

# SharingBymagntiude

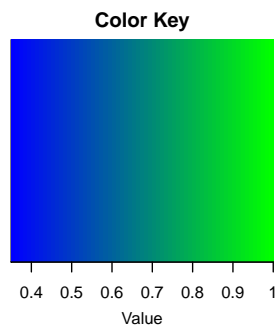
Perform the analysis with global:

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

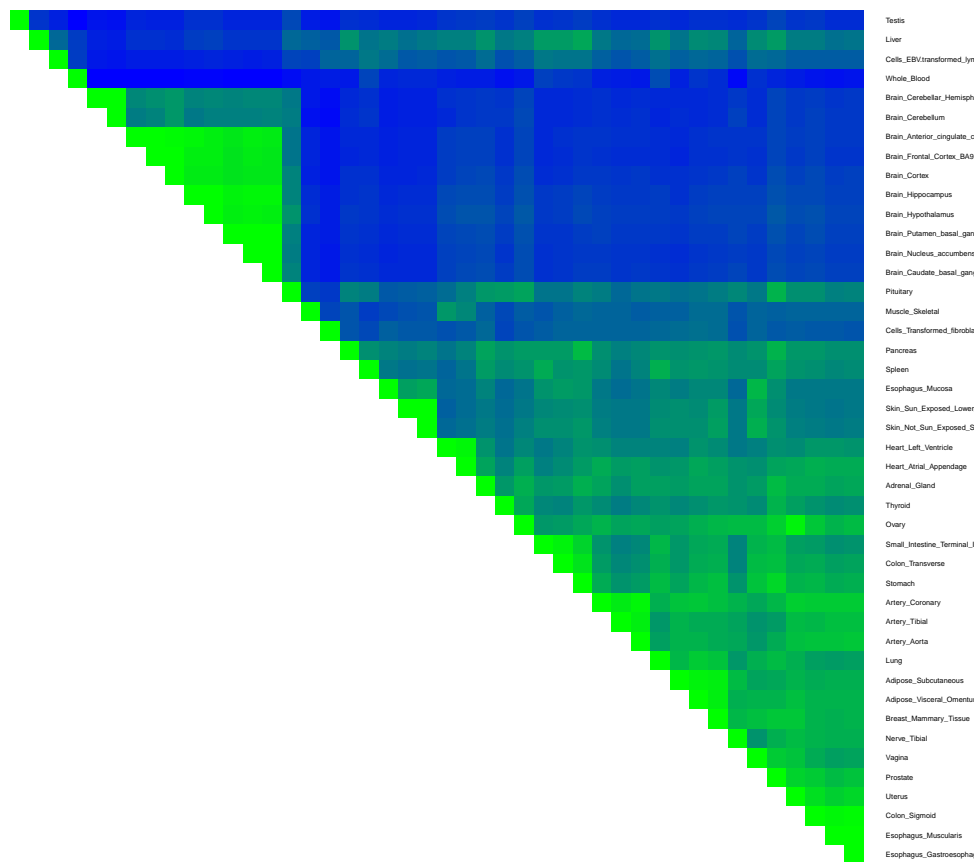
Generate Plot with corrplot:

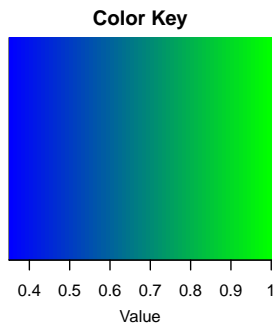
```
## Warning: package 'corrplot' was built under R version 3.2.5
```

Now do with heatmap2:

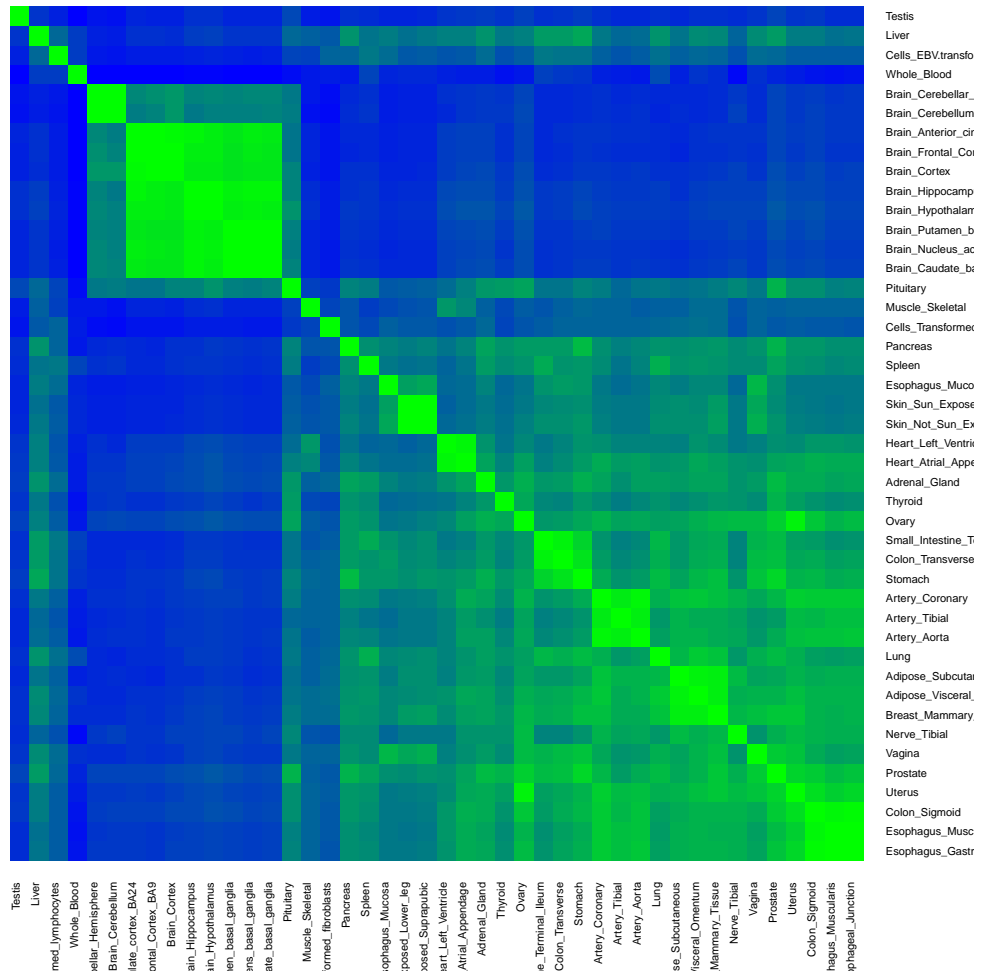


## Pairwise Sharing by Magnitude





## Pairwise Sharing by Magnitude



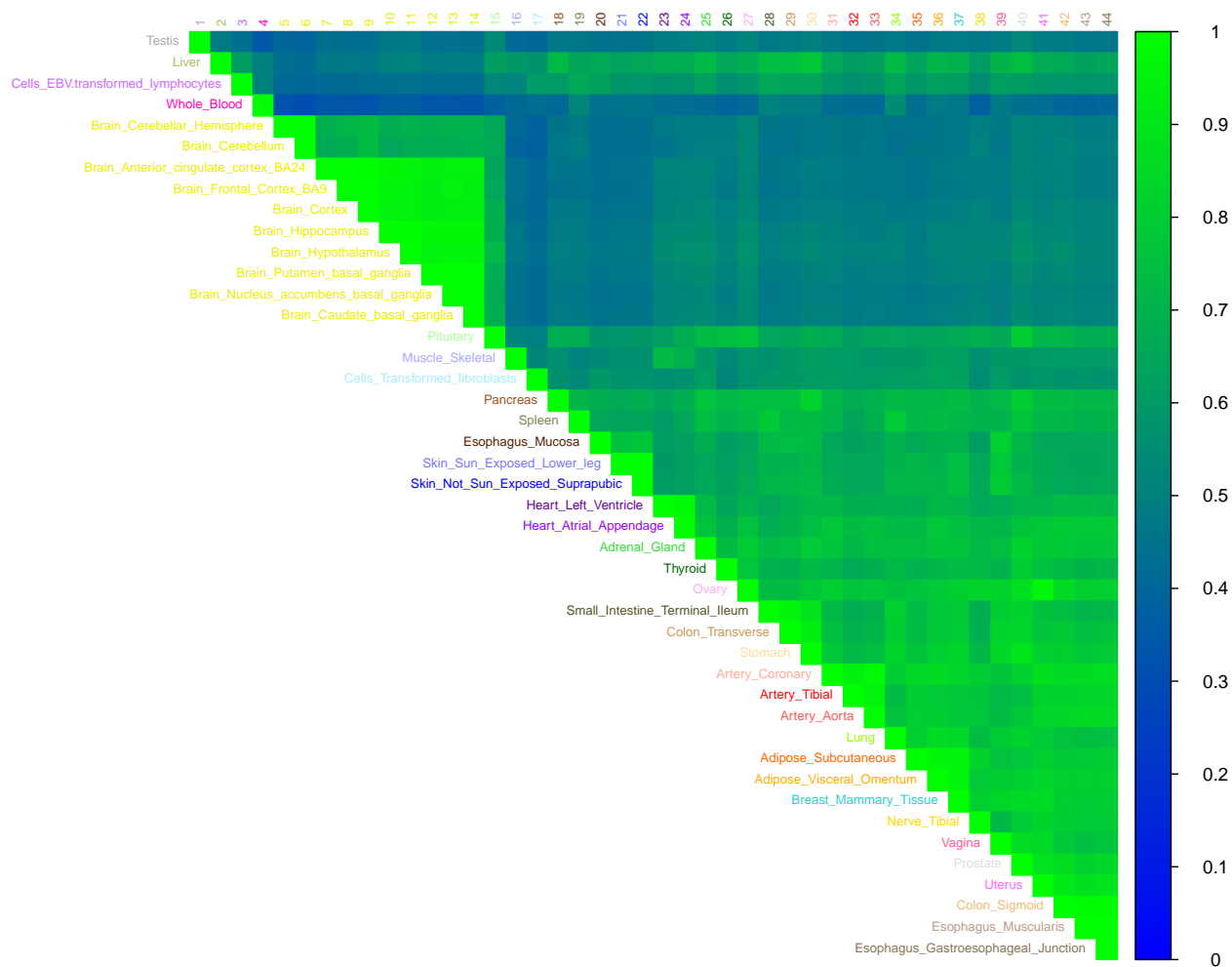
Now do with corrrplot:

```
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
```

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



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

