

# Positive selection on genes interacting with SARS-Cov2, bats

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## 1 Data

Analysis were formatted by the script covid\_comp\_script0\_table.Rnw.

```
home<-"/home/adminmarie/Documents/CIRI_BIBS_projects/"
workdir<-paste0(home, "2020_05_Etienne_covid/2020_dginn_covid19/")
```

```
tab<-read.delim(paste0(workdir,
  "out_tab/covid_comp_alldginn.txt"), h=T, sep="\t")
dim(tab)

## [1] 442 56
```

## 2 Bats gene

```
makeFig1 <- function(df){

  # prepare data for colors etc
  colMethods <- c("deepskyblue4", "darkorange", "deepskyblue3", "mediumseagreen",
  nameMethods <- c("BUSTED", "BppM1M2", "BppM7M8", "codemlM1M2", "codemlM7M8", "MEME")
  metColor <- data.frame(Name = nameMethods, Col = colMethods, stringsAsFactors = F)

  # subset for this specific figure
  #df <- df[df$nbY >= 1, ] # to drop genes found by 0 methods (big datasets)
  xt <- df[, c("BUSTED", "BppM1M2", "BppM7M8", "codemlM1M2", "codemlM7M8")]
  xt$Gene <- df$Gene
  nbrMeth <- 5
  # reverse order of dataframe so that genes with the most Y are at the bottom (to be
  xt[,1:5] <- ifelse(xt[,1:5] == "Y", 1, 0)
  # sort and Filter the 0 lines
  xt<-xt[order(rowSums(xt[,1:5]))],
  xt<-na.omit(xt[rowSums(xt[,1:5])>2,])

  row.names(xt)<-xt$Gene
  xt<-xt[,1:5]

  colFig1 <- metColor[which(metColor$Name %in% colnames(xt)), ]
```

```
##### PART 1 : NUMBER OF METHODS
par(xpd = NA , mar=c(2,7,4,0) , oma = c(0,0,0,0) , mgp = c(3,0.3,0))

h = barplot(
  t(xt),
  border = NA ,
  axes = F ,
  col = adjustcolor(colFig1$Col, alpha.f = 1),
  horiz = T ,
  las = 2 ,
  main = "Methods detecting positive selection" ,
  cex.main = 0.85,
  cex.names = min(50/nrow(xt), 1.5)
)

axis(3, line = 0, at = c(0:nbrMeth), label = c("0", rep("", nbrMeth -1), nbrMeth),

legend("bottomleft",
  horiz = T,
  border = colFig1$Col,
  legend = colFig1$Name,
  fill = colFig1$Col,
  cex = 0.8,
  bty = "n",
  xpd = NA
)
}
```

```
dftmp<-tab[,c("bats_File", "bats_Name",
  "Gene.name", "bats_GeneSize",
  "bats_NbSpecies", "bats_omegaM0Bpp",
  "bats_omegaM0codeml", "bats_BUSTED",
  "bats_BUSTED_p.value", "bats_MEME_NbSites",
  "bats_MEME_PSS", "bats_BppM1M2",
  "bats_BppM1M2_p.value", "bats_BppM1M2_NbSites",
  "bats_BppM1M2_PSS", "bats_BppM7M8",
  "bats_BppM7M8_p.value", "bats_BppM7M8_NbSites",
  "bats_BppM7M8_PSS", "bats_codemlM1M2",
```

```

    "bats_codemlM1M2_p.value", "bats_codemlM1M2_NbSites",
    "bats_codemlM1M2_PSS", "bats_codemlM7M8",
    "bats_codemlM7M8_p.value", "bats_codemlM7M8_NbSites" ,
    "bats_codemlM7M8_PSS")])

names(dftmp)<-names(df)
makeFig1(dftmp)

```

