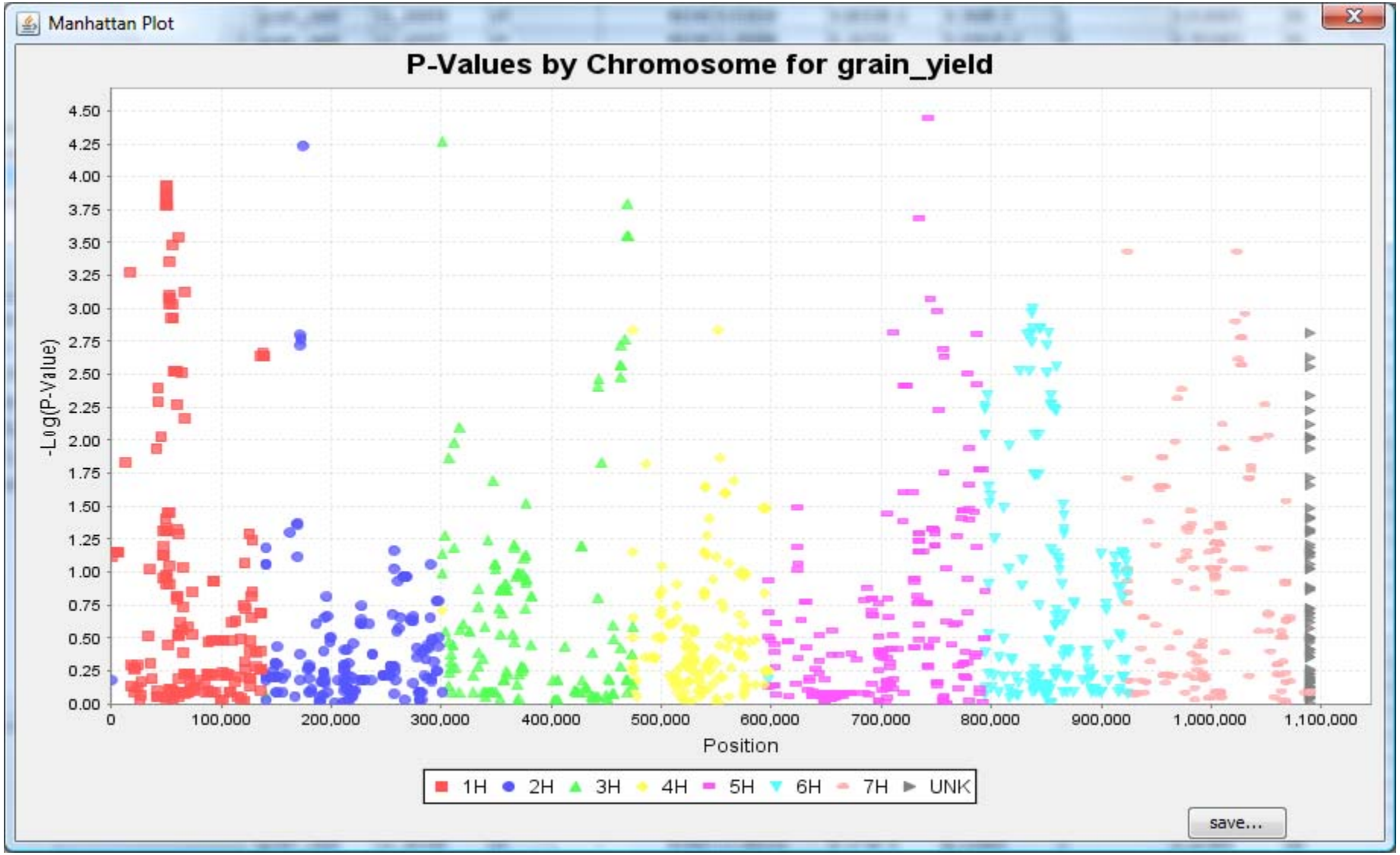
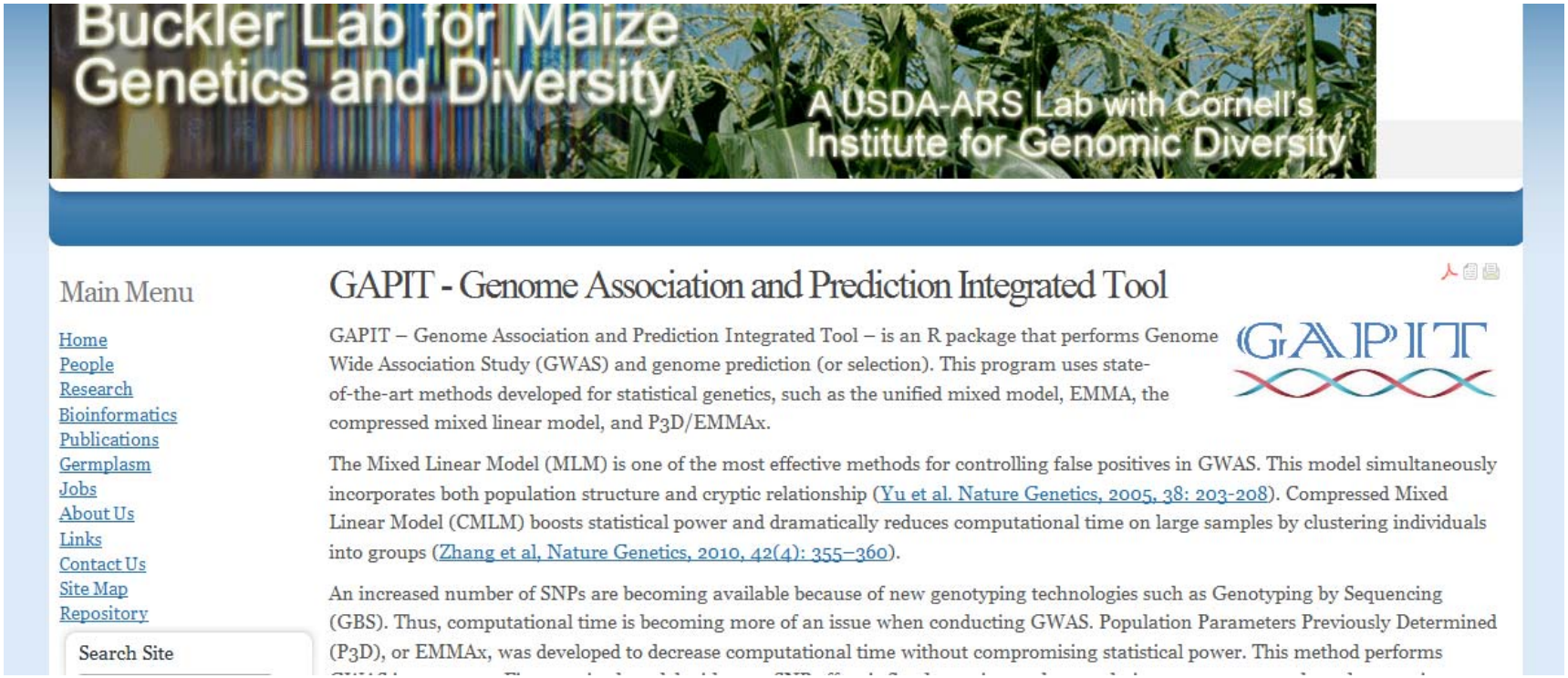
grain_yield	11_10833	1H	52460	2.48536	8.9193E-2	5.4047E-2	2	2.9811E5	87	1.1995E5	2
grain_yield	12_11169	1H	52460	12.09379	7.8841E-4	0.12082	1	1.3329E6	88	1.1021E5	1
grain_yield	12_31272	1H	52460	4.5684	3.5341E-2	4.9352E-2	1	5.4443E5	88	1.1917E5	1
grain_yield	12_31134	1H	52460	8.477E-2	0.77162	9.6237E-4	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


QQ Plot
Expected -Log(P-Value) vs. -Log(P-Value)
-Log(P-Value)
Expected -Log(P-Value)
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00
2.25
2.50
2.75
3.00
3.25
3.50
3.75
4.00
4.25
4.50
grain_yield
Expected Values
save...


Manhattan Plot
P-Values by Chromosome for grain_yield
-Log(P-Value)
4.50
4.25
4.00
3.75
3.50
3.25
3.00
2.75
2.50
2.25
2.00
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00
0
100,000
200,000
300,000
400,000
500,000
600,000
700,000
800,000
900,000
1,000,000
1,100,000
Position
1H
2H
3H
4H
5H
6H
7H
UNK
save...

R Package for Association Analysis and Genomic Selection



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