uk3

Here we plot the correlation matrix and the first 3 eigenvectors of Uk3.

```
library('knitr')
```

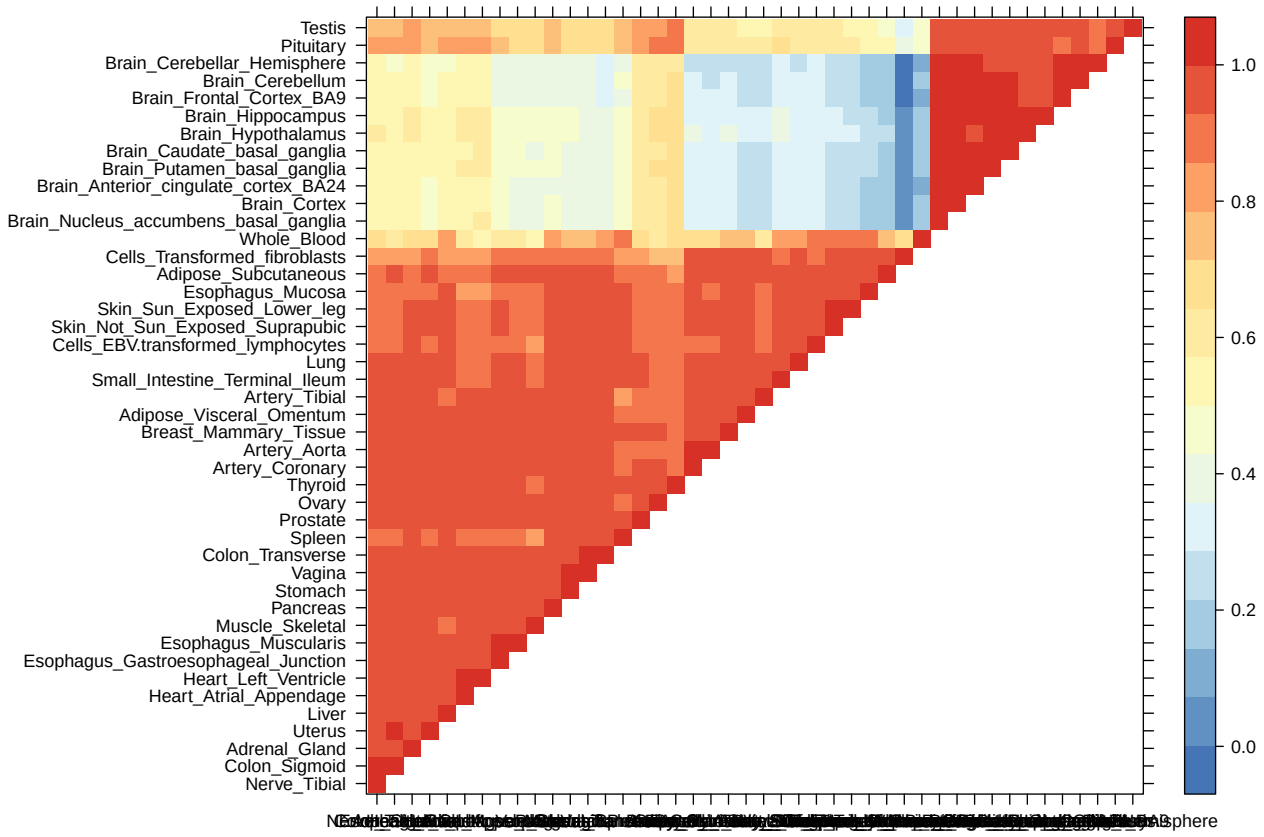
```
## Warning: package 'knitr' was built under R version 3.2.5
```

```
knitr::opts_chunk$set(cache=TRUE)
opts_chunk$set(fig.path = "/Users/sarahurbut/Dropbox/PaperEdits/Paper/ForNatureTechnicalReports/Figures/
covmat=readRDS("../Data/covmatAug13withED.rds")

z.stat=read.table("../Data/maxz.txt")
names=colnames(z.stat)
pis=readRDS("../Data/pisAug13withED.rds")$pihat
pi.mat=matrix(pis,ncol=54,nrow=22,byrow = T)
```

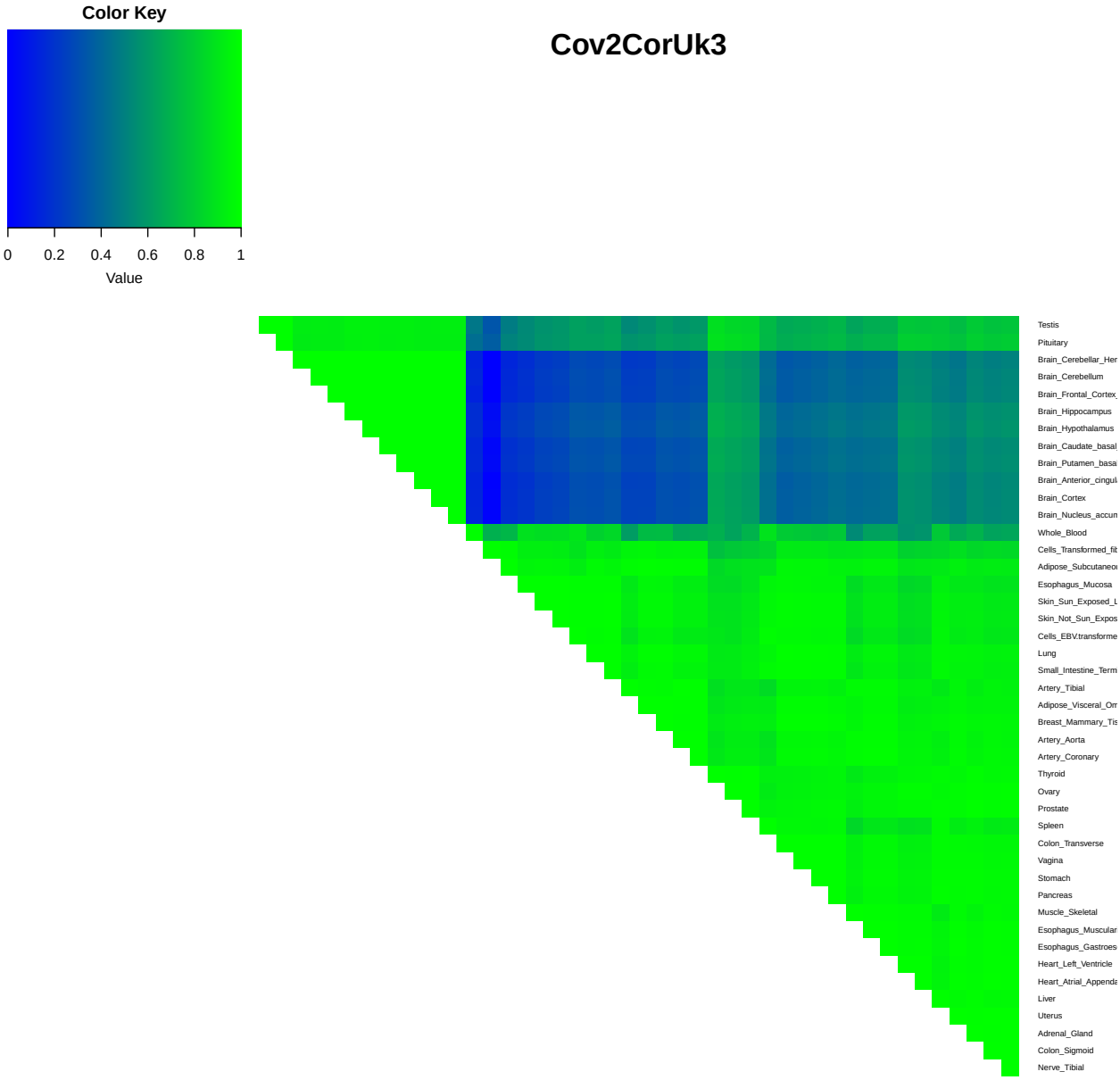
```
library(gplots)
library(ggplot2)
library('colorRamps')
#install.packages("fields")
library(fields)
k=3
hclust.2=function (d, method = "average", members = NULL) {hclust(d, method, members)}
  x=cov2cor(covmat[[k]])
x[x<0]=0
  colnames(x)=names
  rownames(x)=names


h=read.table("../Analysis/uk3rowindices.txt")[,1]
```

heatmap:

```
smat=(x[(h),(h)])
smat[lower.tri(smat)] <- NA

library(lattice)

#print(levelplot(smat,col.regions = jet.colors,xlab = "",ylab = "",colorkey = TRUE))



#clrs <- colorRampPalette(rev(c("purple","#FC8D59","#FEE090","#FFFFBF","#E0F3F8","#91BFDB","#4575B4")))

clrs <- colorRampPalette(rev(c("#D73027","#FC8D59","#FEE090","#FFFFBF",
                               "#E0F3F8","#91BFDB","#4575B4")))(64)
#clrs[63:64] <- "darkviolet"
lat=x[rev(h),rev(h)]
lat[lower.tri(lat)] <- NA
print(levelplot(lat,col.regions = clrs,xlab = "",ylab = "",colorkey = TRUE))
```

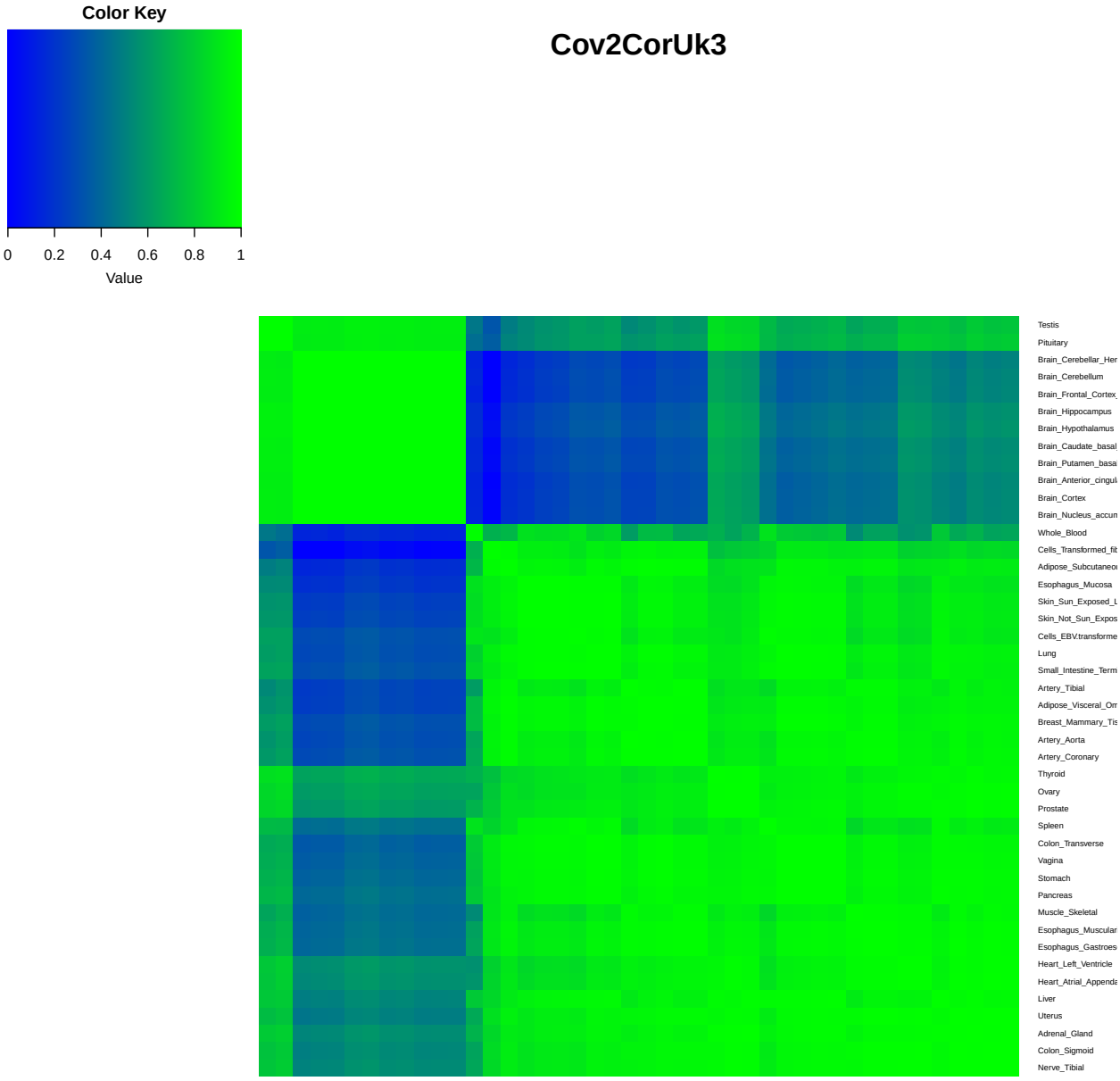



```
heatmap.2(smat,#symm=TRUE,
          Rowv=FALSE,Colv=FALSE,
          dendrogram="none",density="none",trace="none",#col=redblue,
          col=blue2green(256),
          main=paste0("Cov2CorUk3"),
          cexRow=0.5,cexCol=0.5,cex.main=0.5,labCol="")

g=heatmap.2(smat,#symm=TRUE,
          Rowv=FALSE,Colv=FALSE,
          dendrogram="none",density="none",trace="none",#col=redblue,
          col=blue2green(256),
          main=paste0("Cov2CorUk3"),
          cexRow=0.5,cexCol=0.5,cex.main=0.5,labCol="")
```



As square:

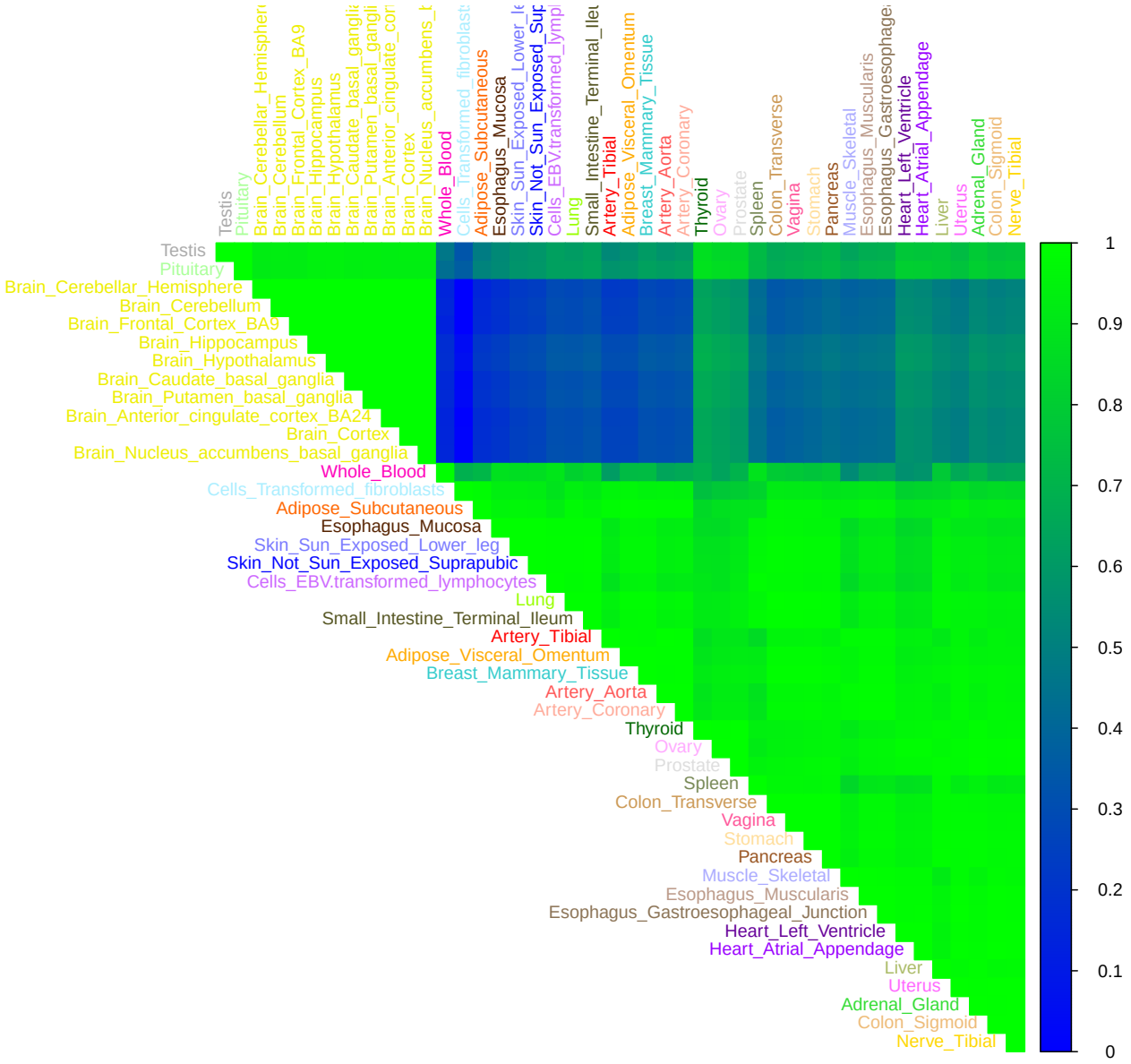
```
smat=(x[h,h])


heatmap.2(smat,#symm=TRUE,
          Rowv=FALSE,Colv=FALSE,
          dendrogram="none",density="none",trace="none",#col=redblue,
          col=blue2green(256),
          main=paste0("Cov2CorUk3"),
          cexRow=0.5,cexCol=0.5,cex.main=0.5,labCol="")
```




```
missing.tissues=c(7,8,19,20,24,25,31,34,37)
color.gtex=read.table("../Data/GTExColors.txt",sep = '\t', comment.char = '')[-missing.tissues,]
col = as.character(color.gtex[,2])

library('corrplot')


corrplot((x[h,h]),type="upper",cl.lim=c(0,1),tl.col=col[h],tl.cex=0.8,method="color",col=rep(blue2green
```

```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```

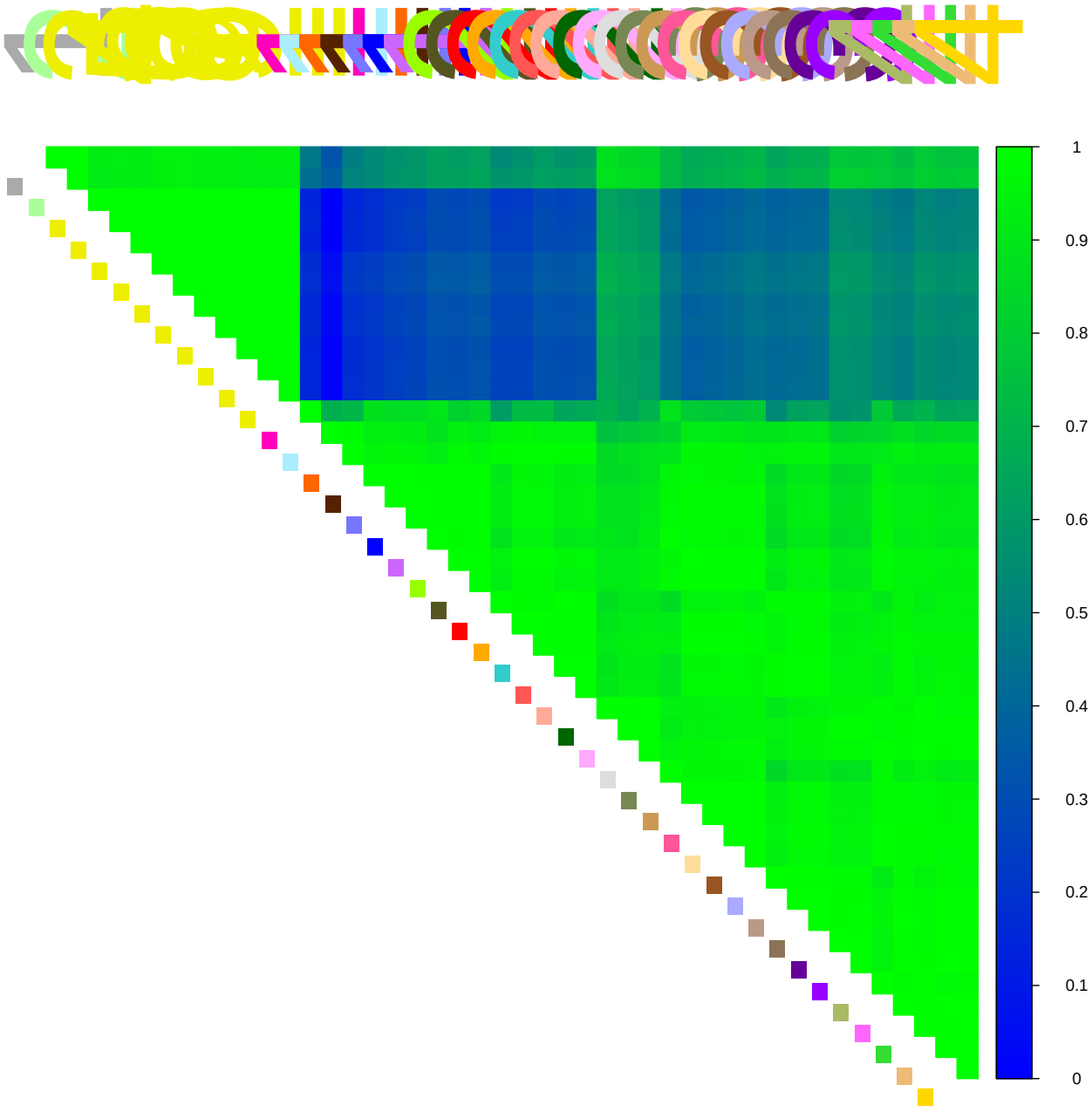
```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```




```
colnames(x)=NULL
rownames(x)=rep(".",44)
corrplot((x[h,h]),type="upper",cl.lim=c(0,1),tl.col=col[h],tl.cex=8,method="color",col=rep(blue2green(25
```

```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```

```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```


1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0