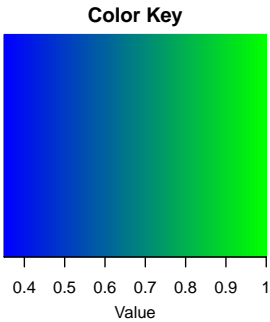


sharingbysignificance

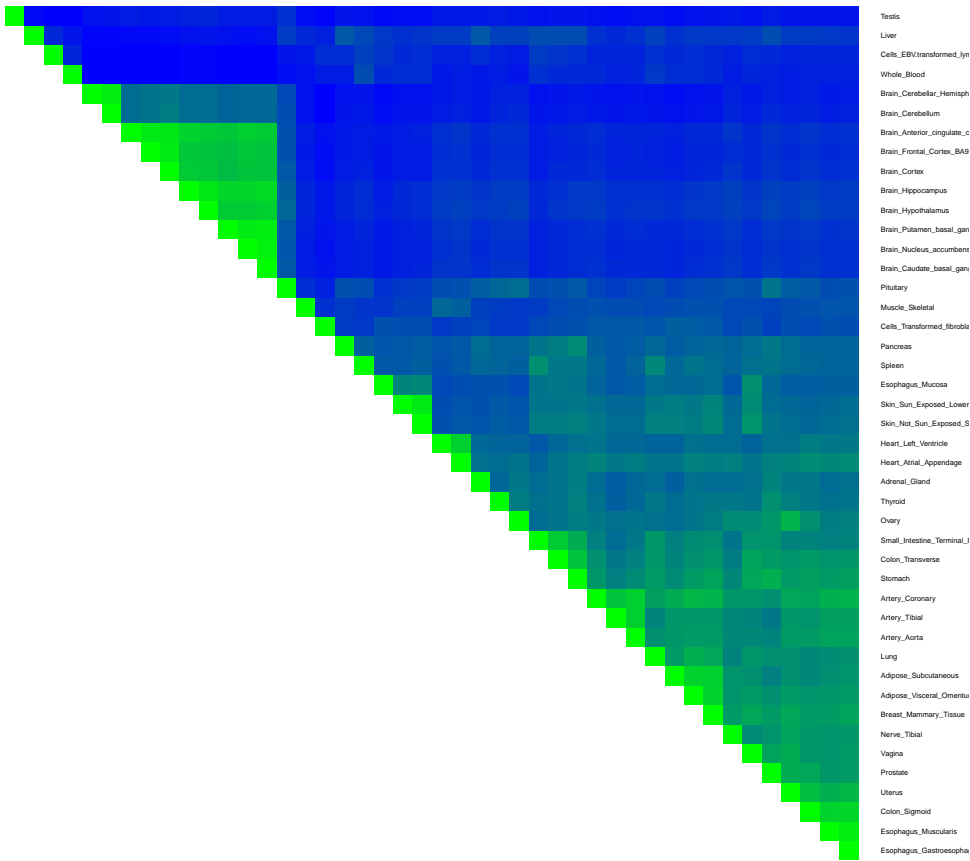
Perform the analysis with global:

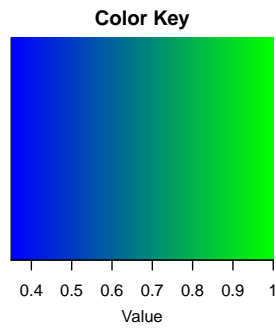
Generate Plot with corrpilot:

Now do with heatmap2:

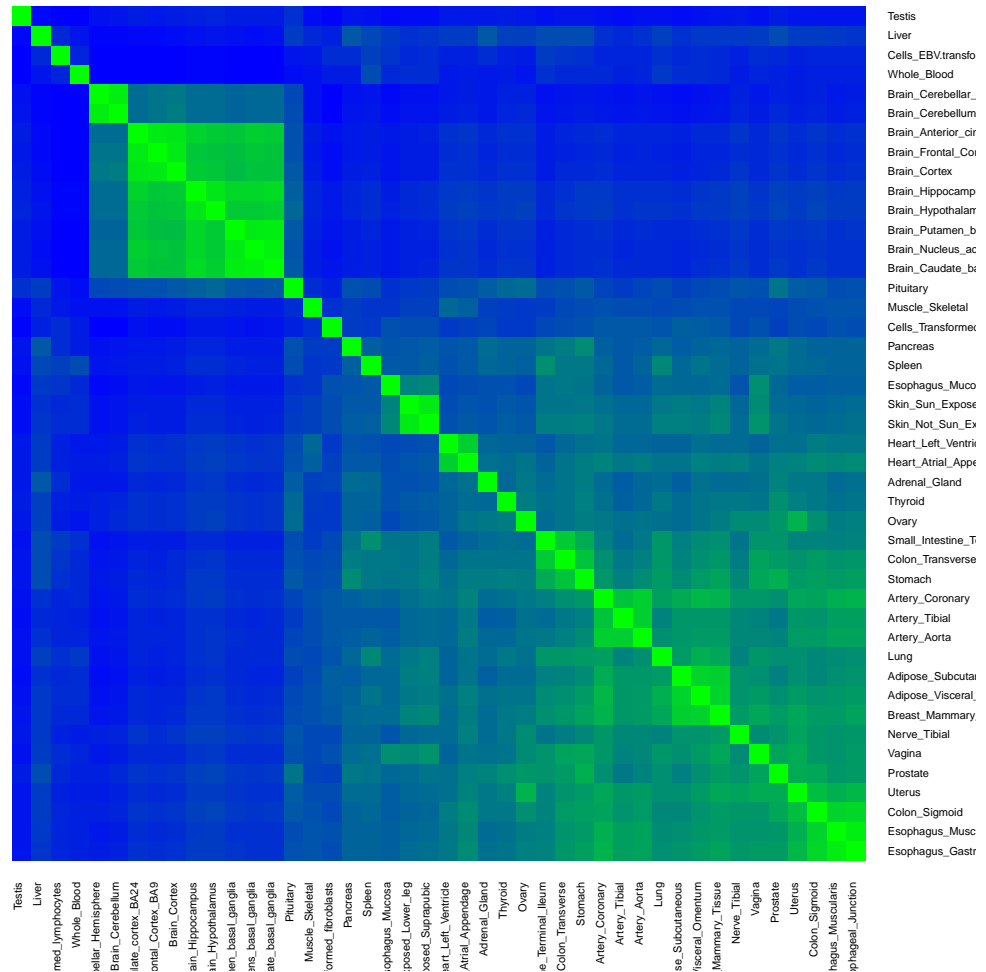


Pairwise Sharing by Significance





Pairwise Sharing by Significance



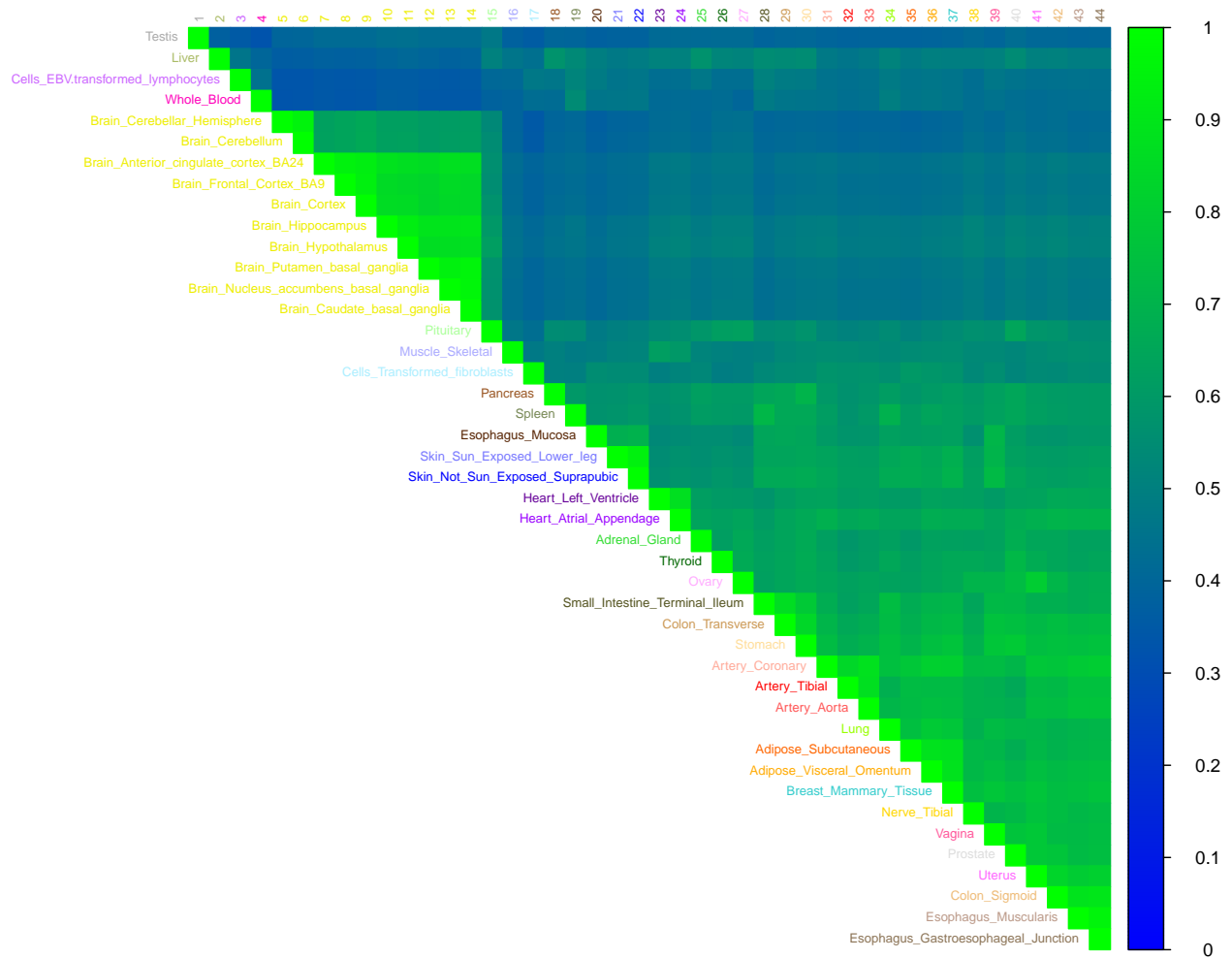
Now do with corrrplot:

```
colnames(shared)=NULL

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

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

```
## 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
```

