

# Marker-assisted selection in Flapjack

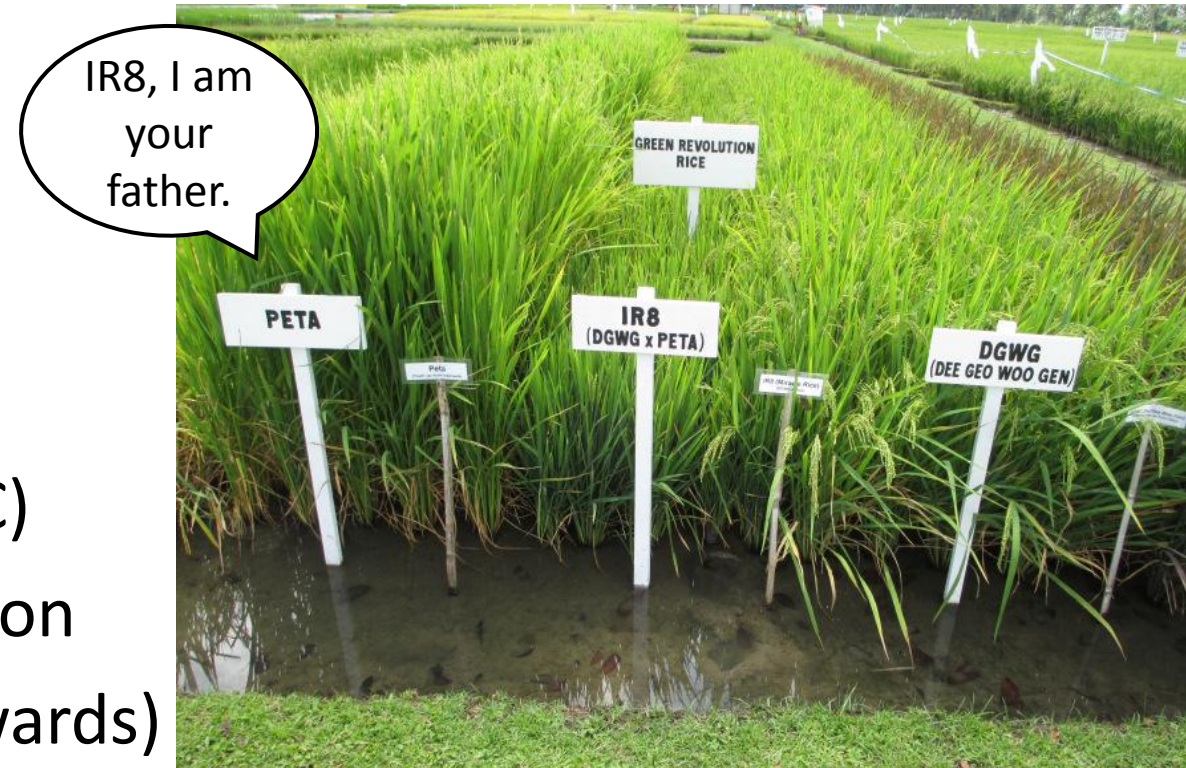
John Carlos Ignacio  
Graduate Research Associate  
Wheat Breeding  
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FJ MAS demo files available @ [flapjack.myddns.me/mas.zip](http://flapjack.myddns.me/mas.zip)

# MAS in Flapjack

- Marker-assisted backcrossing (MABC)
- Pedigree Verification – F1 confirmation
- Pedigree Verification – Lines (F2 onwards)
- Forward Breeding and Indexed Forward Breeding

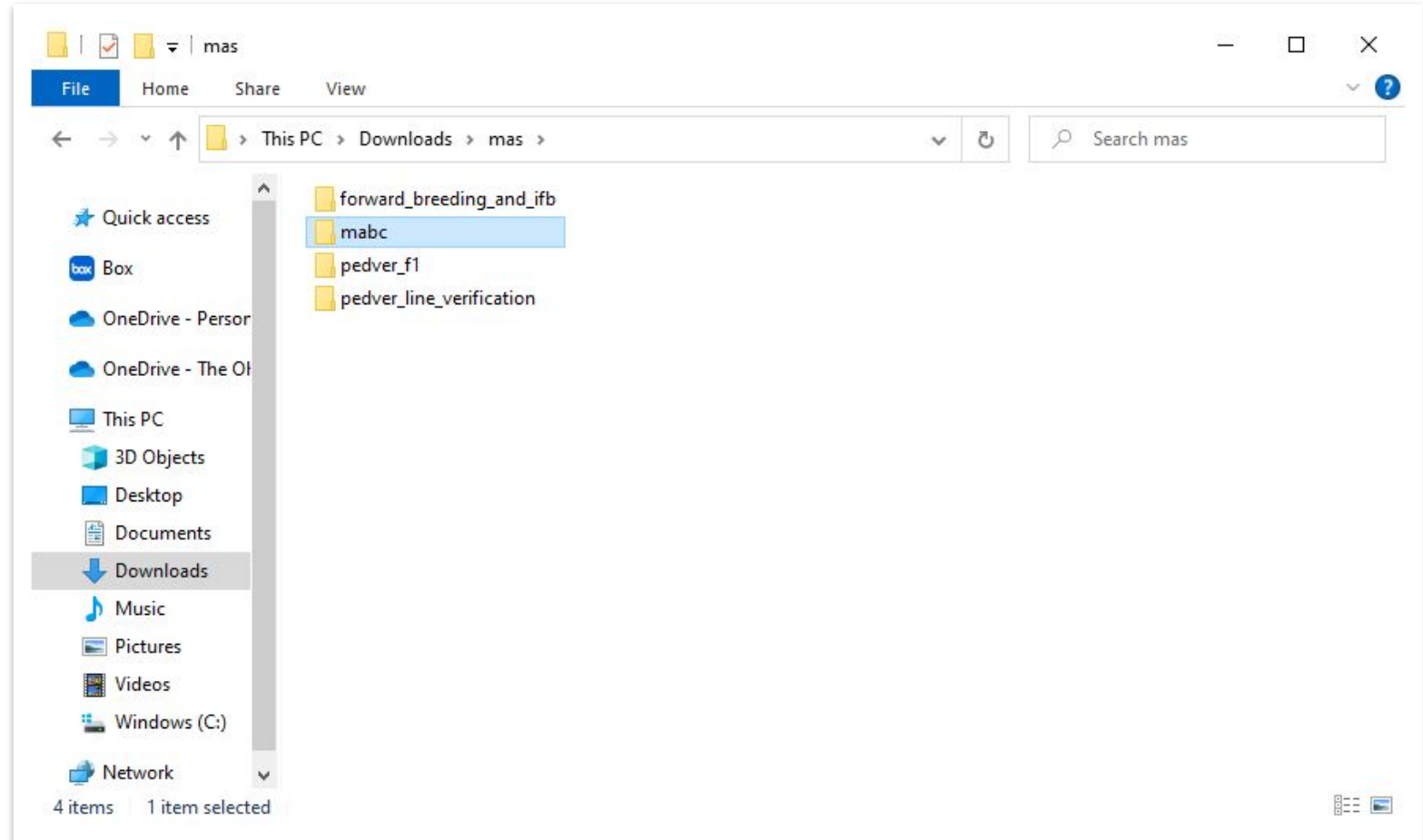


FJ MAS demo files available @ [flapjack.myddns.me/mas.zip](http://flapjack.myddns.me/mas.zip)

# Marker-assisted backcrossing

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Tutorial and Demo



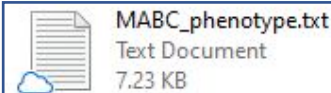
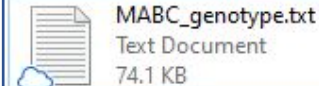
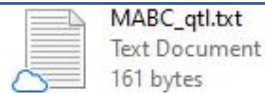
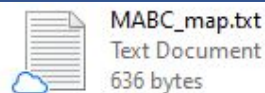
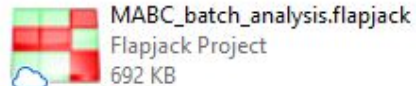
# MABC Input Files

Genotype file: MABC\_genotype.txt

	A	B	C	D	E	F
1	# fjFile = GENOTYPE					
2		m1	m2	m3	m4	m5
3	RP	T	A	T	A	A
4	DP	G	G	G	G	G
5	RP[1]/DP-	T	A	T	A/G	A/G
6	RP[1]/DP-	T	A	T	A/G	A/G
7	RP[1]/DP-4		A		A	A
8	RP[1]/DP-	T	A	T	A	A
9	RP[1]/DP-	T/G	A/G	T/G	A/G	A/G
10	RP[1]/DP-	T	A	T	A	A

Map file: MABC\_map.txt

	A	B	C
1	# fjFile = MAP		
2	m1	1	2
3	m2	1	5
4	m3	1	13
5	m4	1	40
6	m5	1	41
7	m6	1	51
8	m7	1	57
9	m8	1	69
10	m9	1	77
11	m10	1	97



QTL file: MABC\_qtl.txt

	A	B	C	D	E	F	G	H
1	# fjFile = QTL							
2	QTL	Chromosome	Position	Minimum	Maximum	Trait	Experiment	Source
3	QTL1	1	22.5	5	40	TRAIT	EXPERIMENT	DP
4	QTL2	4	157.5	149	166	TRAIT	EXPERIMENT	DP

Phenotype file: MABC\_phenotype.txt  
(Not required)

	A	B	C	D	E
1	# fjFile = phenotype				
2		dnasampl	disease_plant_id	plot_id	
3	RP	A	5	MGZ-054	
4	DP	A	1	DQX-172	
5	RP[1]/DP-2	A	4	ZQL-001	ZQL-18-P01
6	RP[1]/DP-3	A	1	ZQL-002	ZQL-18-P01
7	RP[1]/DP-4	A	1	ZQL-003	ZQL-18-P01
8	RP[1]/DP-5	B	5	ZQL-004	ZQL-18-P01
9	RP[1]/DP-6	B	2	ZQL-005	ZQL-18-P01
10	RP[1]/DP-7	B	5	ZQL-006	ZQL-18-P01
11	RP[1]/DP-8	B	5	ZQL-007	ZQL-18-P01
12	RP[1]/DP-9	B	7	ZQL-008	ZQL-18-P01



# MABC Import Data

Flapjack - 1.21.02.04

File Edit View Visualization Analysis Data Help

New Project Open Project Import Data Find Genotypes Chromosomes

Data Sets (0)

Welcome to Flapjack

Flapjack 1.21.02.04 - © 2007-2021, Information & Computational Sciences, JHI. Feedback Follow

Import Data

Via BrAPI Maps and Genotypes Phenotypes Features (QTL) Graphs Example Data

Use this tab to import map and genotype data into a new or existing Flapjack project.

Data files to import:

Map file (optional): C:\Users\carli\Box\Flapjack\flapjack\_files\mabc\MABC\_map.txt Browse...

Genotype file: C:\Users\carli\Box\Flapjack\flapjack\_files\mabc\MABC\_genotype.txt Browse...

(Genotype files can be in either Flapjack or Intertek format)

Advanced options:

Edit the advanced options to just how Flapjack will process the files being imported.

Advanced options...

Import map/genotypes Cancel Help

Citing Flapjack

Please click here for information on how to cite Flapjack if you use it in your work

The James Hutton Institute

Flapjack Tip: 36x40, 8C, 12T, 114.78MB

**Step 1:**  
Specify Map &  
Genotype files

**Step 2:**  
Set advanced  
options

# MABC Advanced Data Import Settings

Genotype file: MABC\_genotype.txt

	A	B	C	D	E	F
1	# fjFile = GENOTYPE					
2		m1	m2	m3	m4	m5
3	RP	T	A	T	A	A
4	DP	G	G	G	G	G
5	RP[1]/DP-T	A	T	A/G	A/G	A/G
6	RP[1]/DP-T	A	T	A/G	A/G	A/G
7	RP[1]/DP-4	A		A	A	A
8	RP[1]/DP-T	A	T	A	A	A
9	RP[1]/DP-T/G	A/G	T/G	A/G	A/G	A/G
10	RP[1]/DP-T	A	T	A	A	A

Heterozygous data

Missing data

Advanced Data Import Options

Advanced options:

- Duplicate all markers onto a single "All Chromosomes" chromosome for side-by-side viewing (not recommended if you have a large number of markers)
- Don't distinguish between heterozygous alleles (eg, treat A/T the same as T/A)
- Allow data with duplicate line names to be imported (experimental)

Flapjack format specific:

Heterozygous separator string: /

Missing data string:

Genotype data has been transposed from Flapjack default (markers are now rows)

OK Cancel Help

Click OK when done

# MABC Import Data

Flapjack - 1.21.02.04

File Edit View Visualization Analysis **Data** Help

New Project Open Project **Import Data** Find Genotypes Chromosomes

Data Sets (0)

Welcome to Flapjack

Flapjack 1.21.02.04 - © 2007-2021, Information & Computational Sciences, JHI. Feedback Follow

Import Data

Via BrAPI Maps and Genotypes Phenotypes Features (QTL) Graphs Example Data

Use this tab to import map and genotype data into a new or existing Flapjack project.

Data files to import:

Map file (optional): C:\Users\carli\Box\Flapjack\flapjack\_files\mabc\MABC\_map.txt Browse...

Genotype file: C:\Users\carli\Box\Flapjack\flapjack\_files\mabc\MABC\_genotype.txt Browse...

(Genotype files can be in either Flapjack or Intertek format)

Advanced options:

Edit the advanced options to just how Flapjack will process the files being imported.

Advanced options...

Import map/genotypes Cancel Help

Citing Flapjack

Please click here for information on how to cite Flapjack if you use it in your work

The James Hutton Institute

Flapjack Tip: 36x40, 8C, 12T, 114.78MB

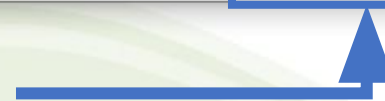
**Step 1:**  
Specify Map &  
Genotype files



**Step 2:**  
Set advanced  
options



**Step 3:**  
Click Import map/genotypes



# MABC Import Data

Step 4:  
Import QTL file

The screenshot shows the Flapjack software interface. The 'Import Data' dialog box is open, with the 'Features (QTL)' tab selected. The 'Features file to import' section contains a text box with the path 'C:\Users\carli\Downloads\mas\mabc\MABC\_qtl.txt' and a 'Browse...' button. Below this is a checkbox labeled 'Apply this file to ALL data sets in the current project'. At the bottom of the dialog, the 'Import features' button is circled in blue. The main window shows a project with 'MABC\_genotype (202x61)' and 'Trait Data' data sets. The 'Import Data' button in the top toolbar is also circled in blue. A zoom slider at the bottom right is highlighted with a blue box and an arrow pointing to it from the text 'Zooming out might help'. The 'Import features' button is also labeled with 'Click when done'.

Import Data

Via BrAPI | Maps and Genotypes | Phenotypes | **Features (QTL)** | Graphs | Example Data

Use this tab to import features (QTL) information into the current project.

Features file to import:

Features file: C:\Users\carli\Downloads\mas\mabc\MABC\_qtl.txt

Apply this file to ALL data sets in the current project

Zoom:

Click when done

Zooming out might help



# MABC Import Data

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The screenshot shows the Flapjack software interface. The main window displays a table of Quantitative Trait Loci (QTLs) under the 'Trait Data' tab. The table has columns for QTL, Chromosome, Position, Minimum, Maximum, Trait, Experiment, Visible, and Source. Two QTLs are listed: QTL1 on chromosome 1 and QTL2 on chromosome 4. A dialog box titled 'Flapjack' is open in the center, providing a summary of the import process.

QTL	Chromosome	Position	Minimum	Maximum	Trait	Experiment	Visible	Source
QTL1	1	22.5	5	40	TRAIT	EXPERIMENT	<input checked="" type="checkbox"/>	DP
QTL2	4	157.5	149	166	TRAIT	EXPERIMENT	<input checked="" type="checkbox"/>	DP

Flapjack

Flapjack has finished importing QTL. A summary is given below:

- Number of QTL read from the file: 2
- Number of QTL added to Flapjack: 2

The number added may be less than the number read if duplicates were detected or if it was impossible to assign QTL to the chromosomes within this data set.

Close

Number of QTLs: 2

Flapjack Tip: Navigate around a view quickly by clicking and dragging on one of the Overview displays

38x42, 8C, 11T, 133.21MB

# MABC Analysis Results

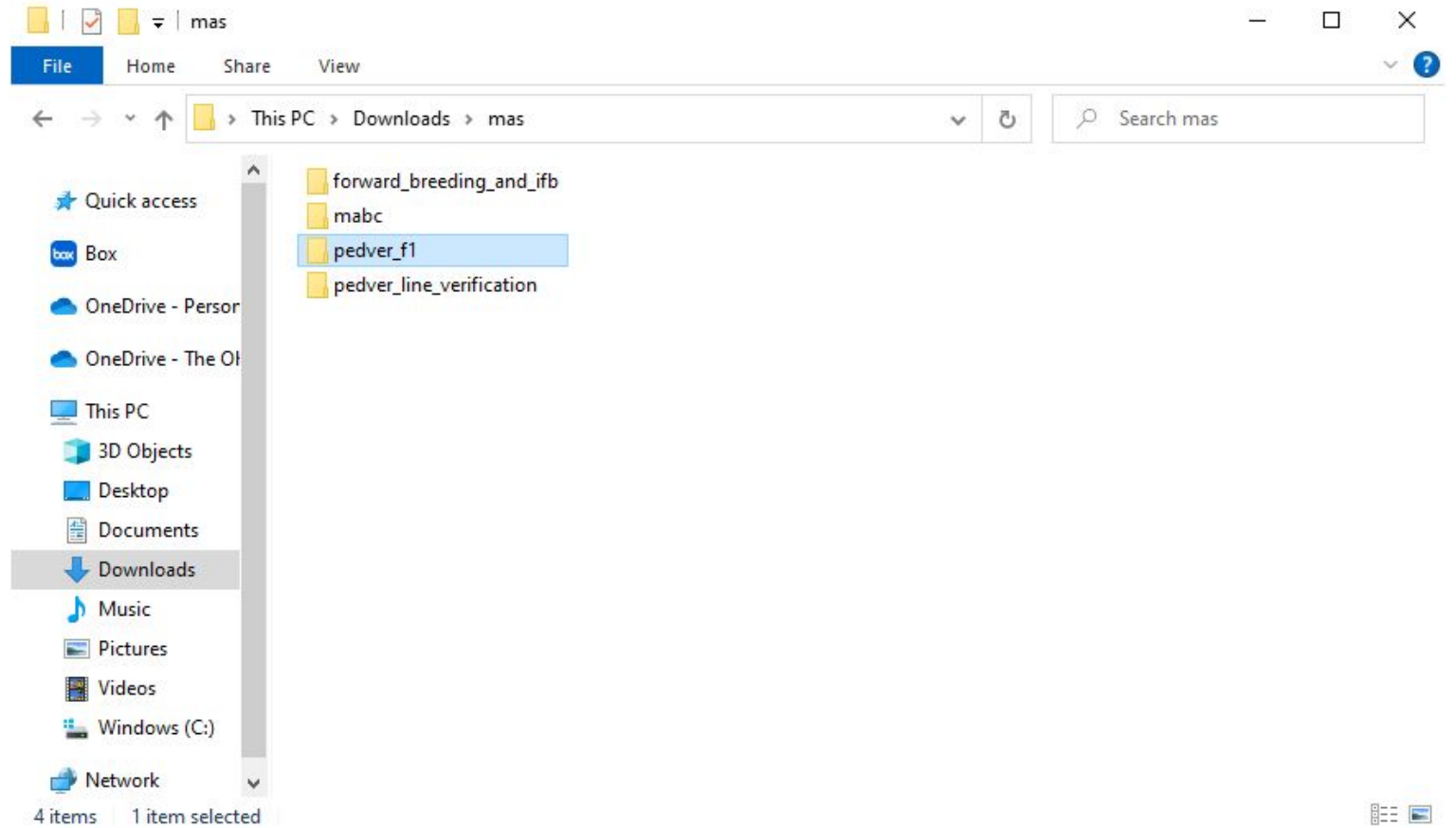
Line	Data Count	% Data	Het Count	% Het	RPP (1)	RPP (2)	RPP (3)	RPP (4)	RPP Total	RPP Coverage	LD (QTL1)	Status (QTL1)	LD (QTL2)	Status (QTL2)	QTL Allele Count
RP	61	100.00	0	0.00	1.00	1.00	1.00	1.00	1.00	0.69	0	0	0	0	0
DP	61	100.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.69	62	2	179	2	4
RP[1]/DP-2	61	100.00	13	21.31	0.92	0.87	0.93	0.90	0.90	0.69	1	0	28	0	0
RP[1]/DP-3	61	100.00	36	59.02	0.67	1.00	0.50	0.69	0.70	0.69	37	0	46	0	0
RP[1]/DP-4	49	80.33	31	63.27	1.00	0.54	0.50	0.71	0.65	0.62	5	0	0	0	0
RP[1]/DP-5	61	100.00	18	29.51	1.00	0.88	0.69	0.91	0.86	0.69	0	0	15	0	0
RP[1]/DP-6	61	100.00	28	45.90	0.50	1.00	0.94	0.63	0.77	0.69	62	1	54	1	2
RP[1]/DP-7	61	100.00	40	65.57	0.75	1.00	0.50	0.50	0.65	0.69	0	0	179	1	1
RP[1]/DP-8	61	100.00	16	26.23	0.74	0.91	1.00	0.77	0.86	0.69	29	0	0	0	0
RP[1]/DP-9	61	100.00	17	27.87	0.96	1.00	0.78	0.75	0.85	0.69	0	0	0	0	0
RP[1]/DP-10	61	100.00	19	31.15	0.96	0.57	0.97	0.85	0.84	0.69	0	0	0	0	0
RP[1]/DP-11	61	100.00	36	59.02	0.87	0.50	0.85	0.67	0.72	0.69	5	0	30	0	0
RP[1]/DP-12	61	100.00	35	57.38	0.50	0.73	0.81	0.70	0.73	0.69	62	1	10	0	1

Results	Description
<b>RPP (1 per chromosome)</b>	Based on map distance if weighted, based on total of markers if unweighted
<b>RPP Total</b>	Average RPP of all chromosomes
<b>RPP Coverage</b>	For weighted model, limits max coverage of a marker
<b>LD (1 per QTL)</b>	Length of donor genome linked to a QTL
<b>Status (1 per QTL)</b>	Count of donor QTL alleles per QTL
<b>QTL Allele Count</b>	Sum of all donor alleles in all QTLs

# Pedigree Verification – F1

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Tutorial and Demo



# PedVer F1 Input Files



Cross\_1.dat

Genotype file: Cross\_1.dat (Required)

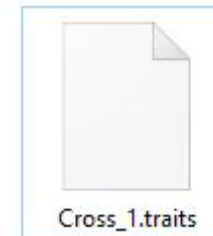
	A	B	C	D	E	F	G	H	I	J
1	# fjFile = GENOTYPE									
2		m1	m2	m3	m4	m5	m6	m7	m8	m9
3	Parent_A	C	T	C	G	G	T	G	C	G
4	Parent_B	C	G	C	G	G	T	G	T	G
5	1_1	C	T	C	G	G	T	G	C	G
6	1_2	C	G/T	C	G	G	T	G	C/T	G
7	1_3	C	G/T	C	G	G	T	G	C/T	G
8	1_4	C	G/T	C	G	G	T	G	C/T	G
9	1_5	C	G/T	C	G	G	T	G	C/T	G
10	1_6	C	G/T	C	G	G	T	G	C/T	G
11	1_7	C	G/T	C	G	G	T	G	C/T	G
12	1_8		G/T			G/A		G	C/T	G
13	1_9	C	G/T	C	G	G	T	G	C/T	G
14	1_10	C	G/T	C	G	G	T	G	C/T	G
15	1_11	C	G/T	C	G	G	T	G	C/T	G
16	1_12	C	G/T	C	G	G	T	G	C/T	G
17	1_13	C	G/T	C	G	G	T	G	C/T	G
18	1_14	C	G/T	C	G	G	T	G	C/T	G
19	1_15	C	G/T	C	G	G	T	G	C/T	G
20	1_16	C	G/T	C	G	G	T	G	C/T	G
21	1_17	C	G/T	C		G	T	G	C/T	G
22	1_18	C	G/T	C	G	G	T	G	C/T	G
23	1_19	C	G/T	C	G	G	T	G	C/T	G
24	1_20	C	T	C	G	G	T	G	C	G



Cross\_1.map

Map file: Cross\_1.map (Not required)

	A	B	C
1	# fjFile = MAP		
2	m1	1	0
3	m2	1	1
4	m3	1	2
5	m4	1	3
6	m5	1	4
7	m6	1	5
8	m7	1	6
9	m8	1	7
10	m9	1	8

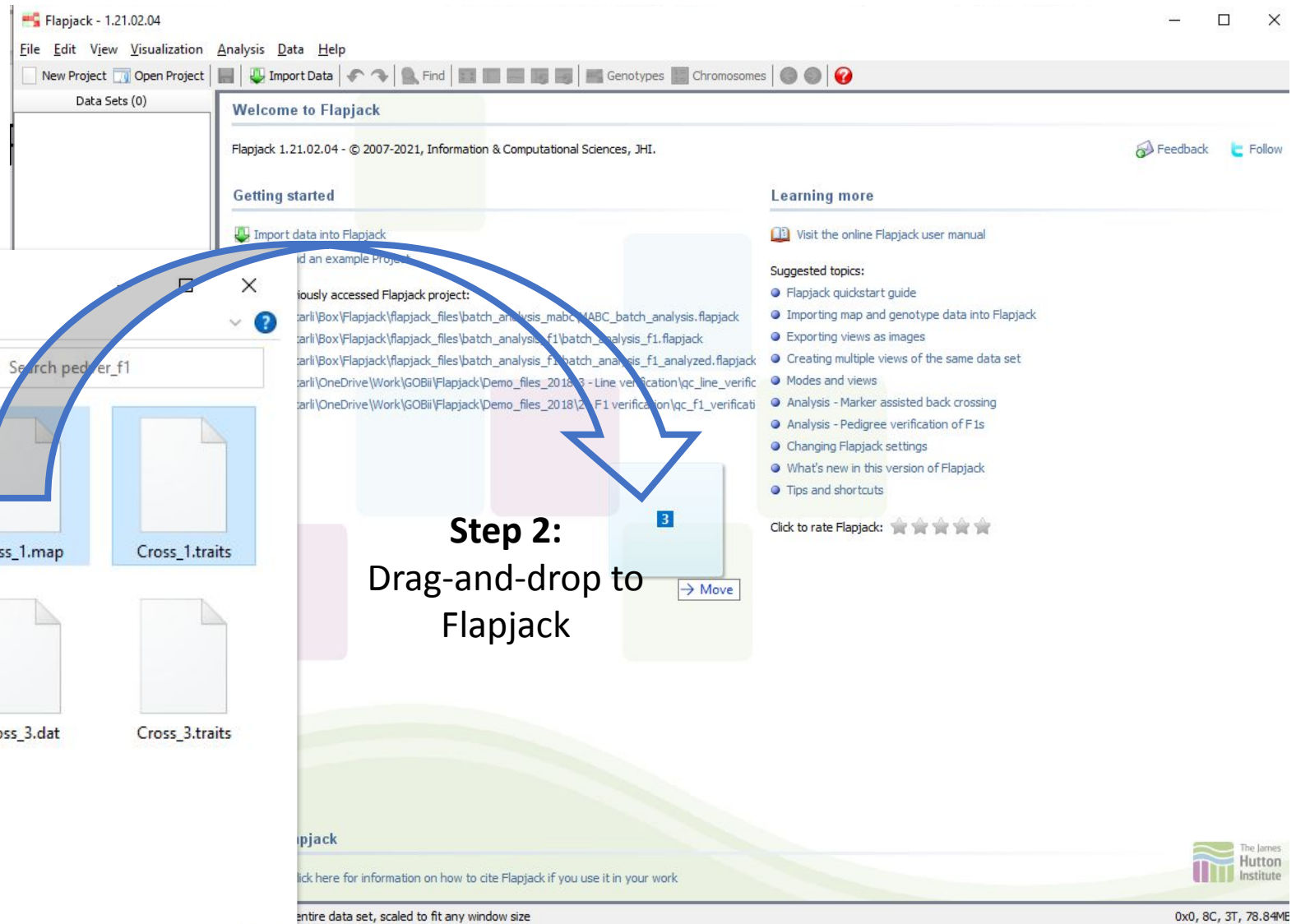
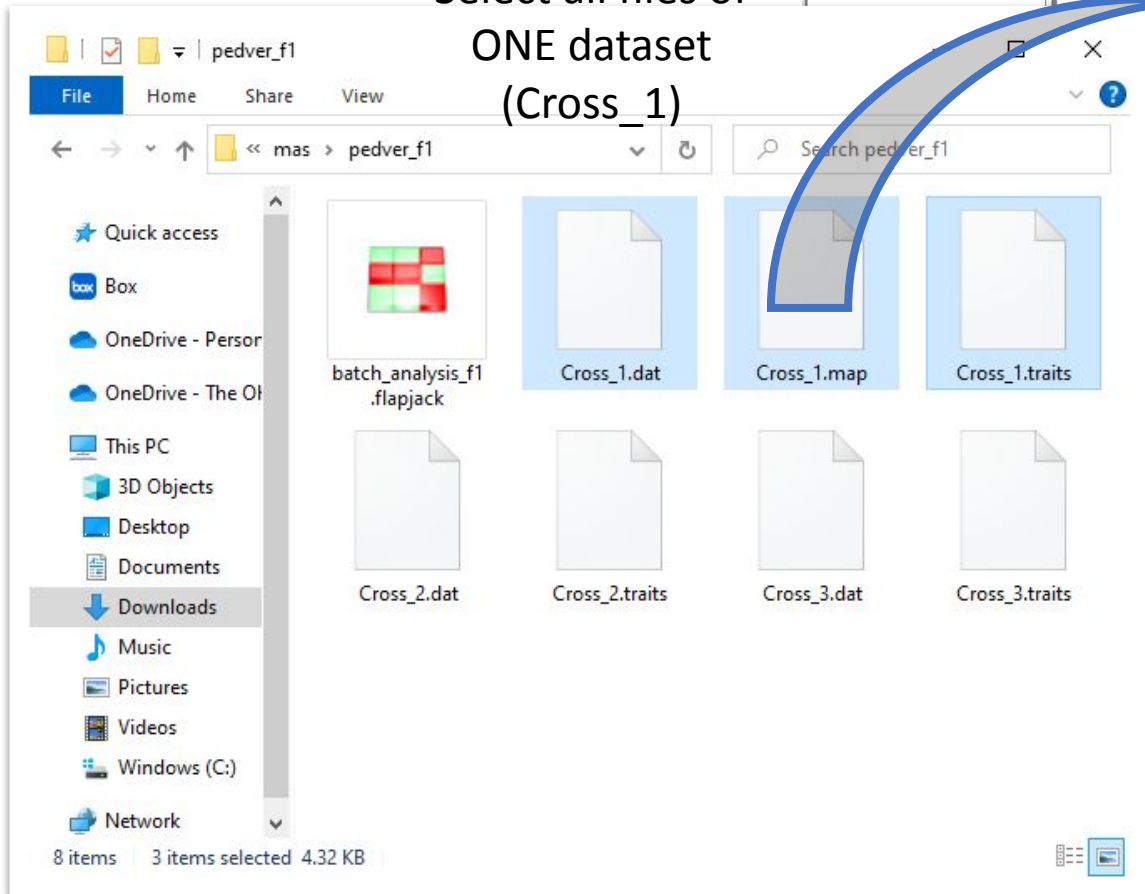


Cross\_1.traits

Pheno file: Cross\_1.traits (Not required)

# Import PedVer F1 Files by Drag-and-Drop

**Step 1:**  
Select all files of  
ONE dataset  
(Cross\_1)



**Step 2:**  
Drag-and-drop to  
Flapjack



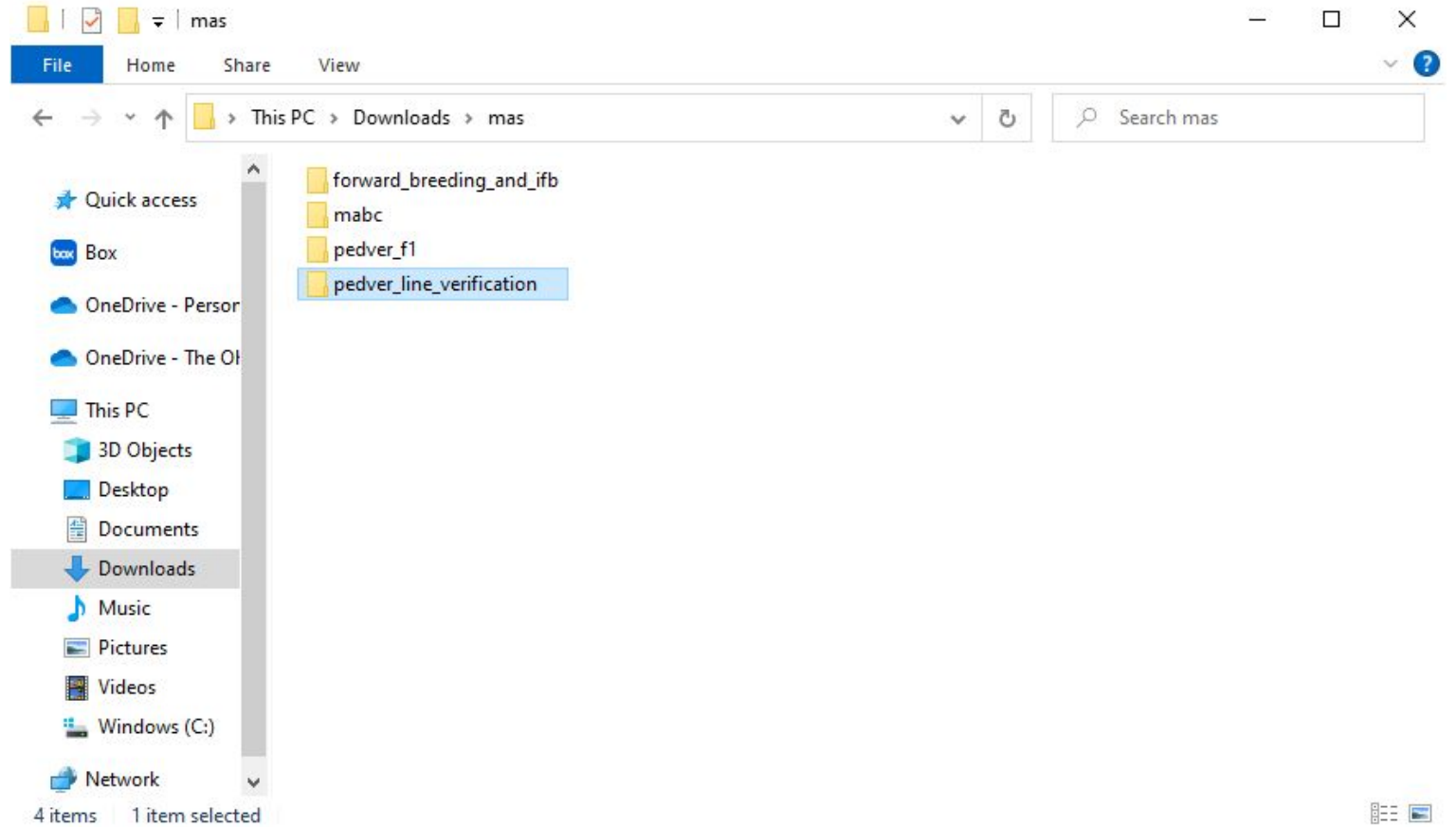
Line	Data Count	% Data	Het Count	% Het	% Het deviation from Expected	% Allele match to P1	% Allele match to P2	% Genotype Match to Expected F1	Rank	Comments	Selected	Decision
Parent_A	9	100.00	0	0.00	22.22	100.00	77.78	77.78	0		FALSE	Parent 1
Parent_B	9	100.00	0	0.00	22.22	77.78	100.00	77.78	0		FALSE	Parent 2
Exp F1:Parent	9	100.00	2	22.22	0.00	88.89	88.89	100.00	0		FALSE	Expected F1
1_1	9	100.00	0	0.00	22.22	100.00	77.78	77.78	0		TRUE	True F1
1_2	9	100.00	0	0.00	22.22	100.00	77.78	77.78	0		TRUE	True F1
1_3	9	100.00	0	0.00	22.22	100.00	77.78	77.78	0		TRUE	True F1
1_4	9	100.00	0	0.00	22.22	100.00	77.78	77.78	0		TRUE	True F1
1_5	9	100.00	0	0.00	22.22	100.00	77.78	77.78	0		TRUE	True F1
1_6	9	100.00	0	0.00	22.22	100.00	77.78	77.78	0		TRUE	True F1
1_7	9	100.00	0	0.00	22.22	100.00	77.78	77.78	0		TRUE	True F1
1_8	5	55.56	0	0.00	22.22	100.00	77.78	77.78	0		TRUE	True F1
1_9	9	100.00	0	0.00	22.22	100.00	77.78	77.78	0		TRUE	True F1
1_10	9	100.00	0	0.00	22.22	100.00	77.78	77.78	0		TRUE	True F1

Column	Definition
Data Count	# of markers scored
% Data	% of all markers scored
Het Count	# markers that were heterozygous
% Het	% markers that were heterozygous
% Het deviation from Expected	The difference in % hets between the expected F1 and the sampled F1
% Allele match to P1	% of markers where the allele matches an allele in P1
% Allele match to P2	% of markers where the allele matches an allele in P2
% Genotype Match to Expected F1	
Rank	
Comments	
Selected	
Decision	

# Pedigree Verification – Lines

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Tutorial and Demo



# PedVer Lines Input Files

## Genotype file: line\_ver\_genotype.txt (Required)

	A	B	C	D	E	F	G	H	I	J	K
1	# fjFile = GENOTYPE										
2		m1	m2	m3	m4	m5	m6	m7	m8	m9	m10
3	P1	A	G	T	+	C	C	T	G	+	-
4	P2	C	A	G	-	C		C	T	-	+
5	P3	A	G	G		T	T	C	G	-	+
6	s1	C	G	T	+	C	C	T	G	+/-	-
7	s2		G	T	-	C	C	T	G	-	-/+
8	s3	C	A	G	+	C	C	T/C	G	+	-
9	s4	C	G/A	T/G		C		T	G/T	-	-
10	s5	A	A	G	+	C		C	T	+	+
11	s6	C	G	T	+/-	C			G	-	+
12	s7	A	G	G	+		C/T	C	G	+	+
13	s8	C	A	G		C		C	G/T		+
14	s9	A	A	G		C	C	T	T	+/-	-
15	s10	A	G/A	G	-	C/C		T	T	-	-/+
16	s11	A/C	G	G	+	C		C	T	+	+
17	s12	A	A	T	-	C	C	T/C	G/T	+	-
18	s13	C	A	G	-	C/C	C	T	T	+	-
19	s14	A	G/A	T/G	+	C		C	G	+	-
20	s15	C	G/A	G	+	C	C	C	G/T	+	+
21	s16	C	A	G	+	C/C		T/C	G	+	-
22	s17	A	G	G	-	C	C	C	T	+	-
23	s18	A		T	-	C		T	T	+/-	-
24	s19	C	A	T	+/-	C	C	T	G	-	-/+
25	s20	C	G	T	+	C/C	C/T	C	G/T	+/-	-/+

## Map file: line\_ver.map (Not required)

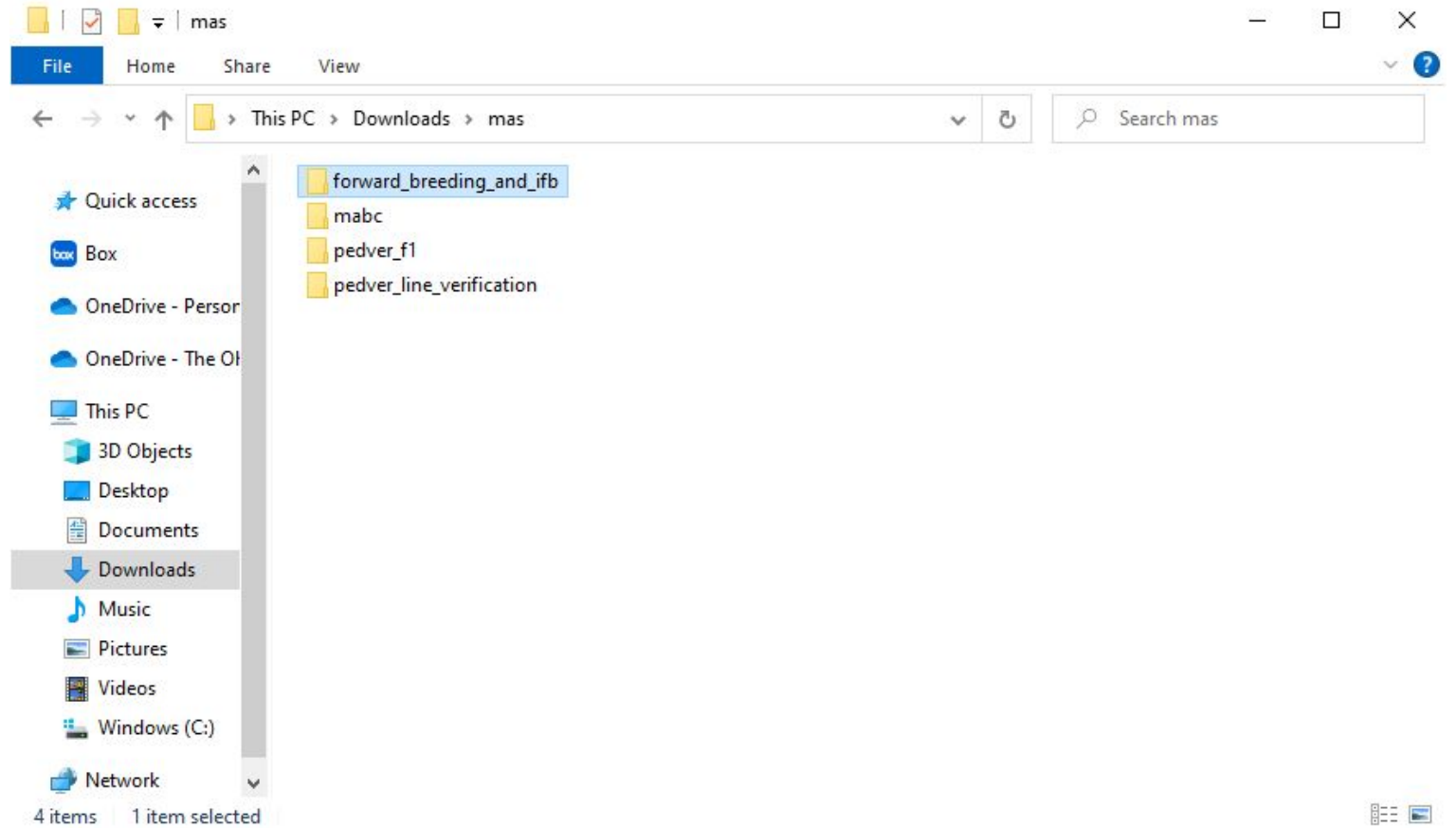
	A	B	C
1	# fjFile = MAP		
2	m1	1	11
3	m2	1	14
4	m3	1	31
5	m4	1	34
6	m5	1	49
7	m6	1	67
8	m7	1	72
9	m8	2	5
10	m9	2	19
11	m10	2	30
12	m11	2	43
13	m12	2	58
14	m13	2	70
15	m14	3	12
16	m15	3	14
17	m16	3	27
18	m17	3	46
19	m18	4	8
20	m19	4	21
21	m20	4	26

Line	Data Count	% Data	Het Count	% Het	% Allele match to P1	% Allele match to P2	% Allele derived P1	% Allele derived P2	% Allele match to P1 / P2	Rank	Comments	Selected	Decision
Parent_A	9	100.00	0	0.00	100.00	77.78	100.00	77.78	100	0		FALSE	Parent 1
Parent_B	9	100.00	0	0.00	77.78	100.00	77.78	100.00	100	0		FALSE	Parent 2
1_1	9	100.00	0	0.00	100.00	77.78	100.00	77.78	100	0		TRUE	Pedigree verified
1_2	9	100.00	2	22.22	88.89	88.89	88.89	88.89	100	0		TRUE	Pedigree verified
1_3	9	100.00	0	0.00	100.00	77.78	100.00	77.78	100	0		TRUE	Pedigree verified
1_4	9	100.00	0	0.00	100.00	77.78	100.00	77.78	100	0		TRUE	Pedigree verified
1_5	9	100.00	0	0.00	100.00	77.78	100.00	77.78	100	0		TRUE	Pedigree verified
1_6	9	100.00	0	0.00	100.00	77.78	100.00	77.78	100	0		TRUE	Pedigree verified
1_7	9	100.00	0	0.00	100.00	77.78	100.00	77.78	100	0		TRUE	Pedigree verified
1_8	5	55.56	2	40.00	88.89	88.89	88.89	88.89	100	0		TRUE	Pedigree verified
1_9	9	100.00	0	0.00	100.00	77.78	100.00	77.78	100	0		TRUE	Pedigree verified
1_10	9	100.00	0	0.00	100.00	77.78	100.00	77.78	100	0		TRUE	Pedigree verified
					<b>Column</b>	<b>Definition</b>							
					<b>Data Count</b>	<b># Markers scored</b>							
					<b>% Data</b>	<b>% of markers scores</b>							
					<b>Het Count</b>	<b># Heterozygous loci</b>							
					<b>% Het</b>	<b>% of Heterozygous loci</b>							
					<b>% Allele match to P1</b>	<b>% of alleles that match alleles in P1</b>							
					<b>% Allele match to P2</b>	<b>% of alleles that match alleles in P2</b>							
					<b>% Allele derived P1</b>	<b>% of alleles that could be derived from P1</b>							
					<b>% Allele derived P2</b>	<b>% of alleles that could be derived from P2</b>							
					<b>% Allele match to P1 / P2</b>	<b>% of alleles that match alleles in P1 or P2</b>							
					<b>Rank</b>								
					<b>Comments</b>								
					<b>Selected</b>								
					<b>Decision</b>								

# Forward Breeding

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Tutorial and Demo





# Forward Breeding Input Files

**Genotype file: Module\_7.1\_genotype.txt (Required)**

	A	B	C	D	E	F	G
1	# fjFile = GENOTYPE						
2		m1	m2	m3	m4	m5	m8
3	s01	A/C	G	+/-		C/G	A
4	s02	A/C	T/G	+	T	C/G	A
5	s03	A	T/G			C/G	
6	s04	A/C	G	+		C	A
7	s05	C	T				A
8	s06	A	G	-		C	A
9	s07		G	+/-	C/T	C/G	A
10	s08		T/G			C/G	
11	s09			+	T		A
12	s10	A/C	G	+/-	C/T	C/G	A
13	s11	C	G	+/-		C	C/A
14	s12		T/G	+		C	A

**GOBii QTL file: gobii-qt1.txt (Required)** – see next slide

Map file: line\_ver.map (Not required)

# GOBii QTL File Format: Used for Forward Breeding and Index Forward Breeding

Indexed Forward Breeding

# ffile= QTL-GOBii											
marker_group_name	marker_name	germplasm_group	platform	fav_allele	unfav_allele	fav_allele_trait_name	unfav_allele_trait_name	breeding_value	model	substitution_effect	relative_weight
QGpc.cd1-1B.1	m1	QG	KASP	C		Q	q	YES	Dominant	2.1	0.4
Sb3	m2	SB	KASP	G		+	-	NO	Additive	1.4	0.2
Sb3	m3	SB	KASP	-		s	S	YES	Recessive	2.4	0.3
Sb3	m4	SB	KASP	T		+	-	NO	Additive	1.4	0.2
Lr68	m5	Leaf Rust	KASP	G		+	-	YES	Additive	2.8	0.2
Hgt-maf-90	m8	Height	KASP	A		+	-	YES	Additive	5	0.2
Hgt-maf-90	m9	Height	KASP	G		+	-	NO	Additive	1	0.2
Hgt-maf-5	m10	Height	KASP	T		+	-	YES	Additive	8	0.8

Forward Breeding

- Second row of column headers is required
- Column names can be different
- But order of columns must be the same

Line	Data Count	% Data	Het Count	% Het	QGpc.cd1-1B.1 - Partial Match	Sb3 - Partial Match	Lr68 - Partial Match	Hgt-maf-90 - Partial Match	Hgt-maf-5 - Partial Match	QGpc.cd1-1B.1 - Complete Match	Sb3 - Complete Match	Lr68 - Complete Match	Hgt-maf-90 - Complete Match	Hgt-maf-5 - Complete Match	Average Weighted Haplotype Match	Selected	Rank	Comments									
s01	8	40	3	37.5	0.50	0.50	0.50	1.00	0.00	0.60	0.00	0.60	1.00	0.00	0.44												
s02	8	40	3	37.5	0.50	0.50	0.50	1.00	0.00	0.60	0.00	0.60	1.00	0.00	0.44												
s03	8	40	2	25	0.00	0.17	0.50	0.50	0.00	0.00	0.00	0.60	0.00	0.00	0.12												
s04	8	40	1	12.5	0.50	0.33	0.00	1.00	0.00	0.60	0.00	0.00	1.00	0.00	0.32												
s05	8	40	0	0	1.00	0.00	0.00	1.00	0.00	1.00	0.00	0.00	1.00	0.00	0.40												
s06	7	35	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20												
s07	8	40	3	37.5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44												
s08	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12												
s09	8	40	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20												
s10	8	40	4	50	0.50	0.50	0.50	1.00	0.00	0.60	0.00	0.60	1.00	0.00	0.56												
s14	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.6	0.44	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s15	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.24	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s16	7	35	2	28.6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.6	0.44	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s17	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.12	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s18	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.44	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s19	7	35	2	28.6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s20	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.32	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s21	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.44	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s22	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.32	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s23	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.24	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s24	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.32	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s25	7	35	2	28.6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.32	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s26	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s27	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.52	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s28	7	35	2	28.6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.24	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s29	8	40	2	25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.6	0.64	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
s30	7	35	2	28.6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.6	0.56	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>								
					Column						Definition																
					Data Count						# markers scored																
					% Data						% markers scored																
					Het Count						# heterozygous markers																
					% Het						% heterozygous markers																
					QGpc.cd1-1B.1 - Partial Match						Partial Match score for each QTL (NOT each marker)						0.6	0.44	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>						
					Sb3 - Partial Match												0	0.24	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>						
					Lr68 - Partial Match												0.6	0.44	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>						
					Hgt-maf-90 - Partial Match												0	0.12	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>						
					Hgt-maf-5 - Partial Match												0	0.44	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>						
					QGpc.cd1-1B.1 - Complete Match												0	0.32	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>						
					Sb3 - Complete Match						Complete Match score for each QTL (NOT each marker)						0	0.32	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>						
					Lr68 - Complete Match												0	0.32	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>						
					Hgt-maf-90 - Complete Match												0	0	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>						
					Hgt-maf-5 - Complete Match												0	0.52	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>						
					Average Weighted Haplotype Match												Average of the complete match scores						0.6	0.56	<input checked="" type="checkbox"/>	0	<input type="checkbox"/>
					Selected																						
					Rank																						
					Comments																						