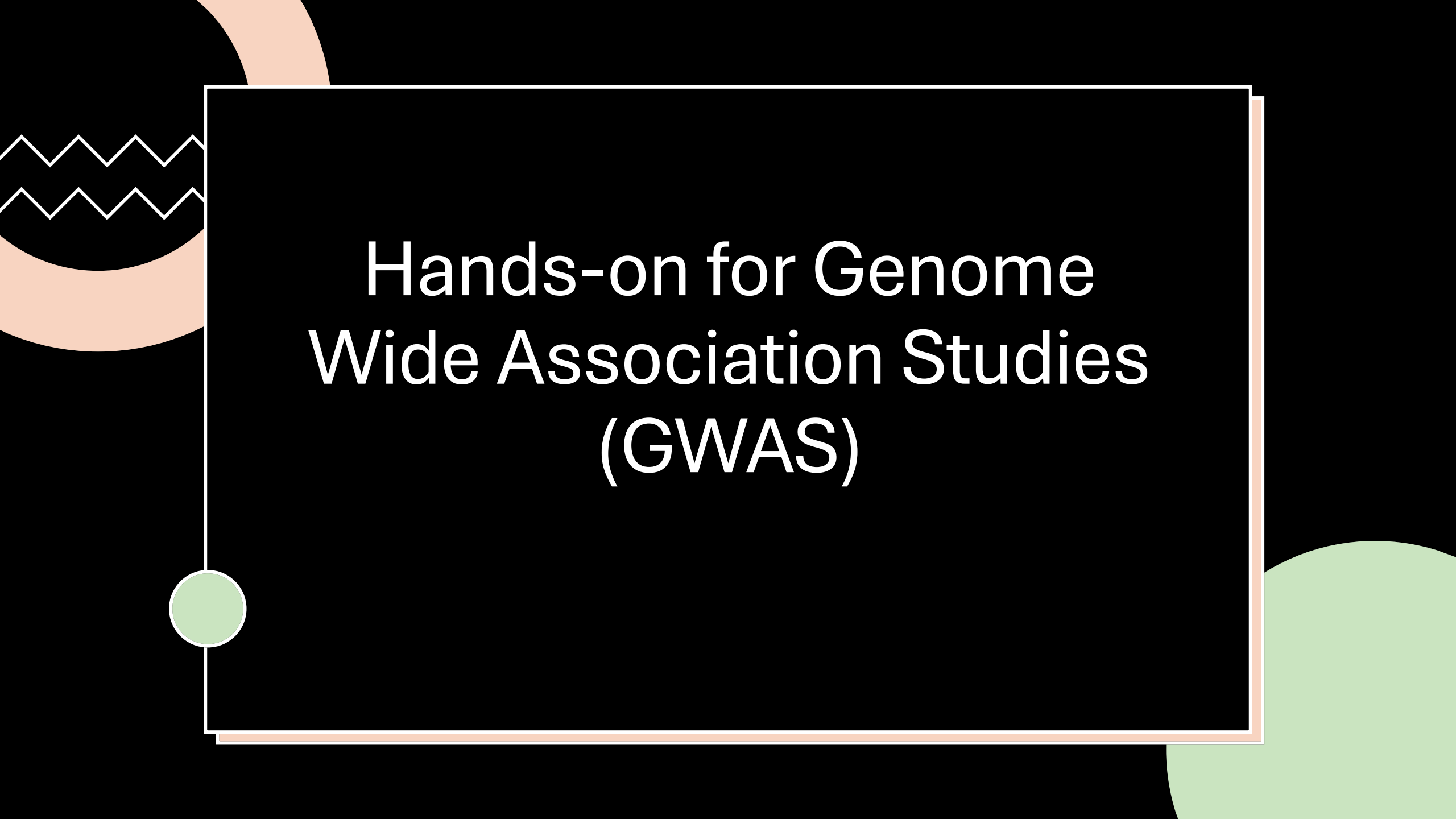




Hands-on for Genome Wide Association Studies (GWAS)

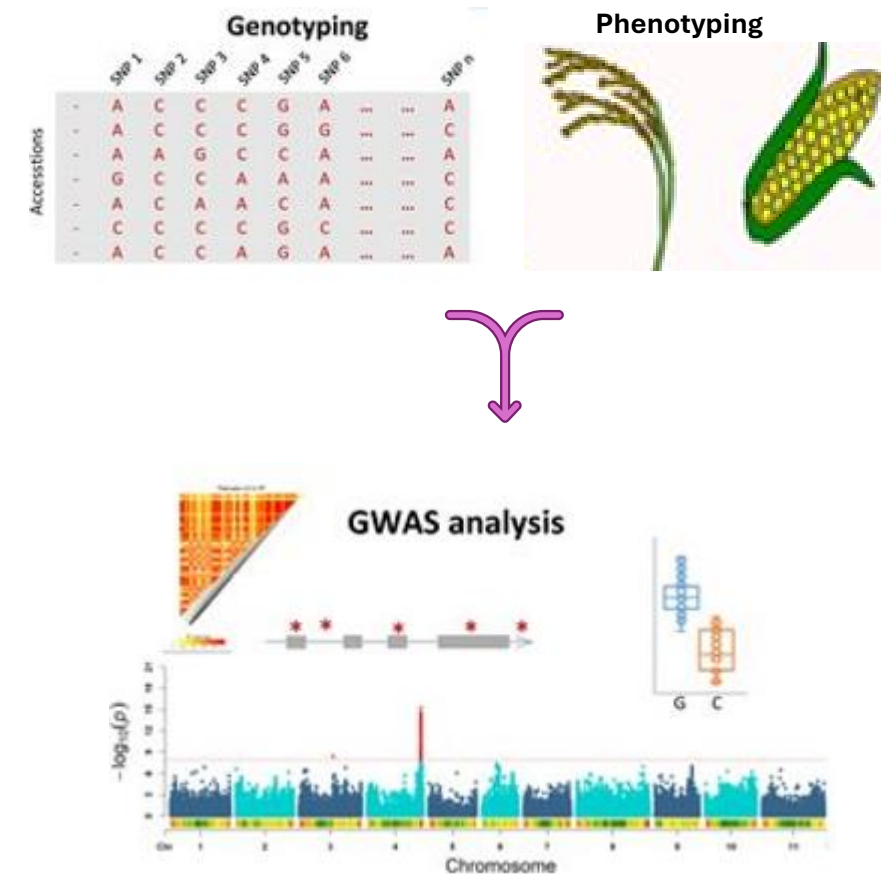
Genome Wide Association Study

- **Goal: find connections between:**

- A phenotype: plant height, disease resistance, ..., trait known to be heritable.
- Whole-genome DNA markers

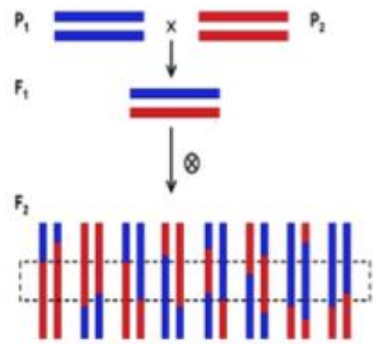
- **Specific goals are distinct:**

1. Identify statistical connections between points (or areas) in the genome and the phenotype
 - Drive hypotheses for biological studies of specific genes/regions in specific context
2. Generate insights on genetic architecture of phenotype
 - Many small genetic effects dispersed across the genome?
 - Few large effects concentrated in one area?

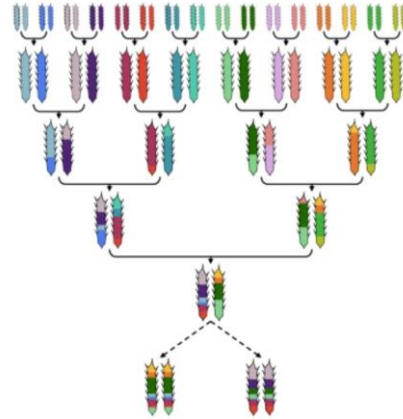


Population required for GWAS

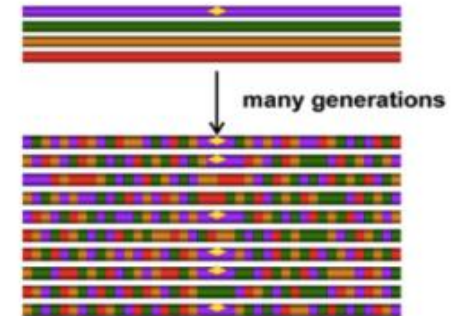
I - QTL analysis



II – Multi-parental QTL



III – GWAS



Resolution

Low

Medium

High

Linkage Blocks

Large

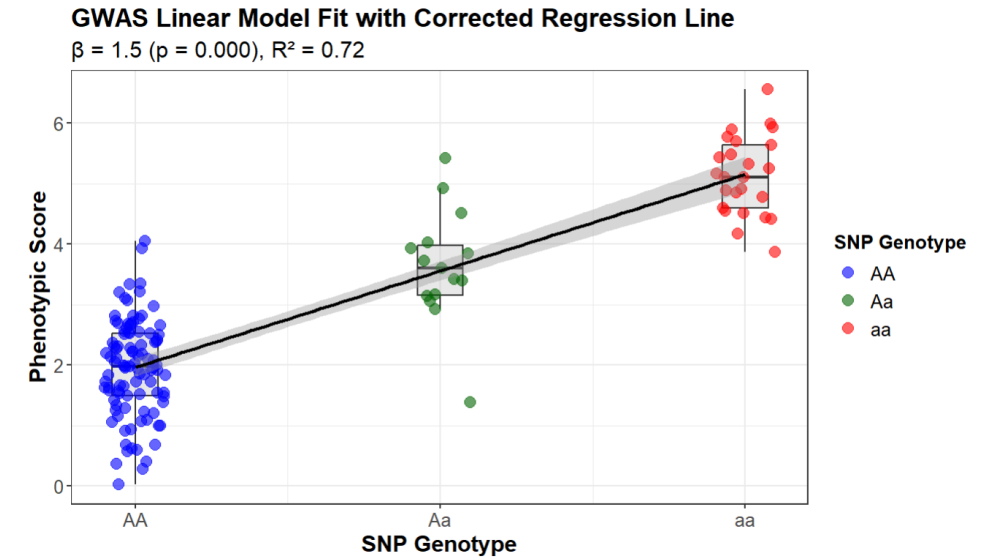
Medium

Small

QTL mapping vs GWAS

At the fundamental level, genetic association and linkage analysis rely on similar principles and assumptions

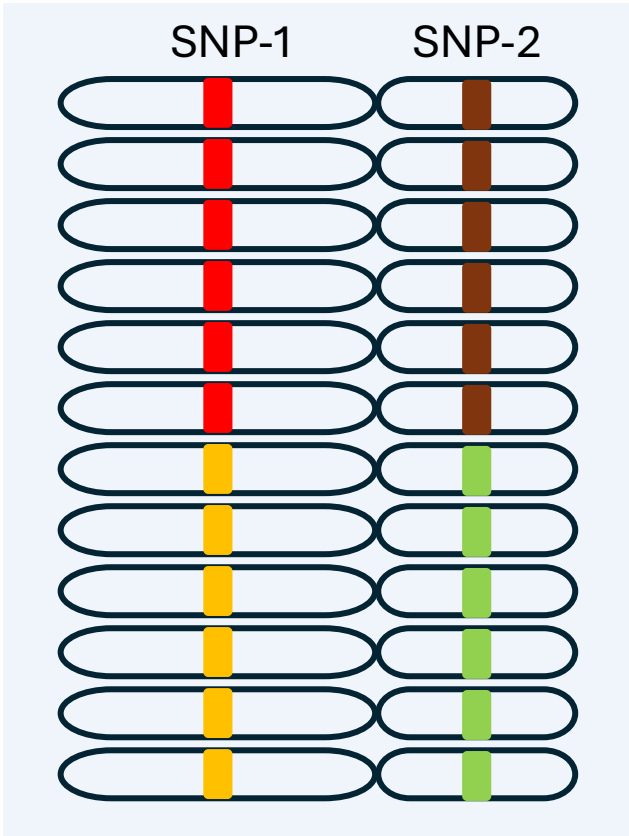
- Both rely on the co-inheritance of adjacent DNA variants, **SHORT-RANGE LINKAGE DISEQUILIBRIUM (LD)**
- **Linkage mapping:** recently generated **LONG-RANGE LD** by identifying haplotypes that are inherited intact over generations in families or pedigrees of known ancestry
- **Association mapping:** historical **SHORT-RANGE LD**, from the retention of adjacent DNA variants over many generations
- Association studies can be regarded as very large linkage studies of unobserved, hypothetical pedigree



Brief introduction of LD

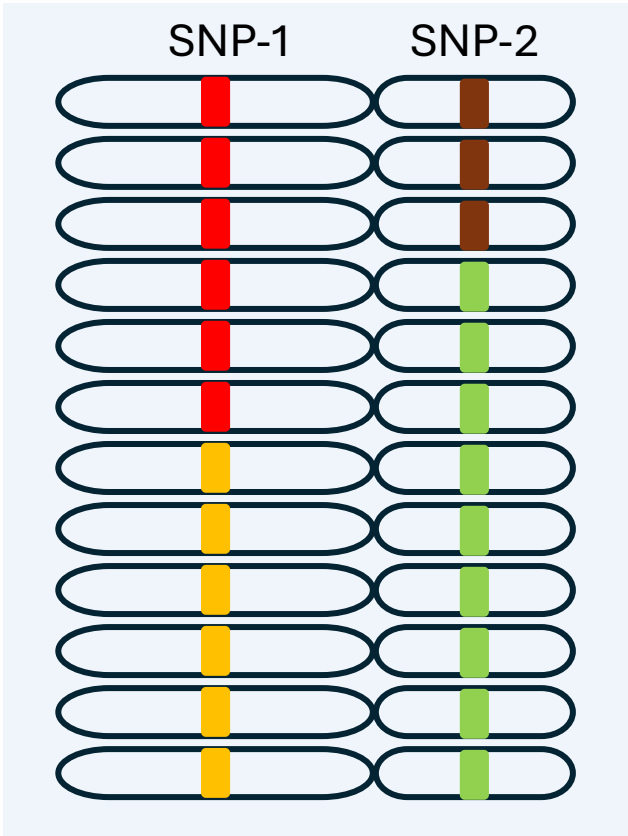
$$D = P(AB) \times P(ab) - P(Ab) \times P(aB)$$

$$r^2 = \frac{D^2}{P(A)P(a)P(B)P(b)}$$



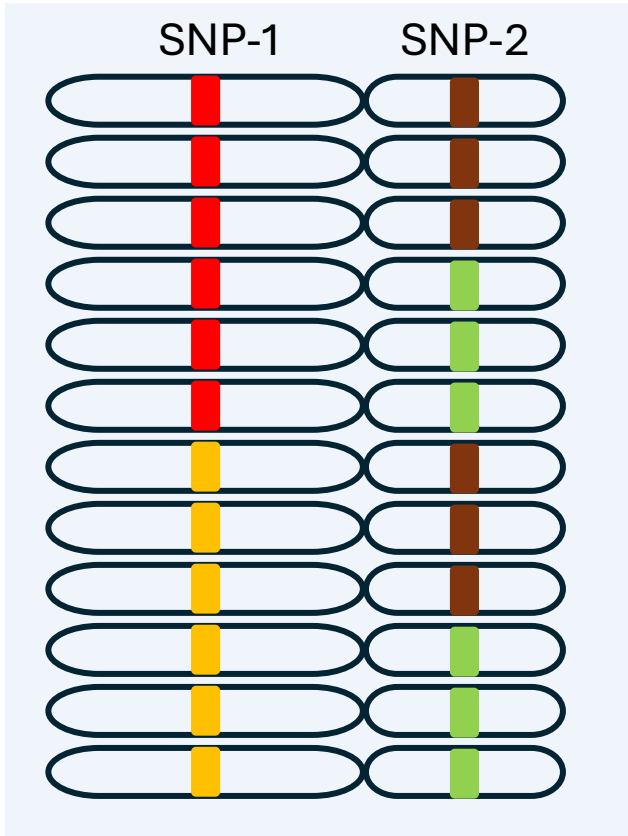
	A	a
B	 6	 0
b	 0	 6

$$D = 0.25$$
$$r^2 = 1$$



	A	a
B	 3	 0
b	 3	 6

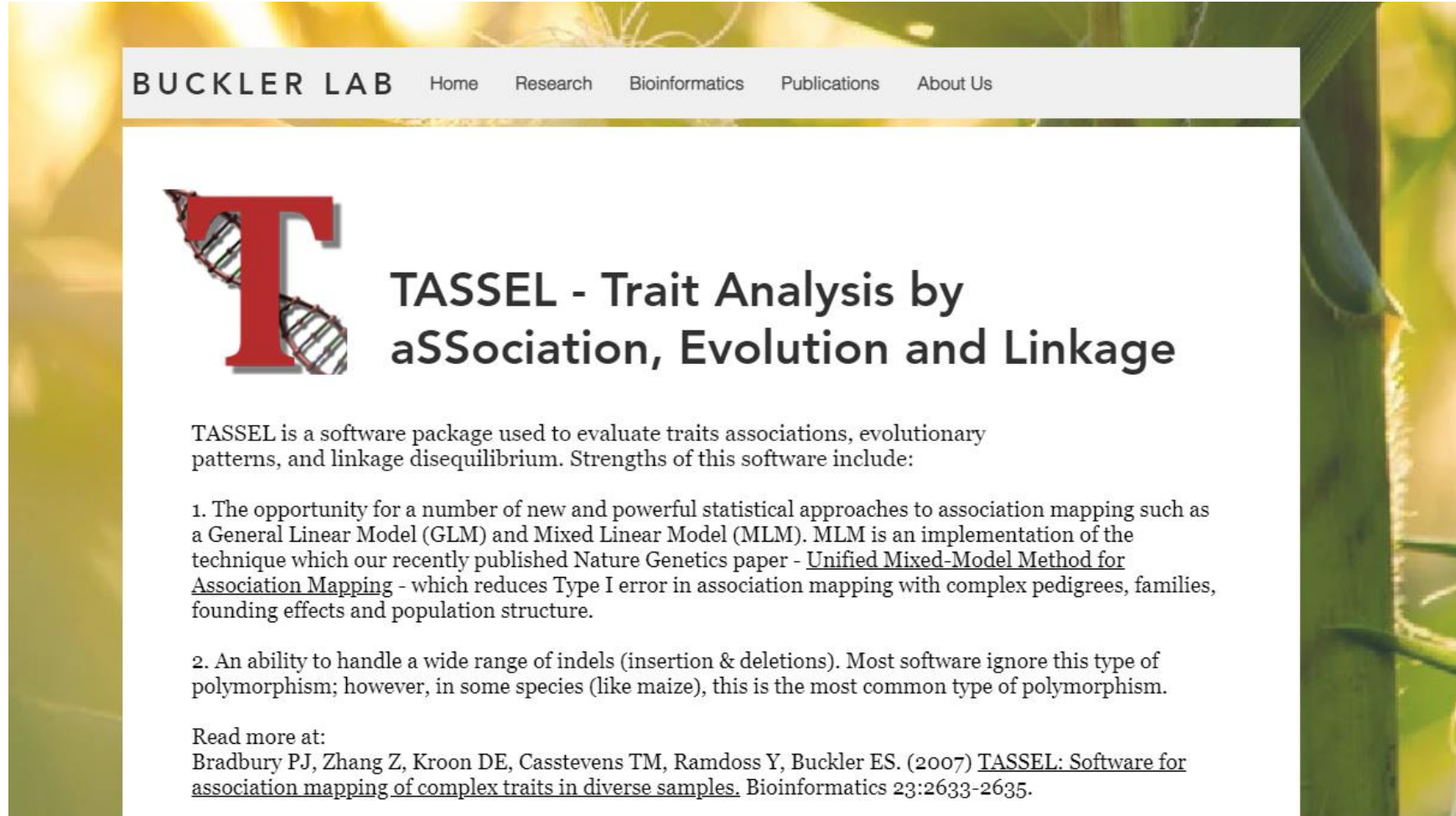
$$D = 0.125$$
$$r^2 = 0.33$$



	A	a
B	 3	 3
b	 3	 3

$$D = 0$$
$$r^2 = 0$$

Tools used for GWAS

A screenshot of the TASSEL website. The header features the text 'BUCKLER LAB' and navigation links: 'Home', 'Research', 'Bioinformatics', 'Publications', and 'About Us'. The main content area has a large red 'T' logo with a DNA double helix. To the right of the logo is the title 'TASSEL - Trait Analysis by aSSociation, Evolution and Linkage'. Below the title, a paragraph describes TASSEL as a software package for evaluating trait associations, evolutionary patterns, and linkage disequilibrium. It lists two strengths: 1. The opportunity for new statistical approaches like GLM and MLM, citing a Nature Genetics paper on the 'Unified Mixed-Model Method for Association Mapping'. 2. The ability to handle indels. At the bottom, it says 'Read more at:' followed by a citation for Bradbury PJ et al. (2007) and a link to the software's association mapping capabilities.

BUCKLER LAB Home Research Bioinformatics Publications About Us

TASSEL - Trait Analysis by aSSociation, Evolution and Linkage

TASSEL is a software package used to evaluate traits associations, evolutionary patterns, and linkage disequilibrium. Strengths of this software include:

1. The opportunity for a number of new and powerful statistical approaches to association mapping such as a General Linear Model (GLM) and Mixed Linear Model (MLM). MLM is an implementation of the technique which our recently published Nature Genetics paper - [Unified Mixed-Model Method for Association Mapping](#) - which reduces Type I error in association mapping with complex pedigrees, families, founding effects and population structure.
2. An ability to handle a wide range of indels (insertion & deletions). Most software ignore this type of polymorphism; however, in some species (like maize), this is the most common type of polymorphism.

Read more at:
Bradbury PJ, Zhang Z, Kroon DE, Casstevens TM, Ramdoss Y, Buckler ES. (2007) [TASSEL: Software for association mapping of complex traits in diverse samples](#). Bioinformatics 23:2633-2635.

<https://www.maizegenetics.net/tassel>



What can TASSEL do?

Genotype and phenotype data editing

- File conversion (e.g., hapmap, VCF, Plink)
- Merging, sorting, filtering
- Phenotype transformation

Genetic analysis

- Diversity
- Relatedness
- Genotype/phenotype association
 - GWAS
 - Genomic selection

Data imputation

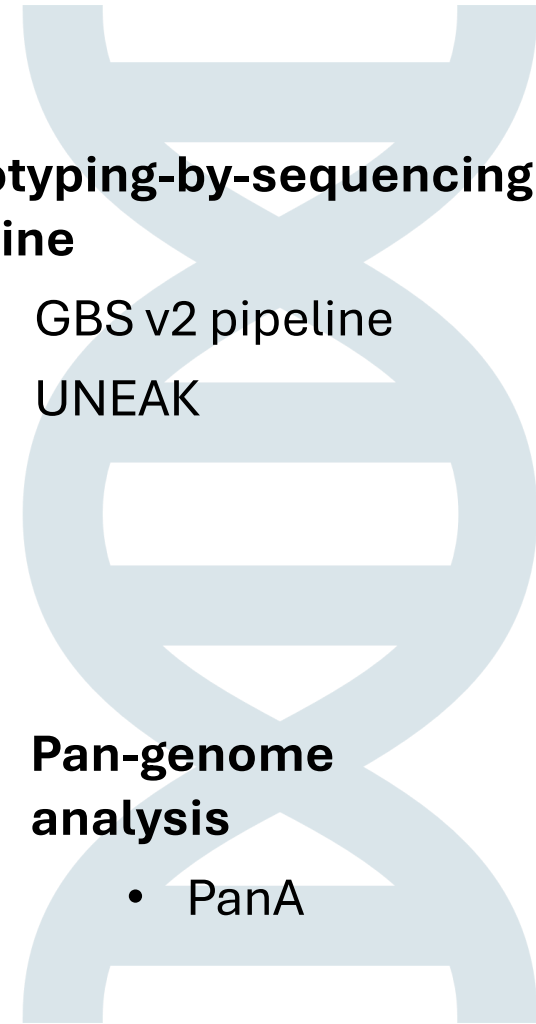
- LD KNNi
- Numerical
- FILLIN, FSFHAP

Genotyping-by-sequencing (GBS) pipeline

- GBS v2 pipeline
- UNEAK

Pan-genome analysis

- PanA



Installation

Homepage: software download & other information

<https://www.maizegenetics.net/tassel>



TASSEL Version 5.0 *(Getting Started!)*
(Build: February 22, 2025 [Requires: Java 1.8](#))

[Tassel 5 Mac OS](#)
[Tassel 5 Windows 64 Bit](#)
[Tassel 5 Windows 32 Bit](#)
[Tassel 5 UNIX](#)

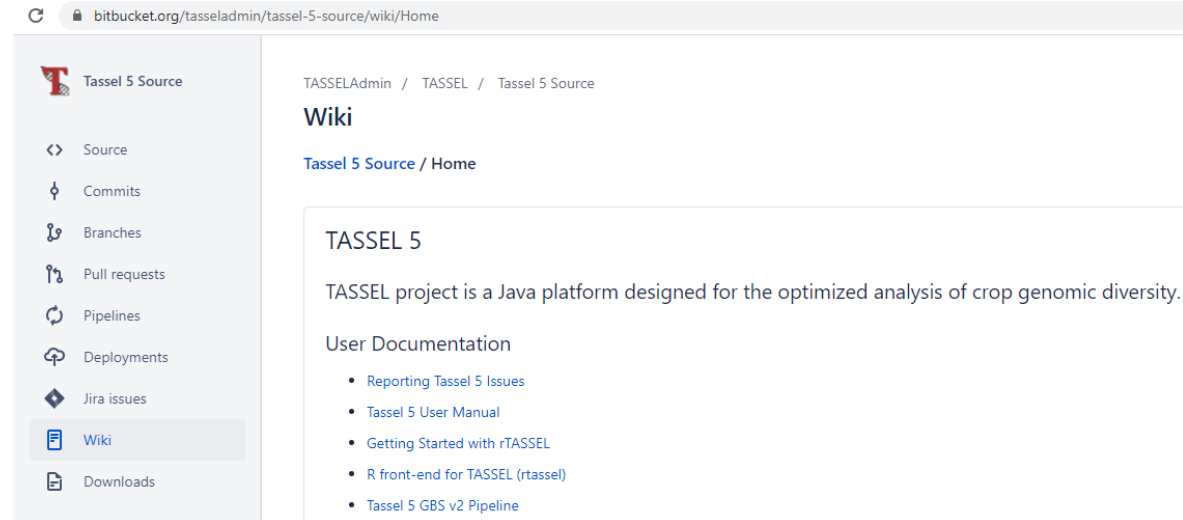
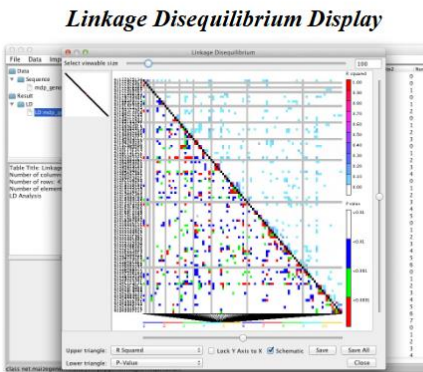
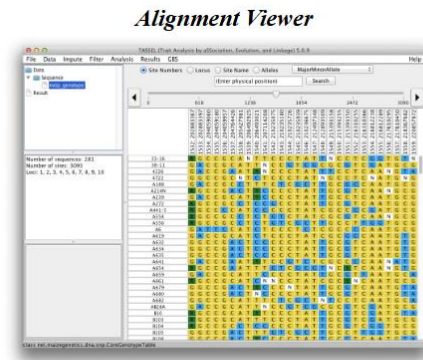
TASSEL Version 5.0 Standalone
(GBS Pipeline V2 - Preferred Version)

[Using Git - Recommended!](#)
[Download \("Tags" are Versions\)](#)

[Archived Versions of TASSEL](#)

TASSEL Documentation

[Tassel 5.0 User's Guide](#)
[R front-end for TASSEL \(rtassel\)](#)
[Tassel 5.0 Youtube Tutorials](#)
[Tassel Tutorial Data](#)
[GBSv2 Test Data .tar .zip](#)
[GBS Test Data](#)
[Visit Tassel User Group](#)
[Tassel 5.0 Change History](#)
[Tassel 5.0 Wiki](#)
[GNU Lesser General Public License](#)



Resources

Wiki: User manual & software information

<https://bitbucket.org/tasseladmin/tassel-5-source/wiki/Home>

User manual

<https://bitbucket.org/tasseladmin/tassel-5-source/wiki/UserManual>

Genotype file format

Hapmap
VCF

Plink

Flapjack

...

- Common output format from genotyping
- Common input format required by e.g., database, imputation software

Hapmap (haplotype map)

11 columns

Individual 1, 2 ...

	rs#	alleles	chrom	pos	strand	assembly#	center	protLSID	assayLSID	panelLSID	QCcode	Parental_1
1	44509	A/G	02	5565755	+	NA	NA	NA	AG	AA	AA	AA
2	38019	G/A	02	43878360	+	NA	NA	NA	GG	GA	GG	GG
3	89440	T/C	04	25220824	+	NA	NA	NA	TC	TT	NN	TT

↑ SNP ID ↙ REF/ALT

xxx.hmp.txt
Can be viewed with NotePad++

Genotype file type – VCF

Meta-
information
line

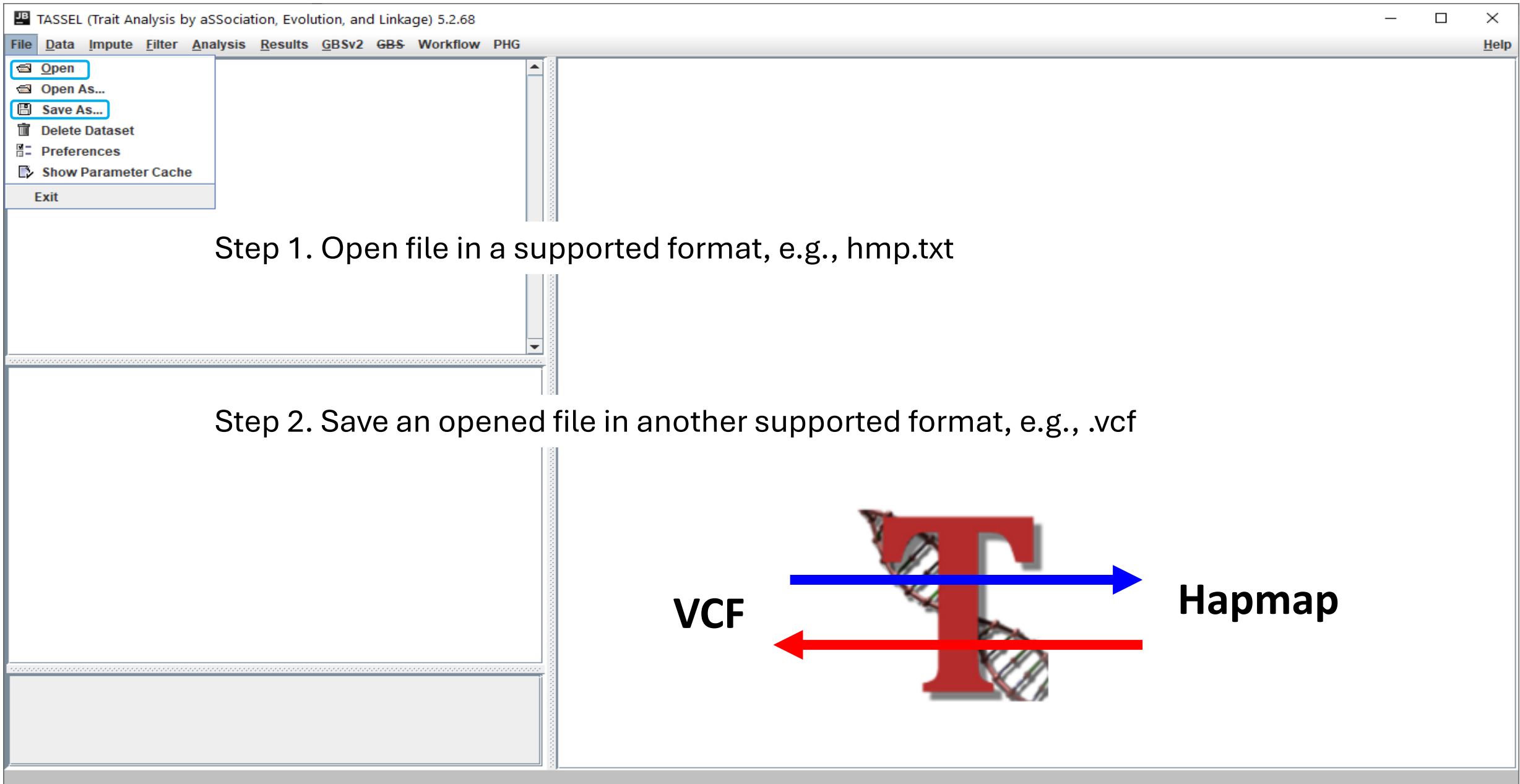
Header line
Data lines

```
##fileformat=VCFv4.0
##fileDate=20160306
##source="Stacks v1.37"
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=AF,Number=.,Type=Float,Description="Allele Frequency">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=AD,Number=1,Type=Integer,Description="Allele Depth">
##FORMAT=<ID=GL,Number=.,Type=Float,Description="Genotype Likelihood">

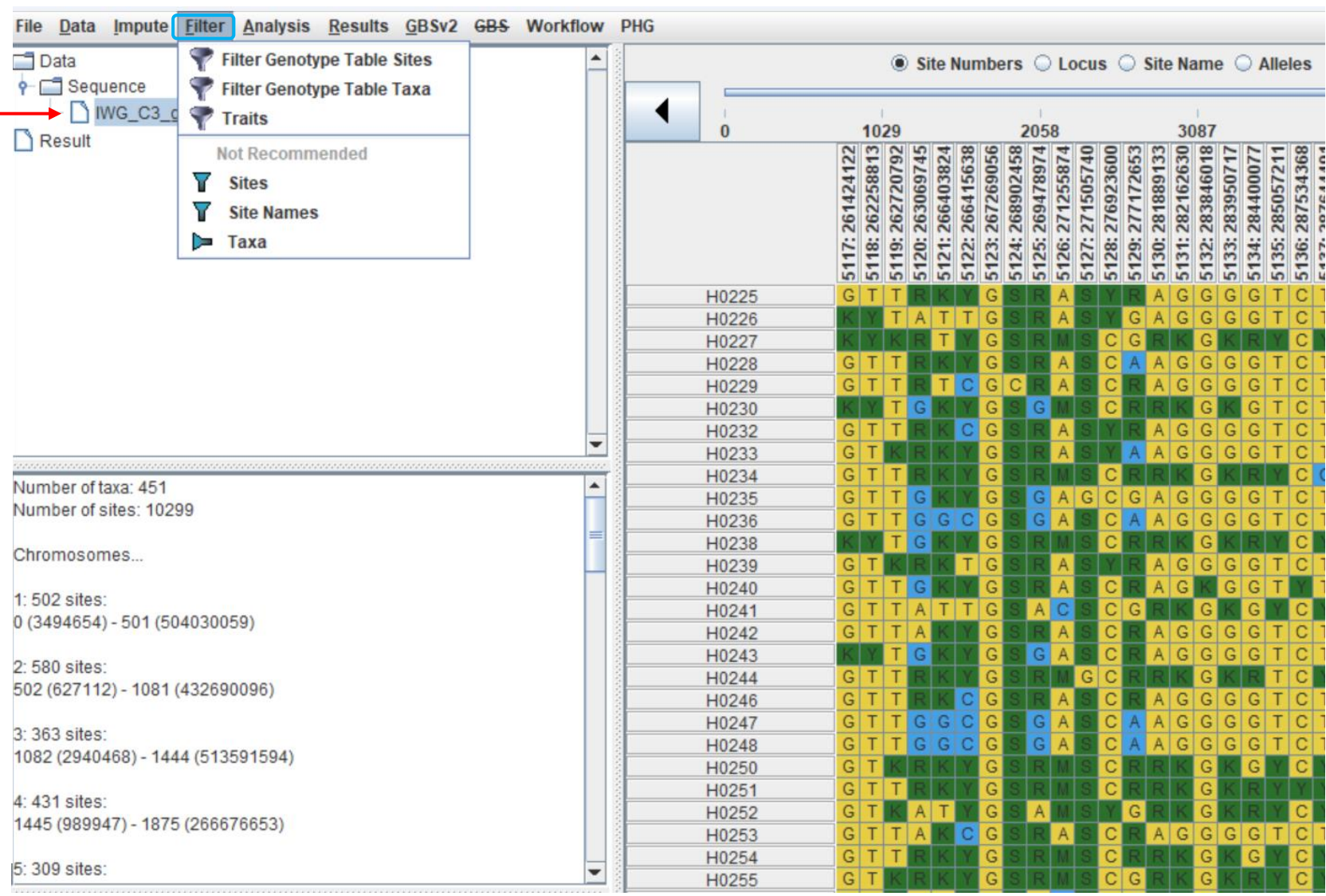
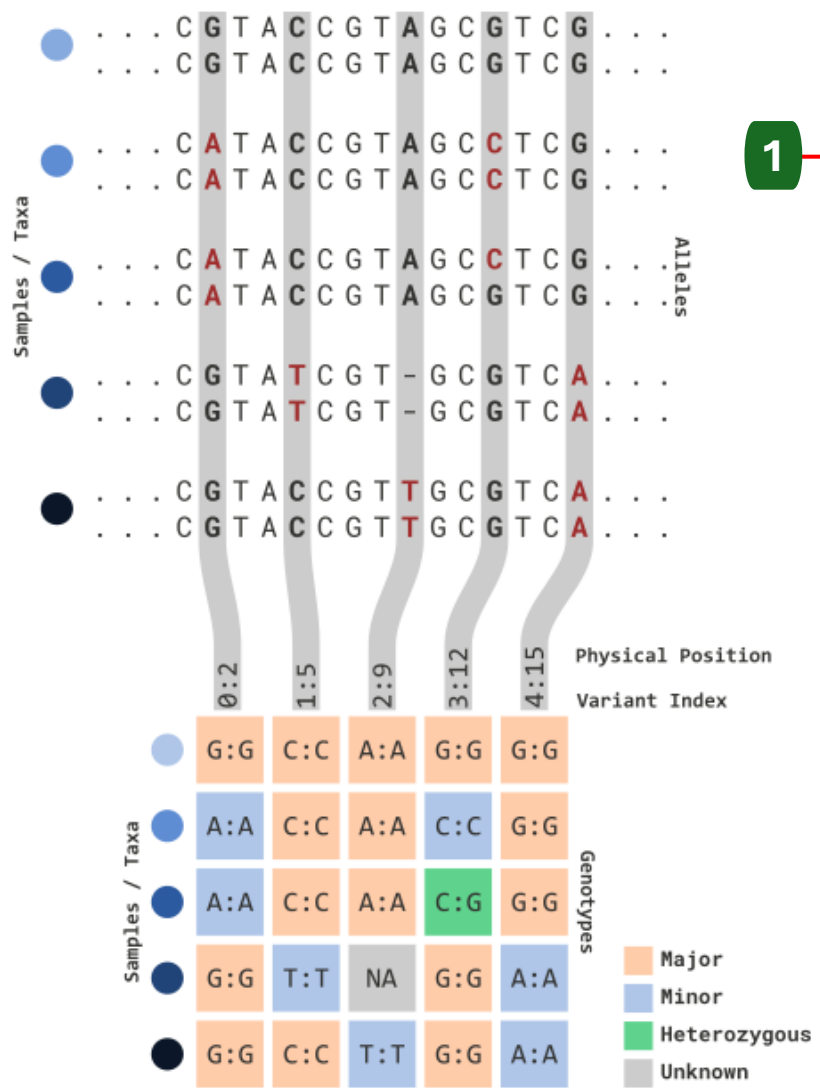
#CHROM    POS      ID       REF      ALT      QUAL     FILTER    INFO      FORMAT    Parental_1
Chr02     5565755  44509    A        G        .        PASS      .        GT:DP:AD:GL  0/1:31:23,8:.,.
```

Code	Meaning
A	Adenine
C	Cytosine
G	Guanine
T	Thymine
R	A or G
Y	C or T
S	G or C
W	A or T
K	G or T
M	A or C
B	C or G or T
D	A or G or T
H	A or C or T
V	A or C or G
N	any base

xxx.vcf
Can be viewed with NotePad++



Filtering Genotype Tables

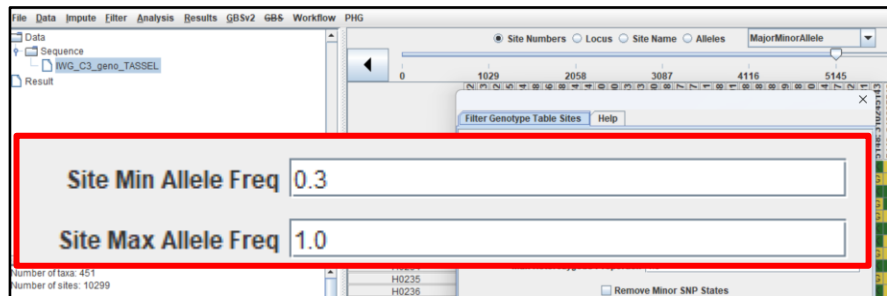
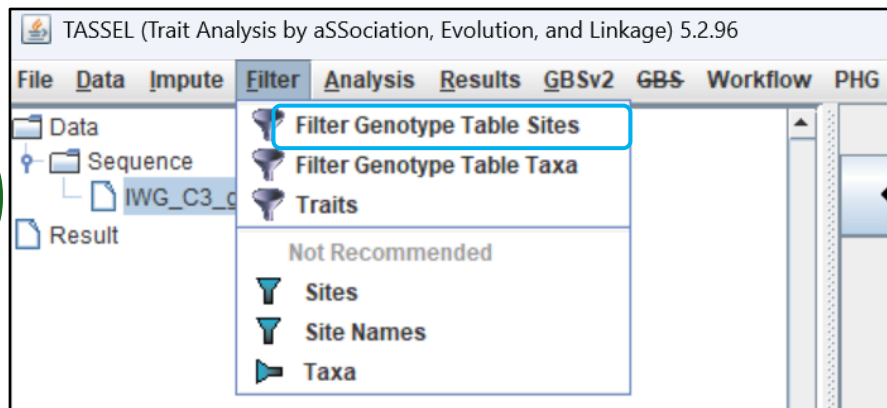


$n \times p$ matrix

Filtering using allelic frequency

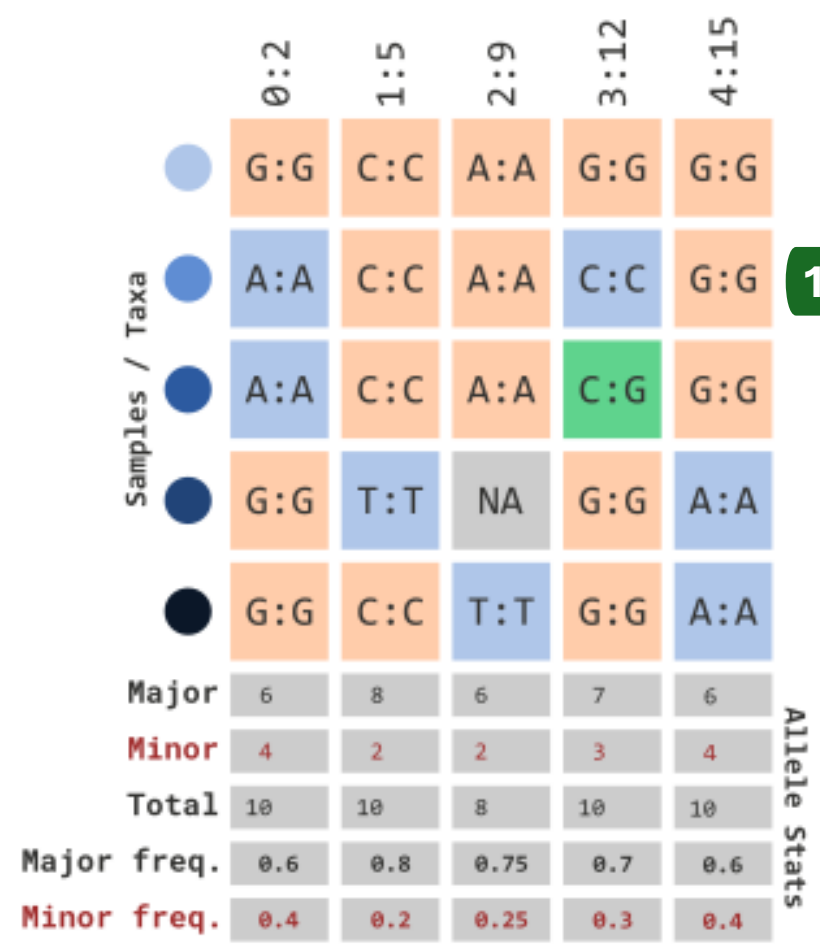
		0:2	1:5	2:9	3:12	4:15
Samples / Taxa	●	G:G	C:C	A:A	G:G	G:G
	●	A:A	C:C	A:A	C:C	G:G
	●	A:A	C:C	A:A	C:G	G:G
	●	G:G	T:T	NA	G:G	A:A
	●	G:G	C:C	T:T	G:G	A:A
	●	G:G	C:C	T:T	G:G	A:A
Major		6	8	6	7	6
Minor		4	2	2	3	4
Total		10	10	8	10	10
Major freq.		0.6	0.8	0.75	0.7	0.6
Minor freq.		0.4	0.2	0.25	0.3	0.4
		Allele Stats				

1

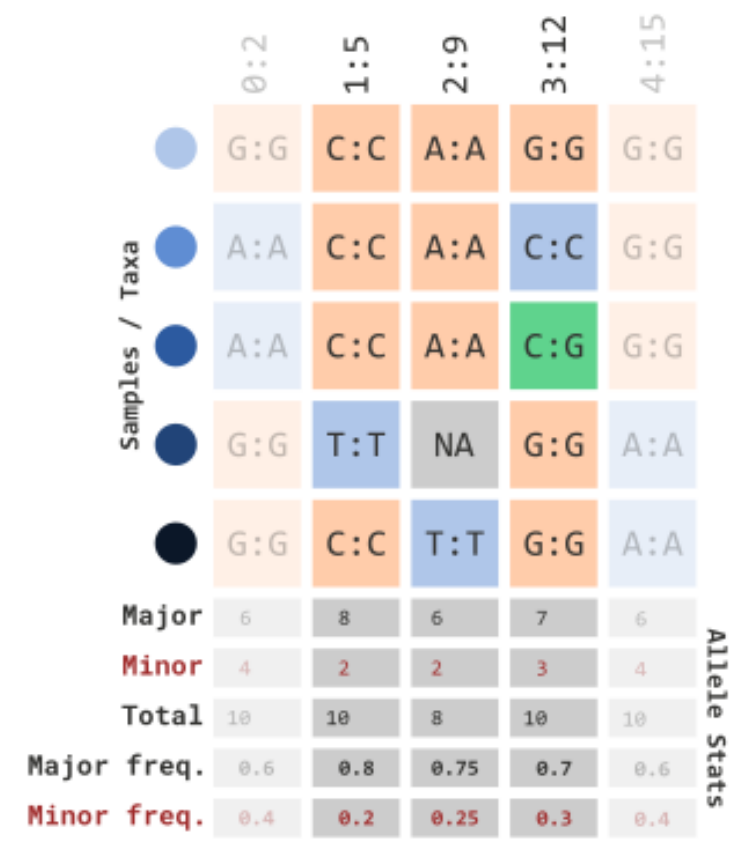
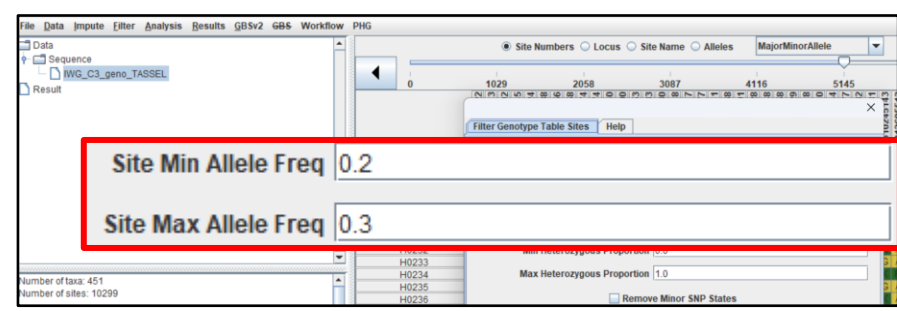
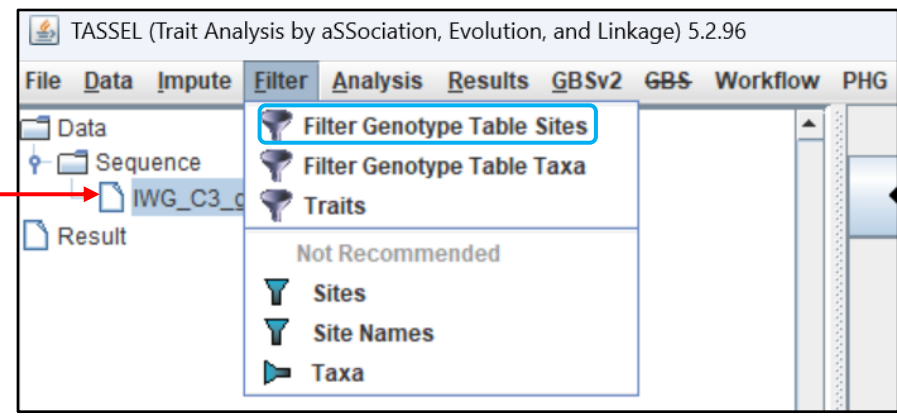


		0:2	1:5	2:9	3:12	4:15
Samples / Taxa	●	G:G	C:C	A:A	G:G	G:G
	●	A:A	C:C	A:A	C:C	G:G
	●	A:A	C:C	A:A	C:G	G:G
	●	G:G	T:T	NA	G:G	A:A
	●	G:G	C:C	T:T	G:G	A:A
	●	G:G	C:C	T:T	G:G	A:A
Major		6	8	6	7	6
Minor		4	2	2	3	4
Total		10	10	8	10	10
Major freq.		0.6	0.8	0.75	0.7	0.6
Minor freq.		0.4	0.2	0.25	0.3	0.4
		Allele Stats				

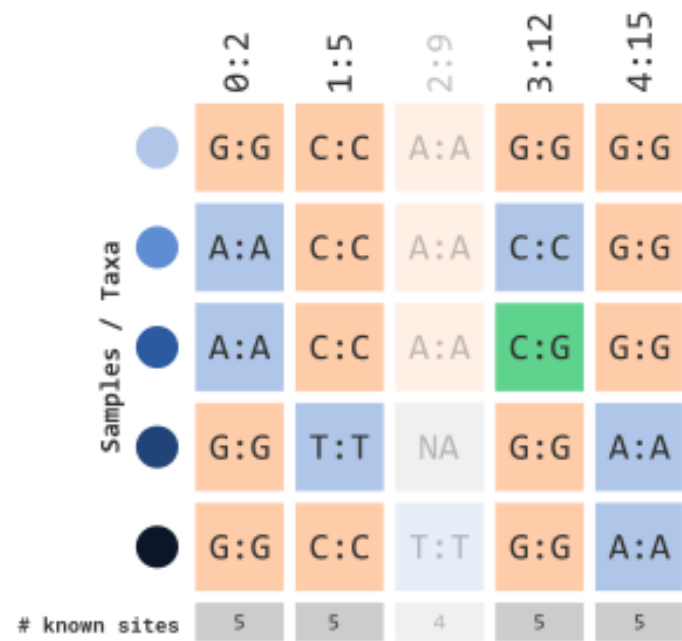
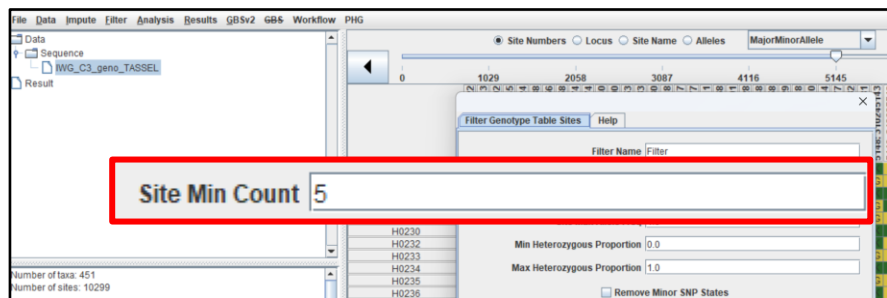
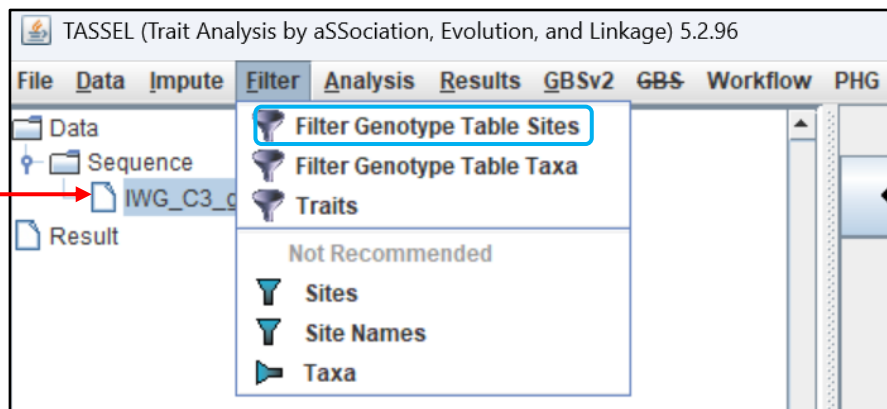
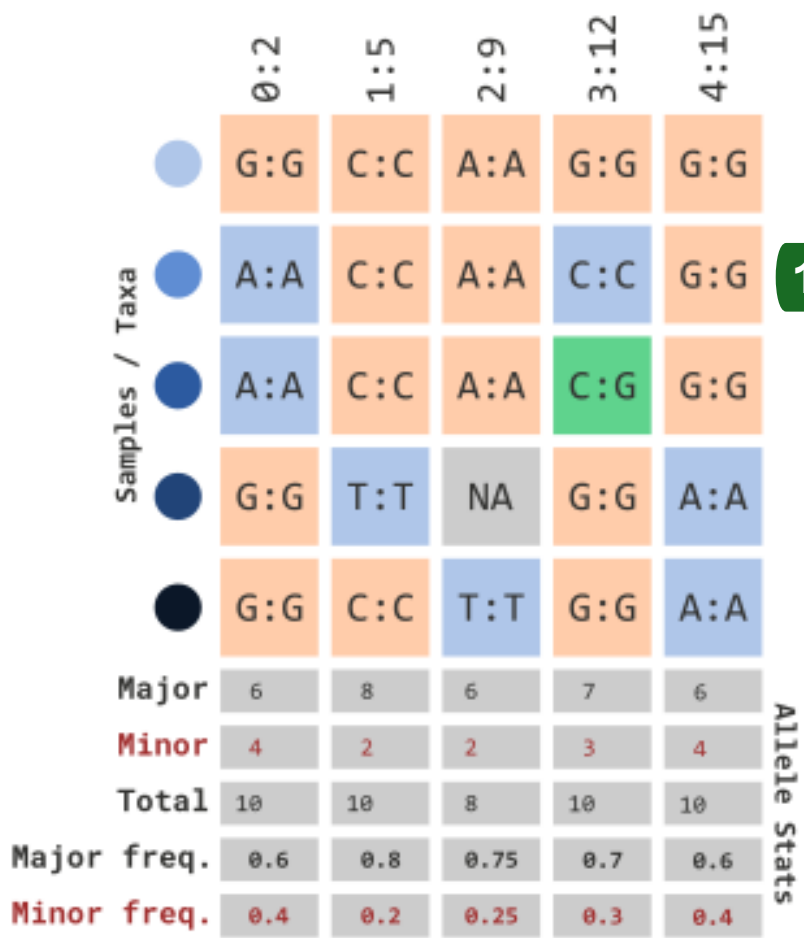
Filtering using allelic frequency



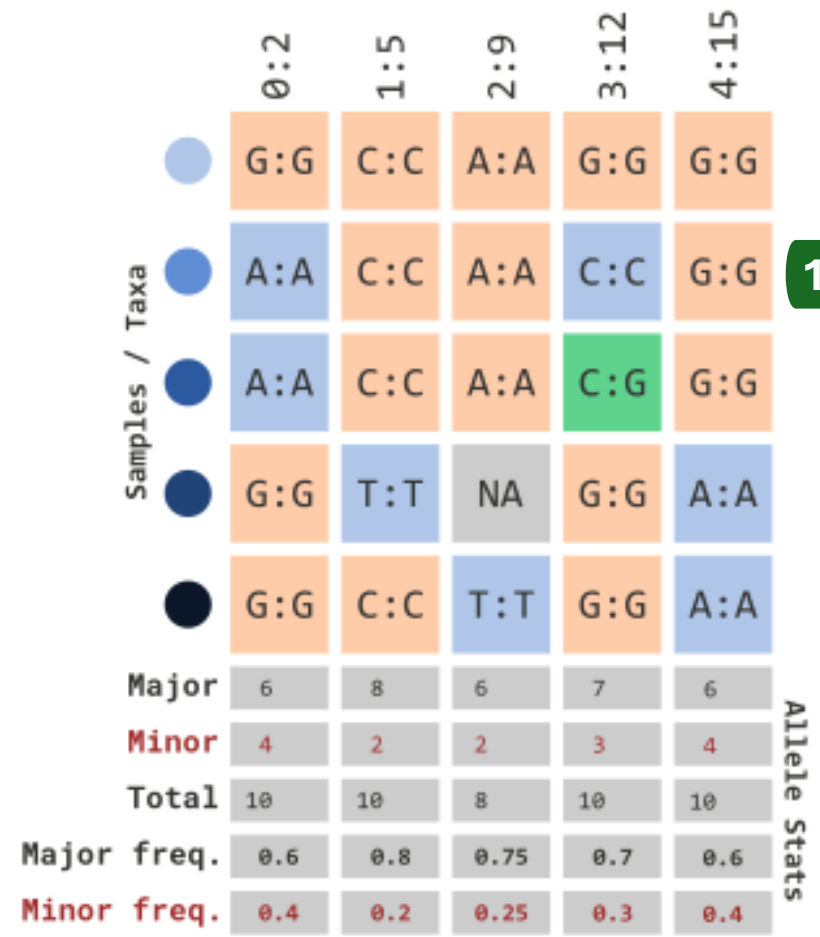
1



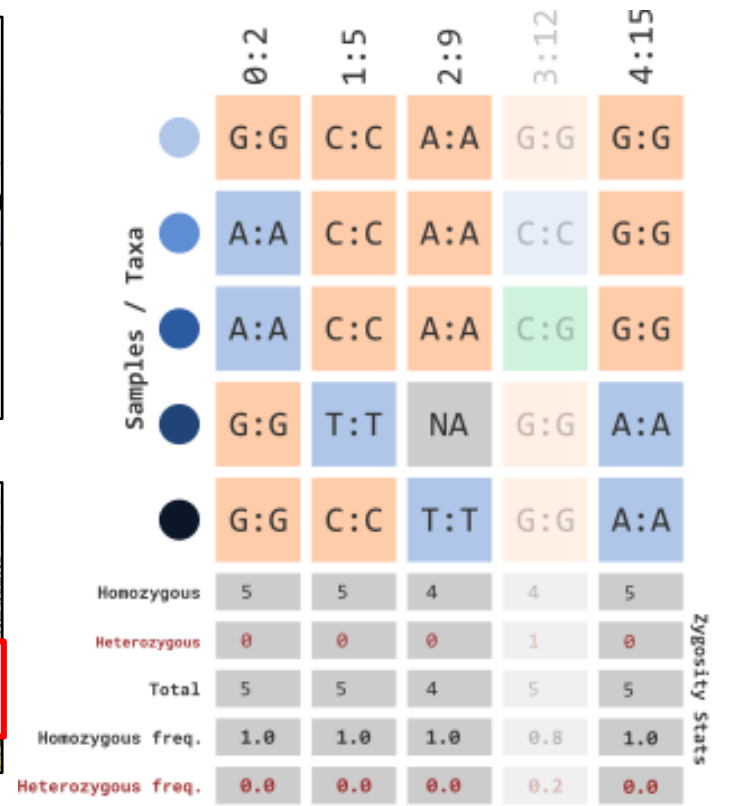
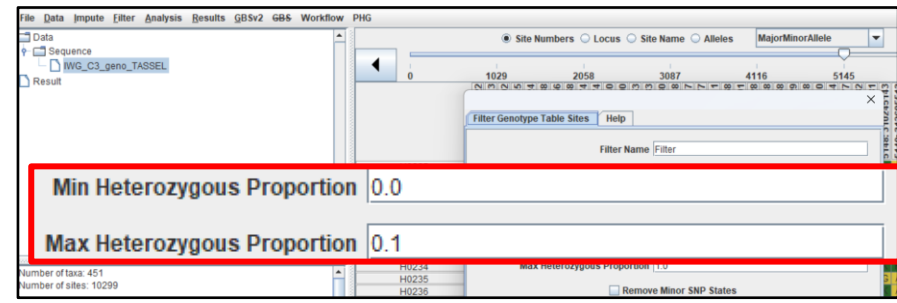
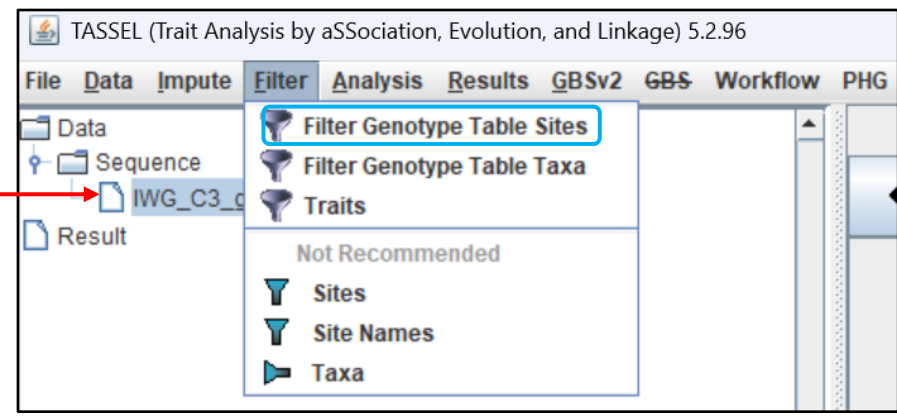
Filtering using NA data



Filtering using heterozygosity frequency



1



Relatedness Analysis

A. Create a kinship matrix object

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 5.2.96

FileDataImputeFilterAnalysisResultsGBSv2GBSWorkflowPHG

Data

Numerical

IWG_C3_Q_matrix

IWG_C3_pheno_for_tassel

Sequence

IWG_C3_geno_TASSEL

Result

Diversity

Relatedness

Association

Distance Matrix

Kinship

Create Tree

Merge Trees

Subset Tree

Remove Tree Branch Lengths

Convert Tree Names

Pedigree Relationship Matrix

Combined A and G Relationship Matrix

MDS

PCA

Remove NaN From Distance Matrix

Subtract Distance Matrix

Add Distance Matrix

Taxa Identity Recognition

Site Numbers

Locus

Site

029

2058

5118: 262258813

5119: 262720792

5120: 263069745

5121: 266403824

5122: 266415638

5123: 267269056

5124: 268902458

5125: 269478974

5126: 271255874

5127: 271505740

5128: 276923600

5129: 277172653

5130: 281889133

T T R K Y G S R A S Y R A

T A T T G S R A S Y G A

K R T Y G S R M S C G R

T T R K Y G S R A S C A A

T T R T C G C R A S C R A

T G K Y G S G M S C R R

T T R K C G S R A S Y R A

T K R K Y G S R A S Y A A

T T R K Y G S R M S C R R

T T G K Y G S G A G C G A

T T G G C G S G A S C A A

K Y T G K Y G S R M S C R R

Number of taxa: 451

Number of sites: 10299

Chromosomes...

Taxa	H0225	H0226	H0227	H0228
H0225	0.87	0.176	0.114	0.117
H0226	0.176	0.914	0.359	0.128
H0227	0.114	0.359	0.861	0.086
H0228	0.117	0.128	0.086	0.841

B. Create a distance matrix

Taxa	H0225	H0226	H0227	H0228
H0225	0	0.301	0.311	0.301
H0226	0.301	0	0.26	0.288
H0227	0.311	0.26	0	0.295
H0228	0.301	0.288	0.295	0

Plotting phylogenetic trees

1

Matrix

IWG_C3_geno_TASSEL

Analysis

Association

Create Tree

2

Clustering Method

Neighbor_Joining

Save Distance Matrix

3

Ok

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 5.2.96

FileDataImputeFilterAnalysisResultsGBSv2GBSWorkflowPHG

Data

Matrix

Centered_IBS_IWG_C3_geno_TASSEL

Matrix:IWG_C3_geno_TASSEL

Matrix:IWG_C3_geno_TASSEL

Numerical

IWG_C3_Q_matrix_structure_k2

IWG_C3_pheno_for_tassel

Sequence

IWG_C3_geno_TASSEL

Tree

Tree:IWG_C3_geno_TASSEL

Result

Number of taxa: 451
Number of sites: 10299
Chromosomes...

Distance Matrix

Kinship

Create Tree

Merge Trees

Subset Tree

Remove Tree Branch Lengths

Convert Tree Names

Dendrogram Relationship Matrix

Site Numbers

029

2058

5118: 262258813

5119: 262720792

5120: 263069745

5121: 266403824

5122: 2664415638

5123: 267269056

5124: 268902458

5125: 269478974

5126: 271255874

T T R K Y G S R A

T A T T G S R A

K R T Y G S R M

T R K Y G S R A

T R T C G C R A

T G K Y G S G M

T R K C G S R A

K R K Y G S R A

T R K Y G S R M

T G K Y G S G A

T G G C G S G A

T T G K Y G S R M

G T K R K T G S R A

G T T C K Y G S R A

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 5.2.96

FileDataImputeFilterAnalysisResultsGBSv2GBSWorkflowPHG

Data

Matrix

Centered_IBS_IWG_C3_geno_TASSEL

Matrix:IWG_C3_geno_TASSEL

Matrix:IWG_C3_geno_TASSEL

Numerical

IWG_C3_Q_matrix_structure_k2

IWG_C3_pheno_for_tassel

Sequence

IWG_C3_geno_TASSEL

Tree

Tree:IWG_C3_geno_TASSEL

Result

Table

Archaeopteryx Tree

LD Plot

Chart

QQ Plot

Manhattan Plot

1

Tree

Tree:IWG_C3_geno_TASSEL

2

Archaeopteryx Tree

Phylogenetic Tree

Phylogenetic Tree

Relatedness Analysis

Plotting PCA

1

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 5.2.96

File

Data

Impute

Filter

Analysis

Results

GBSv2

GBS

Workflow

PHG

Data

Matrix

Centered_IBS_IW

Matrix:IWG_C3_geno_TASSEL

Matrix:IWG_C3_geno_TASSEL

Numerical

IWG_C3_Q_matrix_structure_k2

IWG_C3_pheno_for_tassel

Sequence

IWG_C3_geno_TASSEL

Tree

Tree:IWG_C3_geno_TASSEL

Result

Diversity

Relatedness

Association

Distance Matrix

Kinship

Create Tree

Merge Trees

Subset Tree

Remove Tree Branch Lengths

Convert Tree Names

Pedigree Relationship Matrix

Combined A and G Relationship Matrix

MDS

PCA

Site Numbers

Lo

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5121: 266403824

5122: 266415638

5123: 267269056

5124: 268902458

5125: 269478974

5126: 271255874

T T R K Y G S R A

T T A T T G S R A

K R T Y G S R M

Number of taxa: 451

Number of sites: 10299

Chromosomes...

3

PCA

Help

☒ covariance (alternative = correlation)

limit number of components by

number_of_components

number of components

5

minimum eigenvalue

0.0

total variance

0.5

☒ Return Eigenvalues

☒ Return Eigenvectors

Ok

Cancel

Defaults

User Manual

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 5.2.96

File

Data

Impute

Filter

Analysis

Results

GBSv2

GBS

Workflow

PHG

Data

Matrix

Centered_IBS_IW

Matrix:IWG_C3_geno_TASSEL

Numerical

IWG_C3_Q_matrix_structure

IWG_C3_pheno_for_tassel

PC_IWG_C3_geno_TASSEL

Eigenvalues_IWG_C3_geno_TASSEL

Eigenvectors_IWG_C3_geno_TASSEL

Sequence

Table

Archaeopteryx Tree

LD Plot

Chart

QQ Plot

Manhattan Plot

Taxa

PC1

PC2

H0225

7.912

-8.104

H0226

6.343

2.967

H0227

5.508

3.196

H0228

4.728

-0.212

H0229

5.552

-7.374

H0230

7.517

-3.669

H0232

3.978

3.057

H0233

-3.369

7.352

H0234

-3.655

5.619

H0235

1.508

2.777

H0236

10.411

1.652

H0238

-2.927

-1.466

Graph Type:

XYScatter

Y1

PC2

X

PC1

Y2

None

Line

Regression

2 Y Axes

Save

Properties

PC1 vs. PC2

PC2

10

5

0

-5

-10

-10

-8

-6

-4

-2

0

2

4

6

8

10

12

14

PC1

PC2

Relatedness Analysis

Plotting MDA

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 5.2.96

FileDataImputeFilterAnalysisResultsGBSv2GBSWorkflowPHG

Data

Matrix

Centered_IBS_IW

Matrix:IWG_C3_geno_TASSEL

Numerical

IWG_C3_Q_matrix_structure_k2

IWG_C3_pheno_for_tassel

PC_IWG_C3_geno_TASSEL

Eigenvalues_IWG_C3_geno_TASSEL

Eigenvectors_IWG_C3_geno_TASSEL

Sequence

IWG_C3_geno_TASSEL

Tree

Tree:IWG_C3_geno_TASSEL

Result

Diversity

Relatedness

Association

Distance Matrix

Kinship

Create Tree

Merge Trees

Subset Tree

Remove Tree Branch Lengths

Convert Tree Names

Pedigree Relationship Matrix

Combined A and G Relationship Matrix

MDS

PCA

Taxa

H0225

H0226

H0227

H0228

H0229

H0230

H0232

H0233

H0234

H0235

H0236

H0238

H0239

H0240

H0241

H0242

H0243

H0244

Table Title: Distance Matrix
Number of columns: 452
Number of rows: 451
Matrix size (excludes row headers): 203401

MDS

Help

Number of Axes5

☒ Remove NaNs

OkCancelDefaultsUser Manual

Start from distance matrix

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 5.2.96

FileDataImputeFilterAnalysisResultsGBSv2GBSWorkflowPHG

Data

Matrix

Centered_IBS_IWG_C3_geno_TASSEL

Matrix:IWG_C3_geno_TASSEL

Numerical

IWG_C3_Q_matrix_structure_k2

IWG_C3_pheno_for_tassel

PC_IWG_C3_geno_TASSEL

Eigenvalues_IWG_C3_geno_TASSEL

Eigenvectors_IWG_C3_geno_TASSEL

MDS_PCs_Matrix:IWG_C3_geno_TASSEL

MDS_Eigenvalues_Matrix:IWG_C3_geno_TASSEL

Sequence

IWG_C3_geno_TASSEL

Tree

Tree:IWG_C3_geno_TASSEL

Result

Table

Archaeopteryx Tree

LD Plot

Chart

QQ Plot

Manhattan Plot

Taxa

PC1

PC2

H0225

-0.064

-0.069

H0226

-0.05

0.023

H0227

-0.043

0.026

H0228

-0.037

0.002

H0229

-0.044

-0.061

H0230

-0.059

-0.024

H0232

-0.031

0.024

H0233

0.025

0.056

H0234

0.029

0.044

H0235

-0.012

0.022

H0236

-0.083

0.016

H0238

0.022

-0.006

H0239

0.03

0.056

H0240

0.013

-0.025

H0241

-0.043

0.026

H0242

0.008

0.024

H0243

-0.035

0.045

H0244

-0.051

0.042

Graph Type:XYScatter

Save

Properties

Y1PC2

Y2None

XPC1

☐ Line

☐ Regression

☐ 2 Y Axes

PC1 vs. PC2

PC2

0.05

0.00

-0.05

-0.10

-0.10

-0.08

-0.06

-0.04

-0.02

0.00

0.02

0.04

0.06

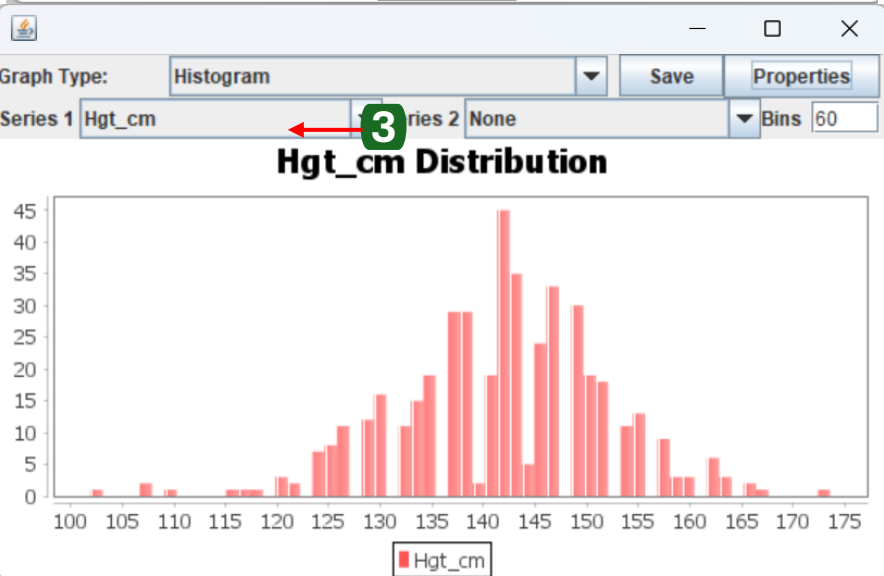
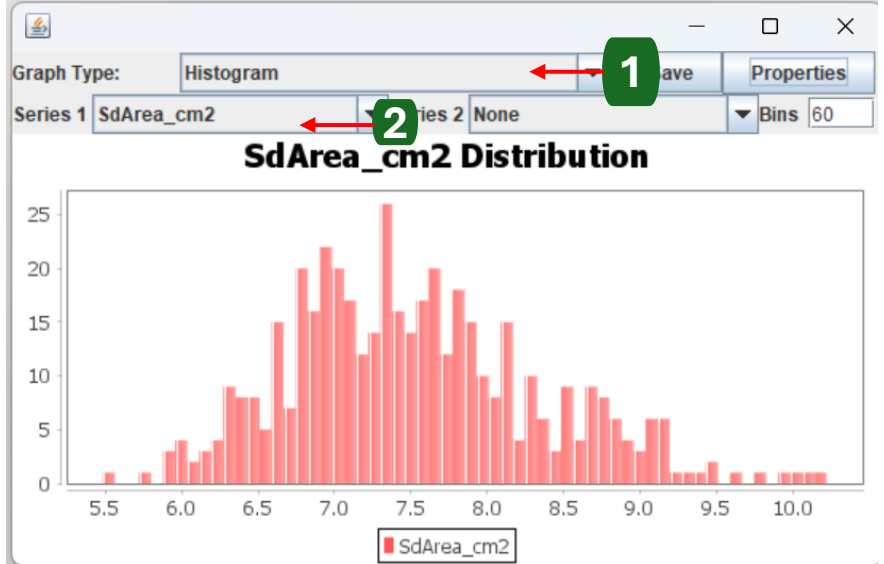
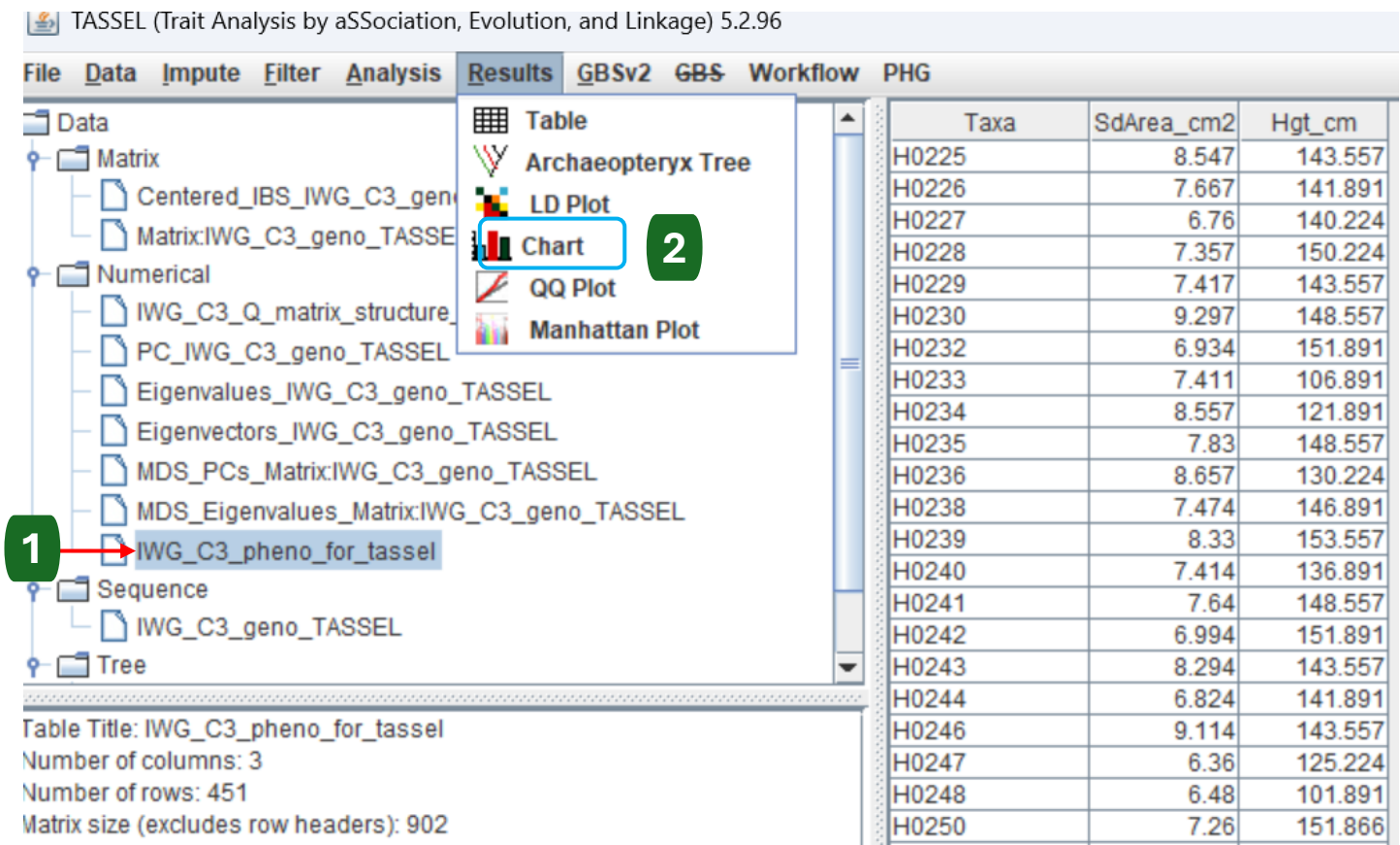
0.08

PC1

PC2

Association Analysis

Checking normality of phenotypic traits



Association Analysis

Genotype Summary

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 5.2.96

FileDataImputeFilterAnalysisResultsGBSv2GBSWorkflowPHG

Get Taxa List

Get Position List

Sort Taxa Alphabetically

Sort Genotype File

Synonymizer

Intersect Join

Union Join

Merge Genotype Tables

Separate

Homozygous Genotype

Change Indels to Unknown

SetLowDepthGenosToMissing

Transform Phenotype

Numerical Genotype

ABH Genotype

Thin Sites by Position

Cluster Genotypes

Mask Genotype

Find Inversions

Create Hybrid Genotypes

Geno Summary

SEL

EL

EL

ASSEL

geno_TASSEL

0

1

5117: 261424122

5118: 262256813

H0225

H0226

H0227

H0228

H0229

H0230

H0232

H0233

H0234

H0235

H0236

H0238

H0239

H0240

H0241

H0242

H0243

H0244

H0246

Stat Type	Value
Number of Taxa	451
Number of Sites	10299
Sites x Taxa	4.6448E6
Number Not Missing	4.6387E6
Proportion Not Missing	0.99867
Number Missing	6176
Proportion Missing	0.00133
Number Gametes	9.2897E6
Gametes Not Missing	9.2773E6
Proportion Gametes Not Missing	0.99867
Gametes Missing	12352
Proportion Gametes Missing	0.00133
Number Heterozygous	1.6648E6
Proportion Heterozygous	0.35841
Average Minor Allele Frequency	0.23667

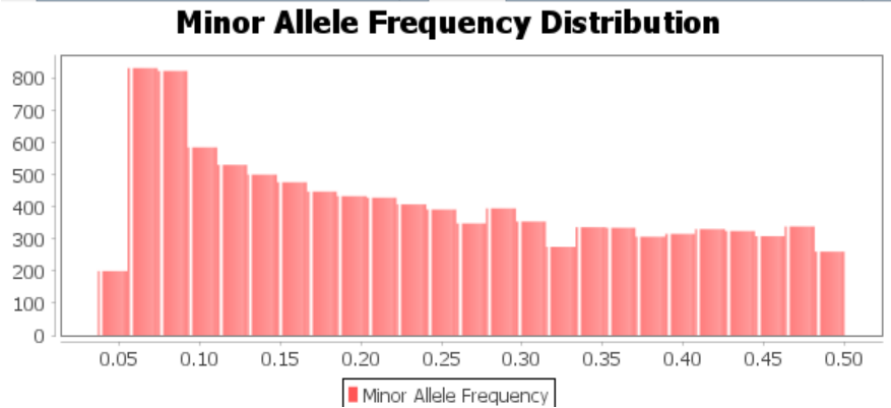
Graph Type: Histogram

Save

Properties

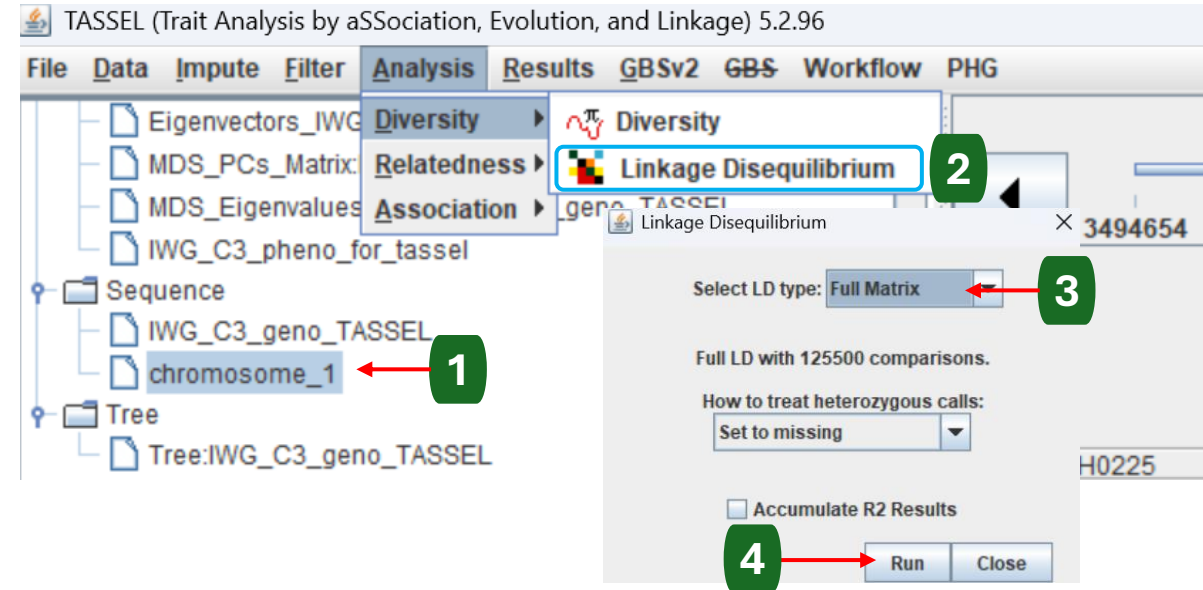
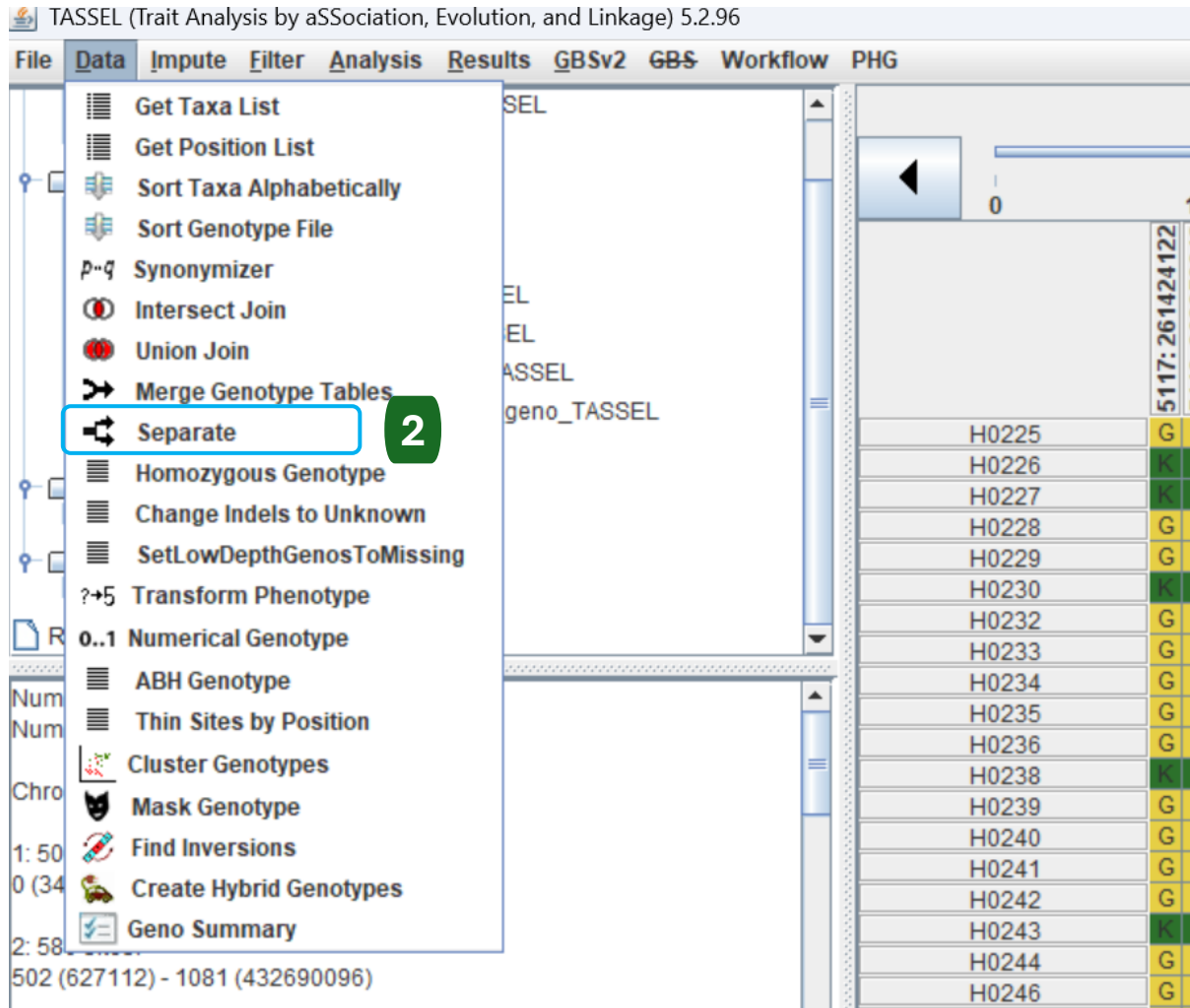
Se... Minor Allele Frequency

Series 2 None



1 Highlight the genotype file

Calculating LD per Chromosome

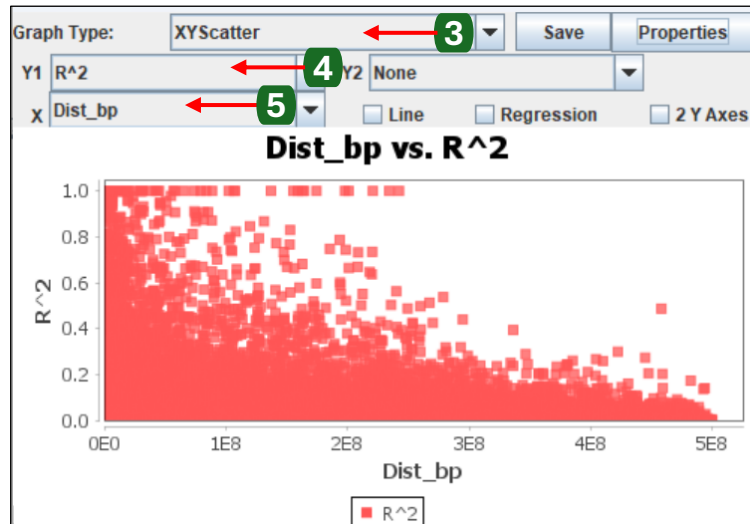
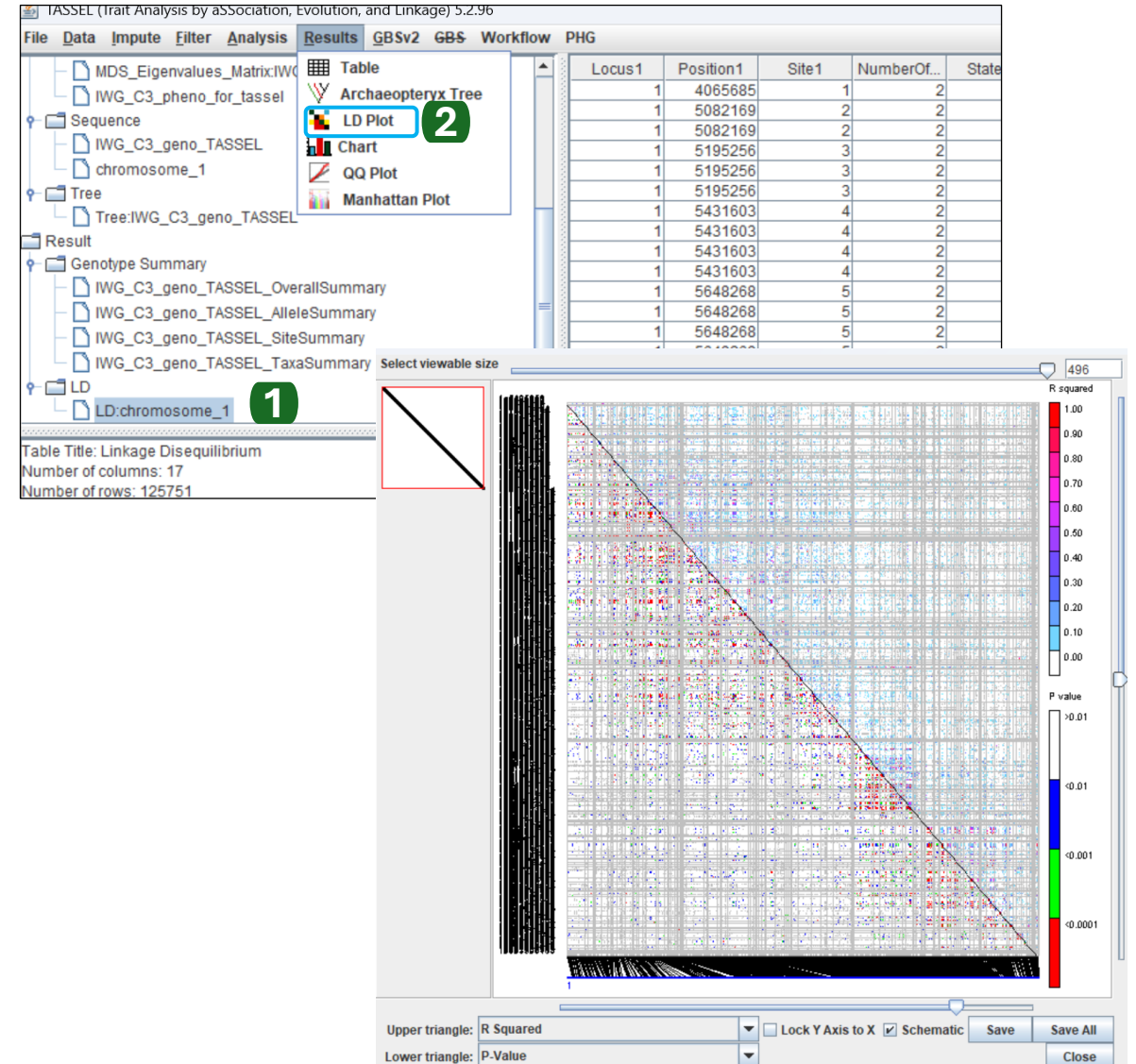
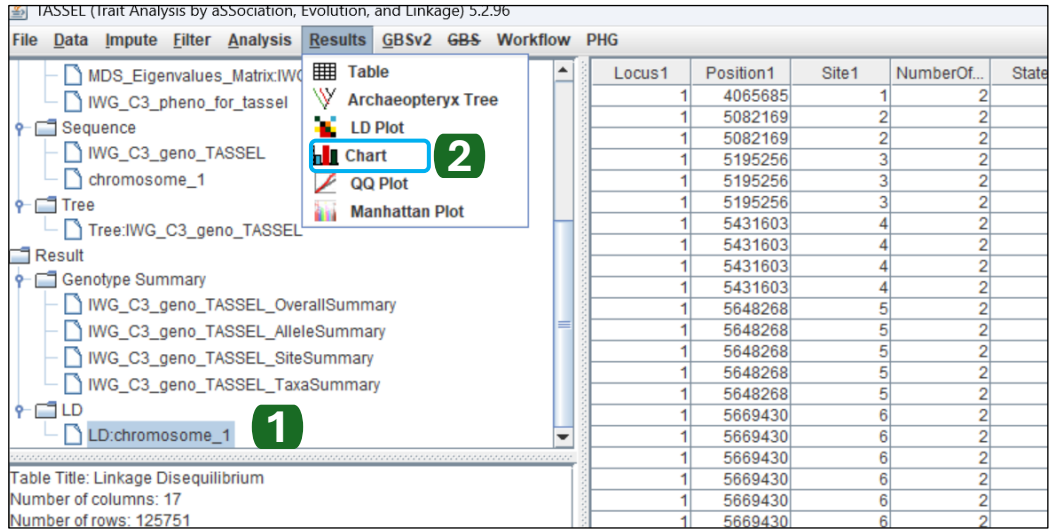


1 Highlight the genotype file

NB: The option `Separate` will list files based on chromosomes. Then `chr1` was retained for demonstration.

Association Analysis

Visualizing LD and LD decay of Chromosome 1



Association Analysis

GWAS: file preparation

Hold Ctrl and left-click to select multiple input files

The screenshot displays the GWAS software interface with the 'Data' menu open. The 'Data' menu is highlighted with a green box and the number '4'. The 'Data' folder is expanded, showing a tree structure of files. Three files are selected with red arrows and green boxes labeled '1', '2', and '3': 'IWG_C3_pheno_for_tassel', 'PC_IWG_C3_geno_TASSEL', and 'IWG_C3_geno_TASSEL'. The 'Intersect Join' option in the 'Data' menu is highlighted with a blue box. The background shows a grid of data with columns labeled 936 and 1872, and rows labeled 5111 through 5124. The grid contains letters (R, Y, A, C, M, Y, G, T, T, R, K) and numbers (250886771, 252078059, 253641525, 254164835, 256483452, 260198457, 261424122, 262258813, 262720792, 263069745, 266403824).

4 Data Impute Filter Analysis Results GBSv2 GBS Workflow PHG

Data

- Matrix
 - Centered_IBS_IWG_C3_geno_TASSEL
 - Matrix:IWG_C3_geno_TASSEL
- Numerical
 - IWG_C3_Q_matrix_structure_k2
 - IWG_C3_pheno_for_tassel
 - PC_IWG_C3_geno_TASSEL
 - Eigenvalues_IWG_C3_geno_TASSEL
 - Eigenvectors_IWG_C3_geno_TASSEL
 - MDS_PCs_Matrix:IWG_C3_geno_TASSEL
 - MDS_Eigenvalues_Matrix:IWG_C3_geno_TASSEL
- Sequence
 - IWG_C3_geno_TASSEL
- Result

File Data Impute Filter Analysis Results GBSv2 GBS Workflow PHG

- Get Taxa List
- Get Position List
- Sort Taxa Alphabetically
- Sort Genotype File
- Synonymizer
- Intersect Join**
- Union Join
- Merge Genotype Tables
- Separate
- Homozygous Genotype
- Change Indels to Unknown
- SetLowDepthGenosToMissing
- Transform Phenotype
- Numerical Genotype
- ABH Genotype
- Thin Sites by Position
- Cluster Genotypes
- Mask Genotype
- Find Inversions
- Create Hybrid Genotypes
- Geno Summary

Site N

936 1872

5111: 250886771 5112: 252078059 5113: 253641525 5114: 254164835 5115: 256483452 5116: 260198457 5117: 261424122 5118: 262258813 5119: 262720792 5120: 263069745 5121: 266403824

R Y A C M Y G T T R K
R C R T M C K Y T A T
R C R T C T K Y K R T
R Y A C M T G T T R K
R Y R Y C T K Y T G K
R Y A C M Y G T T R K
R Y A C M T G T K R K
R Y R T C T G T T R K

Association Analysis

GWAS: QQ Plot

1

File

Data

Impute

Filter

Analysis

Results

GBSv2

GBS

Workflow

PHG

Data

Matrix

Centered_IBS_IW

Matrix:IWG_C3_genotype_TASSEL

Numerical

IWG_C3_Q_matrix_structure_k2

IWG_C3_pheno_for_tassel

PC_IWG_C3_genotype_TASSEL

Eigenvalues_IWG_C3_genotype_TASSEL

Eigenvectors_IWG_C3_genotype_TASSEL

MDS_PCs_Matrix:IWG_C3_genotype_TASSEL

MDS_Eigenvalues_Matrix:IWG_C3_genotype_TASSEL

IWG_C3_genotype_TASSEL + IWG_C3_pheno_for_tassel + PC_IWG_C3_genotype_TASSEL

Sequence

Diversity

Relatedness

Association

GLM

MLM

WeightedMLM

Genomic Selection

Stepwise

Fast-MT Association

Multivariate Stepwise

VCAP Scan

Taxa	SdArea_cm2	Hgt_cm	PC1	PC2	PC3	PC4	PC5	Genotype
H0225	8.547	143.557	7.912	-8.104	-3.44	-3.754	-1.58	WCRKTRT...
	7.667	141.891	6.343	2.967	4.085	-10.684	-3.309	ACRKTGT...
	6.76	140.224	5.508	3.196	5.693	-8.437	-4.185	ACRKKGT...
	7.357	150.224	4.728	-0.212	8.602	-4.187	-1.641	ACGKGR...
	7.417	143.557	5.552	-7.374	-2.71	-2.947	-0.928	WCRKTG...
	9.297	148.557	7.517	-3.669	8.887	0.267	-1.443	ACGKKG...
	6.934	151.891	3.978	3.057	5.276	-9.21	-5.106	ACRGTGT...
	7.411	106.891	-3.369	7.352	1.581	-0.674	-8.422	ACGGTGT...
	8.557	121.891	-3.655	5.619	1.749	-0.731	-9.462	ACGKKG...
	7.83	148.557	1.508	2.777	-1.062	5.046	-3.022	ACGKKG...
	8.657	130.224	10.411	1.652	5.286	1.938	-3.363	ACGKKRT...
	7.474	146.891	-2.927	-1.466	7.725	9	-6.068	ACGKKG...
H0239	8.33	153.557	-3.964	7.279	1.905	0.167	-9.557	ACGGTGT...
H0240	7.414	136.891	-1.494	-2.775	-5.27	2.948	-4.655	WCGGTGT...
H0241	7.64	148.557	5.464	3.397	-2.187	4.497	2.694	ACRGTGT...
H0242	6.994	151.891	-0.945	2.924	-1.363	4.628	-3.228	ACRKKRT...
H0243	8.294	143.557	4.35	5.523	-1.073	3.45	0.003	AYRGTGT...

1

File

Data

Impute

Filter

Analysis

Results

GBSv2

GBS

Workflow

PHG

IWG_C3_pheno_for_tassel

PC_IWG_C3_genotype_TASSEL

Eigenvalues_IWG_C3_genotype_TASSEL

Eigenvectors_IWG_C3_genotype_TASSEL

MDS_PCs_Matrix:IWG_C3_genotype_TASSEL

MDS_Eigenvalues_Matrix:IWG_C3_genotype_TASSEL

IWG_C3_genotype_TASSEL + IWG_C3_pheno_for_tassel + PC_IWG_C3_genotype_TASSEL

Sequence

IWG_C3_genotype_TASSEL

Association

GLM Stats IWG_C3_genotype_TASSEL + IWG_C3_pheno_for_tassel + PC_IWG_C3_genotype_TASSEL

GLM Genotypes IWG_C3_genotype_TASSEL + IWG_C3_pheno_for_tassel

Table

Archaeopteryx Tree

LD Plot

Chart

QQ Plot

Manhattan Plot

Trait	Marker
SdArea_cm2	Chr01_349...
SdArea_cm2	Chr01_406...
SdArea_cm2	Chr01_508...
SdArea_cm2	Chr01_519...
SdArea_cm2	Chr01_543...
SdArea_cm2	Chr01_564...
SdArea_cm2	Chr01_566...
SdArea_cm2	Chr01_606...
SdArea_cm2	Chr01_646...
SdArea_cm2	Chr01_705...
SdArea_cm2	Chr01_720...
SdArea_cm2	Chr01_958...
SdArea_cm2	Chr01_986...
SdArea_cm2	Chr01_122...
SdArea_cm2	Chr01_129...

QQ Plot Options

Available Traits

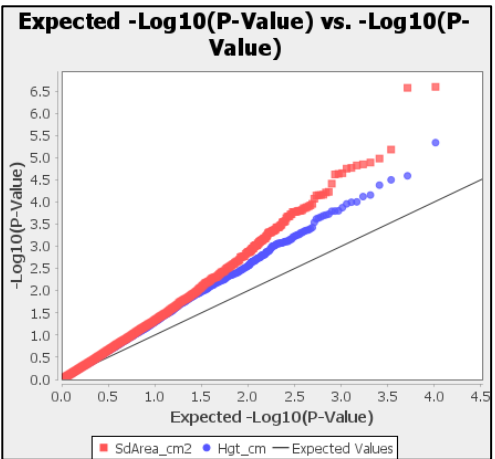
Traits to Plot

Plot Density: 102 of 10299 points per trait.

4

Okay

Cancel



Association Analysis

GWAS: Manhattan Plot

