

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

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's navigation bar with 'Select', 'Analyze', 'Download', 'Browse', 'Reports', 'Manage', and 'Resources' options. The 'Select' dropdown is expanded, showing various selection methods: 'Wizard (Lines, Traits, Trials)', 'Lines by Properties', 'Lines by Phenotype', 'Lines by Haplotype', 'Lines by Genotype Experiment' (which is highlighted with a red box), 'Traits and Trials', 'Markers', 'Subset by Marker Polymorphisms', 'Genetic Map', and 'Clear selection'. Below this is a search bar. To the right, there's a section titled 'Select Lines by Genotype Experiment' with a note about using the selection for analysis or download. It shows a list of platforms: 'Illumina 9K', 'IgenGate', 'restriction site', 'GBS sequence capture', 'Infinium 90K', and 'DArT'. A specific experiment, 'UC Davis WorldwideDiversityPanel_9K', is selected and highlighted with a blue border. On the far right, a list of accessions is shown: ATLAS66, NW03666, SD07220, LOUISE, CITR14695, PI94530, PI173442, PI119350, and PI48147. At the bottom, it says 'found 2259 lines' and has a 'Save selection' button.

2. Go to Select => Genetic Map

The screenshot shows a table titled 'Map Sets' with the following data:

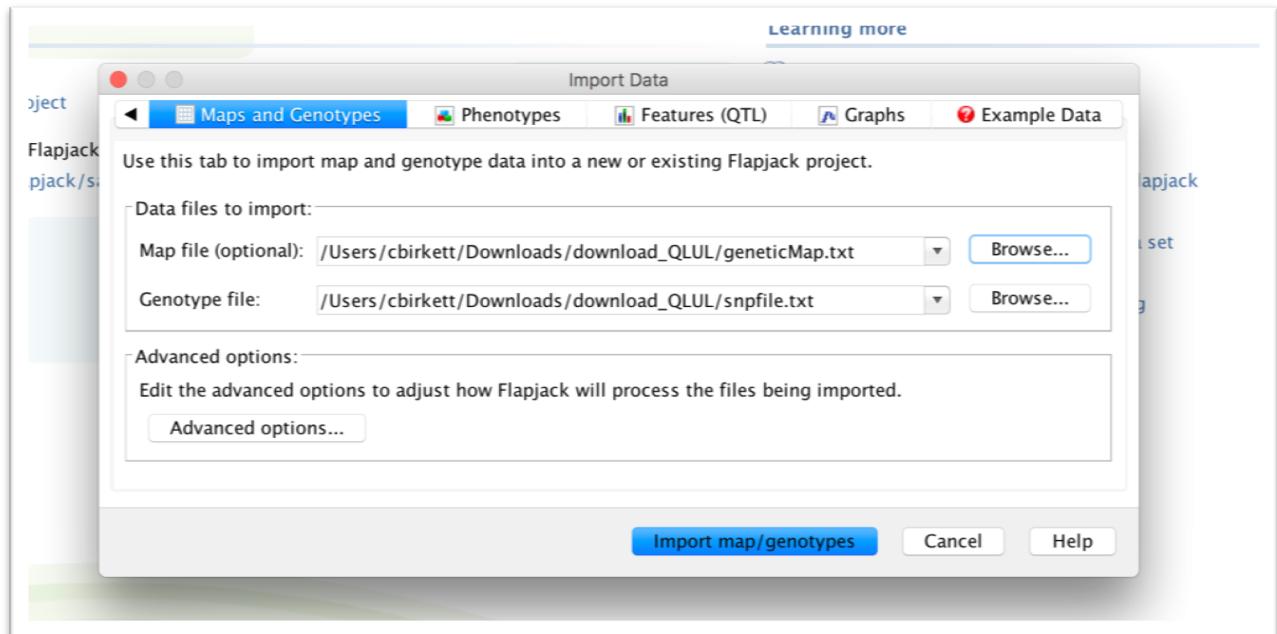
select	markers (total)	markers (in selected lines)	map set name	comment (select item for complete table)
<input checked="" type="radio"/>	877		Aegilops tauschii, 2009	From Luo et al, (2009) PNAS 106(37)
<input checked="" type="radio"/>	19720		SynOp GBS BinMap, 2012	Bin map of Synthetic W9784 x Opata bet
<input checked="" type="radio"/>	1485		SynOp GBS AntMap, 2012	Genetic linkage map of Synthetic W9
<input checked="" type="radio"/>	1625		KleinProteo x KleinChaja, 2012	Contacts: Jorge Dubcovsky, Luxmi Tr
<input checked="" type="radio"/>	3503		wsnp 2013 Consensus	Consensus wsnp map from C.R. Cav
<input checked="" type="radio"/>	38832		90K Array Consensus	From: Wang et. al. (2014) Characteri
<input checked="" type="radio"/>	125340		CSS POPSEQ 2014	A genetic map created by locating th
<input checked="" type="radio"/>	3393777		CSS GBS 2014	A physical map of GBS markers start a
<input checked="" type="radio"/>	168455		RefSeq v1.0	A physical map from IWGSC RefSeq
<input checked="" 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"

The screenshot shows a software interface for managing genotype and phenotype data. At the top, there's a navigation bar with links: Download, Browse, Reports, Manage, and Resources. Below this, a sidebar titled 'Genotype and Phenotype Data' lists several options: SNP Alleles and Sequences, Marker Annotation, Bulk Download, Android Field Book, Weather Data, and Genetic Maps. The main area displays a table with columns for Lines, Markers, Traits, and Trials. Under 'Lines', a list of entries like ATLAS66, NW03666, SD07220, LOUISE, CITR14695, PI94530, PI173442, PI119350, and PI48147 is shown. Under 'Markers', it says 'All' and 'none selected'. Under 'Traits', it says 'none selected'. Under 'Trials', it says 'none selected'. Below the table, there are filtering options: 'Minimum MAF ≥ 5 %' and 'Remove markers missing > 50 % of data'. A summary section shows 'Removed by filtering' (73 markers removed) and 'Remaining' (6232 markers). At the bottom, there are six 'Create file' buttons, each associated with a specific file format and tool:

- 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 converted to integer
- 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”



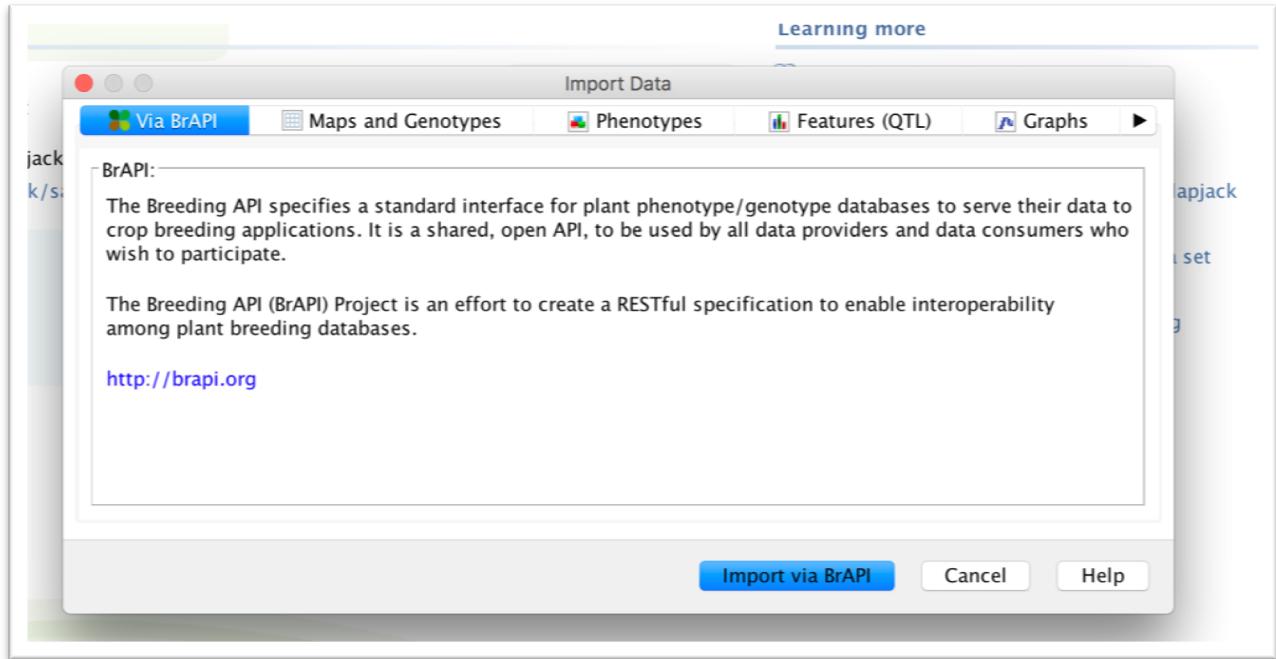
6. On the “Map file” line select “GeneticMap.txt” file.

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

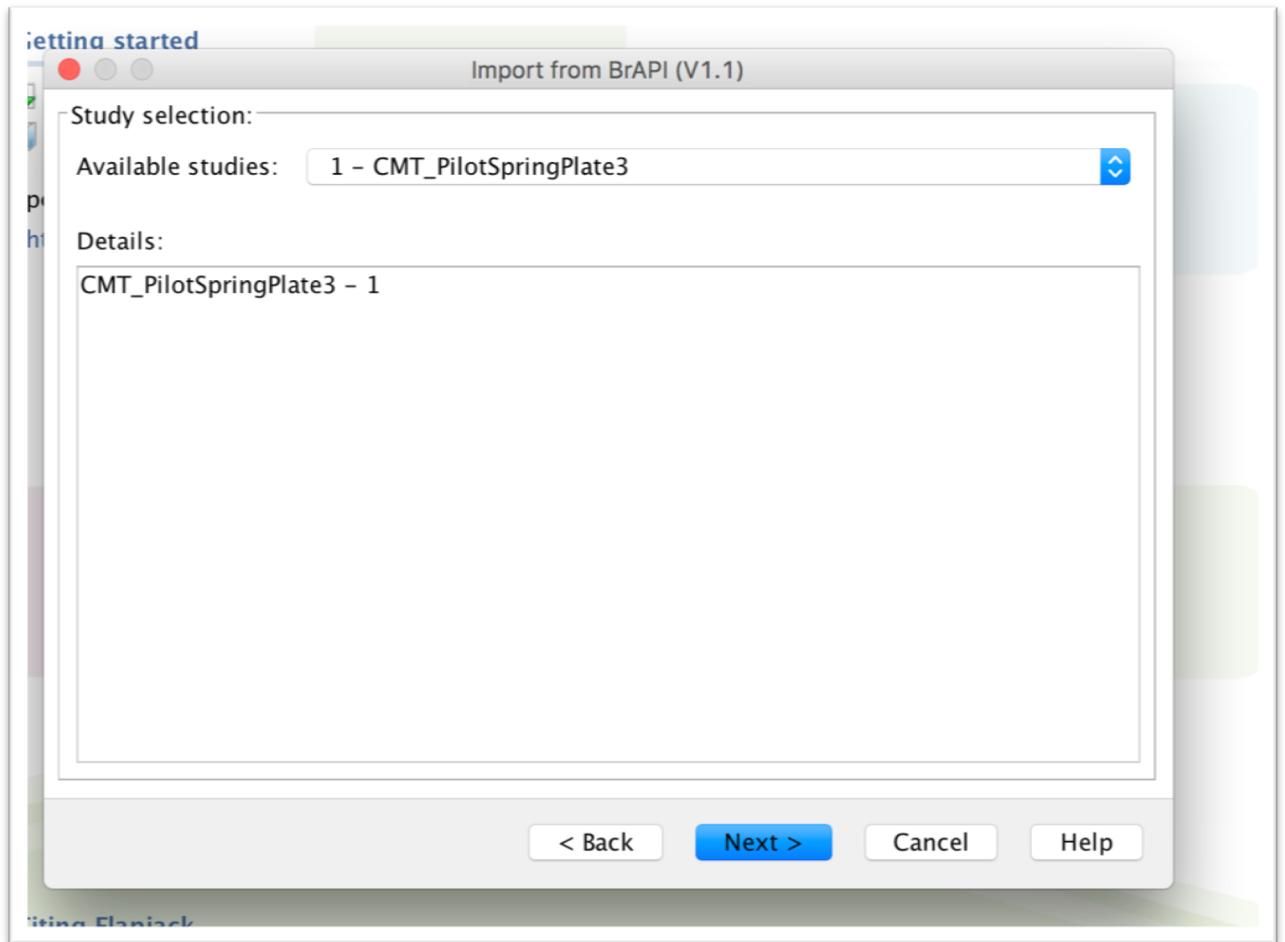


Use BrAPI to directly import data from T3 into Flapjack

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.