

# Package ‘geneNR’

May 8, 2026

**Title** Automated Gene Identification for Post-GWAS and QTL Analysis

**Version** 2.0.1

**Description** Facilitates the post-Genome Wide Association Studies (GWAS) and Quantitative Trait Loci (QTL) analysis of identifying candidate genes within user-defined search window, based on the identified Single Nucleotide Polymorphisms (SNPs) as given by Mazumder AK (2024) <[doi:10.1038/s41598-024-66903-3](https://doi.org/10.1038/s41598-024-66903-3)>. It supports candidate gene analysis for wheat and rice. Just import your GWAS result as explained in the sample\_data file and the function does all the manual search and retrieve candidate genes for you, while exporting the results into ready-to-use output.

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**Encoding** UTF-8

**RoxygenNote** 7.3.2

**Depends** R (>= 3.5)

**LazyData** TRUE

**Imports** readr, stringr, utils, httr, rvest, xml2, writexl, vcfR, ggplot2, ggrepel

**Suggests** knitr, rmarkdown, devtools

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2025-03-29 16:50:02 UTC

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geneQTL	<i>Identifies Candidate Genes based on identified Quantitative Trati Loci (QTL) analysis</i>
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### Description

Identifies Candidate Genes based on identified Quantitative Trati Loci (QTL) analysis

### Usage

```
geneQTL(data_file, crop = "wheat")
```

### Arguments

data_file	The input data in .csv format. (sample_data_wheat_qtl or sample_data_rice_qtl for demo purpose)
crop	Either "wheat" or "rice". (by default it will be wheat)

### Value

A data frame containing traits, QTL, gene\_id, gene\_size, and gene\_type.

**Examples**

```
load(system.file("extdata", "precomputed_sample_results_qtl.rda", package = "geneNR"))
message(sample_results)

result <- geneQTL("sample_data_wheat_qtl", crop="wheat")
result <- geneQTL("sample_data_rice_qtl", crop="rice")
#result <- geneQTL("your_results.csv", crop="wheat")
```

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geneSNP	<i>Identifies Candidate Genes based on identified Single Nucleotide Polymorphisms (SNPs) from Genome Wide Association Studies (GWAS) Analysis</i>
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**Description**

Identifies Candidate Genes based on identified Single Nucleotide Polymorphisms (SNPs) from Genome Wide Association Studies (GWAS) Analysis

**Usage**

```
geneSNP(data_file, upstream = 1e+06, downstream = 1e+06, crop = "wheat")
```

**Arguments**

data_file	The input data in .csv format. (sample_data_wheat or sample_data_rice for demo purpose)
upstream	The search window upstream of the current position of the SNP. (default: 1000000)
downstream	The search window downstream of the current position of the SNP. (default: 1000000)
crop	Either "wheat" or "rice". (default: wheat)

**Value**

A data frame containing traits, SNP, gene\_id, gene\_size, and gene\_type.

**Examples**

```
load(system.file("extdata", "precomputed_sample_results.rda", package = "geneNR"))
message(sample_results)

result <- geneSNP("sample_data_wheat", 10000, 10000, crop = "wheat")
result <- geneSNP("sample_data_rice", 10000, 10000, crop = "rice")
```

---

geneSNPcustom	<i>Identifies Candidate Genes based on identified Single Nucleotide Ploymorphisms (SNPs) from Genome Wide Association Stuides (GWAS) Analysis</i>
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### Description

Identifies Candidate Genes based on identified Single Nucleotide Ploymorphisms (SNPs) from Genome Wide Association Stuides (GWAS) Analysis

### Usage

```
geneSNPcustom(data_file, crop = "wheat")
```

### Arguments

data_file	The input data in .csv format. (sample_data_wheat_custom for demo purpose)
crop	Either "wheat" or "rice". (default: wheat)

### Value

A data frame containing traits, SNP, gene\_id, gene\_size, and gene\_type.

### Examples

```
load(system.file("extdata", "precomputed_sample_results_custom.rda", package = "geneNR"))
message(sample_results)

result <- geneSNPcustom("sample_data_wheat_custom", crop = "wheat")
```

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import_hmp	<i>Imports Hapmap genotypic data file</i>
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---

### Description

Imports Hapmap genotypic data file

### Usage

```
import_hmp(file_path, header = TRUE, sep = "\t", stringsAsFactors = FALSE)
```

**Arguments**

file\_path        Provide the actual path of Hapmap genotypic data file  
header            by default it will be True  
sep                by default it will be tab separated  
stringsAsFactors  
                  by default it will be False

**Value**

Hampmap genotypic data

**Examples**

```
demo_SNP <- system.file("extdata", "demo_SNP.hmp.txt", package = "geneNR")  
hapmap_data <- import_hmp(demo_SNP)  
head(hapmap_data)
```

---

import\_vcf

*Imports VCF (Variant Call Format) data file*

---

**Description**

Imports VCF (Variant Call Format) data file

**Usage**

```
import_vcf(file_path)
```

**Arguments**

file\_path        Provide the actual path of the VCF file

**Value**

A vcfR object containing the imported data

**Examples**

```
demo_SNP <- system.file("extdata", "demo_SNP.vcf", package = "geneNR")  
vcf_data <- import_vcf(demo_SNP)  
vcf_data
```

---

`plot_SNP`*Plot SNP Distribution on Chromosome Map*

---

**Description**

Plots SNP positions across chromosomes with centromere markers using given chromosome details and SNP data.

**Usage**

```
plot_SNP(  
  chromosome_details,  
  data,  
  chromosome_color = "steelblue",  
  title = "Chromosome map with SNPs",  
  label_color = "black",  
  image_width = 10,  
  image_height = 10  
)
```

**Arguments**

<code>chromosome_details</code>	A data frame containing chromosome details with columns Chr, start and stop
<code>data</code>	A data frame containing SNP data with columns Chr, Pos, and SNP.
<code>chromosome_color</code>	Color of the chromosome bars (default: "skyblue").
<code>title</code>	Title of the chromosome plot depicting the identified SNPs
<code>label_color</code>	Color of the SNP labels (default: "black").
<code>image_width</code>	width of the chromosome plot
<code>image_height</code>	height of the chromosome plot

**Value**

A ggplot object for the SNP distribution plot.

**Examples**

```
chromosome_details <- read.csv(system.file("extdata", "chromosome_details.csv", package = "geneNR"))  
data <- read.csv(system.file("extdata", "identified_SNP.csv", package = "geneNR"))  
chromosome_plot <- plot_SNP(chromosome_details = chromosome_details, data = data,  
  chromosome_color = "steelblue", title = "Chromosome map with SNPs", label_color = "black",  
  image_width = 15, image_height = 10)  
print(chromosome_plot)
```

---

plot\_summariseSNP      *Plot SNP Distribution Across Chromosomes*

---

### Description

Creates a bar chart representing the distribution of SNPs across chromosomes. Allows customization of bar color, label size, and label color. Saves the plot to a user-specified directory or a temporary directory.

### Usage

```
plot_summariseSNP(  
  snp_distribution,  
  file_name = "snp_bar_chart.jpeg",  
  output_dir = tempdir(),  
  bar_color = "lightblue",  
  label_size = 3,  
  label_color = "black"  
)
```

### Arguments

snp_distribution	A data frame with columns Chr and SNP_Count.
file_name	The name of the file to save the plot (default: "snp_bar_chart.jpeg").
output_dir	The directory to save the file (default: tempdir()).
bar_color	The color of the bars (default: "lightblue").
label_size	The size of the text labels on the bars (default: 3).
label_color	The color of the text labels on the bars (default: "black").

### Value

A ggplot object for the created bar chart.

### Examples

```
demo_SNP <- system.file("extdata", "demo_SNP.hmp.txt", package = "geneNR")  
data <- import_hmp(demo_SNP)  
snp_distribution <- summariseSNP(data)  
plot <- plot_summariseSNP(snp_distribution, bar_color = "skyblue",  
  label_size = 3, label_color = "red")  
print(plot)
```

---

sample\_data\_rice      *Sample Data*

---

**Description**

A dataset containing sample data related to genetic markers and associated traits.

**Usage**

```
sample_data_rice
```

**Format**

A data frame with columns:

**SNP** SNP identifier, character.

**Chr** Chromosome location, character.

**Pos** Position on the chromosome, numeric.

**traits** Associated traits, character.

**Source**

Basha FTM, Sar P, Bhowmick PK, Mahato A, Bisht DS, Iquebal MA, Chakraborty K, Banerjee A, Verma BC, Bhaduri D, Kumar J, Ngangkham U, Saha S, Priyamedha, Mandal NP, Roy S. Genome-wide association study identified QTLs and genes underlying early seedling vigour in aus rice (*Oryza sativa* L.). *Mol Genet Genomics*. 2024 Dec 3;299(1):112. doi: 10.1007/s00438-024-02204-8. PMID: 39625651.

**Examples**

```
data(sample_data_rice)    #lazy loading
```

---

sample\_data\_rice\_qtl    *Sample Data*

---

**Description**

A dataset containing sample data related to genetic markers and associated traits.

**Usage**

```
sample_data_rice_qtl
```

**Format**

A data frame with columns:

**traits** Associated traits, character.

**Chr** Chromosome location, character.

**start** Position on the chromosome where QTL starts, numeric.

**stop** Position on the chromosome where QTL stops, numeric.

**Source**

Generated for demonstration purposes

**Examples**

```
data(sample_data_rice_qtl) #lazy loading
```

---

sample_data_wheat	<i>Sample Data</i>
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---

**Description**

A dataset containing sample data related to genetic markers and associated traits.

**Usage**

```
sample_data_wheat
```

**Format**

A data frame with columns:

**SNP** SNP identifier, character.

**Chr** Chromosome location, character.

**Pos** Position on the chromosome, numeric.

**traits** Associated traits, character.

**Source**

Generated for demonstration purposes

**Examples**

```
data(sample_data_wheat) #lazy loading
```

sample\_data\_wheat\_custom

*Sample Data*

---

### **Description**

A dataset containing sample data related to genetic markers and associated traits.

### **Usage**

```
sample_data_wheat_custom
```

### **Format**

A data frame with columns:

**traits** Associated traits, character.

**SNP** SNP identifier, character.

**Chr** Chromosome location, character.

**start** Position on the chromosome where search window starts, numeric.

**stop** Position on the chromosome where search window stops, numeric.

### **Source**

Generated for demonstration purposes

### **Examples**

```
data(sample_data_wheat_custom) #lazy loading
```

---

sample\_data\_wheat\_qtl *Sample Data*

---

### **Description**

A dataset containing sample data related to genetic markers and associated traits.

### **Usage**

```
sample_data_wheat_qtl
```

**Format**

A data frame with columns:

**traits** Associated traits, character.

**Chr** Chromosome location, character.

**start** Position on the chromosome where QTL starts, numeric.

**stop** Position on the chromosome where QTL stops, numeric.

**Source**

Generated for demonstration purposes

**Examples**

```
data(sample_data_wheat_qtl) #lazy loading
```

---

summariseSNP

*Distribution of SNPs Across Chromosomes*

---

**Description**

Distribution of SNPs Across Chromosomes

**Usage**

```
summariseSNP(data)
```

**Arguments**

**data** A data frame containing a column named Chr

**Value**

A data frame with chromosome names and the count of SNPs for each chromosome

**Examples**

```
demo_SNP <- system.file("extdata", "demo_SNP.hmp.txt", package = "geneNR")
data <- import_hmp(demo_SNP)
snp_distribution <- summariseSNP(data)
print(snp_distribution)
```

---

summariseSNP\_vcf      *Distribution of SNPs Across Chromosomes from VCF*

---

**Description**

Distribution of SNPs Across Chromosomes from VCF

**Usage**

```
summariseSNP_vcf(vcf_data)
```

**Arguments**

vcf\_data      A vcfR object containing VCF data.

**Value**

A data frame with chromosome names and the count of SNPs for each chromosome.

**Examples**

```
demo_SNP <- system.file("extdata", "demo_SNP.vcf", package = "geneNR")
vcf_data <- import_vcf(demo_SNP)
snp_distribution <- summariseSNP_vcf(vcf_data)
print(snp_distribution)
```

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