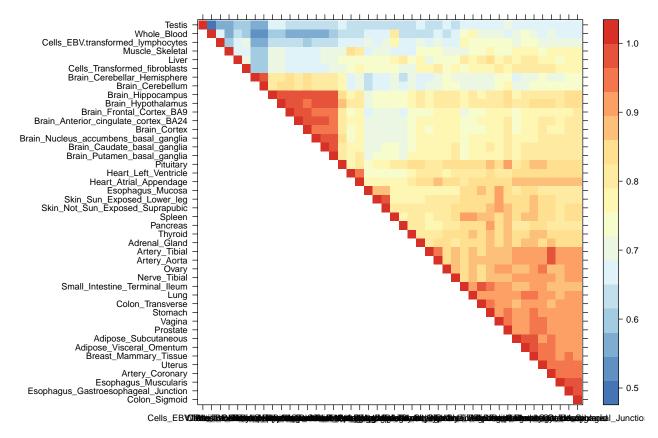
## Uk2

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)
##
## Attaching package: 'gplots'
## The following object is masked from 'package:stats':
##
##
       lowess
## Loading required package: spam
## Loading required package: grid
## Spam version 1.4-0 (2016-08-29) is loaded.
## Type 'help( Spam)' or 'demo( spam)' for a short introduction
## and overview of this package.
## Help for individual functions is also obtained by adding the
## suffix '.spam' to the function name, e.g. 'help( chol.spam)'.
##
## Attaching package: 'spam'
## The following objects are masked from 'package:base':
##
##
       backsolve, forwardsolve
## Loading required package: maps
## [1] 0.2004572
```

Here we make the lattice plot:



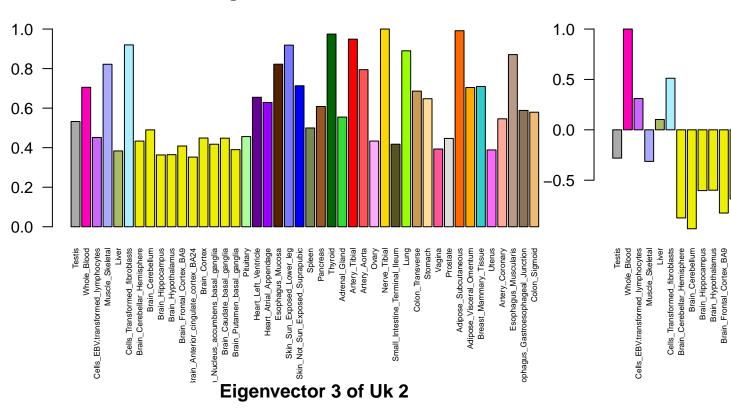
```
#print(levelplot(lat,col.regions = clrs,xlab = "",ylab = "",colorkey = TRUE))
```

And the SVD Plots:

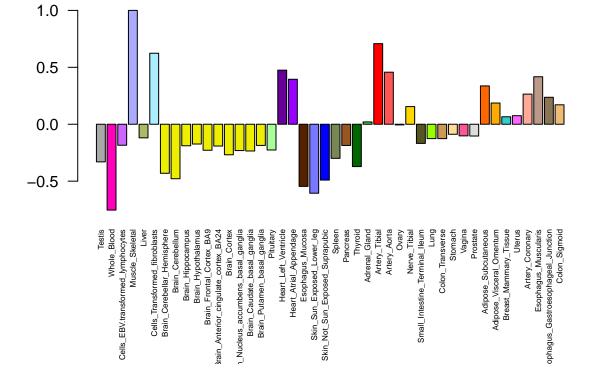
```
missing.tissues=c(7,8,19,20,24,25,31,34,37)
color.gtex=read.table("../../Data/GTExColors.txt",sep = '\t', comment.char = '')[-missing.tissues,]
col = as.character(color.gtex[,2])

k=2
h=read.table(paste0("../../Data/uk",k,"rowIndices.txt"))[,1]
for(g in 1:3){
v=svd(covmat[[k]])$v[h,];d=svd(covmat[[k]])$d
#rownames(v)=colnames(v)=names[h]
```

## Eigenvector 1 of Uk 2







 $(d^2/sum(d^2))[1:3]$ 

**##** [1] 0.995080705 0.001505785 0.000828585