

# SharingBySign

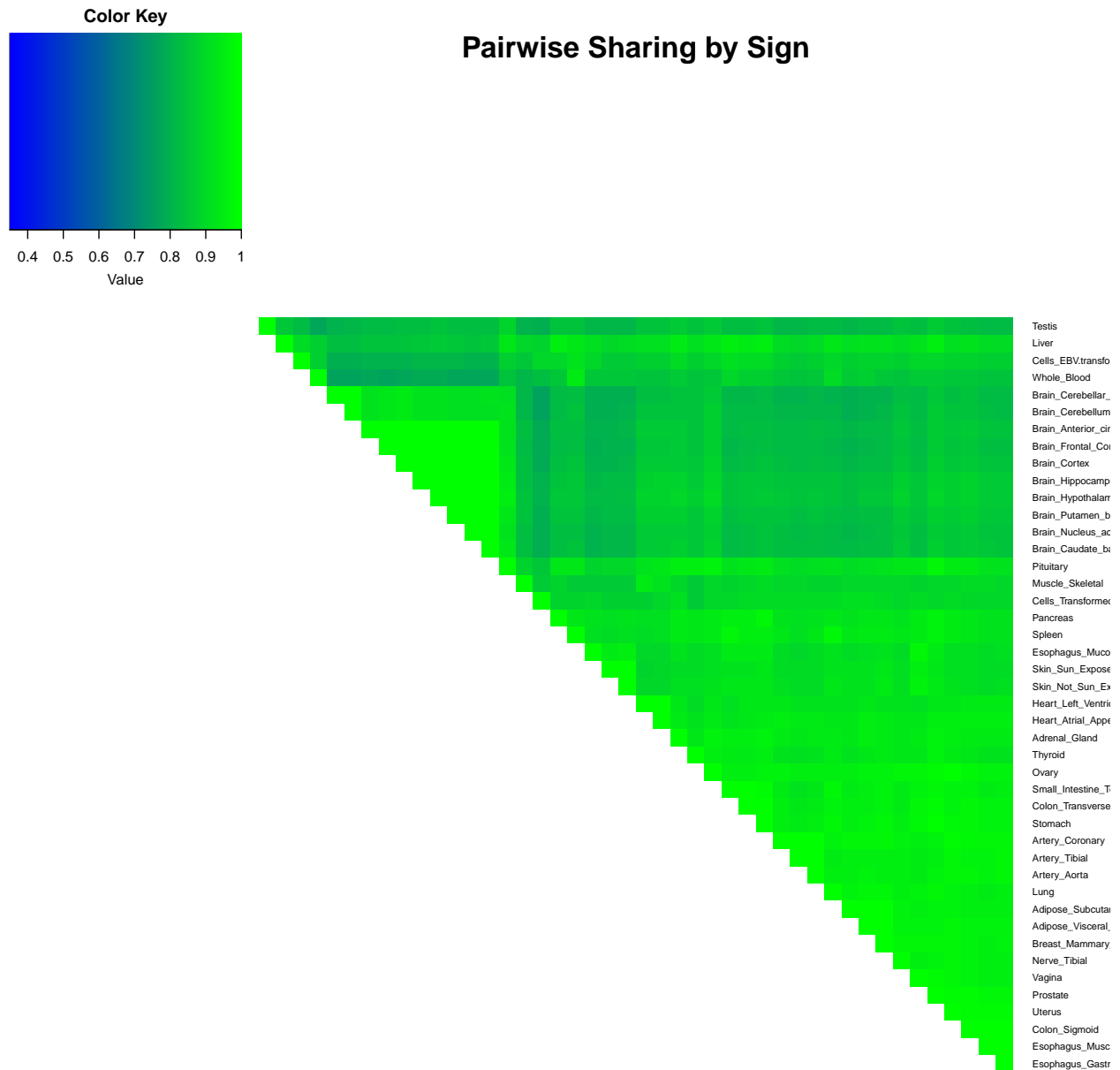
Perform the analysis with global:

```
##  
## Attaching package: 'gplots'  
  
## The following object is masked from 'package:stats':  
##  
##      lowess
```

Generate Plot with corrplot:

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

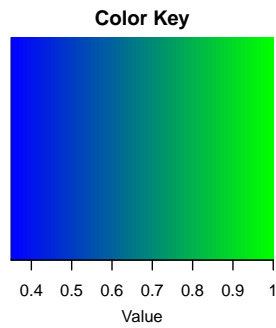
Now do with heatmap.2:



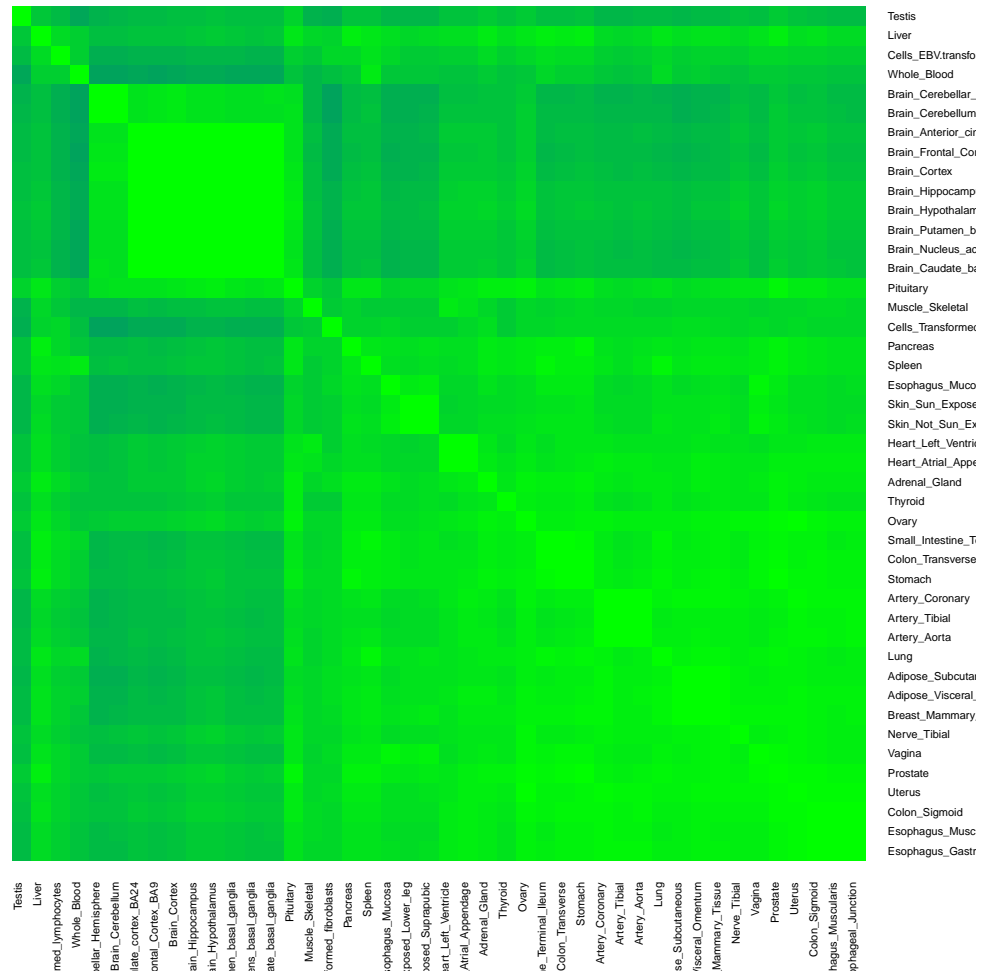
Do as square:

```
smat=shared.fold.size[(all.tissue.order),(all.tissue.order)]

heatmap.2(smat,Rowv=FALSE,Colv=FALSE,
  symm=TRUE,dendrogram="none",density="none",trace="none",#col=redblue,
  col=blue2green,main=paste0("Pairwise Sharing by Sign"),
  cexRow=0.6,cexCol=0.6,cex.main=0.5,breaks=seq(0.35,1,0.01))
```



## Pairwise Sharing by Sign



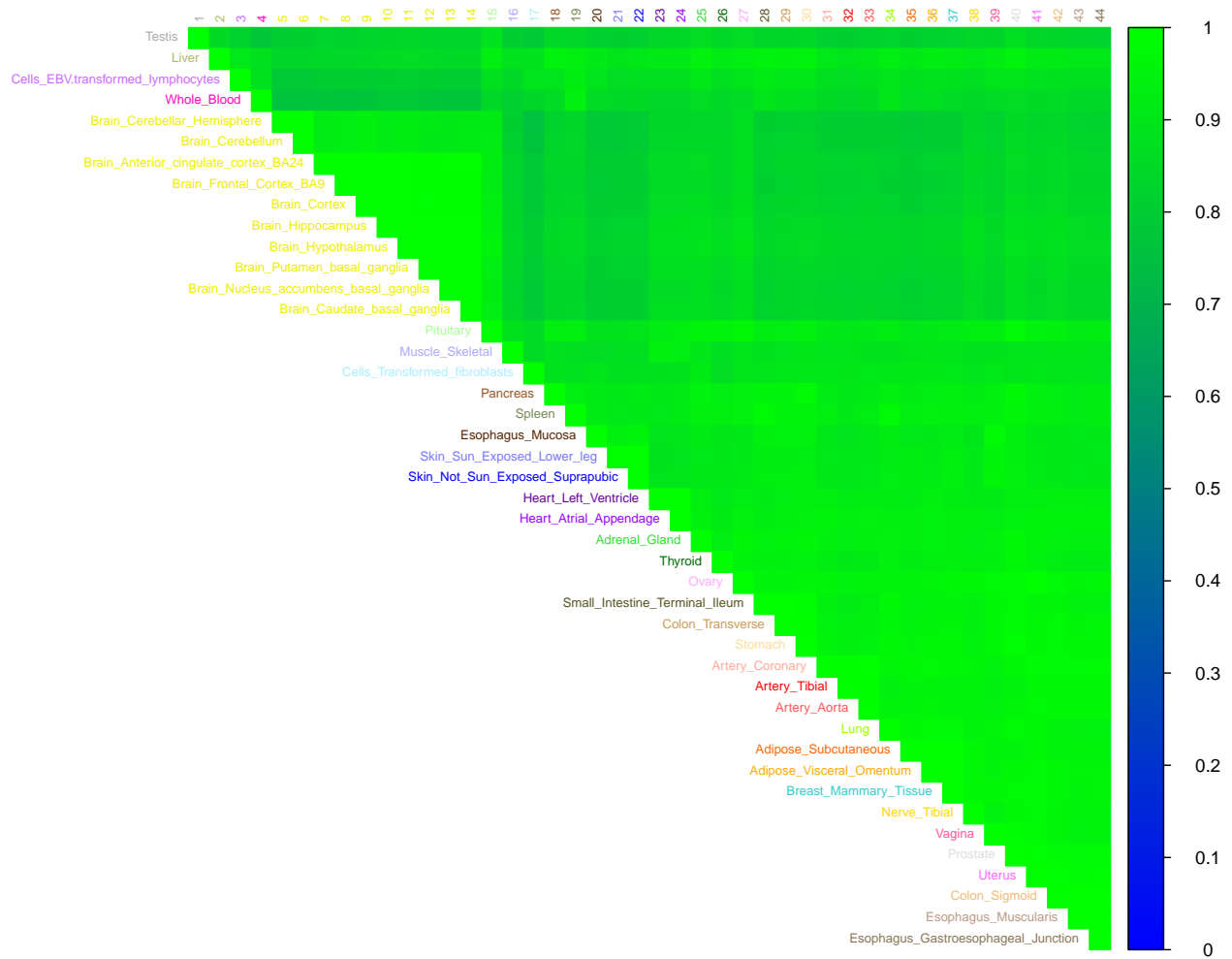
Now do with corrrplot:

```
colnames(shared.fold.size)=NULL

corrrplot(shared.fold.size[(all.tissue.order),all.tissue.order],method="color",type="upper",cl.lim=c(0,1))

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

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## used
```



```
rownames(shared.fold.size)=rep(".",44)
corrplot(shared.fold.size[(all.tissue.order),all.tissue.order],method="color",type="upper",cl.lim=c(0,1))
```

```
## 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
```

