

COVID-19 Specimen Data
Processing:
pangolin_code.R

IMPORTANT: All pangolin file names should follow the same formatting.

<YYYYMMDD>_pangolin_<Plate_<#>_<#>.csv

YYYYMMDD = Date when the pangolin file was made

= 1, 2, 3, ..., n ; Plate number as assigned in the lab that correspond to the samples contained in each particular file

Libraries Needed:
library(tidyverse)
library(lubridate)
library(janitor)

Overview: This code file pulls in all pangolin files as generated by the lab. Those files are processed and then a summary file is output.

Created as empty dataframe first, then gets filled in later in our process.

