SharingBySign

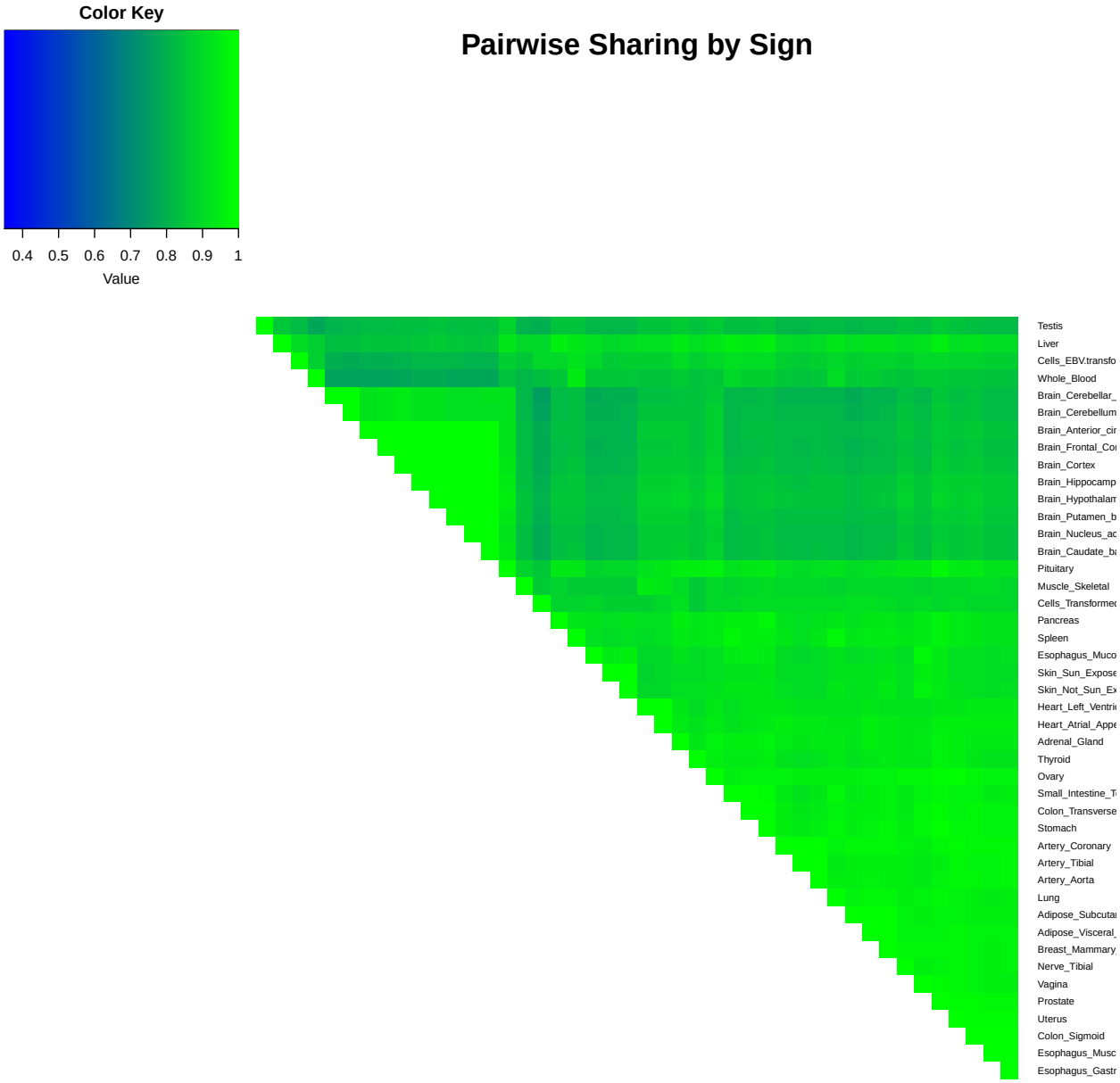
Perform the analysis with global:

```
##
## Attaching package: 'gplots'

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

Generate Plot with corrplot:

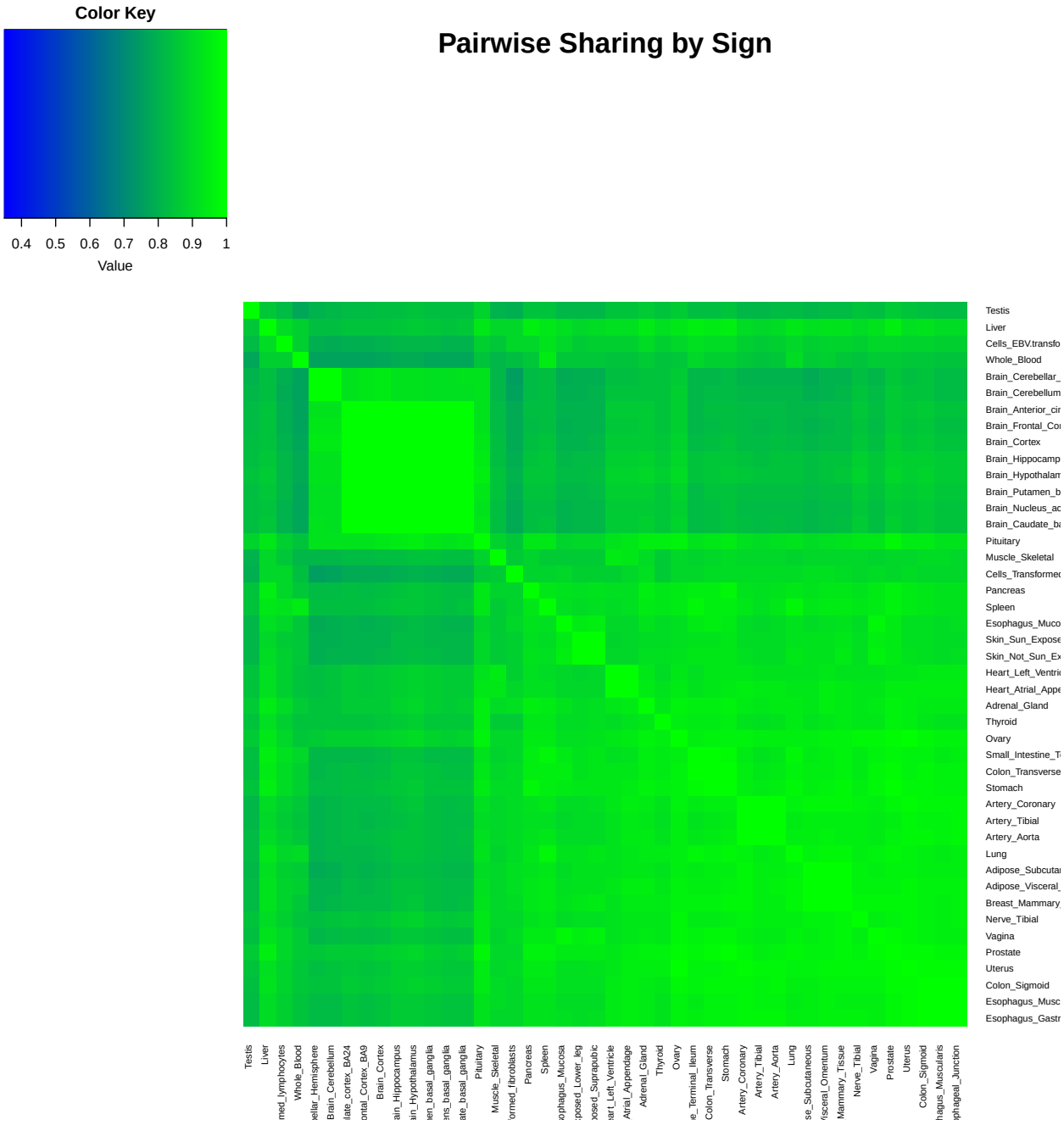
Now do with heatmap.2:



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))
```



Now do with corrplot:

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

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

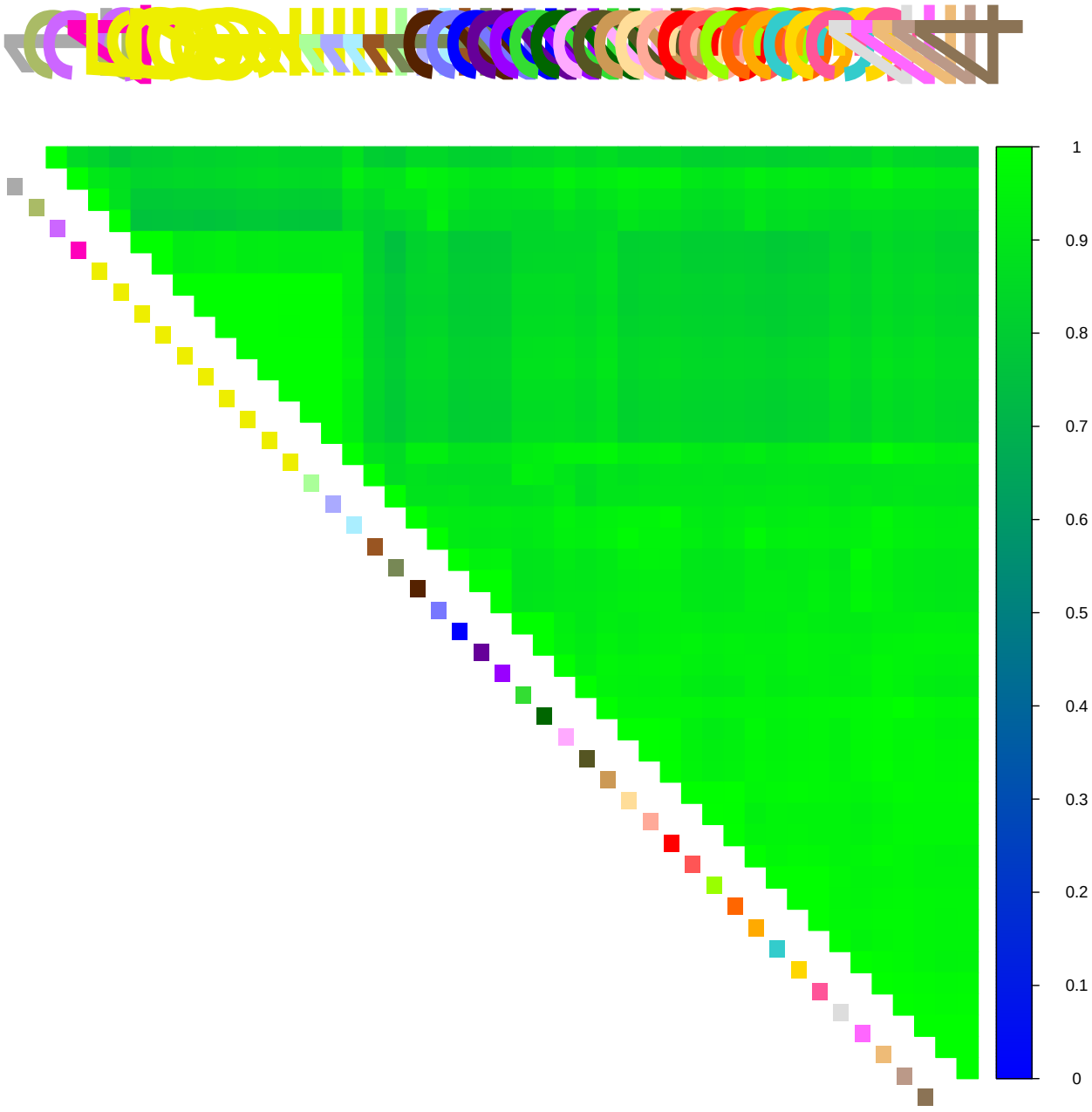
```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```

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

```
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
```


1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0