

Uk2

Here we plot the correlation matrix and the first 3 eigenvectors of Uk2. Recall, UK2 is the second most common pattern of sharing.

```
library('knitr')

knitr::opts_chunk$set(cache=TRUE)
opts_chunk$set(fig.path = "/Users/sarahurbut/Dropbox/PaperEdits/Paper/NGRevision/Figureswithres/")
covmat=readRDS("../Data_vhat/covmatwithvhat.rds")

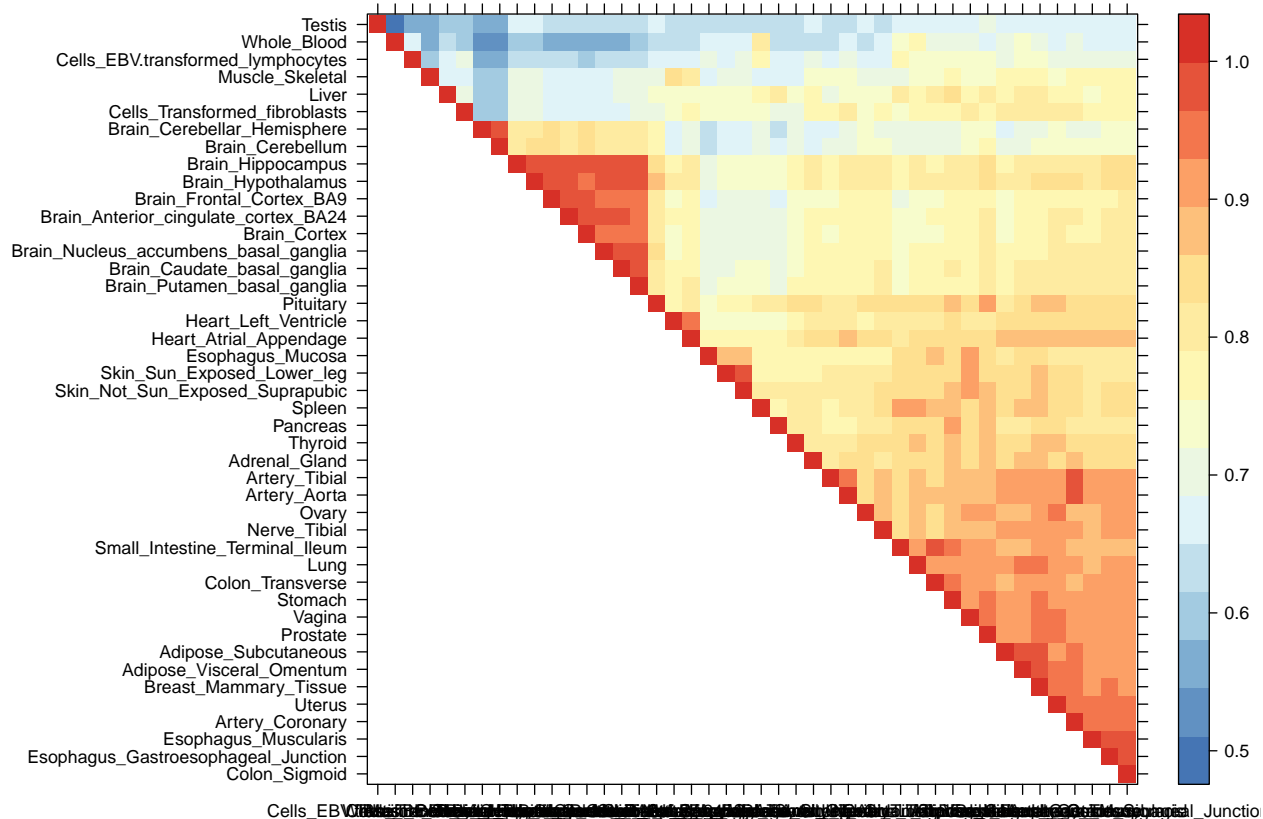
z.stat=read.table("../Data/maxz.txt")
names=colnames(z.stat)
pis=readRDS("../Data_vhat/piswithvhat.rds")$pihat
pi.mat=matrix(pis[-length(pis)],ncol=54,nrow=22,byrow = T)
```

```
## [1] 0.2004572
```

Here we make the lattice plot:

```
library(lattice)

clrs <- colorRampPalette(rev(c("#D73027", "#FC8D59", "#FEE090", "#FFFFBF",
                              "#E0F3F8", "#91BFDB", "#4575B4")))(64)
#clrs[63:64] <- "darkviolet"
lat=x[rev(h),rev(h)]
#lat=x[h,h]
lat[lower.tri(lat)] <- NA
n=nrow(lat)
print(levelplot(lat[n:1,],col.regions = clrs,xlab = "",ylab = "",colorkey = TRUE))
```



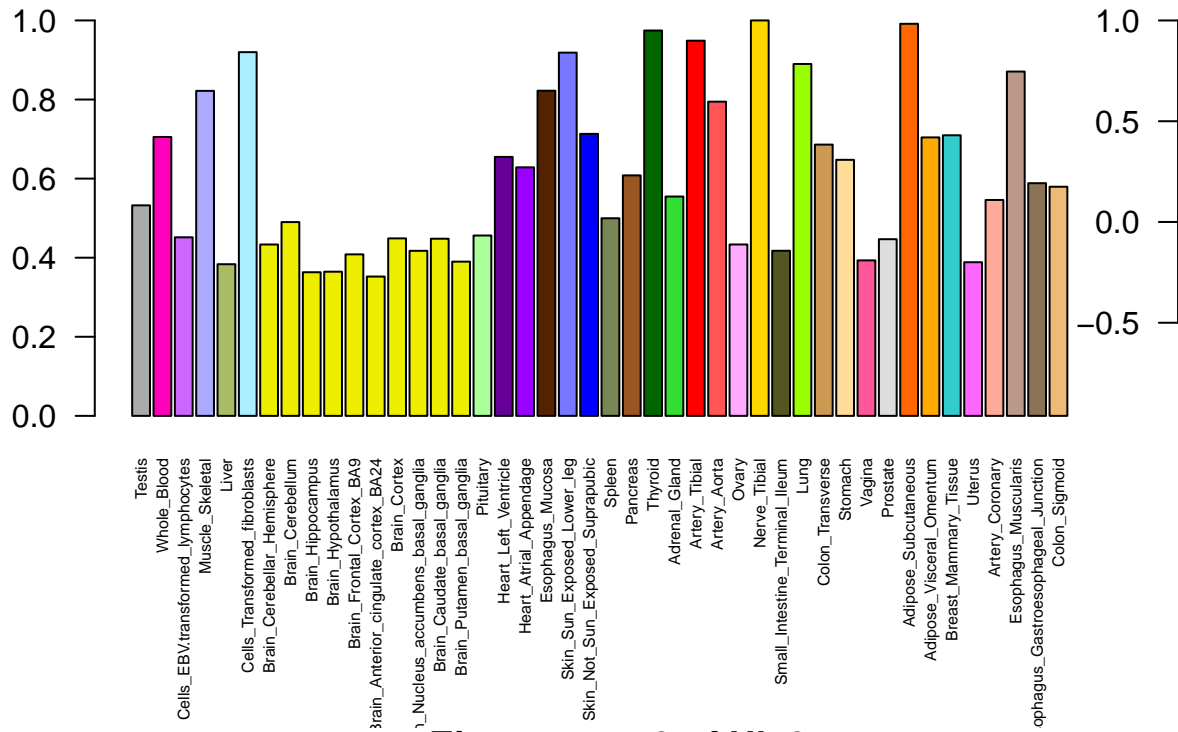
```
#print(levelplot(lat,col.regions = clr, xlab = "", ylab = "", colorkey = TRUE))
```

And the SVD Plots:

```
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])

k=2
h=read.table(paste0("../Data/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

