

StructureEigenUk2

Here we plot the correlation matrix and the first 3 eigenvectors of Uk2.

```
library('knitr')

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

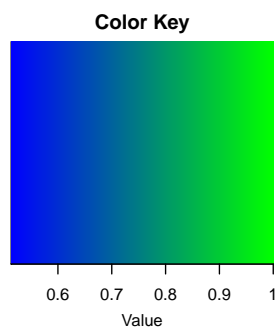
z.stat=read.table("../Data/maxz.txt")
names=colnames(z.stat)
pis=readRDS("../..../Dropbox/withzero/piswithzero.rds")$pihat[-1189]
pi.mat=matrix(pis,ncol=54,nrow=22,byrow = T)
```

```
library(gplots)
library(ggplot2)
library('colorRamps')
#install.packages("fields")
library(fields)
k=2
colSums(pi.mat)[k]
```

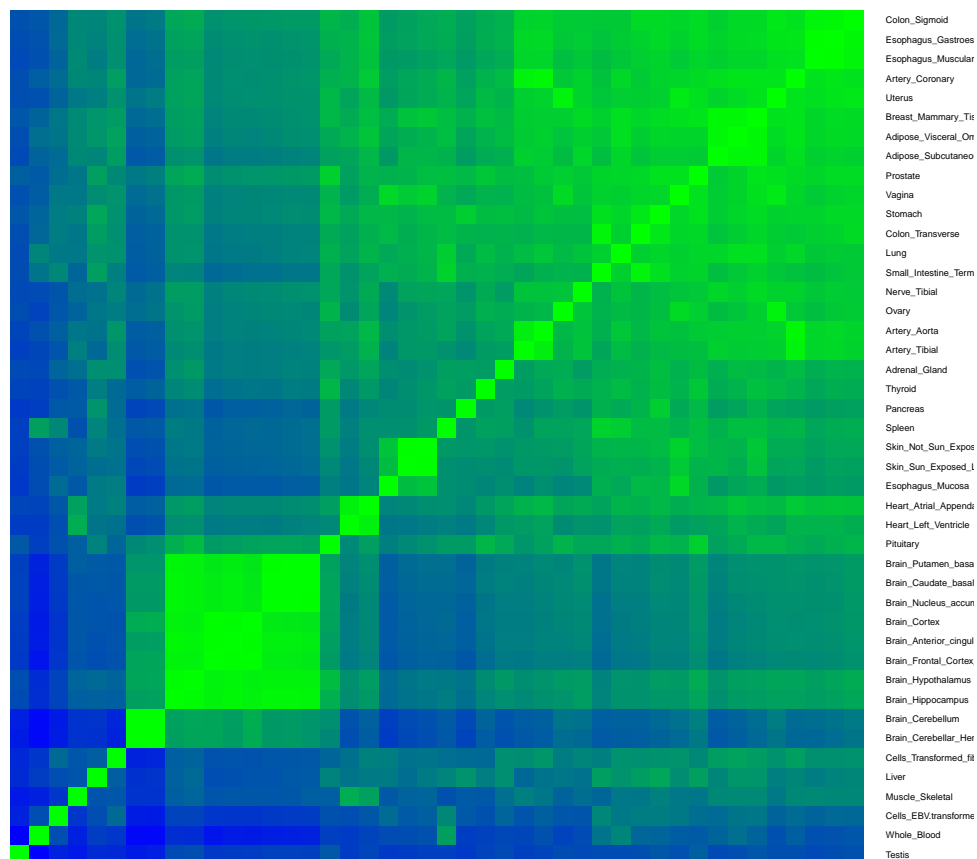
```
## [1] 0.1617467
```

```
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="")
```

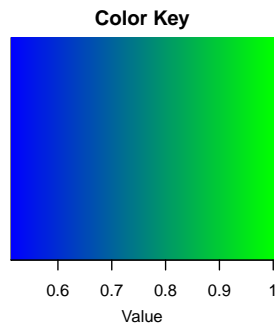


Cov2CorUk2

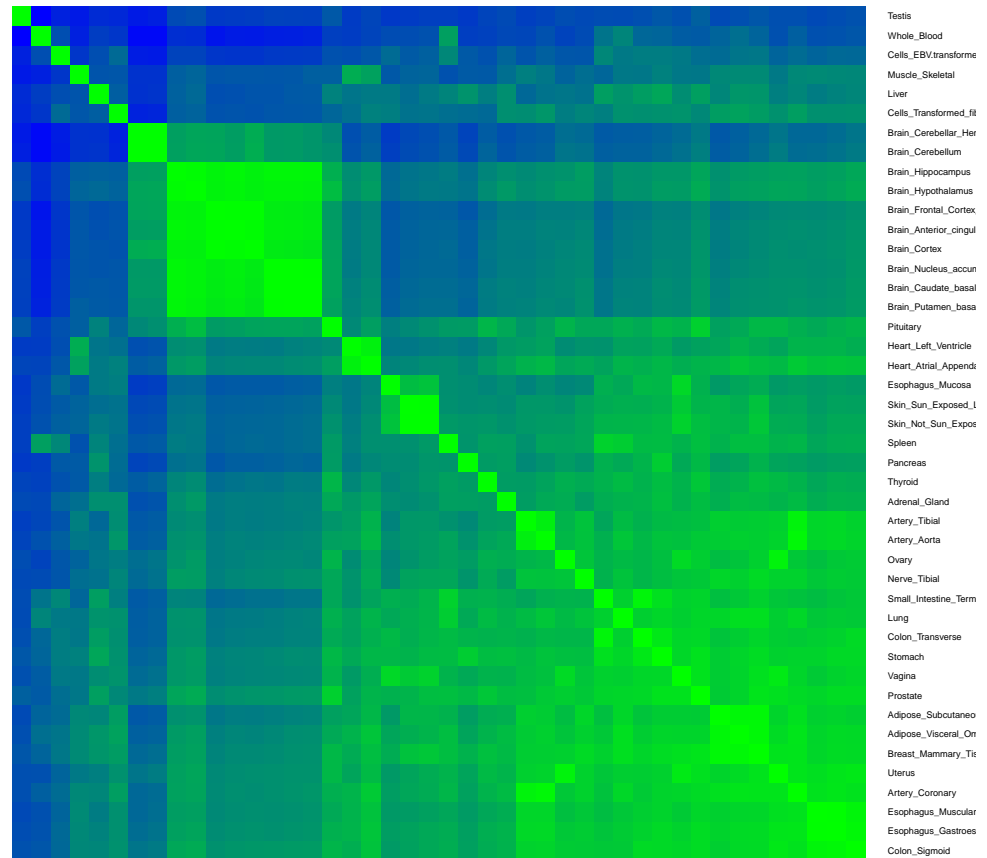


###transpose map

```
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="")
```



Cov2CorUk2

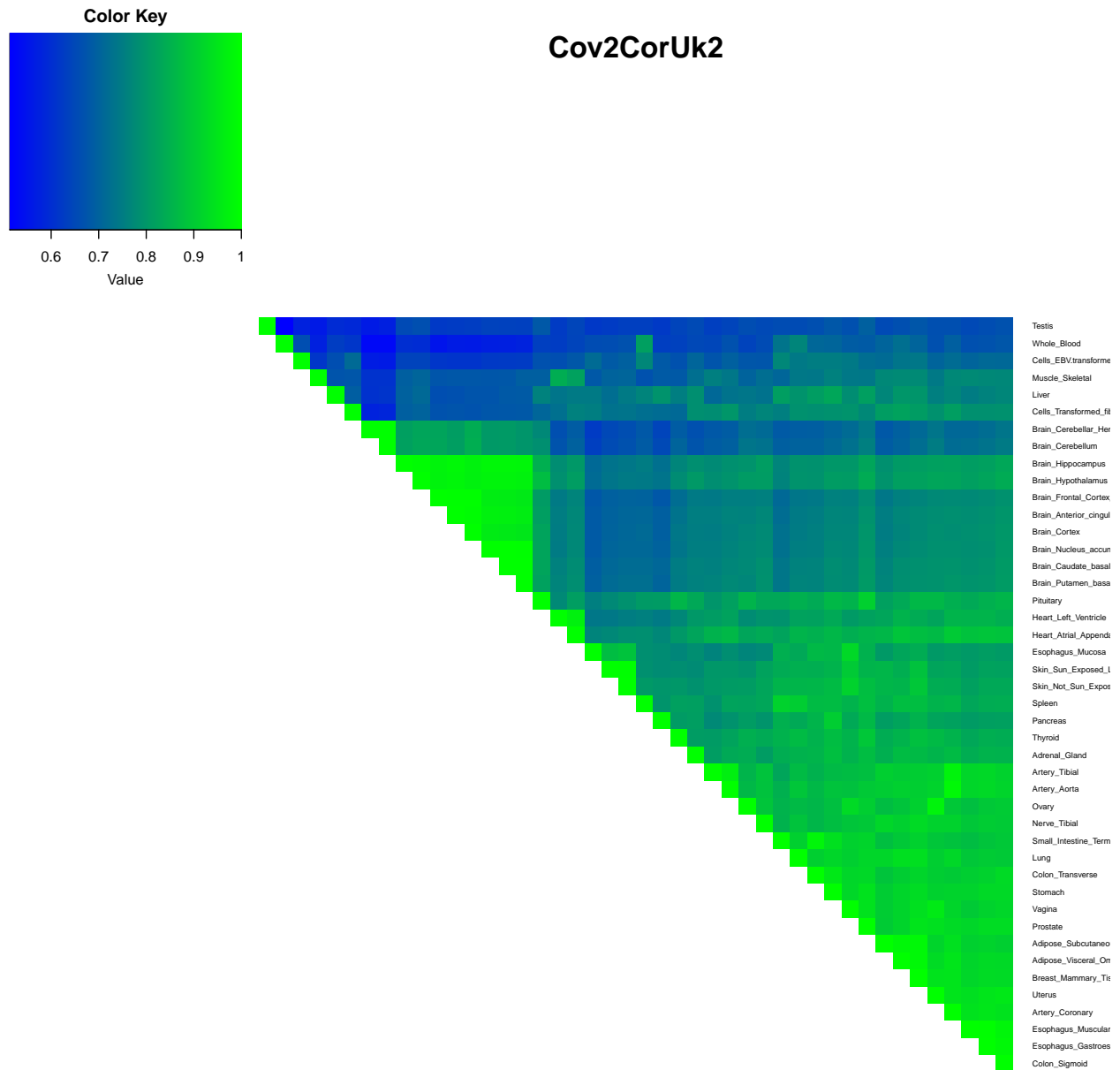


```
write.table(h$rowInd,file = paste0("uk",k,"rowIndices.txt"))
h=read.table(paste0("uk",k,"rowIndices.txt"))[,1]
```

heatmap:

```
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="")
```



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("Cov2Coruk2"),
#           cexRow=0.5,cexCol=0.5,cex.main=0.5,labCol="")

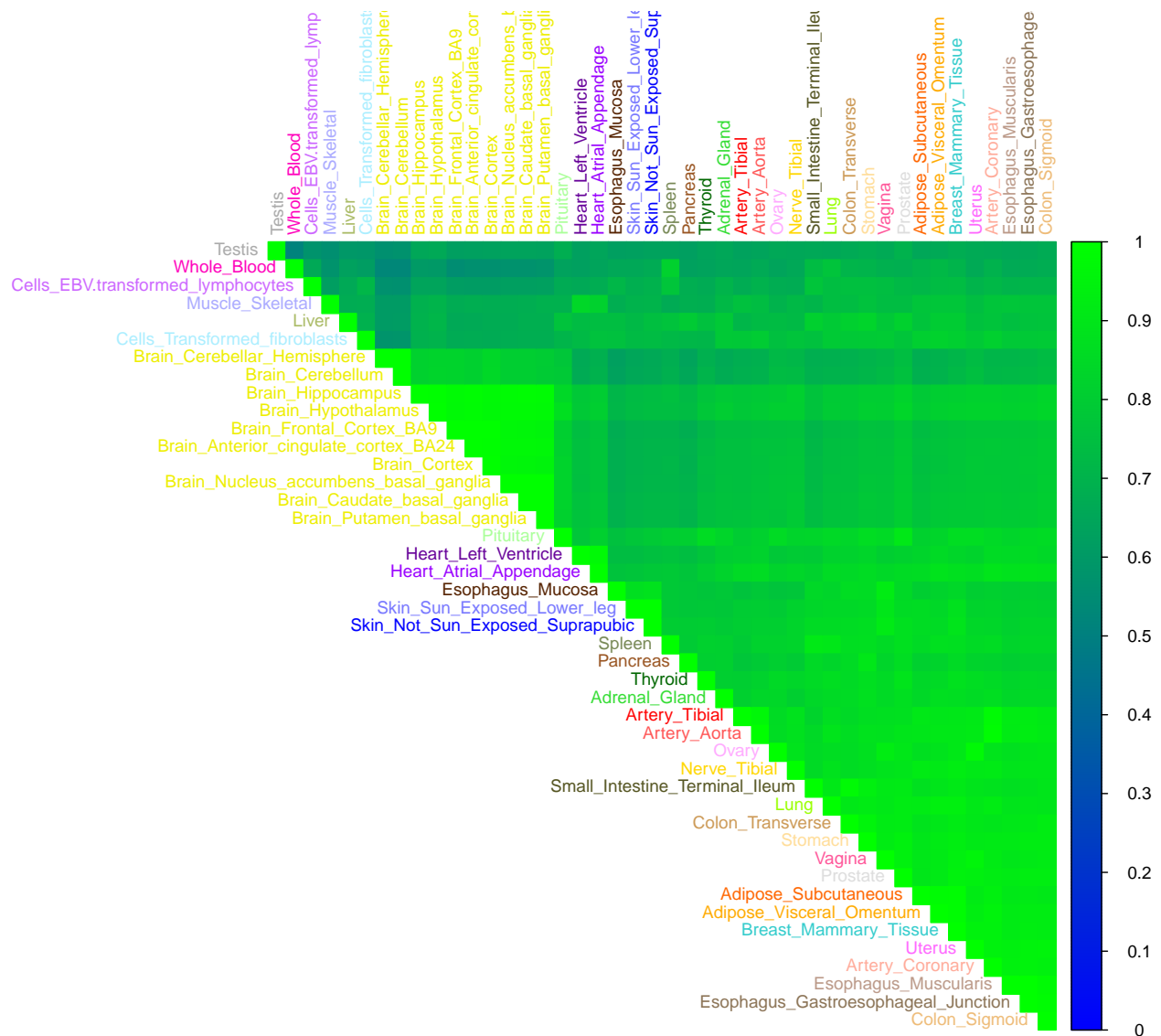
missing.tissues=c(7,8,19,20,24,25,31,34,37)
color.gtex=read.table("../Data/GTExColors.txt",sep = '\t', comment.char = '')[-missing.tissues,]
col = as.character(color.gtex[,2])
```

```
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(200),44))
```

```
## 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
```

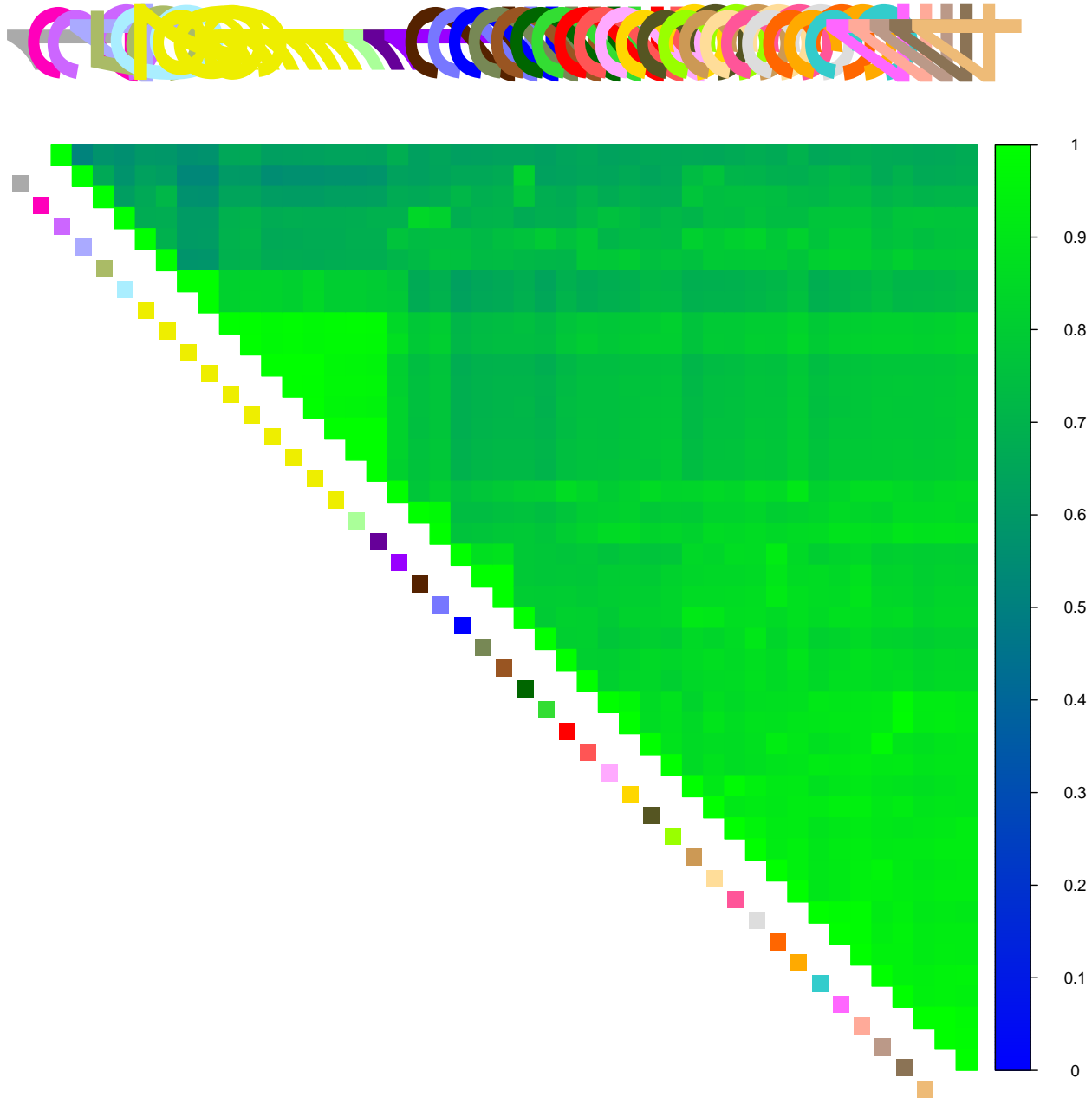
```
rownames(x)=rep(".",44)
```

```
corrplot((x[h,h]),type="upper",cl.lim=c(0,1),tl.col=col[h],tl.cex=8,method="color",col=rep(blue2green(200),44))
```

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

```
## used
```

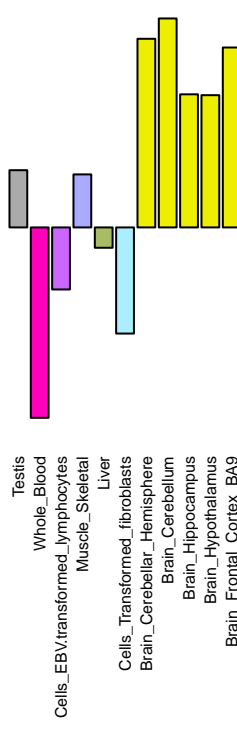
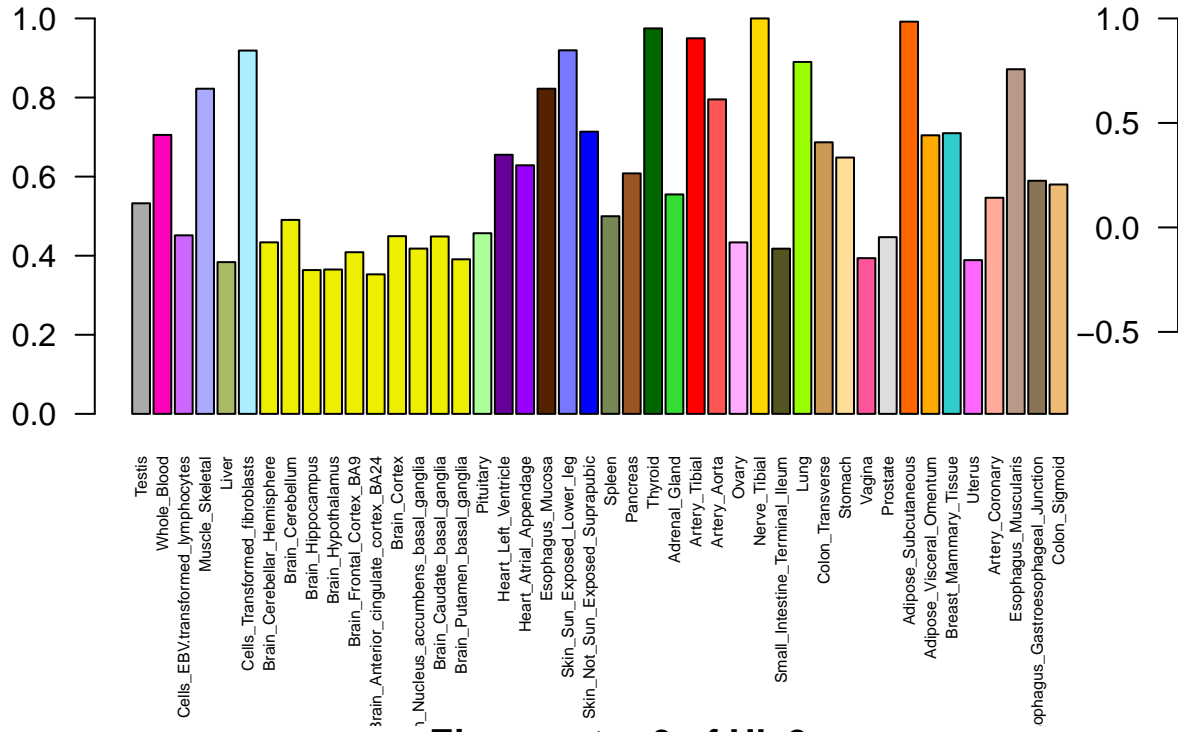
```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```



And the SVD Plots:

```
k=2
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 2



Eigenvector 3 of Uk 2

