plotsforUk5

Here we plot the correlation matrix and the first 3 eigenvectors of Uk5.

```r
library('knitr')

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

z.stat=read.table("../Data/maxz.txt")
names=colnames(z.stat)
pis=readRDS("../../Dropbox/withzero/piswithzero.rds")$pihat[-1189]
pi.mat=matrix(pis,ncol=54,nrow=22,byrow = T)
```
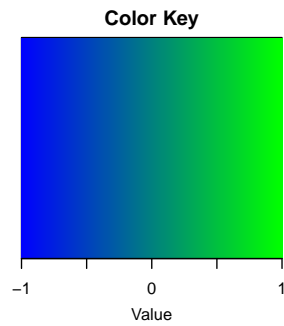
```r
library(gplots)
library(ggplot2)
library('colorRamps')
#install.packages("fields")
library(fields)
k=5
colSums(pi.mat)[k]
```
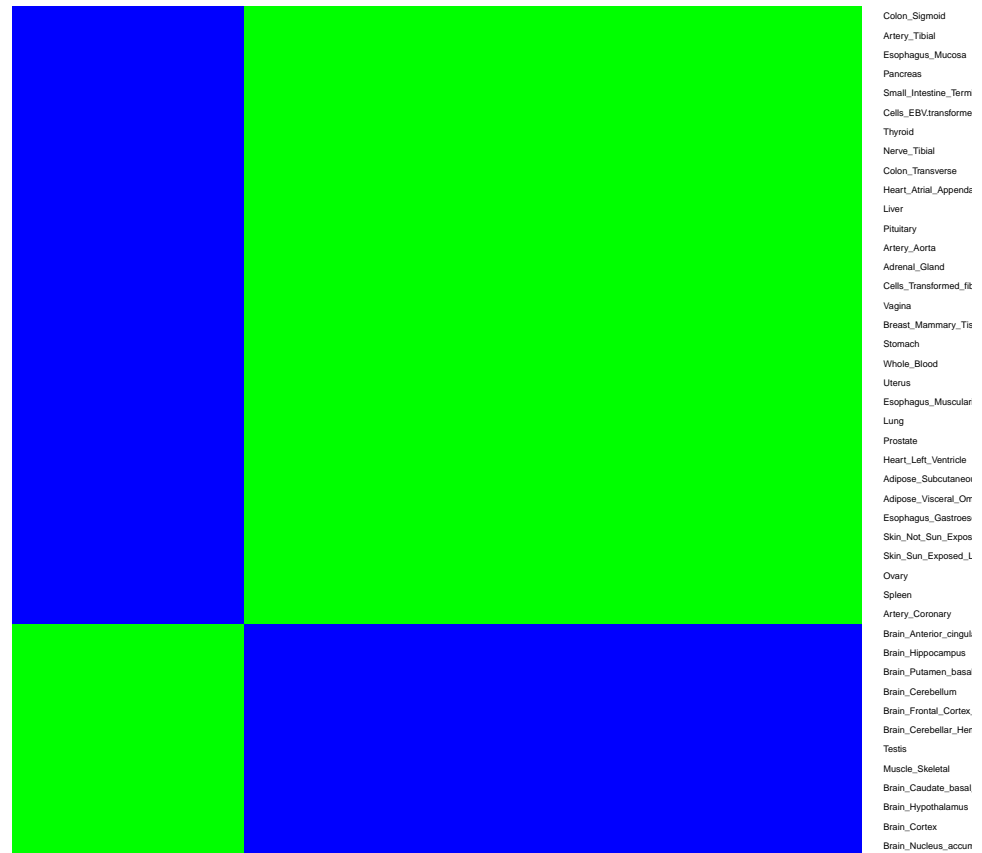
```
## [1] 0.04728692
```

```r
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


##generate indices
h=heatmap.2(x,#symm=TRUE,
          #Rowv=FALSE,Colv=FALSE,
          dendrogram="none",density="none",trace="none",#col=redblue,
          col=blue2green(256),
          main=paste0("Cov2CorUk",k),
          cexRow=0.5,cexCol=0.5,cex.main=0.5,labCol="")
```

Color Key

−1　0　1

Value

Cov2CorUk5

Colon_Sigmoid
Artery_Tibial
Esophagus_Mucosa
Pancreas
Small_Intestine_Term
Cells_EBV.transforme
Thyroid
Nerve_Tibial
Colon_Transverse
Heart_Atrial_Appenda
Liver
Pituitary
Artery_Aorta
Adrenal_Gland
Cells_Transformed_fib
Vagina
Breast_Mammary_Tis
Stomach
Whole_Blood
Uterus
Esophagus_Muscular
Lung
Prostate
Heart_Left_Ventricle
Adipose_Subcutaneo
Adipose_Visceral_Om
Esophagus_Gastroes
Skin_Not_Sun_Expos
Skin_Sun_Exposed_L
Ovary
Spleen
Artery_Coronary
Brain_Anterior_cingula
Brain_Hippocampus
Brain_Putamen_basa
Brain_Cerebellum
Brain_Frontal_Cortex
Brain_Cerebellar_Her
Testis
Muscle_Skeletal
Brain_Caudate_basal
Brain_Hypothalamus
Brain_Cortex
Brain_Nucleus_accum

```r
###transpose map

heatmap.2(x[h$rowInd,h$rowInd],#symm=TRUE,
          Rowv=FALSE,Colv=FALSE,
          dendrogram="none",density="none",trace="none",#col=redblue,
          col=blue2green(256),
          main=paste0("Cov2CorUk",k),
          cexRow=0.5,cexCol=0.5,cex.main=0.5,labCol="")
```
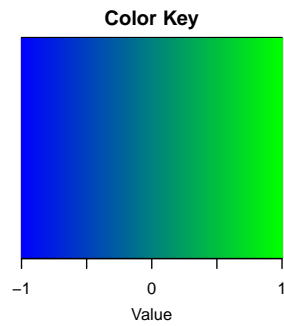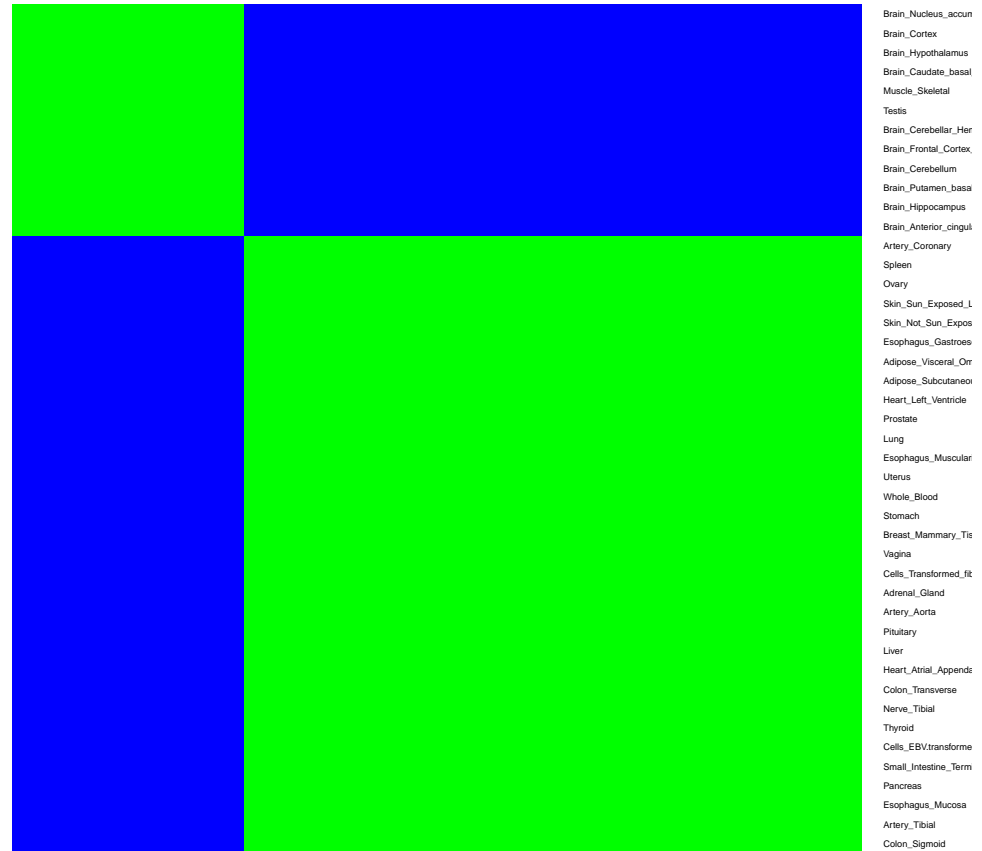
Color Key

Cov2CorUk5

Brain_Nucleus_accun
Brain_Cortex
Brain_Hypothalamus
Brain_Caudate_basal
Muscle_Skeletal
Testis
Brain_Cerebellar_Her
Brain_Frontal_Cortex_
Brain_Cerebellum
Brain_Putamen_basa
Brain_Hippocampus
Brain_Anterior_cinguli
Artery_Coronary
Spleen
Ovary
Skin_Sun_Exposed_L
Skin_Not_Sun_Expos
Esophagus_Gastroes
Adipose_Visceral_Om
Adipose_Subcutaneo
Heart_Left_Ventricle
Prostate
Lung
Esophagus_Muscular
Uterus
Whole_Blood
Stomach
Breast_Mammary_Tis
Vagina
Cells_Transformed_fib
Adrenal_Gland
Artery_Aorta
Pituitary
Liver
Heart_Atrial_Append
Colon_Transverse
Nerve_Tibial
Thyroid
Cells_EBV.transforme
Small_Intestine_Term
Pancreas
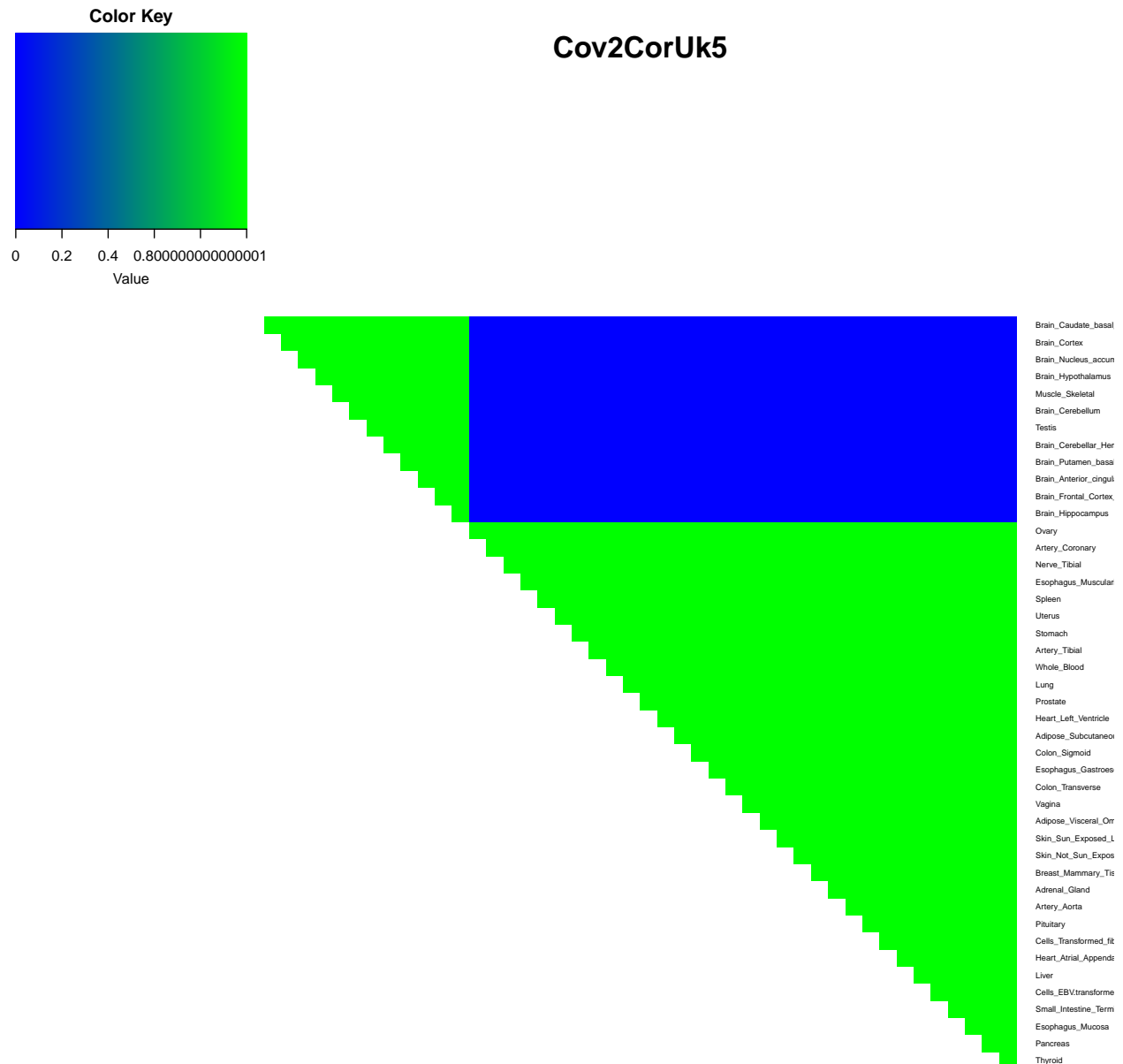Esophagus_Mucosa
Artery_Tibial
Colon_Sigmoid

```r
write.table(h$rowInd,file = paste0("uk",k,"rowIndices.txt"))
h=read.table(paste0("uk",k,"rowIndices.txt"))[,1]
```

heatmap:

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


heatmap.2(smat,#symm=TRUE,
          Rowv=FALSE,Colv=FALSE,
          dendrogram="none",density="none",trace="none",#col=redblue,
          col=blue2green(256),
          main=paste0("Cov2CorUk",k),
          cexRow=0.5,cexCol=0.5,cex.main=0.5,labCol="")
```

Color Key

0   0.2   0.4   0.800000000000001

Value

Cov2CorUk5

Brain_Caudate_basal
Brain_Cortex
Brain_Nucleus_accun
Brain_Hypothalamus
Muscle_Skeletal
Brain_Cerebellum
Testis
Brain_Cerebellar_Her
Brain_Putamen_basal
Brain_Anterior_cinguli
Brain_Frontal_Cortex
Brain_Hippocampus
Ovary
Artery_Coronary
Nerve_Tibial
Esophagus_Muscular
Spleen
Uterus
Stomach
Artery_Tibial
Whole_Blood
Lung
Prostate
Heart_Left_Ventricle
Adipose_Subcutaneo
Colon_Sigmoid
Esophagus_Gastroes
Colon_Transverse
Vagina
Adipose_Visceral_Orr
Skin_Sun_Exposed_L
Skin_Not_Sun_Expos
Breast_Mammary_Tis
Adrenal_Gland
Artery_Aorta
Pituitary
Cells_Transformed_fit
Heart_Atrial_Appenda
Liver
Cells_EBV.transforme
Small_Intestine_Term
Esophagus_Mucosa
Pancreas
Thyroid

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])
```
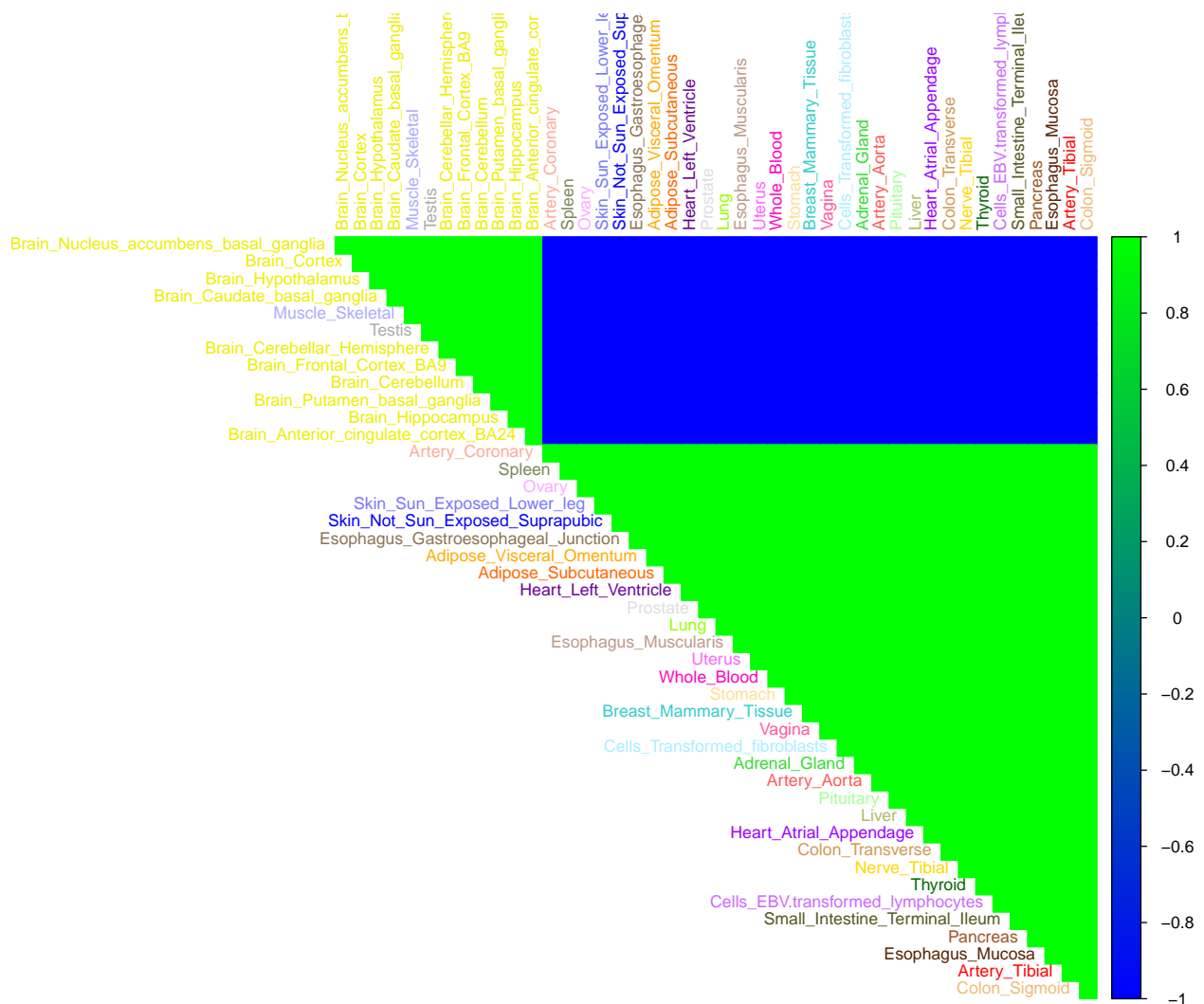
4

```r
library('corrplot')
```

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

```r
corrplot((x[h,h]),type="upper",#cl.lim=c(-1,1),
         tl.col=col[h],tl.cex=0.8,method="color",col=rep(blue2green(256),2))
```

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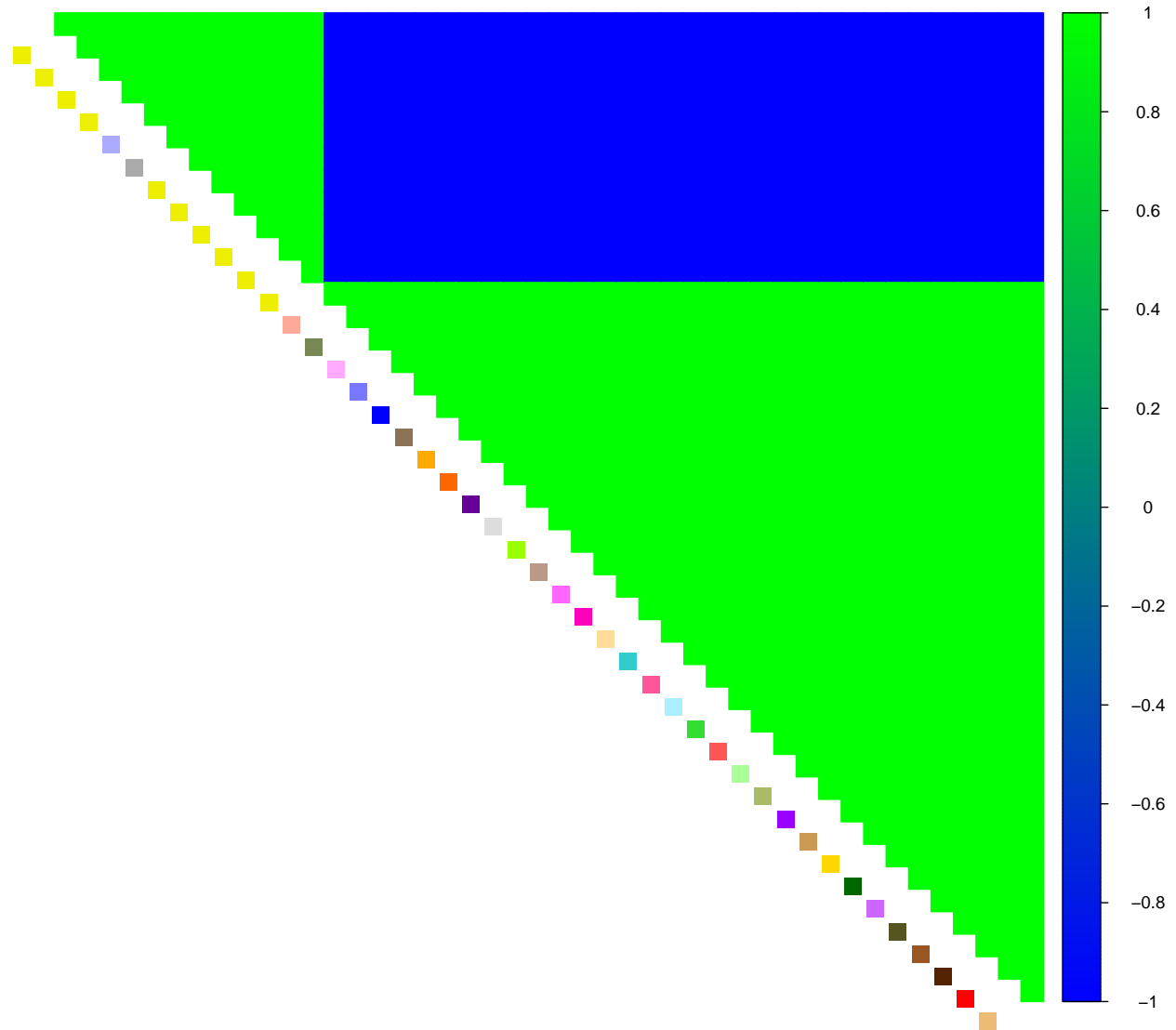
```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```



```r
colnames(x)=NULL
rownames(x)=rep(".",44)
corrplot((x[h,h]),type="upper",#cl.lim=c(-1,1),
         tl.col=col[h],tl.cex=8,method="color",col=rep(blue2green(256),2))
```

```
## 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
```
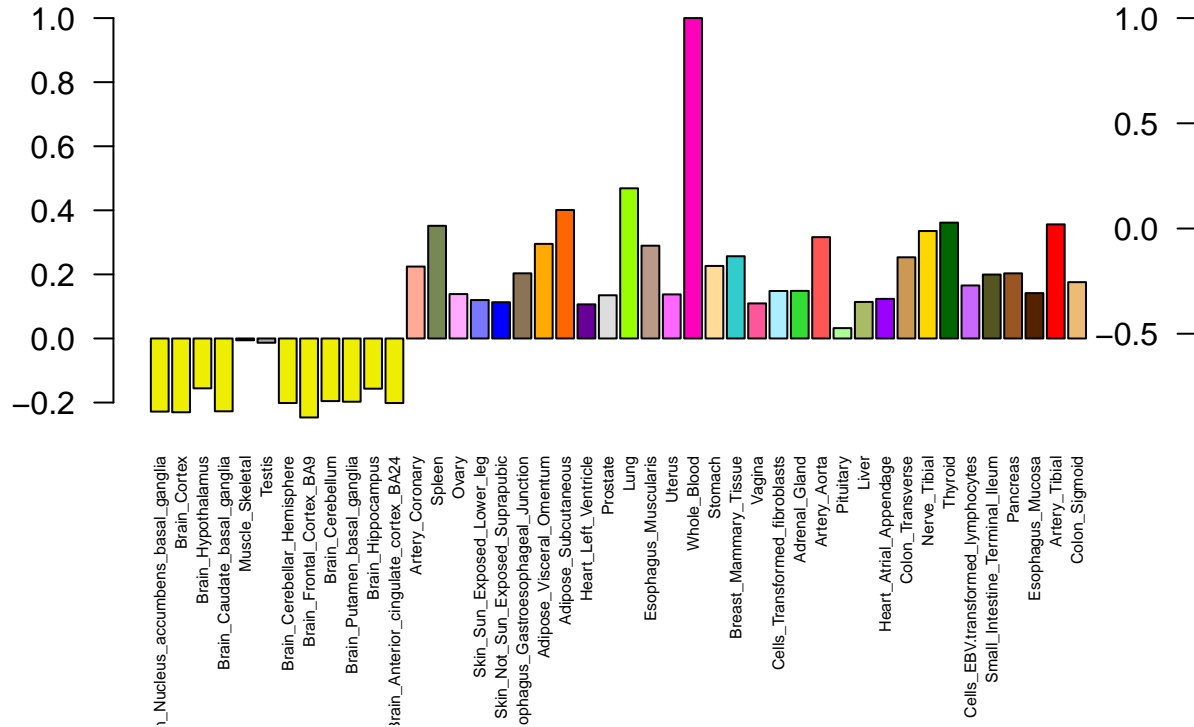

And the SVD Plots:

```
k=5
h=read.table(paste0("uk",k,"rowIndices.txt"))[,1]
for(g in 1:3){
v=svd(covmat[[k]])$v[h,]
rownames(v)=colnames(v)=names(h)
```

```
par(mar=c(8,4.1,4.1,2.1))
barplot(v[,g]/v[which.max(abs(v[,g])),g],las=2,main=paste("Eigenvector",g,"of Uk",k),cex.names = 0.5,col
```

Eigenvector 1 of Uk 5

Eigenvector 3 of Uk 5