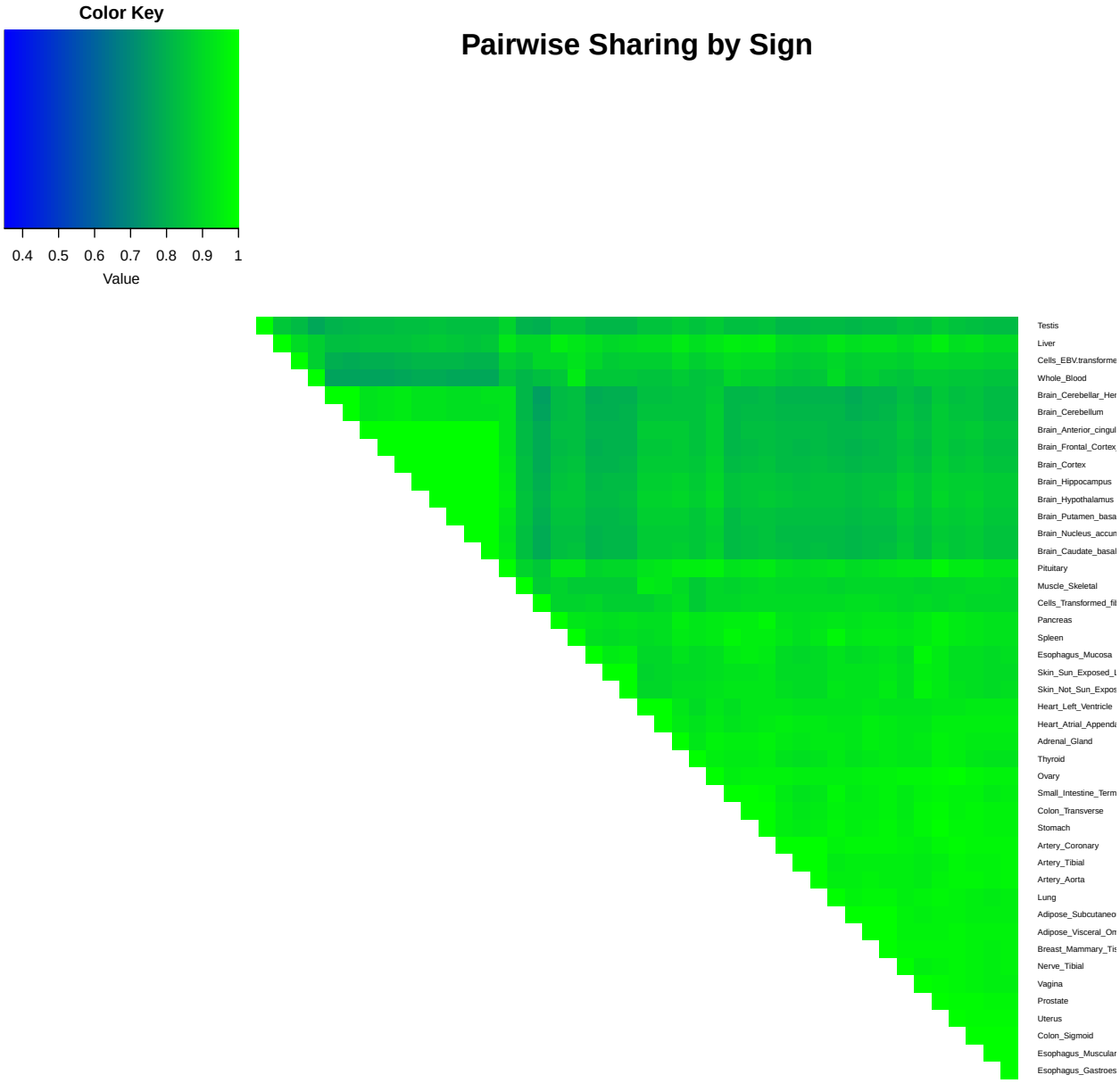
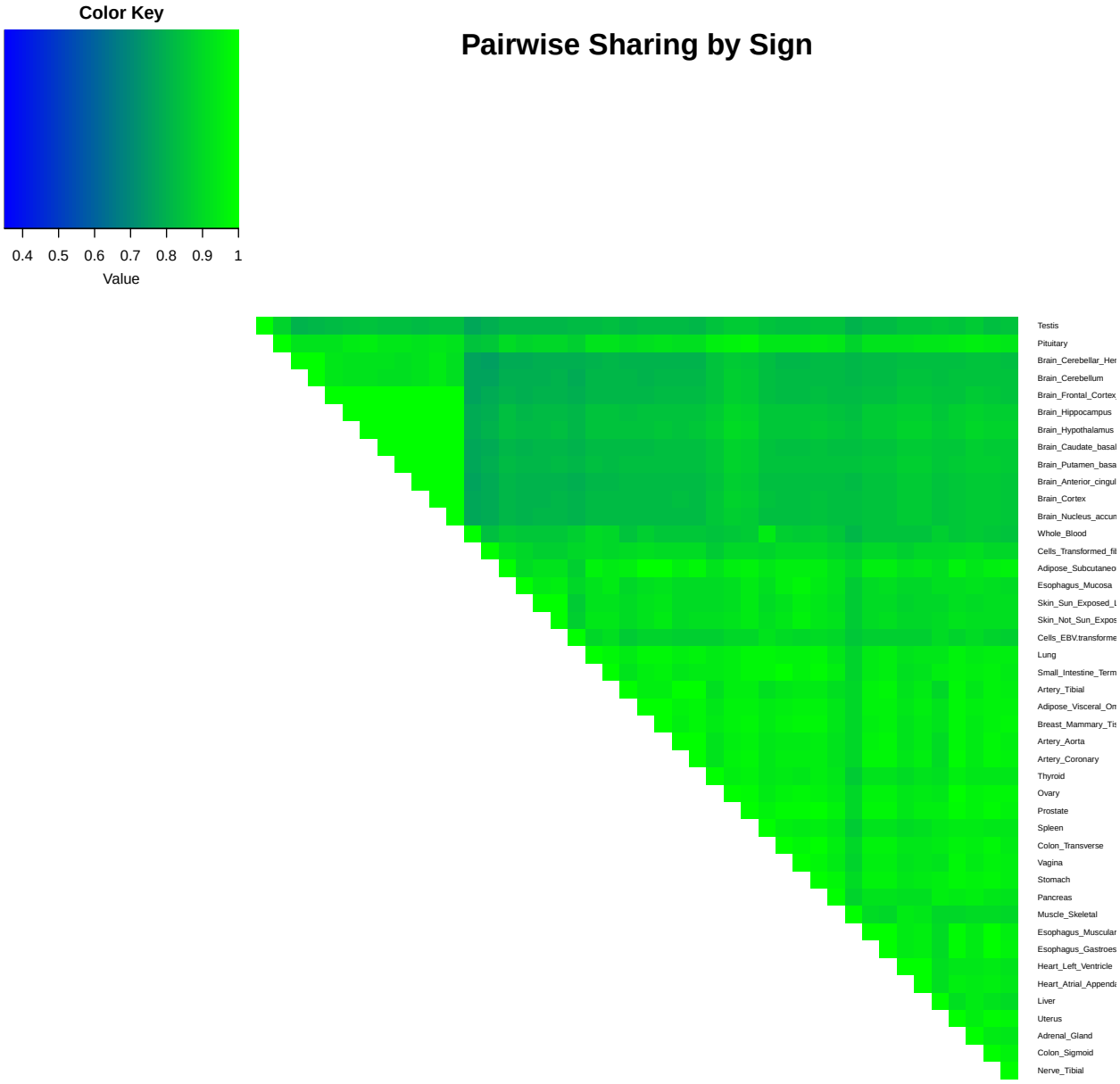
sharedsign

Perform the analysis with separate analyses:

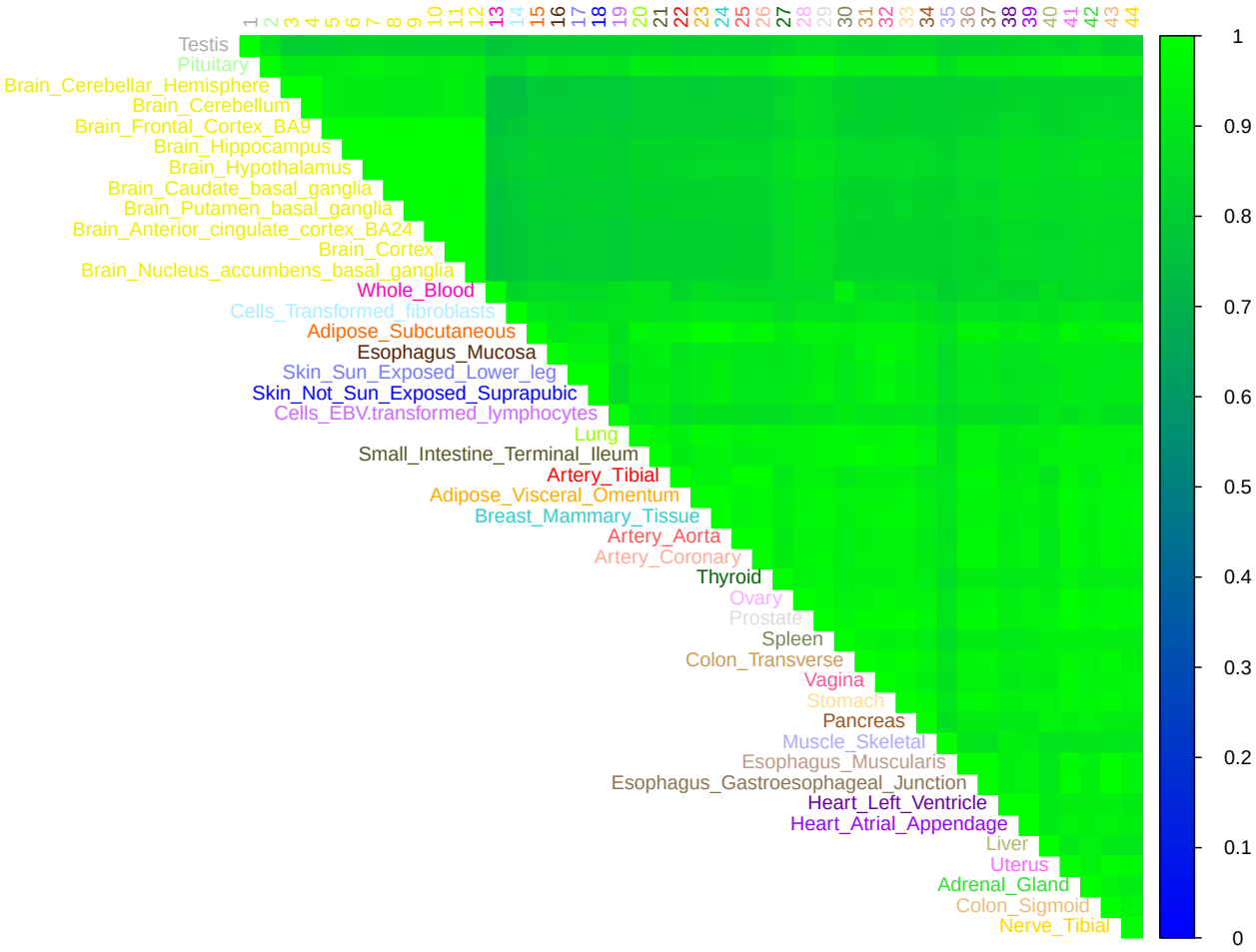
```
##
## Attaching package: 'gplots'

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

We could also try this with the orders induced from sharing by effect size:

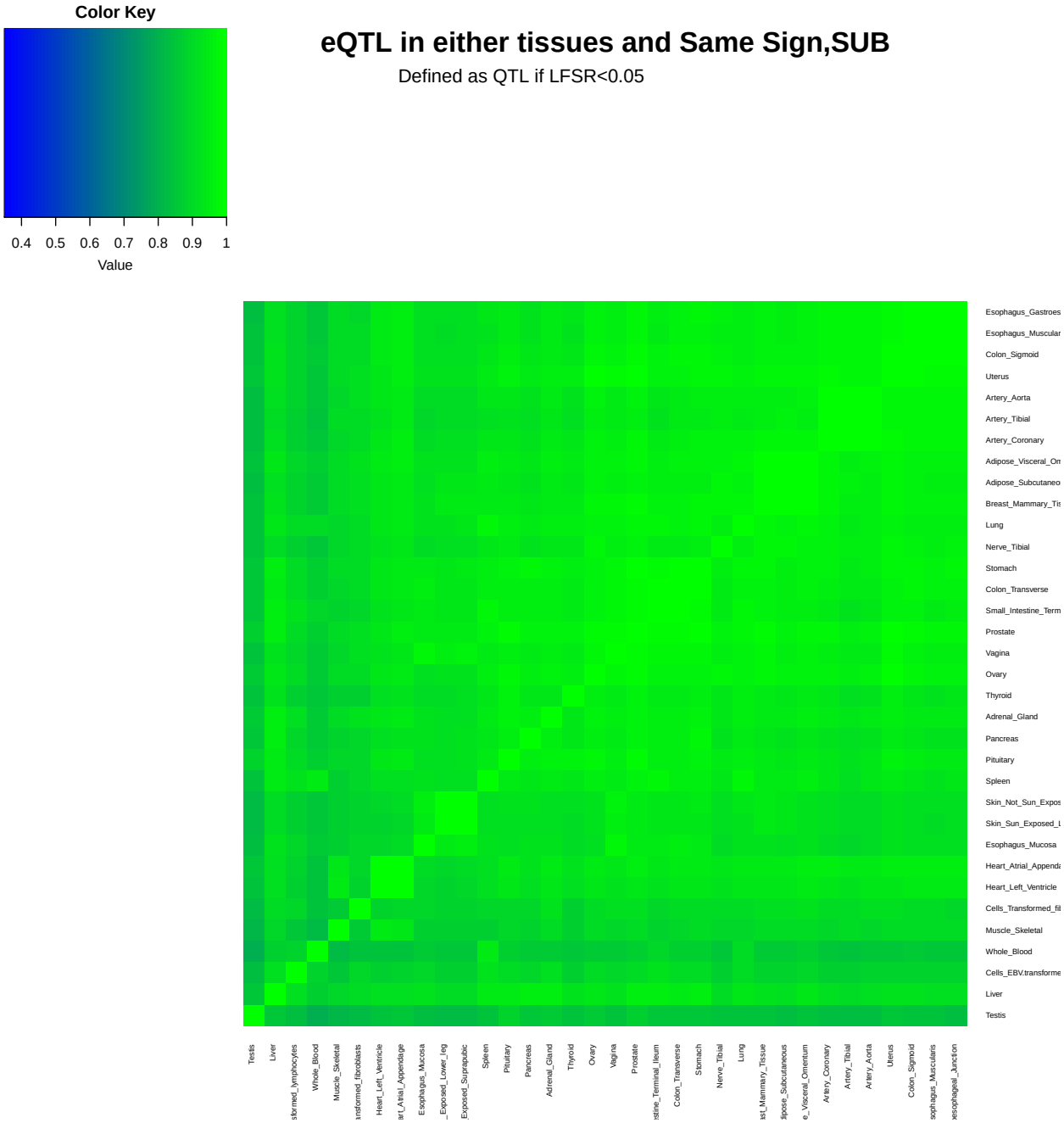




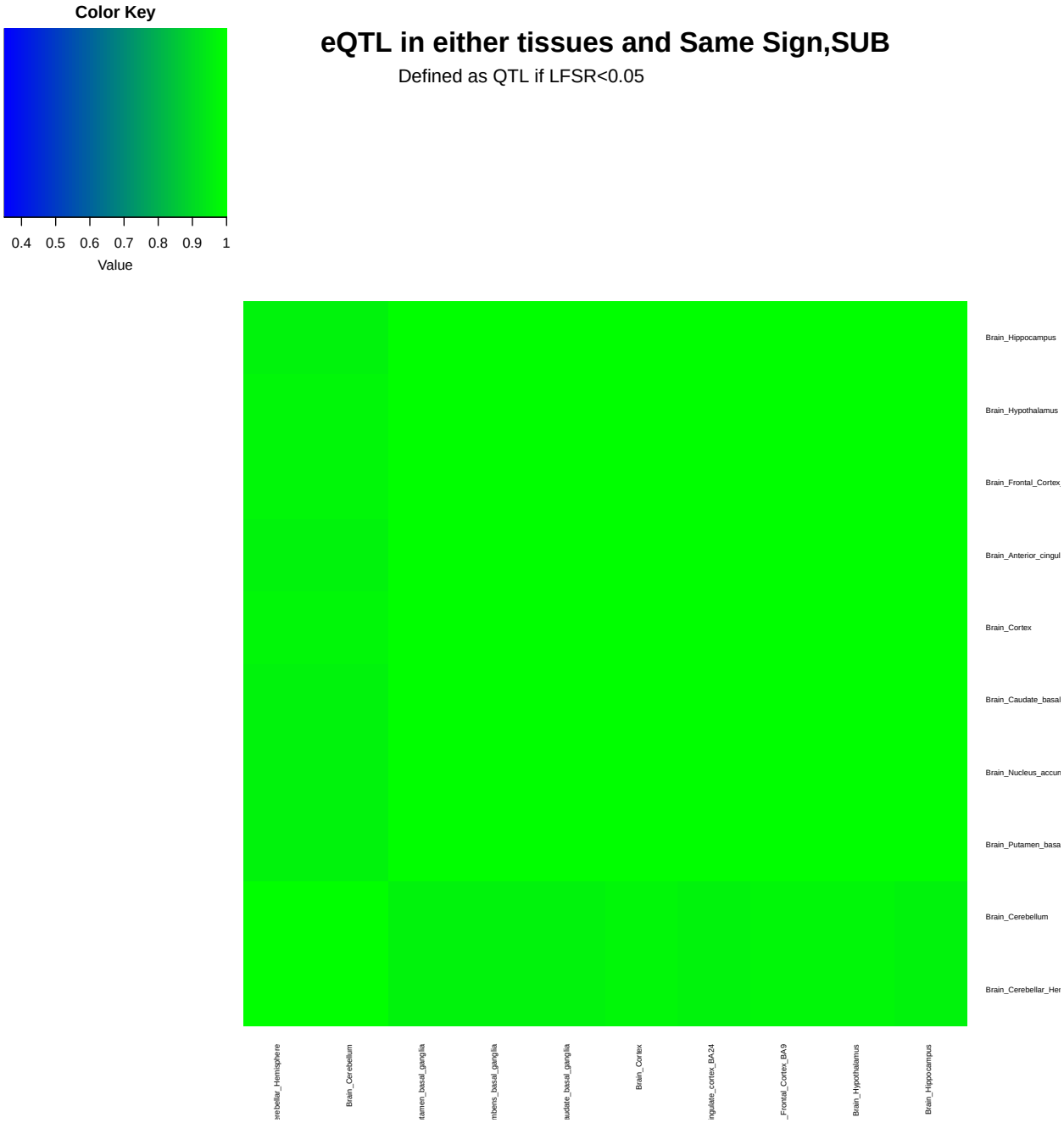

```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used

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




```
##  [1] 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12
## [24] 11 10  9  8  7  6  5  4  3  2  1
```

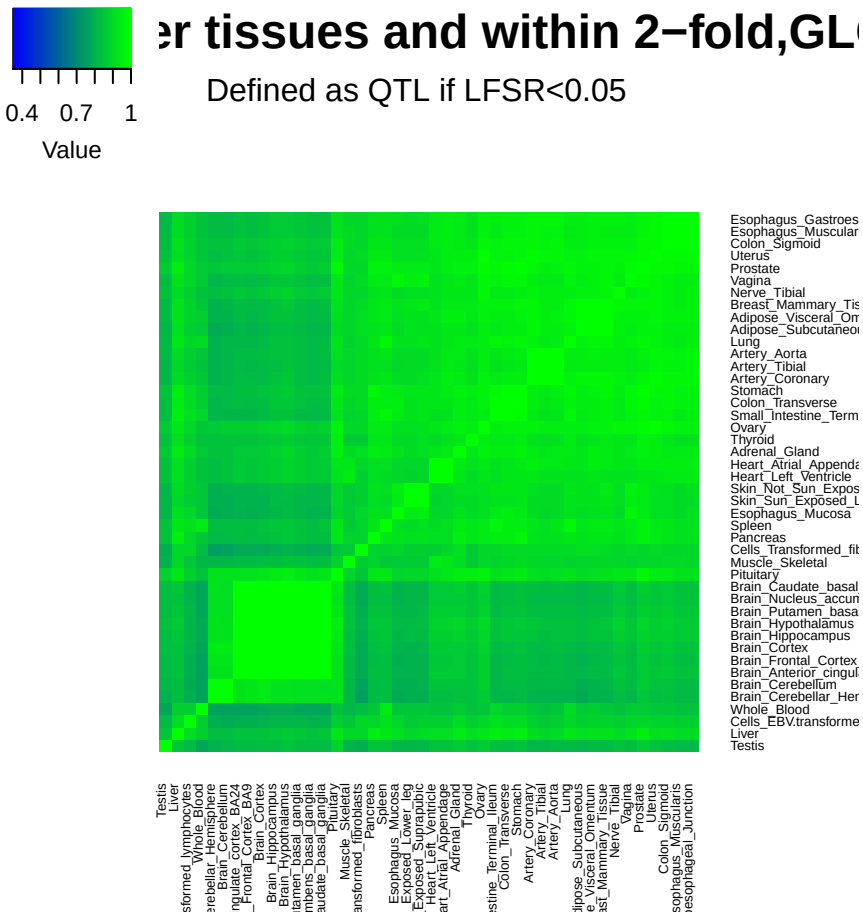



```
##  [1] 10  9  8  7  6  5  4  3  2  1
```

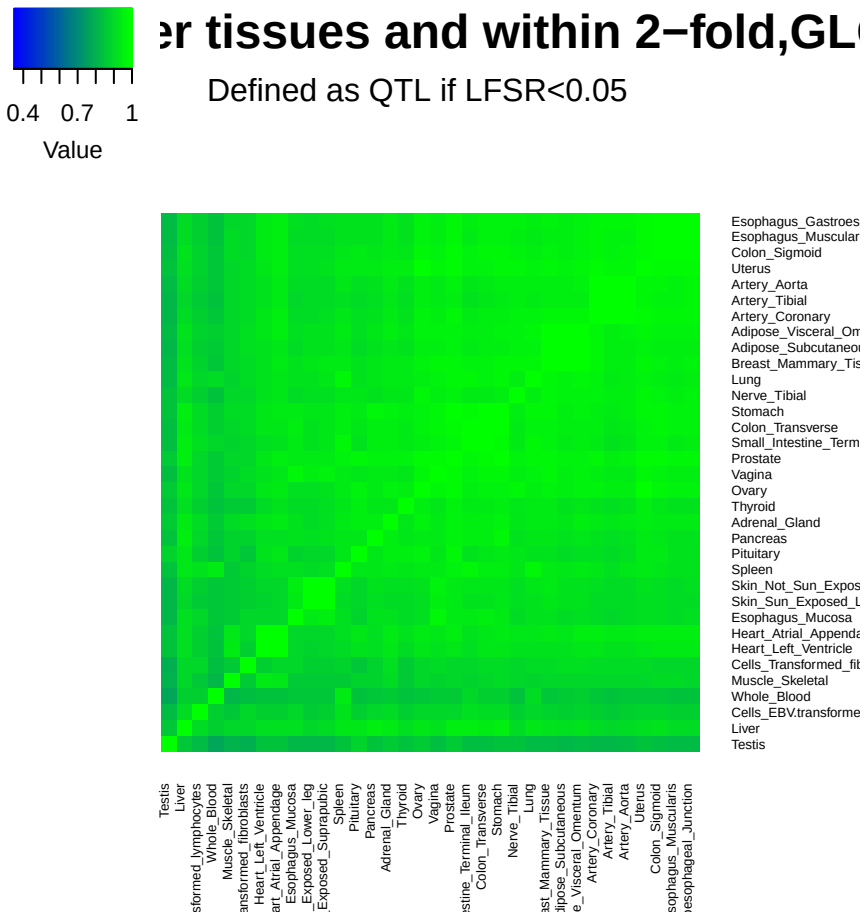


Repeat with all

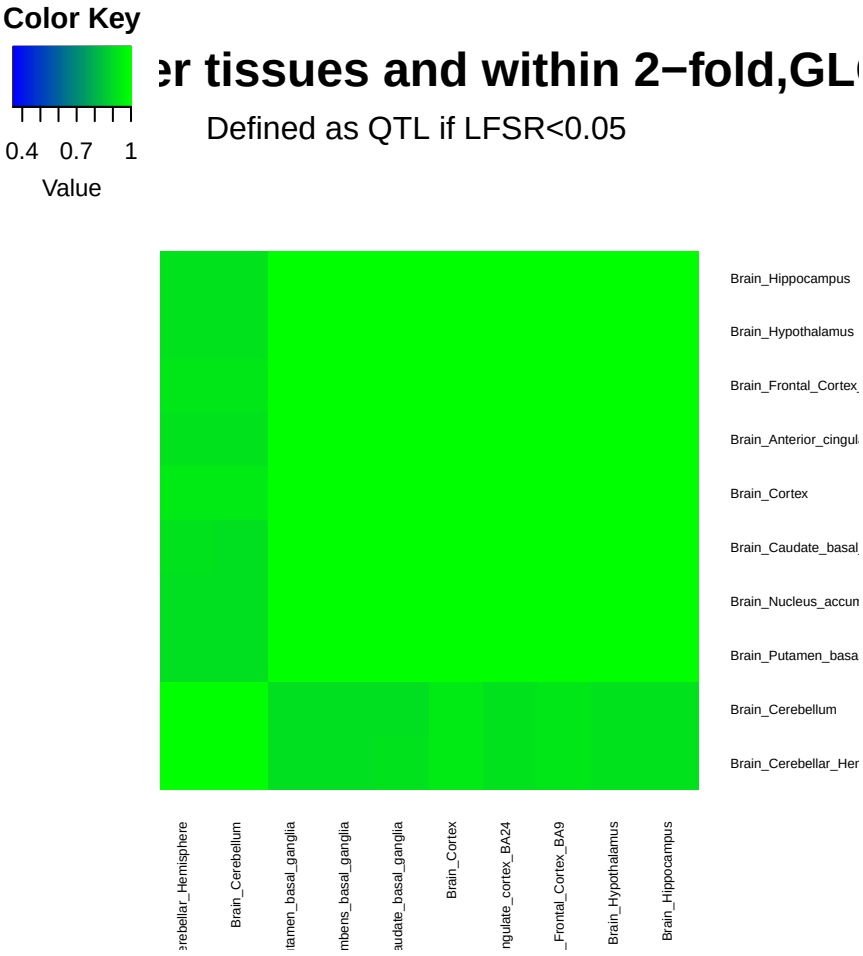
We could also try this with the orders induced from sharing by effect size:



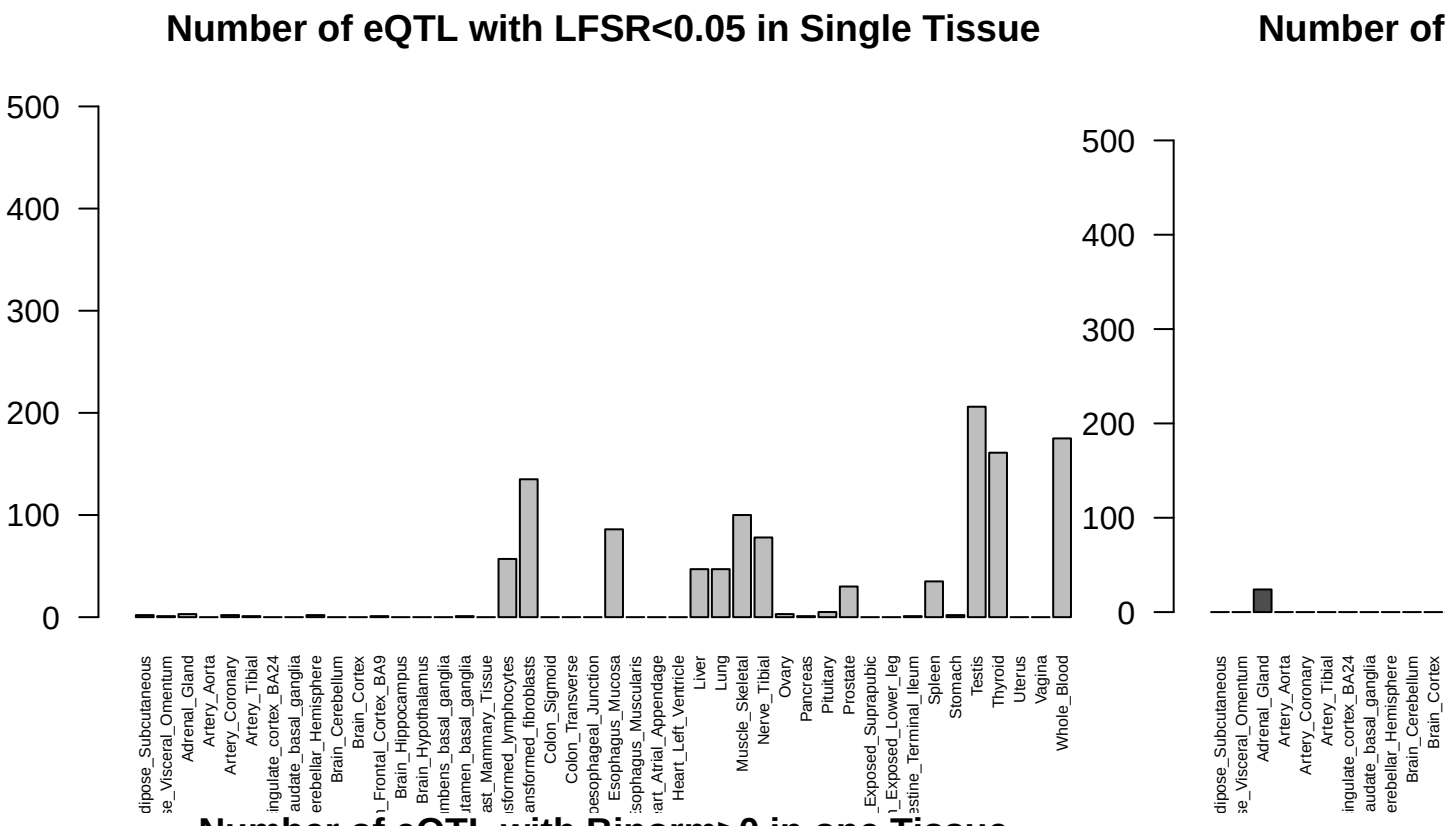

```
##  [1] 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12
## [24] 11 10  9  8  7  6  5  4  3  2  1
```

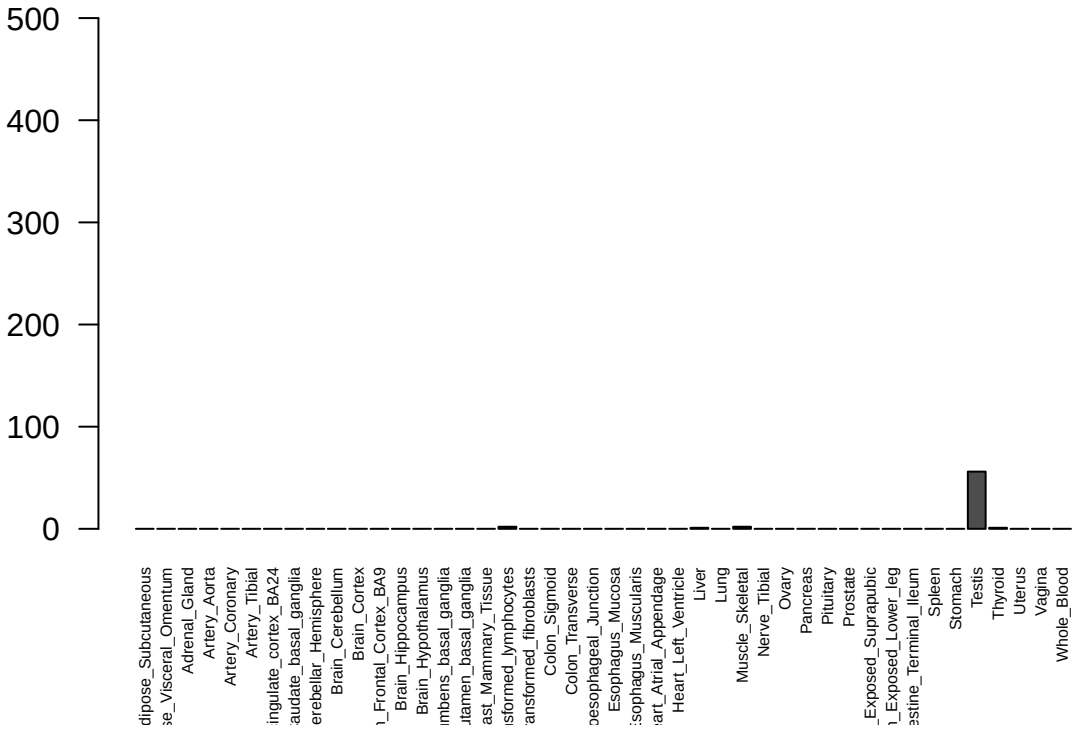



```
##  [1] 10  9  8  7  6  5  4  3  2  1
```



Tissuespecific by effect:





Also, plot the number of tissues in which a gene has the same sign:

```
samesign=apply(pm.mash.beta.norm,1,function(x){sum(x>0)})
hist(samesign,main="",xlab="NumberofTissues",breaks=0.5:44.5,col="grey",freq=FALSE,xaxt="n")
axis(1, at=seq(1, 44, by=1), labels=c(1:44))
```