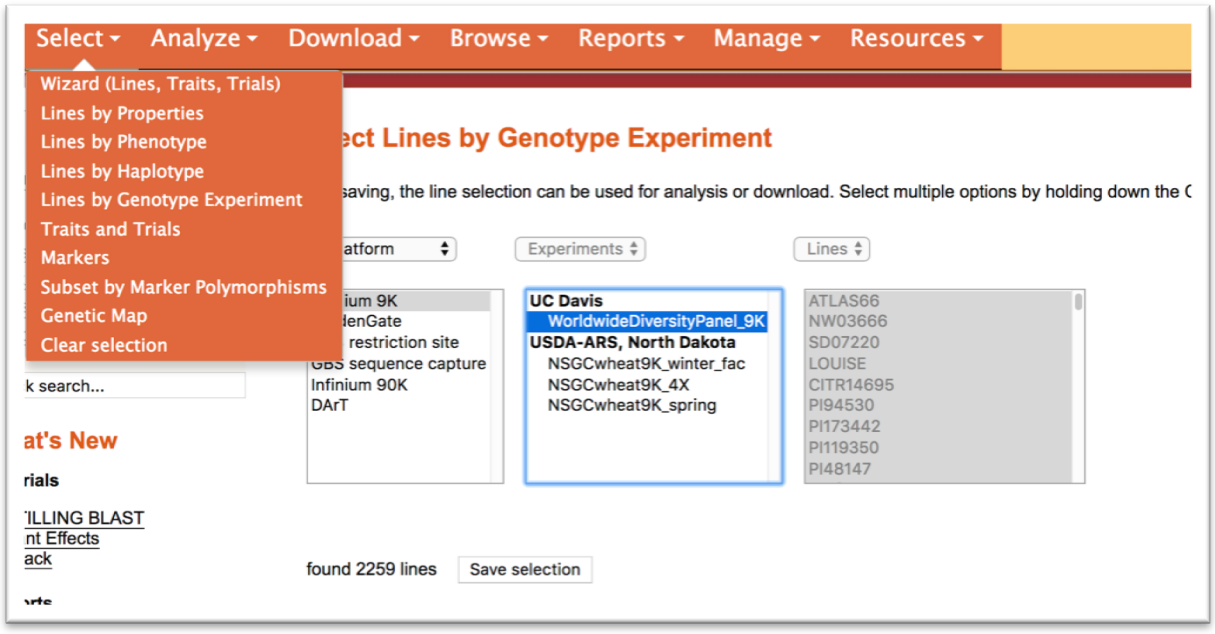
Flapjack is a visualization and analysis program for genotype data. The software is provided by The James Hutton Institute (JHI) and runs on Windows, Linux and MacOS. The program is available from [Flapjack Download]. Data from T3 website can be accessed by

1. Saving from T3 then importing into Flapjack or
2. Using BrAPI to import directly into Flapjack

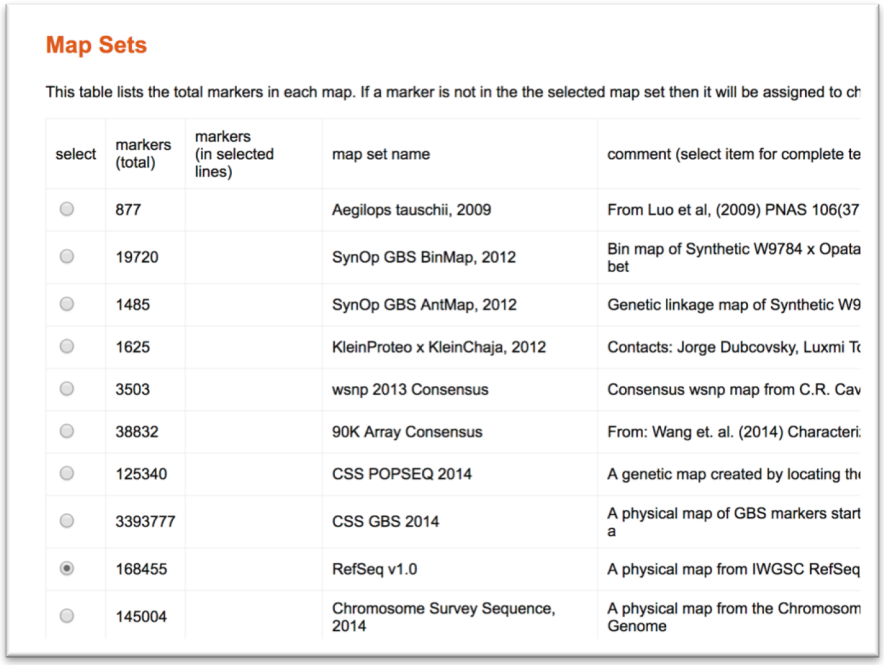
Requirements: Flapjack allows importing genotype, map, and phenotype files.

Download data from T3 website then import the data into Flapjack

1. The data can be selected by Select => Wizard or Select => Lines by Genotype Experiment



2. Go to Select => Genetic Map

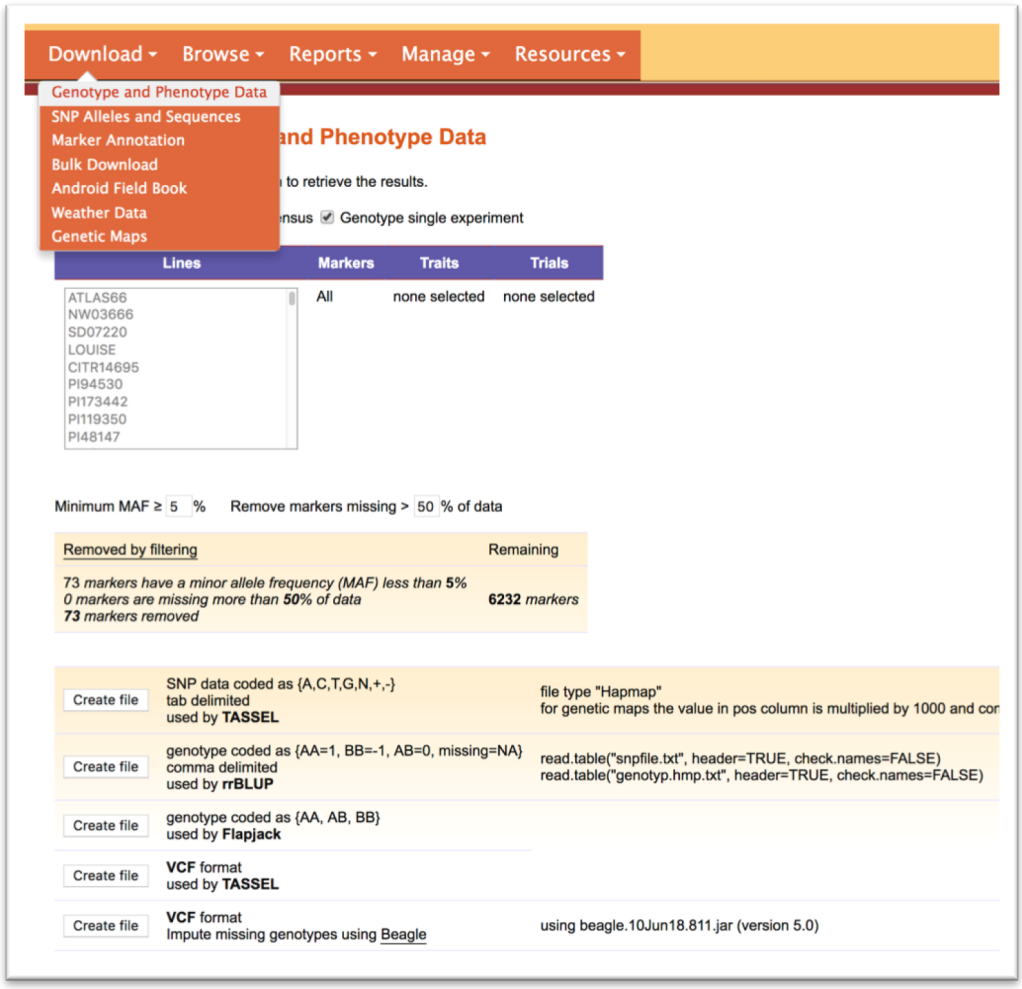


Map Sets

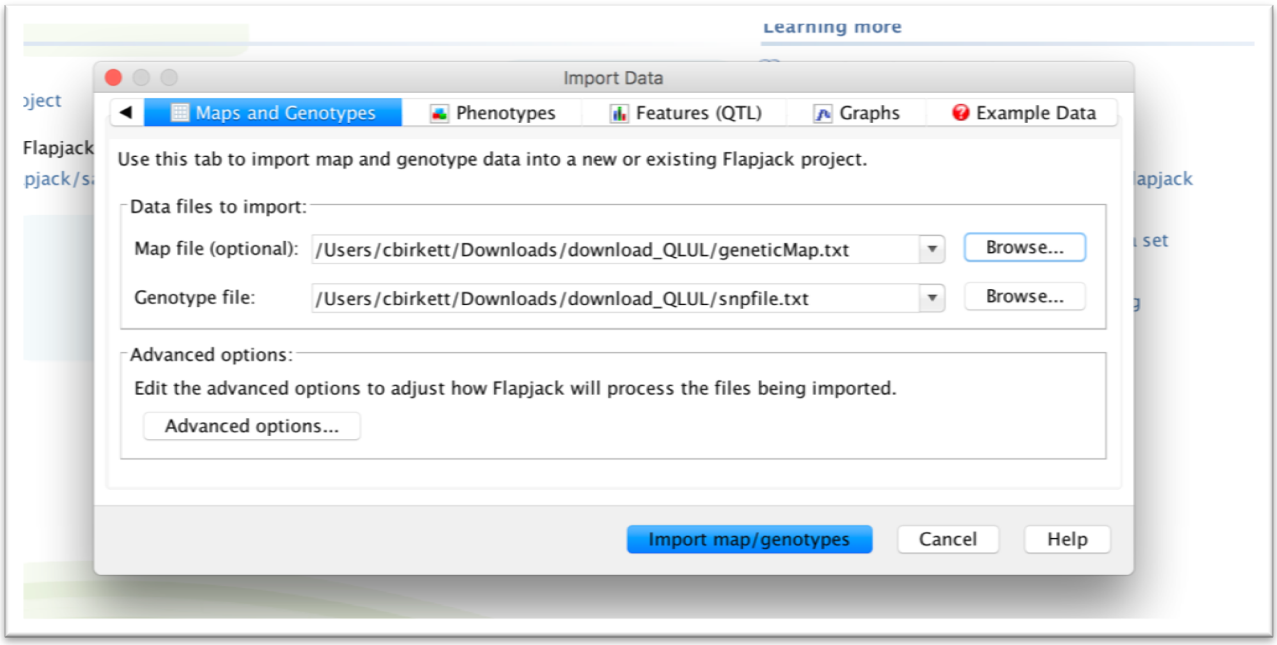
This table lists the total markers in each map. If a marker is not in the the selected map set then it will be assigned to ch

select	markers (total)	markers (in selected lines)	map set name	comment (select item for complete te
○	877		Aegilops tauschii, 2009	From Luo et al, (2009) PNAS 106(37
○	19720		SynOp GBS BinMap, 2012	Bin map of Synthetic W9784 x Opata bet
○	1485		SynOp GBS AntMap, 2012	Genetic linkage map of Synthetic W9
○	1625		KleinProteo x KleinChaja, 2012	Contacts: Jorge Dubcovsky, Luxmi Tc
○	3503		wsnp 2013 Consensus	Consensus wsnp map from C.R. Cav
○	38832		90K Array Consensus	From: Wang et. al. (2014) Characteri
○	125340		CSS POPSEQ 2014	A genetic map created by locating th
○	3393777		CSS GBS 2014	A physical map of GBS markers start a
◉	168455		RefSeq v1.0	A physical map from IWGSC RefSeq
○	145004		Chromosome Survey Sequence, 2014	A physical map from the Chromosom Genome

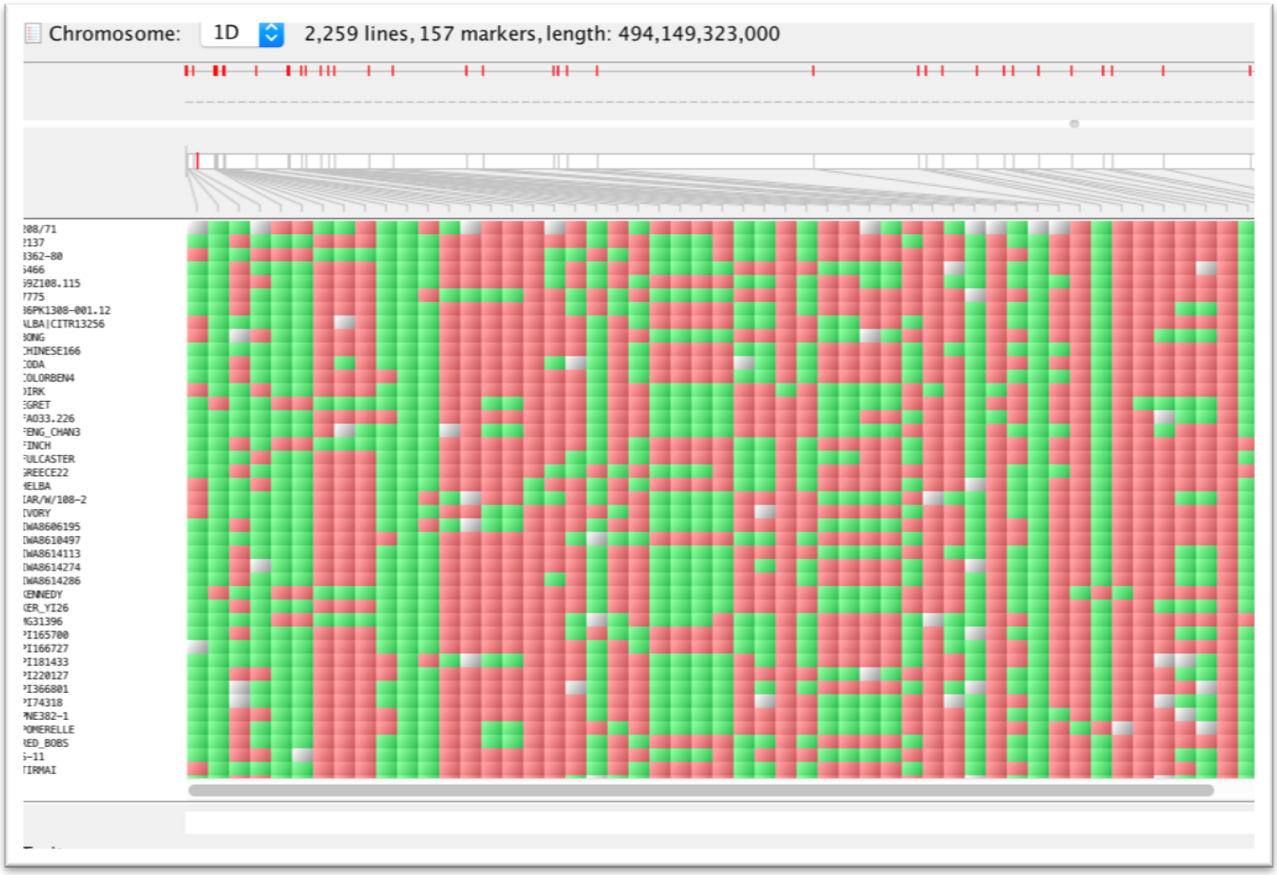
3. Go to Download => Genotype and Phenotype Data - Select Flapjack format
4. Select “Create File”


Download
Browse
Reports
Manage
Resources
Genotype and Phenotype Data
SNP Alleles and Sequences
Marker Annotation
Bulk Download
Android Field Book
Weather Data
Genetic Maps
and Phenotype Data
to retrieve the results.
nsus
Genotype single experiment
Lines
Markers
Traits
Trials
ATLAS66
NW03666
SD07220
LOUISE
CITR14695
PI94530
PI173442
PI119350
PI48147
All
none selected
none selected
Minimum MAF ≥ 5 %
Remove markers missing > 50 % of data
Removed by filtering
Remaining
73 markers have a minor allele frequency (MAF) less than 5%
0 markers are missing more than 50% of data
73 markers removed
6232 markers
Create file
SNP data coded as {A,C,T,G,N,+,-}
tab delimited
used by TASSEL
file type "Hapmap"
for genetic maps the value in pos column is multiplied by 1000 and cor
Create file
genotype coded as {AA=1, BB=-1, AB=0, missing=NA}
comma delimited
used by rrBLUP
read.table("snpfile.txt", header=TRUE, check.names=FALSE)
read.table("genotyp.hmp.txt", header=TRUE, check.names=FALSE)
Create file
genotype coded as {AA, AB, BB}
used by Flapjack
Create file
VCF format
used by TASSEL
Create file
VCF format
Impute missing genotypes using Beagle
using beagle.10Jun18.811.jar (version 5.0)

5. In Flapjack Program select “Import Data”

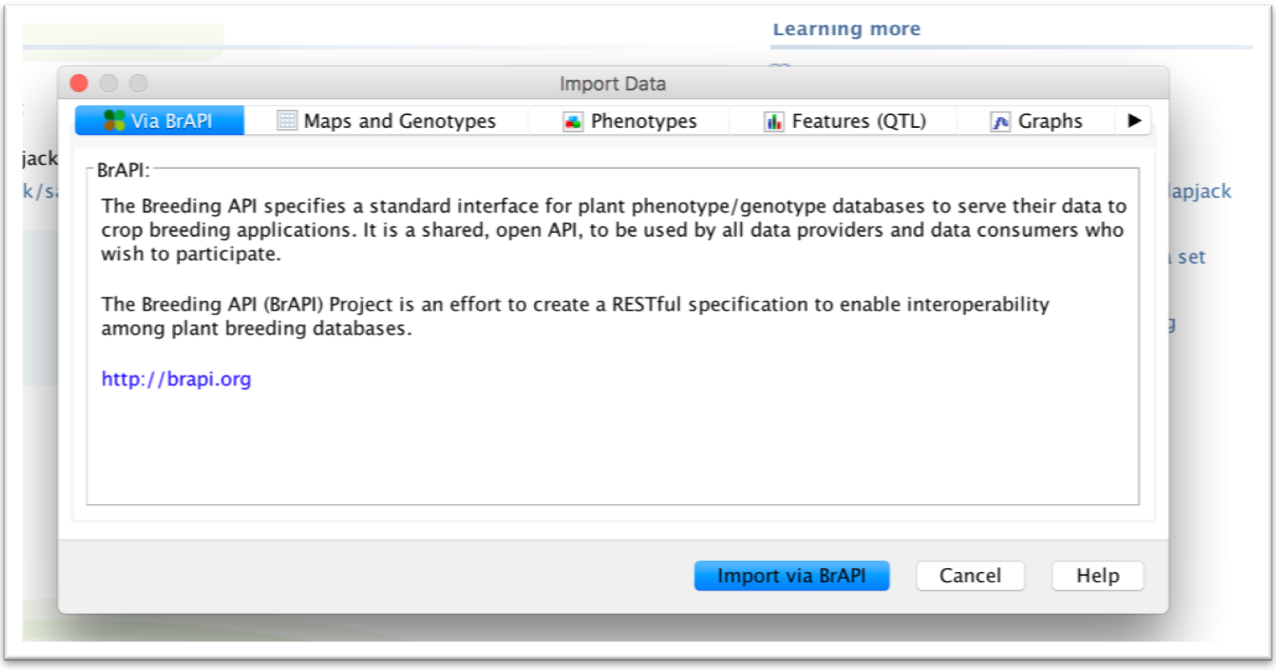


6. On the “Map file” line select “GeneticMap.txt” file.
7. On the “Genotype file” line select “Browse” then select the “snpfile.txt” file.

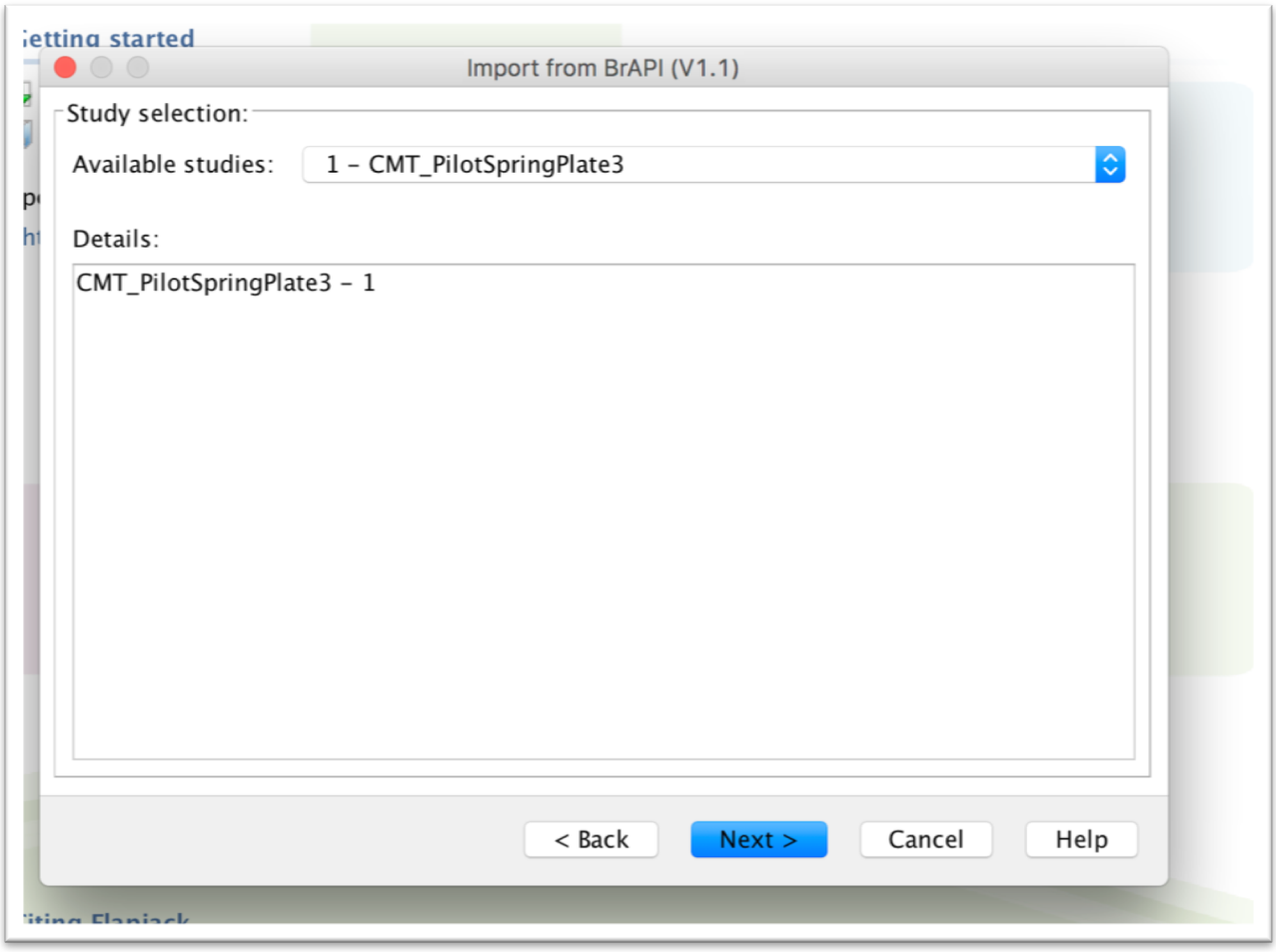


Use BrAPI to directly import data from T3 into Flapjack

1. In Flapjack Program select “Import Data” then select left arrow so Via BrAPI is visible.
2. Select “Import via BrAPI”



3. In the Category select “Triticeae Toolbox, The” then “Next” then “Next” again.
4. Select from the list of studies then “Next”



5. Select from the list of Maps then “Next”
6. The Importing data step may take several minutes for large studies or maps.