

Supplementary 2

vPCR tests for high throughput SARS-CoV-2 screening

```
library(tidyverse)

## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.4
## v forcats    1.0.0      v stringr   1.5.1
## v ggplot2     3.4.4      v tibble    3.2.1
## v lubridate  1.9.3      v tidyr     1.3.0
## v purrr      1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

packageVersion("tidyverse")

## [1] '2.0.0'

library(stringr)
packageVersion("stringr")

## [1] '1.5.1'

library(data.table)

##
## Attaching package: 'data.table'
##
## The following objects are masked from 'package:lubridate':
##
##     hour, isoweek, mday, minute, month, quarter, second, wday, week,
##     yday, year
##
## The following objects are masked from 'package:dplyr':
##
##     between, first, last
##
## The following object is masked from 'package:purrr':
##
##     transpose

packageVersion("data.table")

## [1] '1.14.8'

library(sf)

## Linking to GEOS 3.12.1, GDAL 3.7.3, PROJ 9.2.1; sf_use_s2() is TRUE
```

```

packageVersion("sf")

## [1] '1.0.16'

library(viridis)

## Loading required package: viridisLite

packageVersion("viridis")

## [1] '0.6.4'

library(scico)
packageVersion("scico")

## [1] '1.5.0'

library(ggpubr)
packageVersion("ggpubr")

## [1] '0.6.0.999'

# Tables T04 & T03 were retrived on 2022-07-13
t04 <- read.csv("./T04B_merge.csv", header = T)
t042 <- t04 %>%
  mutate(date = ifelse(Fecha.de.hisopado %in% "", Fecha.de.diagnóstico,
    Fecha.de.hisopado))

filt <- t042 %>%
  filter(date > "2020-11-01" & date < "2021-10-01")
filt <- filt[order(filt$date, decreasing = T), ]
head(filt)

##      Identificador.de.Consorcio Identificador.de.Laboratorio Laboratorio
## 5046          CUY29-005475          77253          LDM
## 5049          CUY29-005480          440953    Americano
## 5050          CUY29-005481          440950    Americano
## 5056          CUY29-005487          440624    Americano
## 5057          CUY29-005488          440839    Americano
## 5058          CUY29-005489          440827    Americano
##      Kit.de.Diagnóstico Ct.diagnóstico País Fecha.de.diagnóstico
## 5046                    21.9          2021-09-30
## 5049                    20          2021-10-01
## 5050                    20          2021-10-01
## 5056                    25          2021-09-30
## 5057                    22          2021-09-30
## 5058                    24          2021-09-30
##      Fecha.de.hisopado Departamento Localidad      Sexo Edad Hospitalización
## 5046                    NA
## 5049      2021-09-30      Rocha      Masculino    50
## 5050      2021-09-30      Rocha      Femenino    47
## 5056      2021-09-30    Colonia      Masculino    71
## 5057      2021-09-30  Canelones      Masculino    40
## 5058      2021-09-30  Canelones      Femenino    24
##      Link.Epidemiológico Síntomas Outcome Comentarios      Semana PCR.Variantes
## 5046                    4/10/2021          Si

```

```

## 5049 4/10/2021 Si
## 5050 4/10/2021 Si
## 5056 4/10/2021 Si
## 5057 4/10/2021 Si
## 5058 4/10/2021 Si
##      Status.qPCR Secuenciación Status.Seq Variante.por.PCR ID.de.secuenciación
## 5046 B.1.617.2
## 5049 Si B.1.617.2 SEQ-027
## 5050 Si B.1.617.2 SEQ-027
## 5056 Si B.1.617.2 SEQ-027
## 5057 Si B.1.617.2 SEQ-027
## 5058 B.1.617.2
##      Linaje.por.secuenciación QC_FINAL Vacuna Laboratorio.Vacuna.1era.dosis
## 5046
## 5049 AY.20 PASS_0-10
## 5050 AY.20 PASS_0-10
## 5056 AY.20 PASS_0-10
## 5057 AY.43 PASS_0-10
## 5058
##      Fecha.1era.dosis Laboratorio.Vacuna.2nda.dosis Fecha.2nda.dosis date
## 5046 NA NA 2021-09-30
## 5049 NA NA 2021-09-30
## 5050 NA NA 2021-09-30
## 5056 NA NA 2021-09-30
## 5057 NA NA 2021-09-30
## 5058 NA NA 2021-09-30

```

```
# Filter relevant dates
```

```
filtc <- t042 %>%
```

```
  filter(date > "2021-07-01" & date < "2021-10-01")
```

```
filtc$Variante.por.PCR <- gsub("No-VOC", "B.1.617.2", filtc$Variante.por.PCR) #non-voc samples were as
```

```
filt <- filt[!filt$Identificador.de.Consorcio %in% filtc$Identificador.de.Consorcio,
]
```

```
filt <- as.data.frame(rbind(filt, filtc))
```

```
dim(as.data.frame(unique(filt$Identificador.de.Consorcio)))
```

```
## [1] 5099 1
```

```
filt <- filt[order(filt$date, decreasing = T), ]
```

```
head(filt)
```

```

##      Identificador.de.Consorcio Identificador.de.Laboratorio Laboratorio
## 11841 CUY29-005475 77253 LDM
## 11871 CUY29-005480 440953 Americano
## 11881 CUY29-005481 440950 Americano
## 11941 CUY29-005487 440624 Americano
## 11951 CUY29-005488 440839 Americano
## 11961 CUY29-005489 440827 Americano
##      Kit.de.Diagnóstico Ct.diagnóstico País Fecha.de.diagnóstico
## 11841 21.9 2021-09-30
## 11871 20 2021-10-01
## 11881 20 2021-10-01
## 11941 25 2021-09-30
## 11951 22 2021-09-30

```

```

## 11961          24          2021-09-30
##      Fecha.de.hisopado Departamento Localidad      Sexo Edad Hospitalización
## 11841          NA
## 11871      2021-09-30      Rocha      Masculino      50
## 11881      2021-09-30      Rocha      Femenino      47
## 11941      2021-09-30      Colonia      Masculino      71
## 11951      2021-09-30      Canelones      Masculino      40
## 11961      2021-09-30      Canelones      Femenino      24
##      Link.Epidemiológico Síntomas Outcome Comentarios      Semana PCR.Variantes
## 11841          4/10/2021          Si
## 11871          4/10/2021          Si
## 11881          4/10/2021          Si
## 11941          4/10/2021          Si
## 11951          4/10/2021          Si
## 11961          4/10/2021          Si
##      Status.qPCR Secuenciación Status.Seq Variante.por.PCR ID.de.secuenciación
## 11841          B.1.617.2
## 11871          Si          B.1.617.2          SEQ-027
## 11881          Si          B.1.617.2          SEQ-027
## 11941          Si          B.1.617.2          SEQ-027
## 11951          Si          B.1.617.2          SEQ-027
## 11961          B.1.617.2
##      Linaje.por.secuenciación QC_FINAL Vacuna Laboratorio.Vacuna.1era.dosis
## 11841
## 11871          AY.20 PASS_0-10
## 11881          AY.20 PASS_0-10
## 11941          AY.20 PASS_0-10
## 11951          AY.43 PASS_0-10
## 11961
##      Fecha.1era.dosis Laboratorio.Vacuna.2nda.dosis Fecha.2nda.dosis
## 11841          NA          NA
## 11871          NA          NA
## 11881          NA          NA
## 11941          NA          NA
## 11951          NA          NA
## 11961          NA          NA
##      date
## 11841 2021-09-30
## 11871 2021-09-30
## 11881 2021-09-30
## 11941 2021-09-30
## 11951 2021-09-30
## 11961 2021-09-30

```

```

# Get samples that were screened by the vPCR

```

```

vPCR <- filt[which(filt$PCR.Variantes == "Si"), ]
head(vPCR)

```

```

##      Identificador.de.Consorcio Identificador.de.Laboratorio Laboratorio
## 11841      CUY29-005475      77253      LDM
## 11871      CUY29-005480      440953      Americano
## 11881      CUY29-005481      440950      Americano
## 11941      CUY29-005487      440624      Americano
## 11951      CUY29-005488      440839      Americano

```

```

## 11961          CUY29-005489          440827  Americano
##      Kit.de.Diagnóstico Ct.diagnóstico País Fecha.de.diagnóstico
## 11841          21.9          2021-09-30
## 11871          20          2021-10-01
## 11881          2021-10-01
## 11941          25          2021-09-30
## 11951          22          2021-09-30
## 11961          24          2021-09-30
##      Fecha.de.hisopado Departamento Localidad      Sexo Edad Hospitalización
## 11841          NA
## 11871      2021-09-30      Rocha      Masculino      50
## 11881      2021-09-30      Rocha      Femenino      47
## 11941      2021-09-30      Colonia      Masculino      71
## 11951      2021-09-30      Canelones      Masculino      40
## 11961      2021-09-30      Canelones      Femenino      24
##      Link.Epidemiológico Síntomas Outcome Comentarios      Semana PCR.Variantes
## 11841          4/10/2021          Si
## 11871          4/10/2021          Si
## 11881          4/10/2021          Si
## 11941          4/10/2021          Si
## 11951          4/10/2021          Si
## 11961          4/10/2021          Si
##      Status.qPCR Secuenciación Status.Seq Variante.por.PCR ID.de.secuenciación
## 11841          B.1.617.2
## 11871          Si          B.1.617.2          SEQ-027
## 11881          Si          B.1.617.2          SEQ-027
## 11941          Si          B.1.617.2          SEQ-027
## 11951          Si          B.1.617.2          SEQ-027
## 11961          B.1.617.2
##      Linaje.por.secuenciación QC_FINAL Vacuna Laboratorio.Vacuna.1era.dosis
## 11841
## 11871          AY.20 PASS_0-10
## 11881          AY.20 PASS_0-10
## 11941          AY.20 PASS_0-10
## 11951          AY.43 PASS_0-10
## 11961
##      Fecha.1era.dosis Laboratorio.Vacuna.2nda.dosis Fecha.2nda.dosis
## 11841          NA          NA
## 11871          NA          NA
## 11881          NA          NA
## 11941          NA          NA
## 11951          NA          NA
## 11961          NA          NA
##      date
## 11841 2021-09-30
## 11871 2021-09-30
## 11881 2021-09-30
## 11941 2021-09-30
## 11951 2021-09-30
## 11961 2021-09-30

```

```

# Distribution by departamento
table(vPCR$Departamento)

```

```
##
```

##		Artigas	Canelones	Cerro Largo	Colonia
##	664	168	329	124	119
##	Durazno	Flores	Florida	Lavalleja	Maldonado
##	15	55	46	48	202
##	Montevideo	Paysandú	Río Negro	Rivera	Rocha
##	1174	292	227	113	378
##	Salto	San José	Soriano	Tacuarembó	Treinta y Tres
##	331	216	82	404	94

```

filtc <- vPCR %>%
  filter(date > "2021-07-01" & date < "2021-10-01")
dim(filtc)

```

```
## [1] 1236 32
```

```

filtc$Variante.por.PCR <- gsub("No-VOC", "B.1.617.2", filt$Variante.por.PCR) #se marcaron todas las n
unique(filtc$Variante.por.PCR)

```

```
## [1] "B.1.617.2" "Descartada" "No concluyente" "P.1/B.1.351"
```

```

filtd <- vPCR %>%
  filter(date > "2021-03-01" & date < "2021-07-15")
dim(filtd)

```

```
## [1] 3996 32
```

```
unique(filtd$Variante.por.PCR)
```

```

## [1] "P.1/B.1.351" "B.1.617.2" "Descartada" "No concluyente"
## [5] "No-VOC"

```

```

gamma <- filtd[which(filtd$Variante.por.PCR == "P.1/B.1.351"), ]
dim(gamma)

```

```
## [1] 3275 32
```

```
dim(gamma) * 100/dim(filtd) #Porcentaje de Gamma entre marzo y mediados de julio
```

```
## [1] 81.95696 100.00000
```

Gamma en Marzo 2021

```

filtm <- vPCR %>%
  filter(date > "2021-03-01" & date < "2021-03-31")
dim(film)

```

```
## [1] 374 32
```

```
unique(film$Variante.por.PCR)
```

```
## [1] "P.1/B.1.351" "No-VOC" "Descartada" "No concluyente"
```

```

gamma <- film[which(film$Variante.por.PCR == "P.1/B.1.351"), ]
dim(gamma)

```

```
## [1] 161 32
```

```
dim(gamma) * 100/dim(film) #Porcentaje de Gamma entre marzo y mediados de julio
```

```
## [1] 43.04813 100.00000
```

```
filtjn <- vPCR %>%
  filter(date > "2021-06-01" & date < "2021-06-30")
dim(filtjn)
```

Gamma in June 2021

```
## [1] 887 32
```

```
unique(filtjn$Variante.por.PCR)
```

```
## [1] "P.1/B.1.351"      "No-VOC"           "No concluyente" "B.1.617.2"
## [5] "Descartada"
```

```
gamma <- filtjn[which(filtjn$Variante.por.PCR == "P.1/B.1.351"), ]
dim(gamma)
```

```
## [1] 818 32
```

```
dim(gamma) * 100/dim(filtjn)
```

```
## [1] 92.22097 100.00000
```

```
filtsp <- vPCR %>%
  filter(date > "2021-09-01" & date < "2021-09-30")
dim(filtsp)
```

Gamma in September

```
## [1] 331 32
```

```
unique(filtsp$Variante.por.PCR)
```

```
## [1] "No concluyente" "B.1.617.2"      "Descartada"      "P.1/B.1.351"
gamma <- filtsp[which(filtsp$Variante.por.PCR == "P.1/B.1.351"), ]
dim(gamma)
```

```
## [1] 12 32
```

```
dim(gamma) * 100/dim(filtsp)
```

```
## [1] 3.625378 100.000000
```

```
filtj <- vPCR %>%
  filter(date > "2021-07-01" & date < "2021-07-31")
dim(filtj)
```

Delta in July

```
## [1] 541 32
```

```
unique(filtj$Variante.por.PCR)
```

```
## [1] "P.1/B.1.351"      "B.1.617.2"       "Descartada"      "No concluyente"
## [5] "No-VOC"
```

```
delta <- filtj[which(filtj$Variante.por.PCR == "B.1.617.2"), ]
dim(delta)
```

```
## [1] 108 32
dim(delta) * 100/dim(filtj) #Porcentaje de delta en julio
```

```
## [1] 19.96303 100.00000
```

```
filts <- vPCR %>%
  filter(date > "2021-09-01" & date < "2021-09-30")
dim(filts)
```

Delta in September

```
## [1] 331 32
```

```
unique(filt$d$Variante.por.PCR)
```

```
## [1] "P.1/B.1.351" "B.1.617.2" "Descartada" "No concluyente"
## [5] "No-VOC"
```

```
delta <- filts[which(filts$Variante.por.PCR == "B.1.617.2"), ]
dim(delta)
```

```
## [1] 252 32
```

```
dim(delta) * 100/dim(filts) #Porcentaje de delta en setiembre
```

```
## [1] 76.13293 100.00000
```

```
list <- vPCR %>%
  group_by(date, Variante.por.PCR) %>%
  tally() %>%
  ungroup()
list <- as.data.frame(list)
list$date <- as.Date(list$date)
head(list)
```

```
##      date Variante.por.PCR n
## 1 2020-11-03      No-VOC 2
## 2 2020-11-13      No-VOC 3
## 3 2020-11-16      No-VOC 7
## 4 2020-11-23      No-VOC 2
## 5 2020-12-01      No-VOC 4
## 6 2020-12-04      No-VOC 1
```

```
# Edit names
```

```
list$Variante.por.PCR <- gsub("Descartada", "Discarded", list$Variante.por.PCR)
list$Variante.por.PCR <- gsub("No concluyente", "Inconclusive", list$Variante.por.PCR)
```

```
list2 <- list %>%
  filter(date > "2021-02-01" & date < "2021-07-31")
unique(list2$Variante.por.PCR)
```

```
## [1] "No-VOC" "Discarded" "P.1/B.1.351" "Inconclusive" "B.1.617.2"
```

```
gamma <- list2[which(list2$Variante.por.PCR == "P.1/B.1.351"), ]
sum(gamma$n)/sum(list2$n) * 100
```

```
## [1] 78.78151
```



```

list3 <- list %>%
  filter(date > "2021-07-01" & date < "2021-09-30")
list3$Variante.por.PCR <- gsub("No-VOC", "B.1.617.2", list3$Variante.por.PCR)
unique(list3$Variante.por.PCR)

## [1] "Discarded"      "Inconclusive" "P.1/B.1.351"  "B.1.617.2"

delta <- list3[which(list3$Variante.por.PCR == "B.1.617.2"), ]
sum(delta$n)/sum(list3$n) * 100

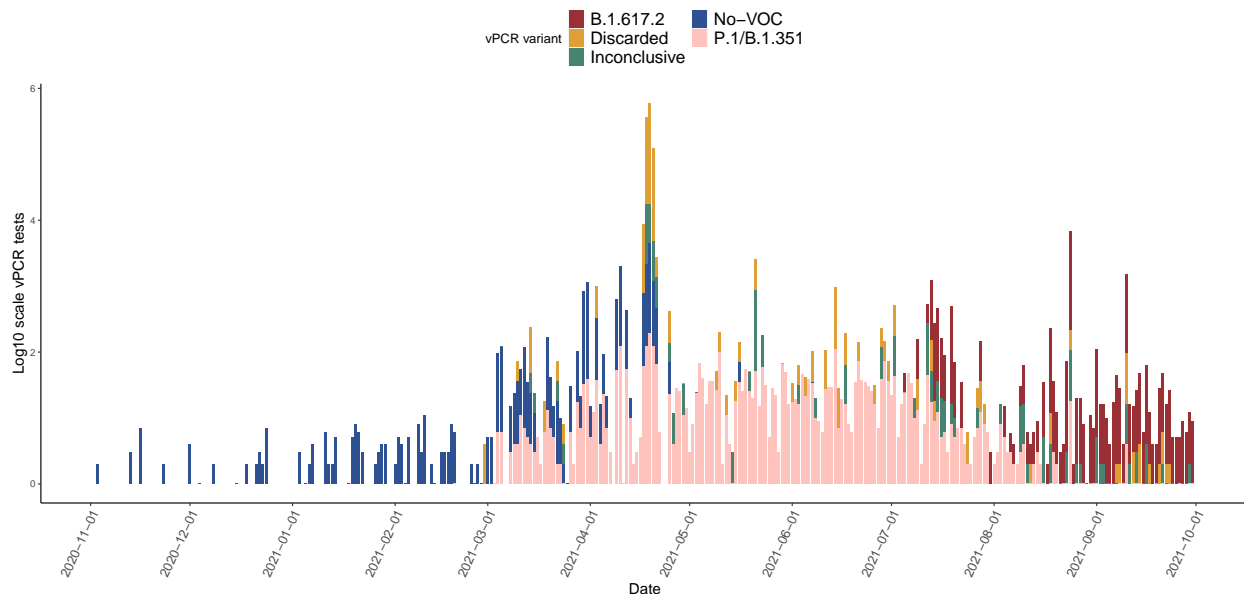
## [1] 46.48693

gamma <- list3[which(list3$Variante.por.PCR == "P.1/B.1.351"), ]
sum(gamma$n)/sum(list3$n) * 100

## [1] 37.5817

s3 <- ggplot(list, aes(fill = Variante.por.PCR, y = log10(n), x = date)) +
  geom_bar(position = "stack", stat = "identity", alpha = 1) + scale_fill_manual(values = c(B.1.617.2 = "#ff9933",
  `P.1/B.1.351` = "#ffcc33", Discarded = "#d9f9d9", Inconclusive = "#468471",
  `No-VOC` = "#2d5192")) + theme(axis.line = element_line(colour = "black"),
  panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
  panel.border = element_blank(), panel.background = element_blank(),
  axis.text.x = element_text(angle = 65, hjust = 1, size = 12), axis.title.x = element_text(size = 14),
  axis.title.y = element_text(size = 14), legend.text = element_text(size = 16),
  legend.title = element_text(size = 12), legend.position = "top", legend.box.just = "center",
  legend.key.width = unit(1, "lines")) + scale_x_date(date_breaks = "1 months") +
  ggtitle("") + guides(fill = guide_legend(title = "vPCR variant", nrow = 3,
  ncol = 2)) + ylab("Log10 scale vPCR tests") + xlab("Date")
s3

```



```

depart_uy <- st_read("ine_depto-20231103T191932Z-001/ine_depto/")

## Reading layer 'ine_depto' from data source
##   '/home/ceciliasalazar/Documentos/trabajo/paper_delta/supplementaries/supplementary_2/datos_input/i
##   using driver 'ESRI Shapefile'

```

```
## Warning in CPL_read_ogr(dsn, layer, query, as.character(options), quiet, : GDAL
## Message 1:
## /home/ceciliasalazar/Documentos/trabajo/paper_delta/supplementaries/supplementary_2/datos_input/ine_
## contains polygon(s) with rings with invalid winding order. Autocorrecting them,
## but that shapefile should be corrected using ogr2ogr for example.

## Simple feature collection with 20 features and 5 fields
## Geometry type: MULTIPOLYGON
## Dimension: XY
## Bounding box: xmin: 366582.2 ymin: 6127919 xmax: 858252.1 ymax: 6671738
## Projected CRS: WGS 84 / UTM zone 21S

# Retrived from
# https://github.com/tereom/taller-mapas-mv/blob/master/material.zip?raw=true

class(depart_uy)

## [1] "sf" "data.frame"

head(depart_uy)

## Simple feature collection with 6 features and 5 fields
## Geometry type: MULTIPOLYGON
## Dimension: XY
## Bounding box: xmin: 368497.6 ymin: 6133499 xmax: 686307.6 ymax: 6671738
## Projected CRS: WGS 84 / UTM zone 21S
## AREA_KM2 PERIMETER DEPTO NOMBRE CDEPTO_ISO
## 1 530 202137.0 1 MONTEVIDEO UYMO
## 2 11928 722385.9 2 ARTIGAS UYAR
## 3 4536 404534.8 3 CANELONES UYCA
## 4 6106 431056.4 5 COLONIA UYCO
## 5 11643 821325.4 6 DURAZNO UYDU
## 6 10417 669409.9 8 FLORIDA UYFD
## geometry
## 1 MULTIPOLYGON (((579197 6136...
## 2 MULTIPOLYGON (((441318.2 66...
## 3 MULTIPOLYGON (((587667.2 61...
## 4 MULTIPOLYGON (((446550.3 61...
## 5 MULTIPOLYGON (((545016.7 62...
## 6 MULTIPOLYGON (((547183.6 62...

dim(depart_uy)

## [1] 20 6

unique(depart_uy$NOMBRE)

## [1] "MONTEVIDEO" "ARTIGAS" "CANELONES"
## [4] "COLONIA" "DURAZNO" "FLORIDA"
## [7] "LAVALLEJA" "PAYSANDU" "RIO NEGRO"
## [10] "RIVERA" "ROCHA" "SALTO"
## [13] "SAN JOSE" "SORIANO" "TREINTA Y TRES"
## [16] "LIMITE CONTESTADO" "TACUAREMBO" "FLORES"
## [19] "MALDONADO" "CERRO LARGO"

df <- read.table("input_vPCR.tsv", sep = "\t", header = T)
table(vPCR$Departamento)
```

```
##
##           Artigas      Canelones      Cerro Largo      Colonia
##           664         168          329          124         119
##           Durazno      Flores          Florida      Lavalleja      Maldonado
##           15          55           46           48          202
##           Montevideo    Paysandú      Río Negro      Rivera          Rocha
##           1174         292          227          113          378
##           Salto        San José        Soriano      Tacuarembó Treinta y Tres
##           331          216           82           404          94
```

```
df$Departament <- toupper(df$Departament)
colnames(df)[1] <- c("NOMBRE")
head(df)
```

```
##           NOMBRE Count      pct
## 1      DURAZNO     15 0.2952175
## 2      FLORIDA     46 0.9053336
## 3    LAVALLEJA     48 0.9446959
## 4      FLORES     55 1.0824641
## 5      SORIANO     82 1.6138555
## 6 TREINTA Y TRES     94 1.8500295
```

```
unique(df$NOMBRE)
```

```
## [1] "DURAZNO"      "FLORIDA"      "LAVALLEJA"    "FLORES"
## [5] "SORIANO"      "TREINTA Y TRES" "RIVERA"        "COLONIA"
## [9] "CERRO LARGO"  "ARTIGAS"      "MALDONADO"     "SAN JOSÉ"
## [13] "RÍO NEGRO"    "PAYSANDÚ"     "CANELONES"     "SALTO"
## [17] "ROCHA"        "TACUAREMBÓ"   ""              "MONTEVIDEO"
```

```
df$NOMBRE <- gsub("RÍO NEGRO", "RIO NEGRO", df$NOMBRE)
df$NOMBRE <- gsub("SAN JOSÉ", "SAN JOSE", df$NOMBRE)
df$NOMBRE <- gsub("TACUAREMBÓ", "TACUAREMBO", df$NOMBRE)
df$NOMBRE <- gsub("PAYSANDÚ", "PAYSANDU", df$NOMBRE)
```

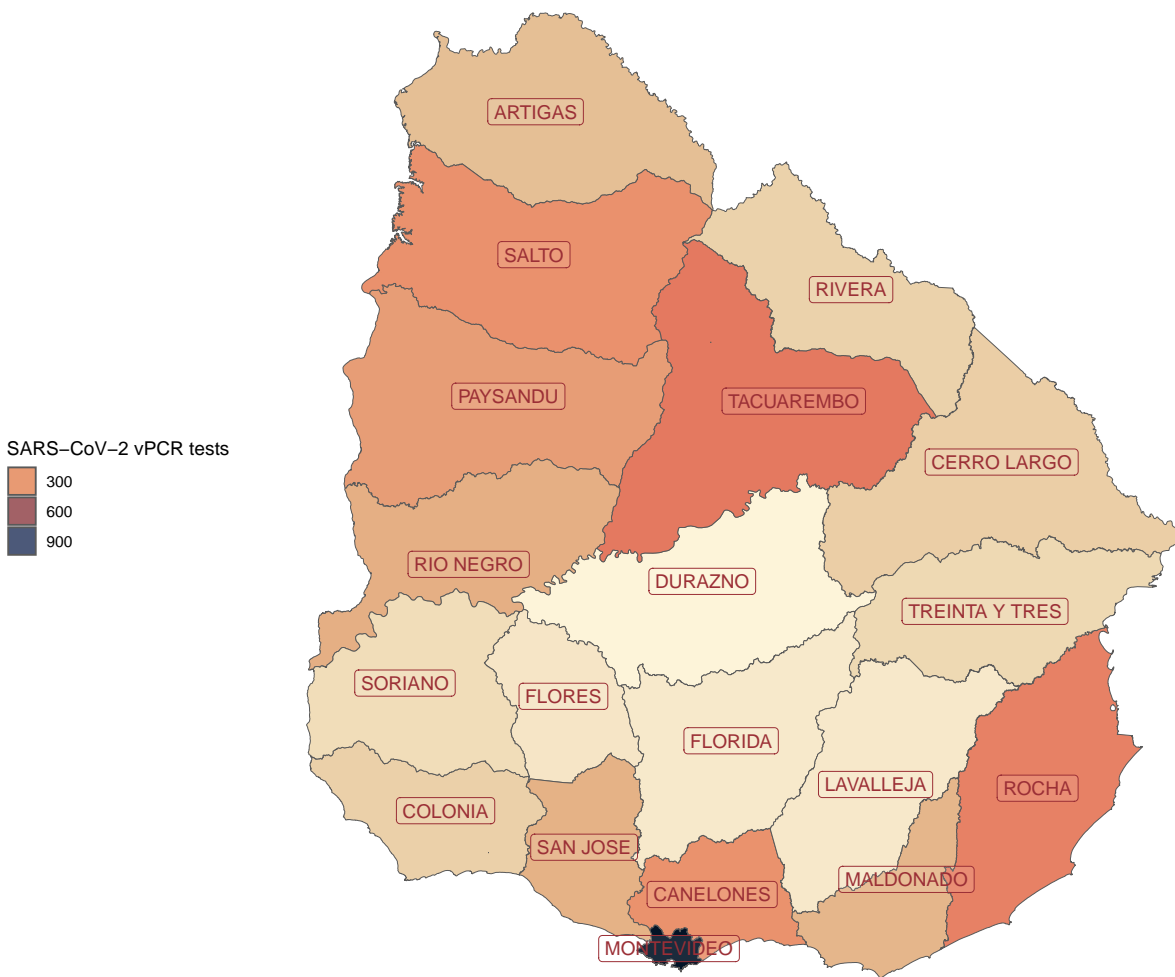
```
depart_uy <- merge(depart_uy, df, by = "NOMBRE")
head(depart_uy)
```

```
## Simple feature collection with 6 features and 7 fields
## Geometry type: MULTIPOLYGON
## Dimension: XY
## Bounding box: xmin: 368497.6 ymin: 6139891 xmax: 858252.1 ymax: 6671738
## Projected CRS: WGS 84 / UTM zone 21S
##           NOMBRE AREA_KM2_ PERIMETER DEPTO CDEPTO_ISO Count      pct
## 1      ARTIGAS     11928   722385.9      2      UYAR     168 3.3064357
## 2    CANELONES     4536   404534.8      3      UYCA     329 6.4751033
## 3  CERRO LARGO    13648   887309.8      4      UYCL     124 2.4404645
## 4      COLONIA     6106   431056.4      5      UYCO     119 2.3420586
## 5      DURAZNO    11643   821325.4      6      UYDU     15 0.2952175
## 6      FLORES     5144   380717.4      7      UYFS     55 1.0824641
##           geometry
## 1 MULTIPOLYGON (((441318.2 66...
## 2 MULTIPOLYGON (((587667.2 61...
## 3 MULTIPOLYGON (((694640.5 64...
## 4 MULTIPOLYGON (((446550.3 61...
## 5 MULTIPOLYGON (((545016.7 62...
```

```
## 6 MULTIPOLYGON (((491438 6242...
```

```
# Create Uruguay Map
```

```
vpcrt <- ggplot(depart_uy) + geom_sf(aes(fill = Count)) + scico::scale_fill_scico(palette = "lipari",
  direction = -1) + geom_sf_label(aes(label = NOMBRE), alpha = 0.1, color = "#9b2f36") +
  theme(axis.line = element_blank(), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), panel.border = element_blank(),
    panel.background = element_blank(), axis.title.x = element_blank(),
    axis.title.y = element_blank(), axis.ticks.x = element_blank(),
    axis.text.x = element_blank(), axis.text.y = element_blank(), axis.ticks.y = element_blank(),
    legend.position = "left") + guides(fill = guide_legend(title = "SARS-CoV-2 vPCR tests"))
vpcrt
```



```
# Rename samples
```

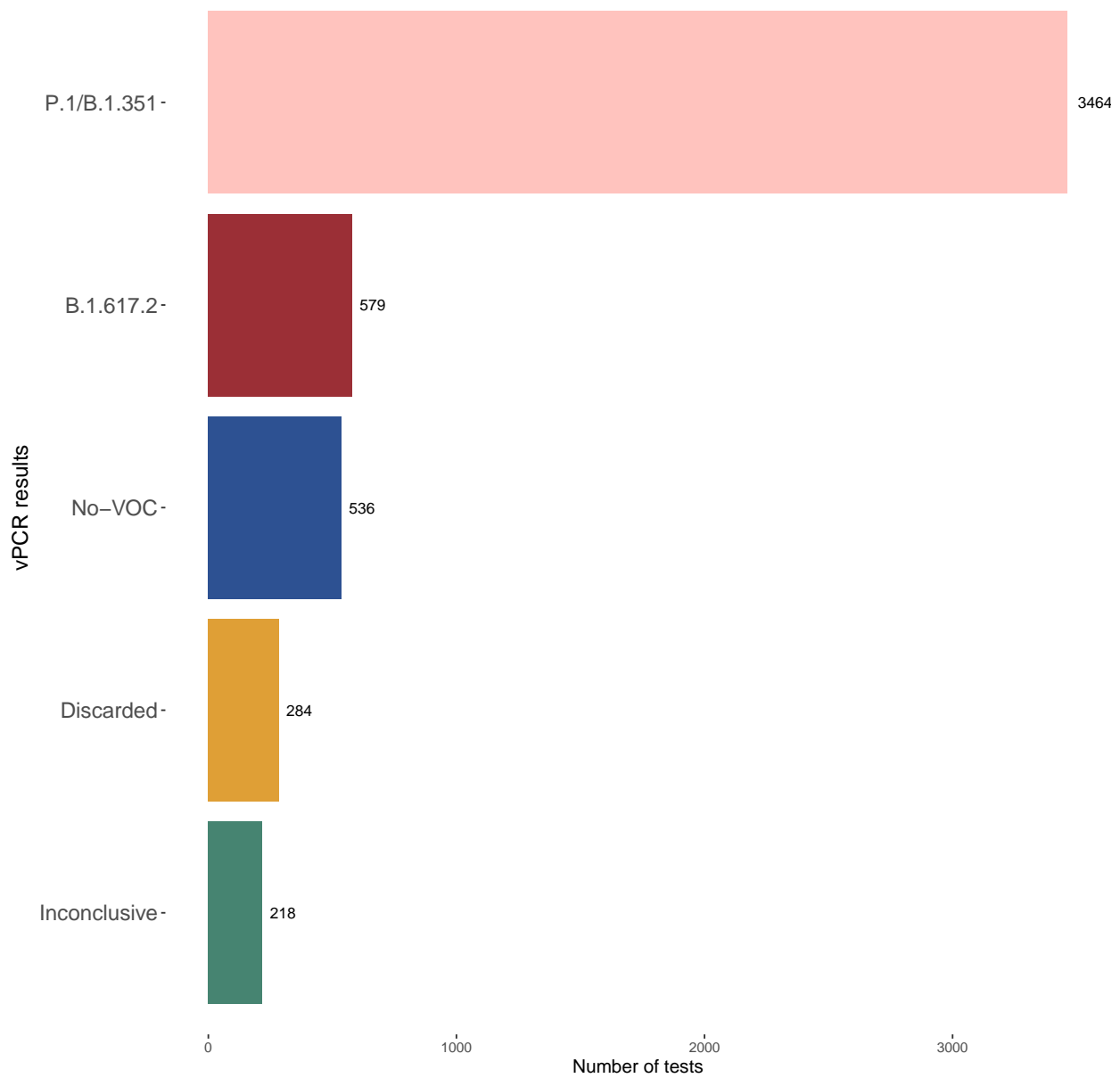
```
vPCRr <- as.data.frame(table(vPCR$Variante.por.PCR))
```

```

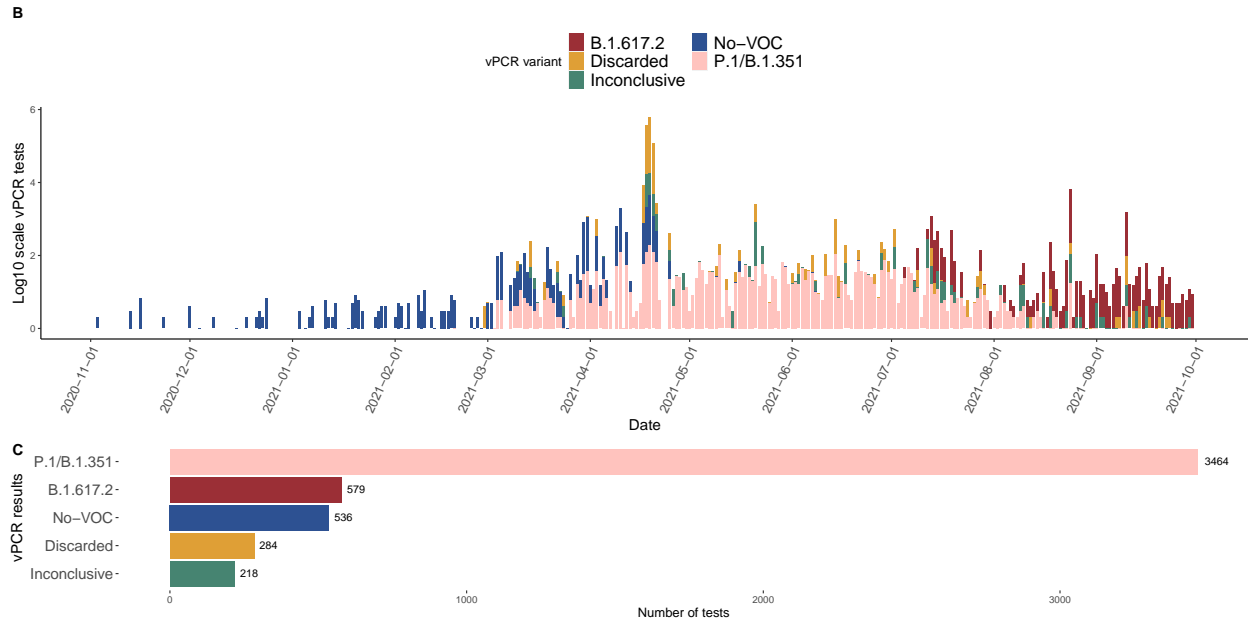
vPCRR <- vPCRR[order(vPCRR$Freq, decreasing = T), ]
vPCRR$Var1 <- gsub("Descartada", "Discarded", vPCRR$Var1)
vPCRR$Var1 <- gsub("No concluyente", "Inconclusive", vPCRR$Var1)

# Create count of vPCR test
bar_c <- ggplot(vPCRR, aes(x = reorder(Var1, Freq), y = Freq, fill = Var1)) +
  geom_bar(stat = "identity") + geom_text(aes(label = Freq), hjust = -0.3,
    size = 3.5) + theme(axis.line = element_blank(), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), panel.border = element_blank(),
    panel.background = element_blank(), axis.text.x = element_text(hjust = 0.5),
    axis.title.x = element_text(size = 12), axis.title.y = element_text(size = 14,
      vjust = 1.5), axis.text.y = element_text(size = 14), legend.position = "none") +
  scale_fill_manual(values = c(B.1.617.2 = "#9b2f36", `P.1/B.1.351` = "#ffc3be",
    Discarded = "#df9f36", Inconclusive = "#468471", `No-VOC` = "#2d5192")) +
  ylab("Number of tests") + xlab("vPCR results") + coord_flip()
bar_c

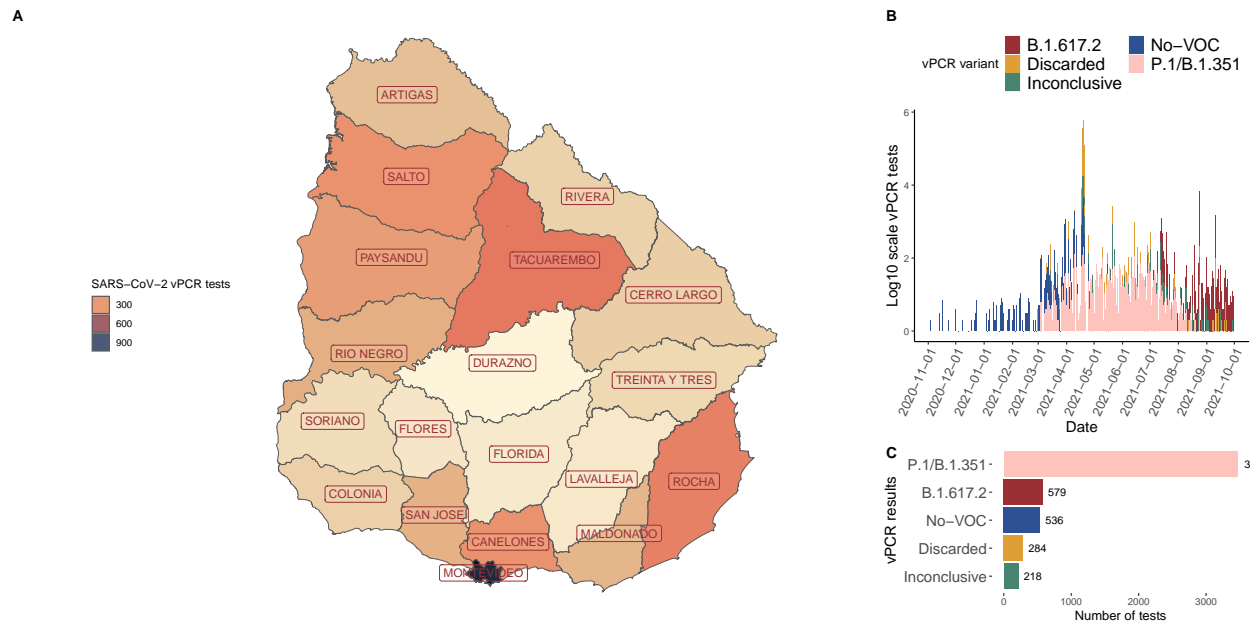
```



```
sup <- ggarrange(s3, bar_c, widths = c(0.7, 0.3), heights = c(0.7, 0.3),
  nrow = 2, labels = c("B", "C"))
sup
```



```
sup1 <- ggarrange(vpcrt, sup, widths = c(0.7, 0.3), heights = c(0.7, 0.3),
  labels = c("A", ""))
sup1
```



```
dir.create("Figures")
```

```
## Warning in dir.create("Figures"): 'Figures' ya existe
```

```
png("../Figures/sup2_vpcr.png", res = 600, height = 25, width = 40, units = "cm")
sup1
dev.off()
```

```
## pdf
## 2
```