```r
## Get file list of all data within directory
setwd("E:/DrugHits/HTS1_Analysis/R/Preswesk/")
directory <- getwd()
output_dir <- "E:/DrugHits/HTS1_Analysis/Analysis/Preswesk/"
##MUST EDIT FILES SO THAT TOP TWO LINES ARE DELETED
##USE NOTEPAD SO AS NOT TO LOSS ANY DATA
files_full <- list.files(directory, full.names = T)

## Read all files into variable
for (i in seq_along(files_full)){
  files <- read.csv(files_full[i])
  well_unique <- unique(files$Section)
  tmp <- seq_along(files_full)
  plate_number <- paste("Plate_", tmp[i], "_", sep="")
  output1 <- vector();output2 <- vector();output3 <- vector()
  output4 <- vector();output5 <- vector();output6 <- vector()
  for (j in seq_along(well_unique)){
    wells <- subset(files, Section==well_unique[j])##Seperates each well
    well_density <- wells[, 3] ##pulls out mean density
    tmp1 <- sort(well_density)
    upper_h <- ((length(tmp1)-1)*0.75)+1
    lower_h <- ((length(tmp1)-1)*0.25)+1
    ##Calculate mean, standard deviation, median, upper and lower quantile, and cell count
    well_mean <- mean(tmp1); well_sd <- sd(tmp1)
    well_median <- median(tmp1,na.rm=T)
    well_upperq <- tmp1[floor(upper_h)]+((upper_h-floor(upper_h))*(tmp1[floor(upper_h)+1]- tmp1[floor(upper_h)]))
    well_lowerq <- tmp1[floor(lower_h)]+((lower_h-floor(lower_h))*(tmp1[floor(lower_h)+1]- tmp1[floor(lower_h)]))
    cell_count <- length(tmp1)
    output1 <- c(output1, well_mean);output2 <- c(output2, well_sd)##Output each variable
    output3 <- c(output3, well_median);output4 <- c(output4, well_upperq)
    output5 <- c(output5, well_lowerq);output6 <- c(output6, cell_count)
  }
  plate <- data.frame(Well = well_unique, Mean = output1, Std = output2, Median = output3, Upper = output4, Lower = output5, Count = output6)
  plate_name <- paste(output_dir, plate_number, sep="")
  write.table(plate, file = paste(plate_name, Sys.Date(), "_Well_Analysis_Prestwick.csv", sep=""),
              sep = ",", append=FALSE, row.names = FALSE, col.names=TRUE)
}
```