

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

The screenshot shows the T3 website interface. At the top, there is a navigation bar with links: Select, Analyze, Download, Browse, Reports, Manage, and Resources. A dropdown menu titled "Wizard (Lines, Traits, Trials)" is open, showing options like Lines by Properties, Lines by Phenotype, Lines by Haplotype, Lines by Genotype Experiment, Traits and Trials, Markers, Subset by Marker Polymorphisms, Genetic Map, and Clear selection. Below this, there is a search bar with placeholder text "Search...". On the right, there is a sidebar with sections for "What's New" and "T3 News". The main content area is titled "Select Lines by Genotype Experiment" and contains a message: "When saving, the line selection can be used for analysis or download. Select multiple options by holding down the C key while selecting." It has three dropdown menus: Platform (Infinium 9K, DenGate, restriction site, GBS sequence capture), Experiments (USDA-ARS, North Dakota, UC Davis, Worldwide Diversity Panel 9K), and Lines (ATLAS66, NW03666, SD07220, LOUISE, CITR14695, PI94530, PI173442, PI119350, PI48147). A button "found 2259 lines" is visible, along with a "Save selection" button.

## 2. Go to Select => Genetic Map

### Map Sets

This table lists the total markers in each map. If a marker is not in 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
<input type="radio"/>	877		Aegilops tauschii, 2009	From Luo et al, (2009) PNAS 106(37
<input type="radio"/>	19720		SynOp GBS BinMap, 2012	Bin map of Synthetic W9784 x Opata bet
<input type="radio"/>	1485		SynOp GBS AntMap, 2012	Genetic linkage map of Synthetic W9
<input type="radio"/>	1625		KleinProteo x KleinChaja, 2012	Contacts: Jorge Dubcovsky, Luxmi T
<input type="radio"/>	3503		wsnp 2013 Consensus	Consensus wsnp map from C.R. Cav
<input type="radio"/>	38832		90K Array Consensus	From: Wang et. al. (2014) Characteri
<input type="radio"/>	125340		CSS POPSEQ 2014	A genetic map created by locating th
<input type="radio"/>	3393777		CSS GBS 2014	A physical map of GBS markers start
<input checked="" type="radio"/>	168455		RefSeq v1.0	A physical map from IWGSC RefSeq
<input type="radio"/>	145004		Chromosome Survey Sequence, 2014	A physical map from the Chromosome 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**

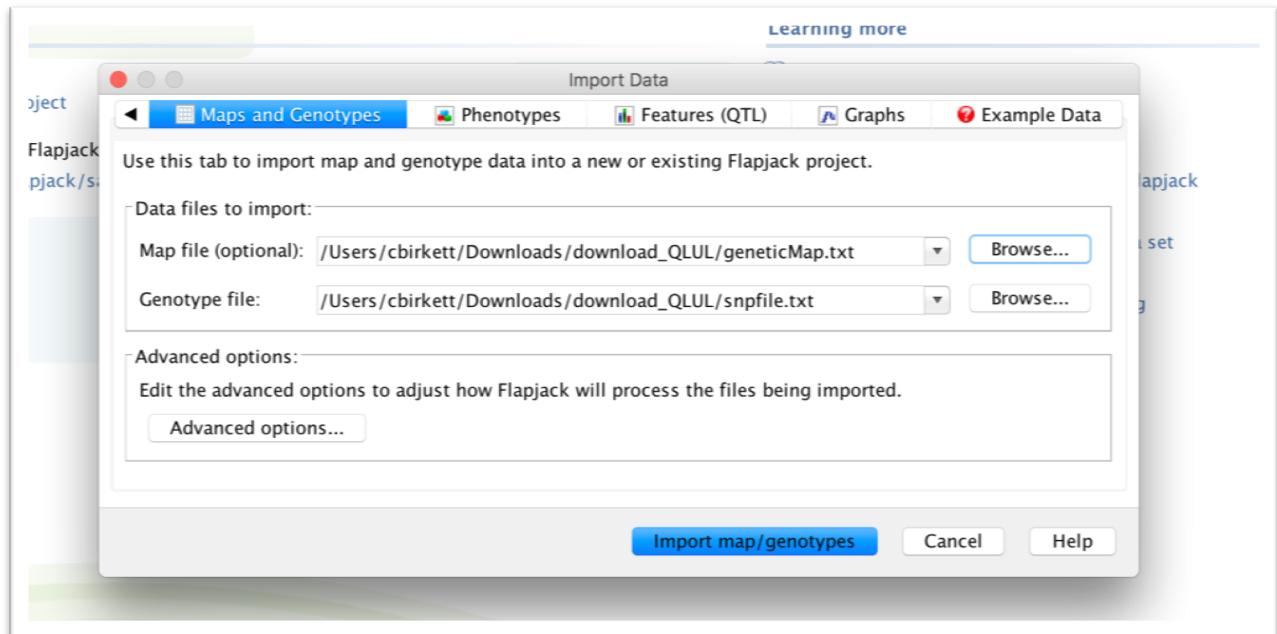
Lines	Markers	Traits	Trials
All	none selected	none selected	
ATLAS66 NW03666 SD07220 LOUISE CITR14695 PI94530 PI173442 PI119350 PI48147			

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 <b>TASSEL</b>	file type "Hapmap" for genetic maps the value in pos column is multiplied by 1000 and converted to integer
Create file	genotype coded as {AA=1, BB=-1, AB=0, missing=NA} comma delimited used by <b>rrBLUP</b>	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 <b>Flapjack</b>	
Create file	<b>VCF</b> format used by <b>TASSEL</b>	
Create file	<b>VCF</b> format Impute missing genotypes using <u><a href="#">Beagle</a></u>	using beagle.10Jun18.811.jar (version 5.0)

5. In Flapjack Program select “Import Data”



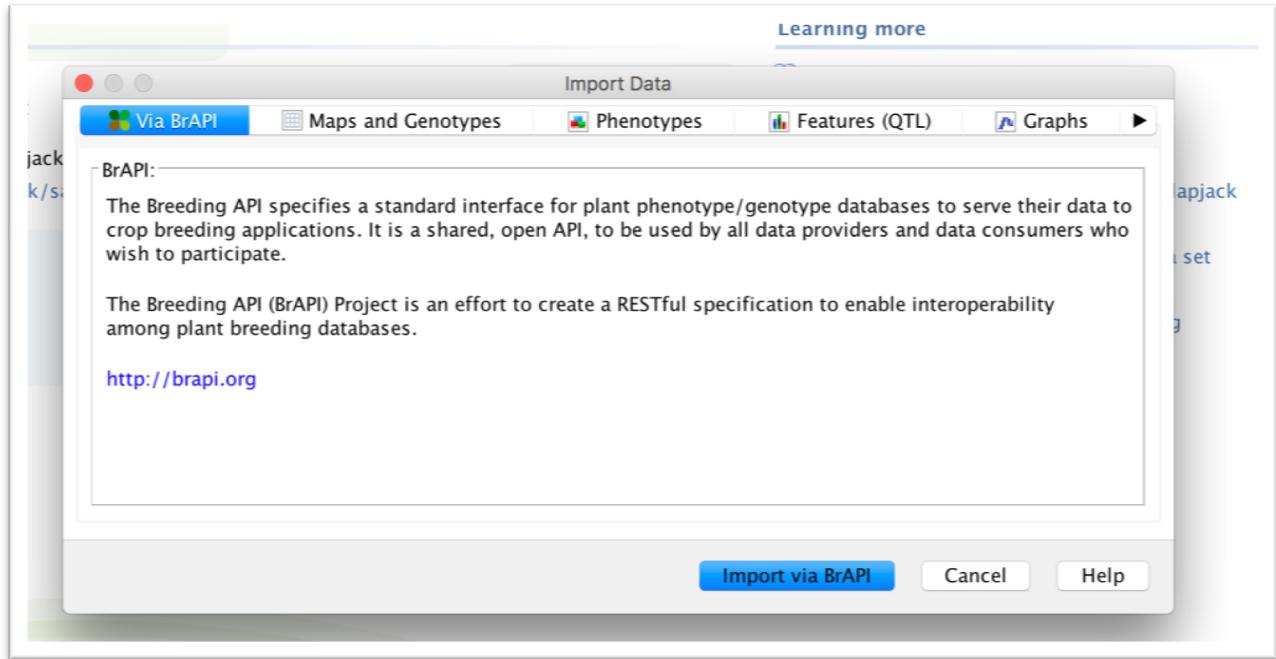
6. On the “Map file” line select “GeneticMap.txt” file.

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

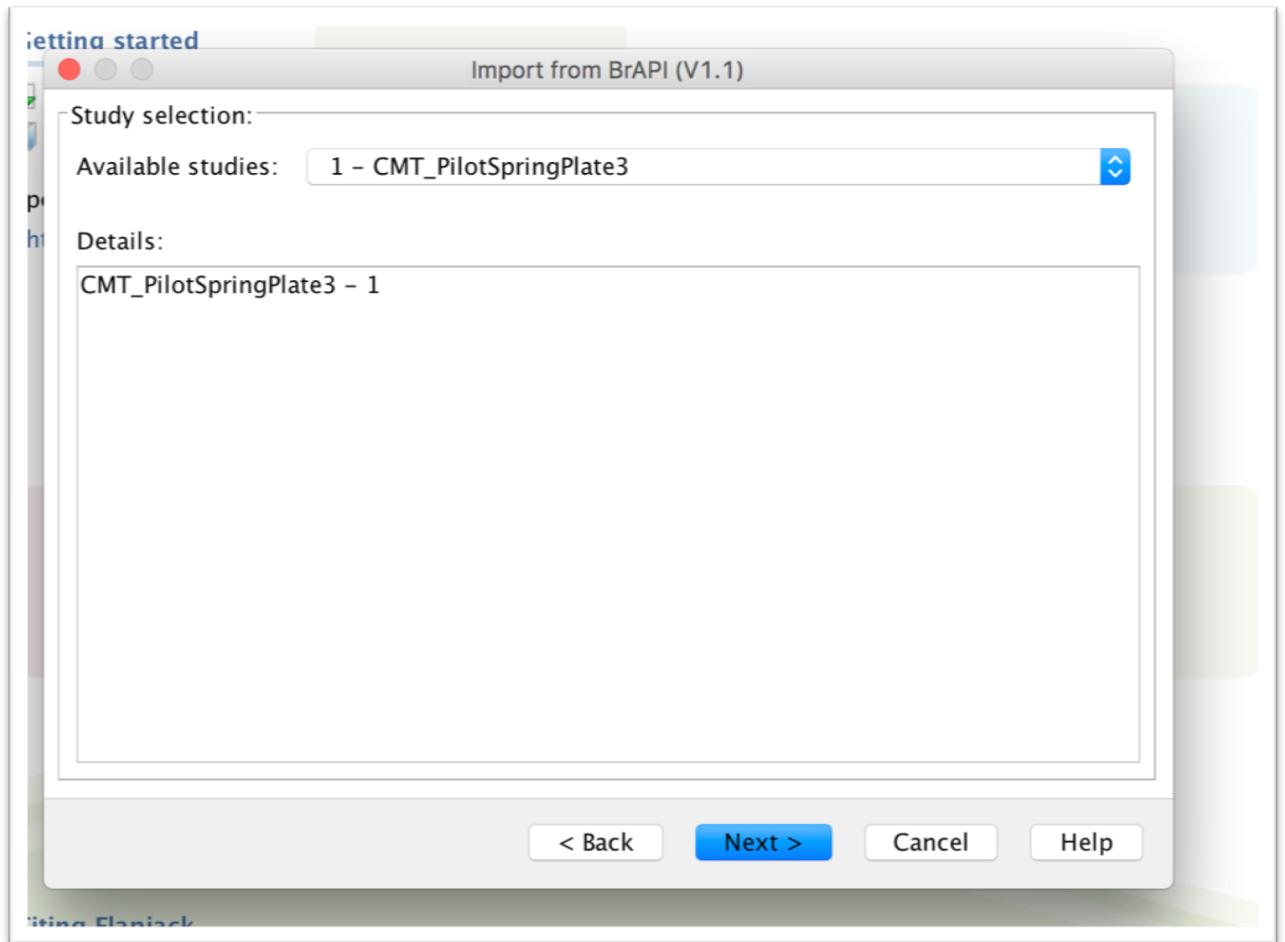


## Use BrAPI to directly import data from T3 into Flapjack

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.