Graphical user interface, application

Description automatically generated

setwd(

#setwd("Please insert your working directory filepath here") # (Example working directory below)

setwd(

# Install and load Boruta with dependency 'Ranger'

install.packages('Boruta')

install.packages('ranger')

library(Boruta)

library(ranger)

# Upload cell line data from your working directory

AB.data.new <- read.csv("AB CNV cells new.csv")

# Execute Boruta algorithm, focusing on response (to rucaparib?)

AB.CNV.Boruta <- Boruta(response~.,AB.data.new)

# View basic results

print(AB.CNV.Boruta)

# Visualise results with a boxplot (significant interactions coloured green)

plot(AB.CNV.Boruta)