This is a data report outlining the a pearson correlation analysis of viral qpcr and clinical score data in the CC lines.

This analysis is based off code documented here:

https://www.r-bloggers.com/r-defining-your-own-color-schemes-for-heatmaps/ (https://www.r-bloggers.com/r-defining-your-own-color-schemes-for-heatmaps/)

```r
library(gplots)
```

```
## Warning: package 'gplots' was built under R version 3.2.5
```

```
##
## Attaching package: 'gplots'
```

```
## The following object is masked from 'package:stats':
##
##     lowess
```

```r
library(ggplot2)
library(reshape2)
```

```
## Warning: package 'reshape2' was built under R version 3.2.5
```

```r
sessionInfo()
```

```
## R version 3.2.3 (2015-12-10)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 14393)
##
## locale:
## [1] LC_COLLATE=English_United States.1252
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] reshape2_1.4.2 ggplot2_2.2.1  gplots_3.0.1
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.12.8       knitr_1.15.1       magrittr_1.5
##  [4] munsell_0.4.3     colorspace_1.3-2   stringr_1.1.0
##  [7] plyr_1.8.4        caTools_1.17.1     tools_3.2.3
## [10] grid_3.2.3        gtable_0.2.0       KernSmooth_2.23-15
## [13] htmltools_0.3.5   gtools_3.5.0       assertthat_0.1
## [16] lazyeval_0.2.0    yaml_2.1.14        rprojroot_1.1
## [19] digest_0.6.11     tibble_1.2         bitops_1.0-6
## [22] evaluate_0.10     rmarkdown_1.3      gdata_2.17.0
## [25] stringi_1.1.2     scales_0.4.1       backports_1.0.4
```

```
set.seed(123)

oas1b_corr_plot <- read.csv(file="C:\\gale_lab\\oas1b_manuscript\\revisions\\qPCR_and_outcome3.c
sv", header=T)



m <- melt(cor(oas1b_corr_plot[,c(5:11)], use="pairwise.complete.obs"))



p <- ggplot(data=m, aes(x=Var1, y=Var2, fill=value)) + geom_tile() + theme(text = element_text(s
ize=20),
axis.text.x = element_text(angle=90, hjust=1))
```

We update the color panel to show those conditions with the highest correlation.

```
#set up a coloring scheme using colorRampPalette
red=rgb(1,0,0); green=rgb(0,1,0); blue=rgb(0,0,1); white=rgb(1,1,1)
RtoWrange<-colorRampPalette(c(red, white ) )
WtoGrange<-colorRampPalette(c(white, green) )

p <- p + scale_fill_gradient2(low=RtoWrange(100), mid=WtoGrange(100), high="gray")

p + theme(text = element_text(size=20),
axis.text.x = element_text(angle=90, hjust=1))
```
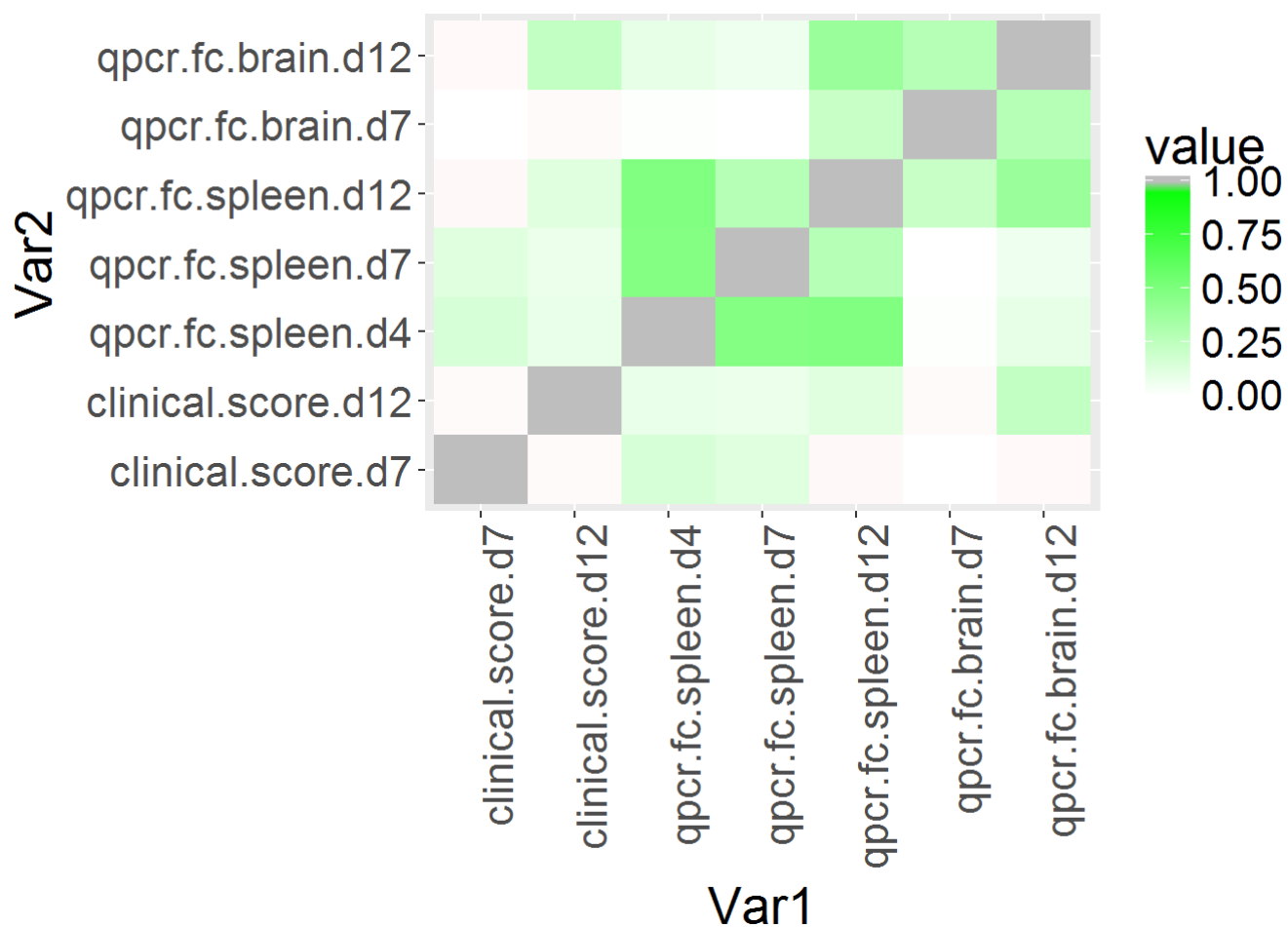
In the correlation heatmap above, there is a relationship between viral load and clinical score at days 4 and 7 post infection. There is also a correlation between clinical score and viral load in the brain at day 12 post infection.