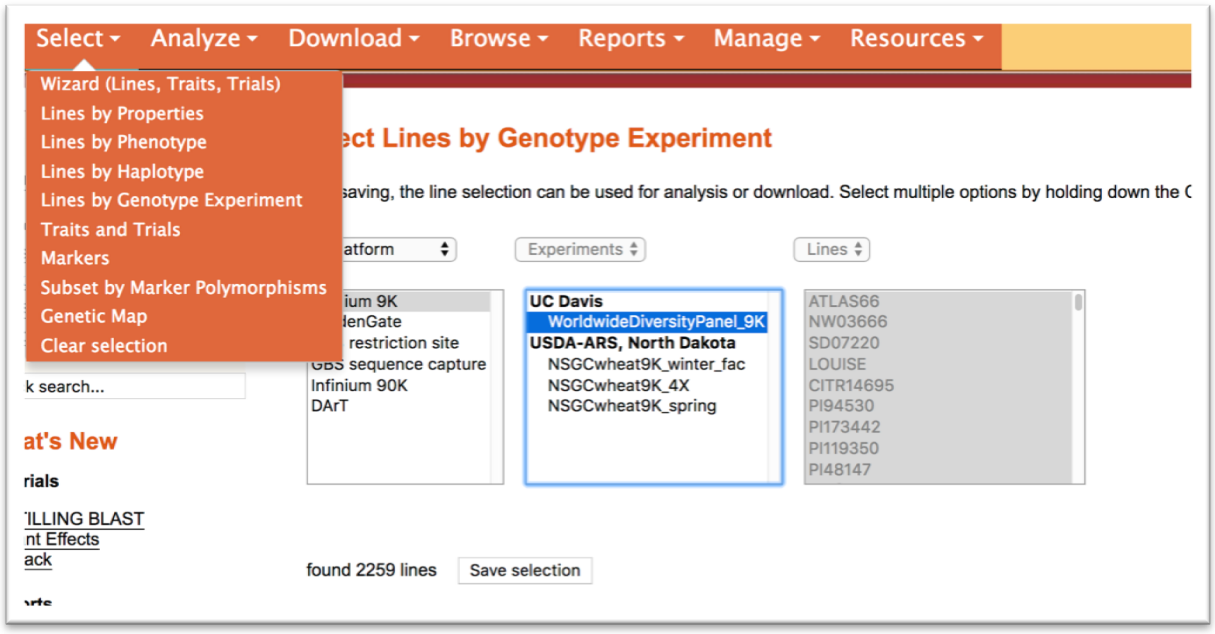
R Script is a programming language widely used among statisticians, data miners, and data analysis. The software is available from CRAN Download R and Microsoft R Open. Data from T3 can be accessed by

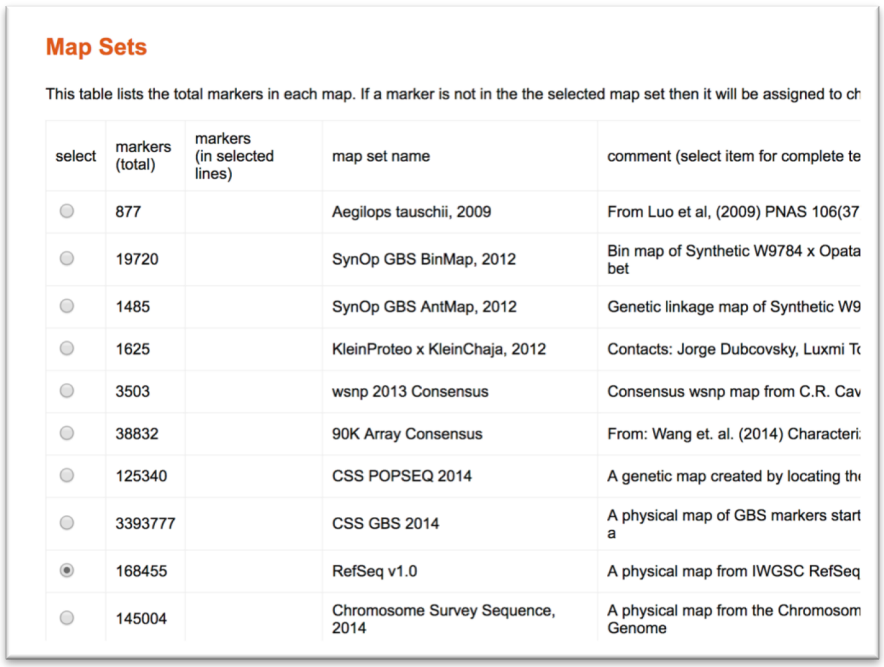
1. Saving from T3 then reading into R
2. Using BrAPI R package to read directly into R

Download data from T3 website then read into R

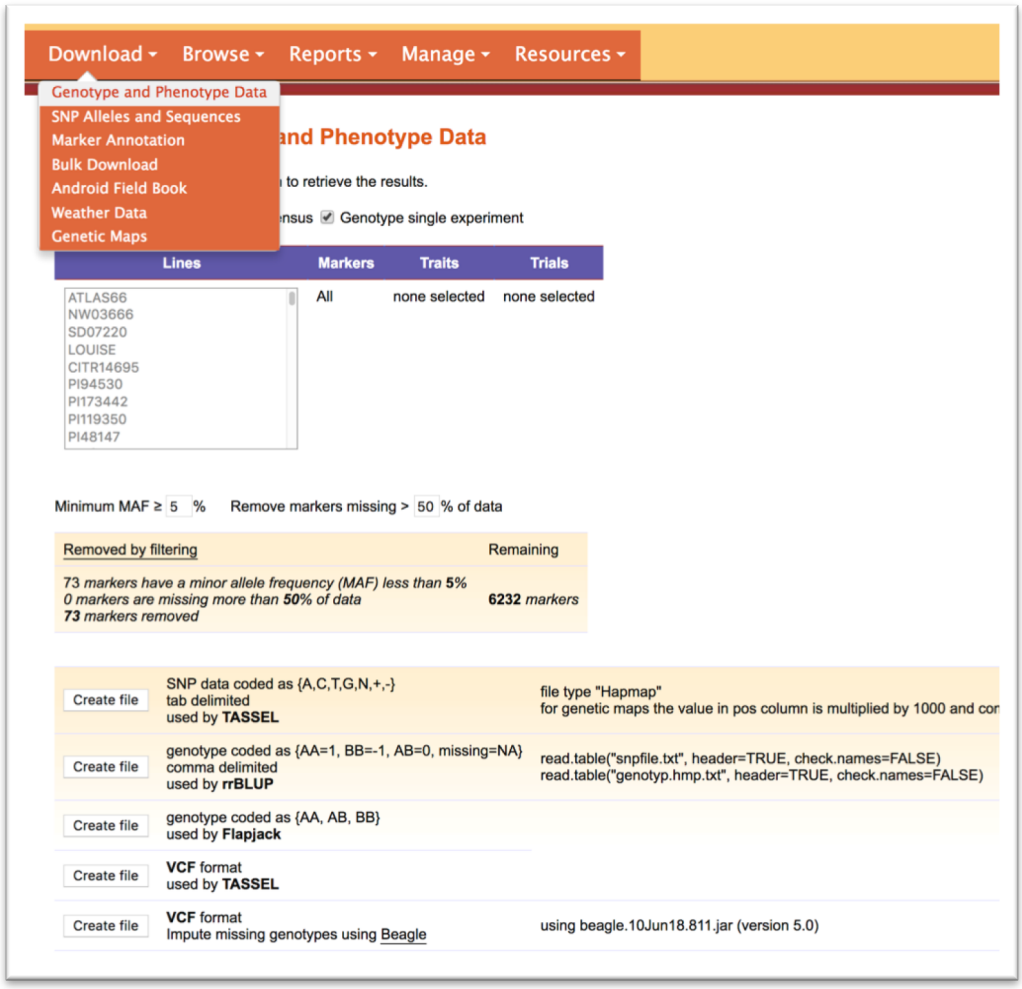
1. The data can be selected by Select => Wizard or Select => Lines by Genotype Experiment



2. Go to Select => Genetic Map



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



5. In the R script read in file

```
R version 3.5.0 (2018-04-23) -- "Joy in Playing"
Copyright (C) 2018 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin15.6.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> snp <- readTable("genotype.hmp.txt", header=TRUE, check.names=FALSE)
```

Use BrAPI R package to directly read data from T3 in R

The documentation for this package is at https://github.com/CIP-RIU/brapi. The current package (Aug 1, 2018) will direct you to t3sandbox.org. This will be fixed soon to point to triticeaetoolbox.org/wheat.

In R execute

```
install.packages("devtools")
devtools::install_github("CIP-RIU/brapi")

library(brapi)
library(magrittr)

t3wheat <= ba_db()$t3s

list available calls
bp_calls(t3wheat)
```