

# gwasExtra cookbook

gwasExtra is an R package or Shiny application specifically designed for Genome-Wide Association Studies (GWAS), aimed at providing additional functionalities and tools to assist researchers in processing, visualizing, and analyzing GWAS data.

## Home page

gwasExtra

Home page

Data check

Plot

SNP Extraction

Gene map

Annotate

Data merge

Help

Software Introduction

gwasExtraFile is a powerful Shiny application designed to help users visualize GWAS results, filter SNP loci, and perform gene localization analysis. Through its intuitive graphical interface, the application enables researchers to efficiently analyze genome-wide association data, quickly identify SNP loci associated with traits, and further localize potential functional genes. By combining the advantages of data processing and visualization, gwasExtraFile provides a convenient tool for genomic research.

PLINK

GEMMA

GAPIT

TASSEL

EMMAX

...

visualization

Significant snp

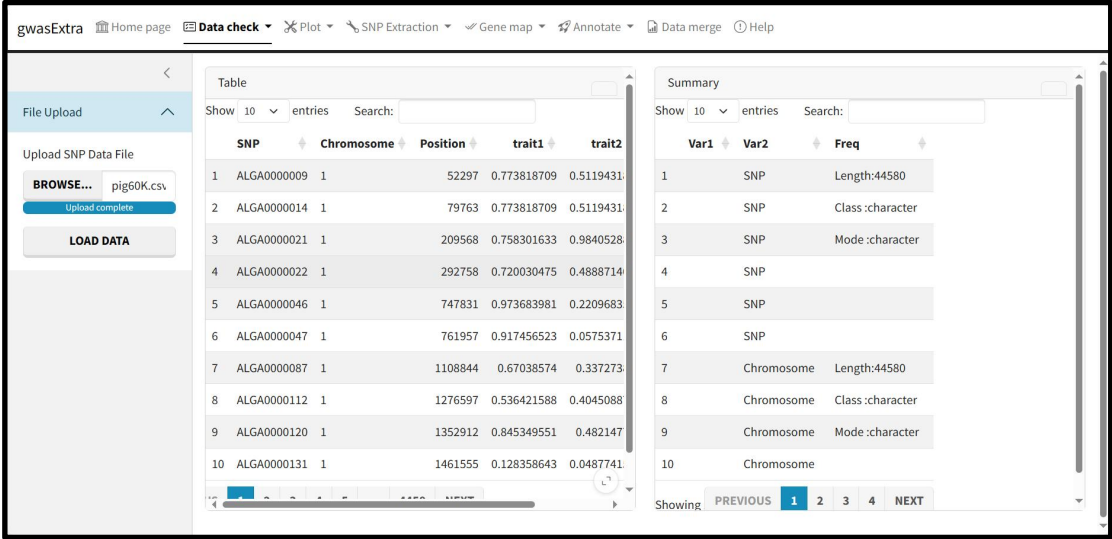
Gene list

Gene	SNP	P-value	chr	pos
BRCA1	rs112494342	1.2e-08	17	43034197
BRCA2	rs112494342	1.2e-08	17	43034197
BRCA3	rs112494342	1.2e-08	17	43034197
BRCA4	rs112494342	1.2e-08	17	43034197
BRCA5	rs112494342	1.2e-08	17	43034197
BRCA6	rs112494342	1.2e-08	17	43034197
BRCA7	rs112494342	1.2e-08	17	43034197
BRCA8	rs112494342	1.2e-08	17	43034197
BRCA9	rs112494342	1.2e-08	17	43034197
BRCA10	rs112494342	1.2e-08	17	43034197

# Data check

Demo data :

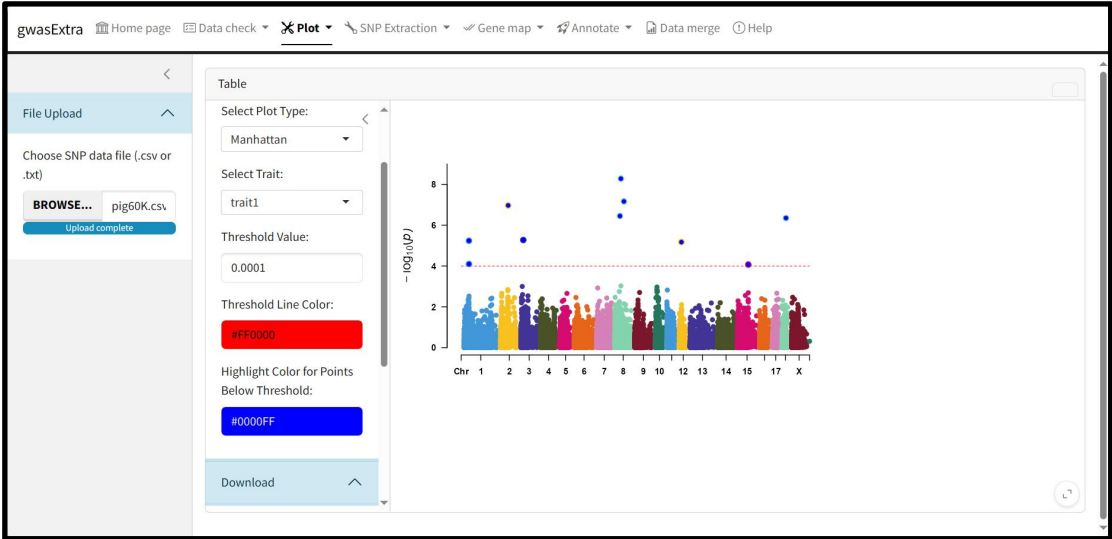
<https://github.com/w1996jy/gwasExtraFile/blob/main/data/pig60K.csv>



# GWAS result plot

Demo data :

<https://github.com/w1996jy/gwasExtraFile/blob/main/data/pig60K.csv>



## SNP extract

Demo data :

<https://github.com/w1996jy/gwasExtraFile/blob/main/data/pig60K.csv>

SNP	Chromosome	Position	P
11681	15	95748847	0.0000853644
13460	3	21472898	0.0000053437
14309	1	43358326	0.0000801322
18698	8	45703730	3.56582e-7
20194	12	18258585	0.00000675211
26779	2	67385863	1.08e-7
29178	1	43201866	0.00000580599
36009	18	3446892	4.48355e-7
40400	8	80539938	6.87e-8
41953	8	53910480	5.26e-9

## Gene map

Demo data :

[https://github.com/w1996jy/gwasExtraFile/blob/main/data/Significant\\_SNP.csv](https://github.com/w1996jy/gwasExtraFile/blob/main/data/Significant_SNP.csv)

[https://github.com/w1996jy/gwasExtraFile/blob/main/data/gene\\_info.csv](https://github.com/w1996jy/gwasExtraFile/blob/main/data/gene_info.csv)

Chromosome	Start	End	Gene	Position	QTL
1 15	95786198	95786198	Gene_13953	95748847	95448847-96048847
2 15	95893560	95893560	Gene_39932	95748847	95448847-96048847
3 15	95541619	95541619	Gene_47648	95748847	95448847-96048847
4 15	95479641	95479641	Gene_51426	95748847	95448847-96048847
5 15	95614402	95614402	Gene_54377	95748847	95448847-96048847
6 1	43510229	43510229	Gene_15717	43358326	43058326-43658326
7 2	67403695	67403695	Gene_4153	67385863	67085863-67605863

## Data merge

Demo data :

[https://github.com/w1996jy/gwasExtraFile/blob/main/data/join\\_df1.xlsx](https://github.com/w1996jy/gwasExtraFile/blob/main/data/join_df1.xlsx)

[https://github.com/w1996jy/gwasExtraFile/blob/main/data/join\\_df2.xlsx](https://github.com/w1996jy/gwasExtraFile/blob/main/data/join_df2.xlsx)

The screenshot displays the 'gwasExtra' web application interface, specifically the 'Data merge' section. The top navigation bar includes links for Home page, Data check, Plot, SNP Extraction, Gene map, Annotate, and Data merge (which is currently selected), along with a Help icon.

On the left side, there is a 'File Upload' panel with two sections: 'Upload the first dataset (CSV or XLSX)' and 'Upload the second dataset (CSV or XLSX)'. Each section has a 'BROWSE...' button and a file name ('join\_df1.xl' and 'join\_df2.xl' respectively) with an 'Upload complete' status.

The main area is titled 'Table of result' and contains a 'Parameter' section on the left with dropdown menus for 'Select Join Type' (set to 'left\_join') and 'Select Join Key Column from Dataset 1' and 'Dataset 2' (both set to 'index'). Below this is a 'Download' section with a 'DOWNLOAD' button.

The central part of the interface shows a table of results with 12 columns: index, mpg, cyl, disp, hp, drat, wt, qsec, vs, am, gear, and carb. The table displays 5 entries, which are rows of car data. Below the table, it indicates 'Showing 1 to 5 of 5 entries' and includes 'PREVIOUS', '1' (current page), and 'NEXT' navigation buttons.

index	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb	
1	Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
2	Valiant	18.1	6	225	105	2.76	3.46	20.22	1	0	3	1
3	Mazda RX4 Wag	21	6	160	110	3.9	2.875	17.02	0	1	4	4
4	Hornet Sportabout	18.7	8	360	175	3.15	3.44	17.02	0	0	3	2
5	Merc 230	22.8	4	140.8	95	3.92	3.15	22.9	1	0	4	2

## contact

If you need help while using the software, please contact me at Email:

[fyliangfei@163.com](mailto:fyliangfei@163.com).