

# SNP to genind object

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## SNP to genind Object

```
# Load data
data <- read.csv("TF_PS_pipits_genotypes.csv", header = TRUE, row.names = 1)

# Check the first few rows
head(data)

##      Island X5239s1 X7259s1 TLR4_1 TLR4_2 TLR4_3 TLR4_4 Sample.1 UTM Easting
## 285      TF      AT      AT      AA      GG      CT      AC      NA      NA
## 286      TF      AA      AA      AA      GG      CT      AC      NA      NA
## 287      TF      AT      AT      AA      GG      CC      CC      NA      NA
## 288      TF      AA      AT      AA      GG      CT      CC      NA      NA
## 289      TF      AA      AA      AA      GG      CT      CC      NA      NA
## 291      TF      AA      TT      AA      GG      CT      CC      NA      NA
##      Northing ALTITUDE MINTEMP PRECIPITATION DISTWATER ASPECT SLOPE DISTFARM
## 285      NA      NA      NA      NA      NA      NA      NA      NA
## 286      NA      NA      NA      NA      NA      NA      NA      NA
## 287      NA      NA      NA      NA      NA      NA      NA      NA
## 288      NA      NA      NA      NA      NA      NA      NA      NA
## 289      NA      NA      NA      NA      NA      NA      NA      NA
## 291      NA      NA      NA      NA      NA      NA      NA      NA
##      DISTPOUL DENSITY VEGTYPE DIST_URB
## 285      NA      NA      NA      NA
## 286      NA      NA      NA      NA
## 287      NA      NA      NA      NA
## 288      NA      NA      NA      NA
## 289      NA      NA      NA      NA
## 291      NA      NA      NA      NA

# Convert to genind object
genind_obj <- df2genind(data[,2:7], ploidy = 2, sep = "", NA.char = "NA")

# Add pop information based on "Island"
pop(genind_obj) <- factor(data$Island)

# Check the structure of the genind object
summary(genind_obj)

##
## // Number of individuals: 780
## // Group sizes: 590 190
## // Number of alleles per locus: 2 2 2 2 2 2
```

```
## // Number of alleles per group: 10 12
## // Percentage of missing data: 0.56 %
## // Observed heterozygosity: 0.32 0.39 0.02 0.1 0.49 0.45
## // Expected heterozygosity: 0.37 0.44 0.02 0.12 0.49 0.45
```

## Plot locality data

```
# Subset data from PS with env data
data_ps <- data[data$UTM == "28N",]

# Subset genind obj from PS
genind_ps <- df2genind(data_ps[,2:7], ploidy = 2, sep = "", NA.char = "NA")

# Place coordinates in spacial object
library(sf)

## Linking to GEOS 3.10.2, GDAL 3.4.1, PROJ 8.2.1; sf_use_s2() is TRUE
library(tmap)

## Breaking News: tmap 3.x is retiring. Please test v4, e.g. with
## remotes::install_github('r-tmap/tmap')
library(terra)

## terra 1.7.83
Sites.sf_ps <- st_as_sf(data_ps, coords=c("Easting", "Northing"))
st_crs(Sites.sf_ps) <- 32628

# Plot with tmap
tmap_mode("plot")

## tmap mode set to plotting
plot(st_geometry(Sites.sf_ps))
```

