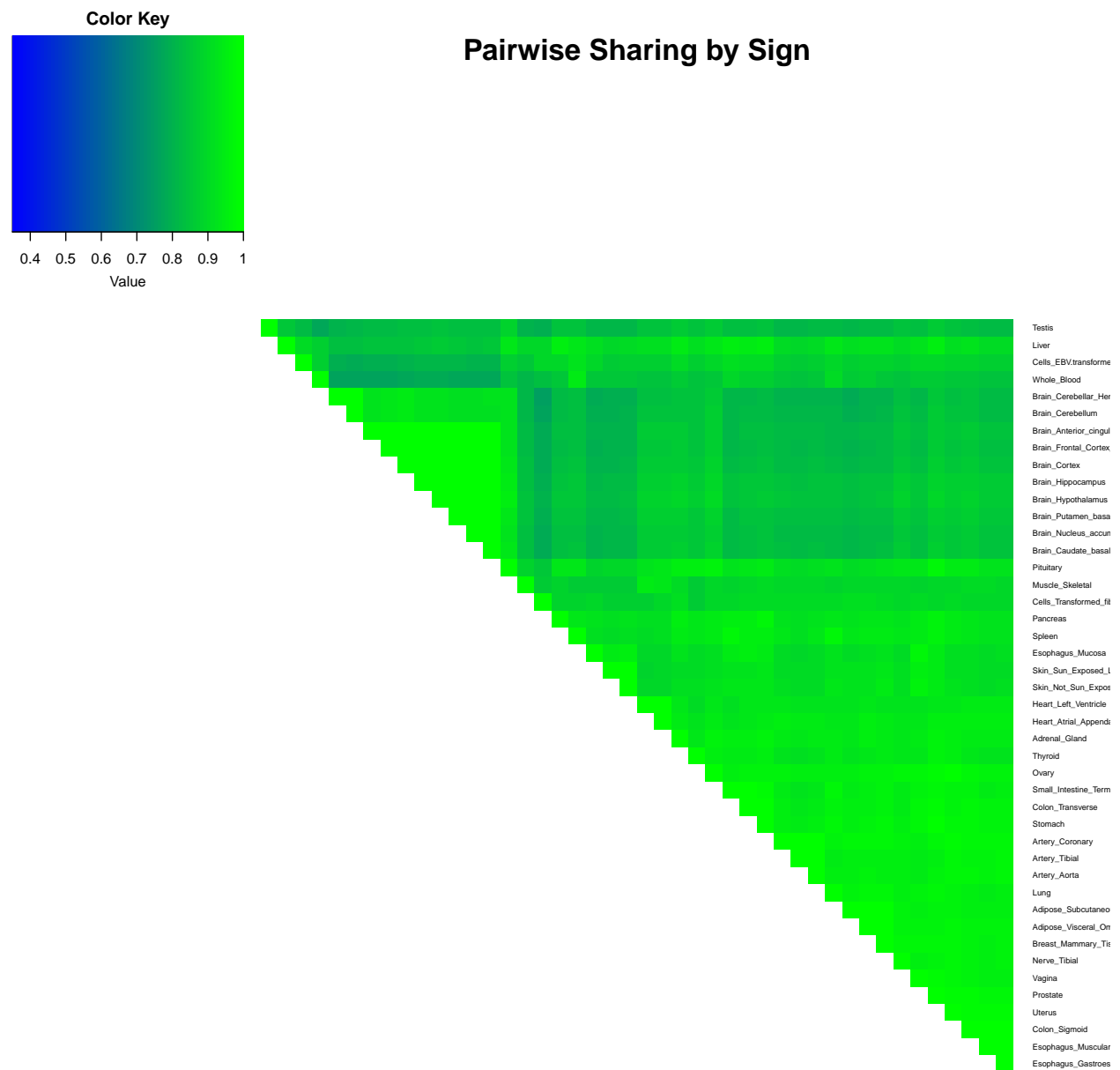


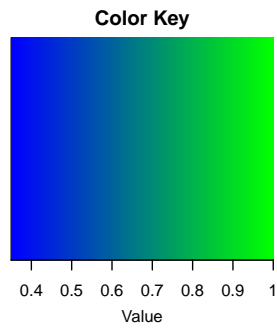
# sharedsign

Perform the analysis with separate analyses:

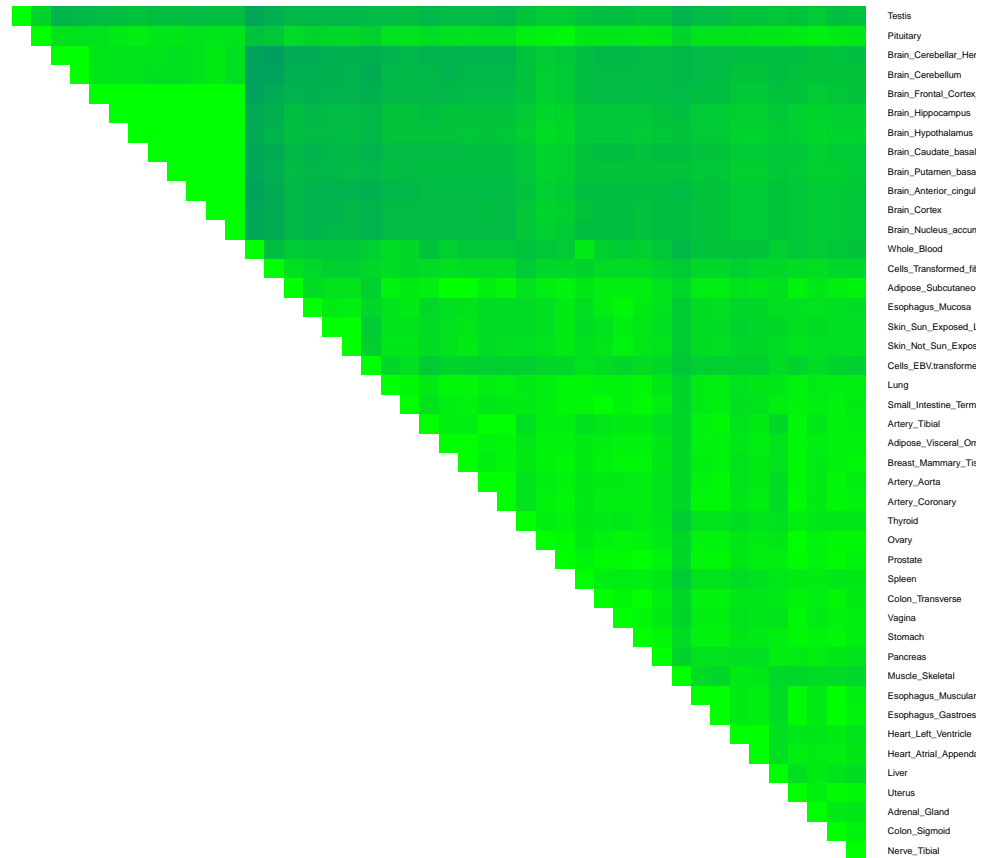
```
##  
## Attaching package: 'gplots'  
  
## The following object is masked from 'package:stats':  
##  
##      lowess
```

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



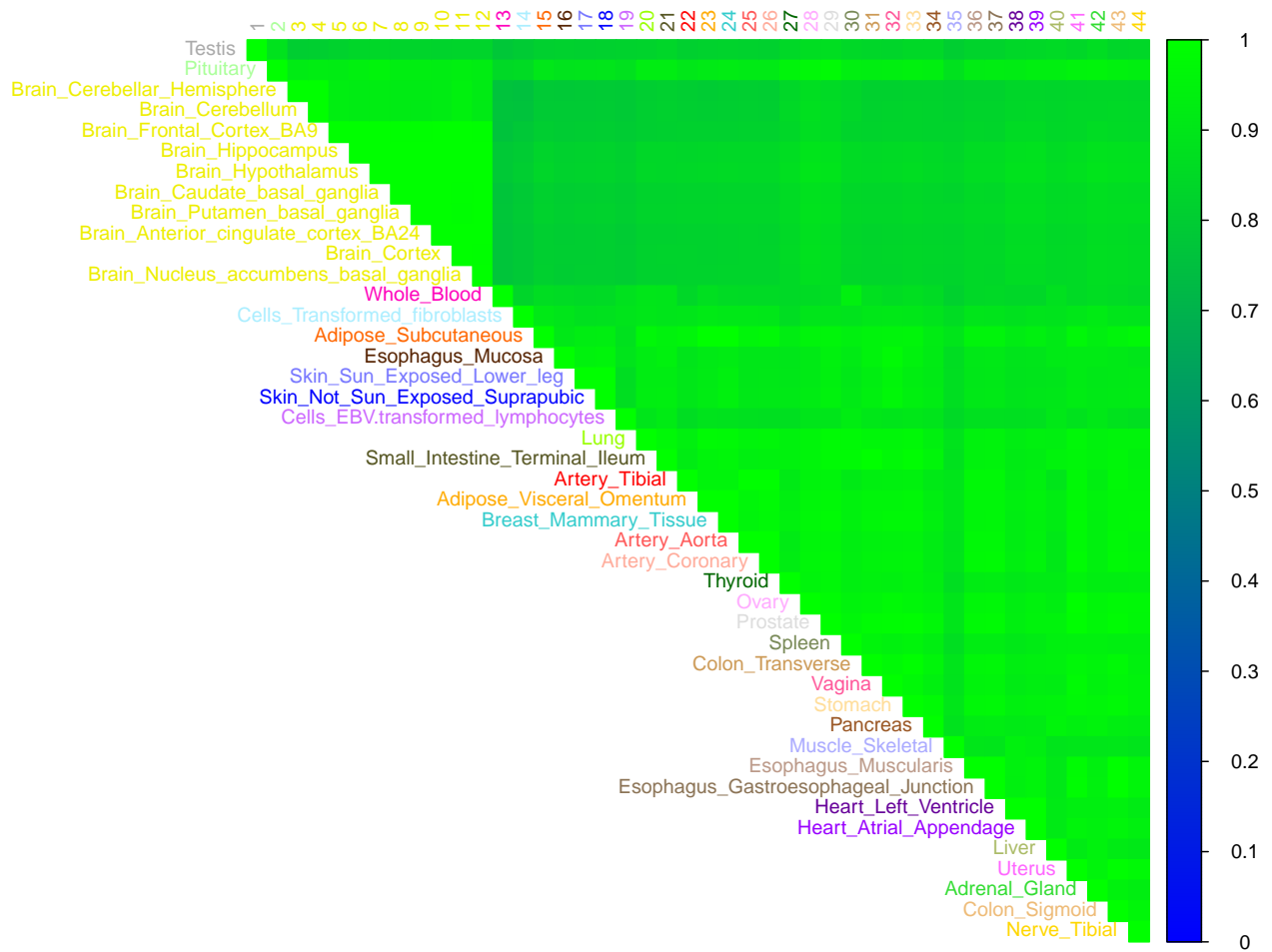


## Pairwise Sharing by Sign

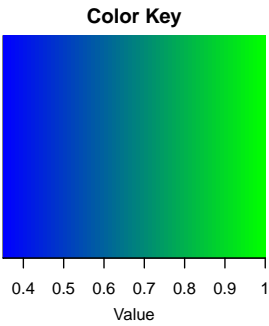


```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```

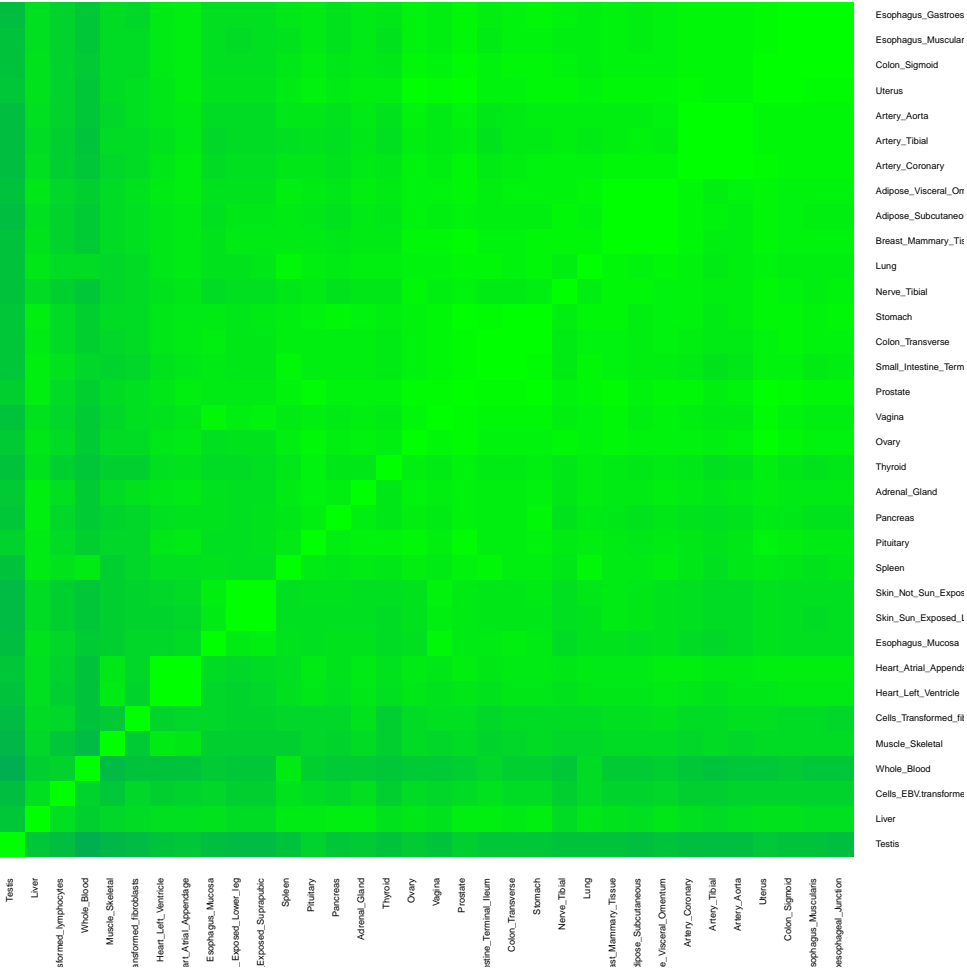
```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```



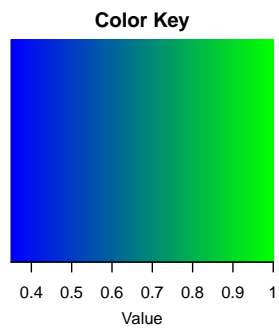
```
## [1] 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12
## [24] 11 10 9 8 7 6 5 4 3 2 1
```



**eQTL in either tissues and Same Sign,SUB**  
Defined as QTL if LFSR<0.05

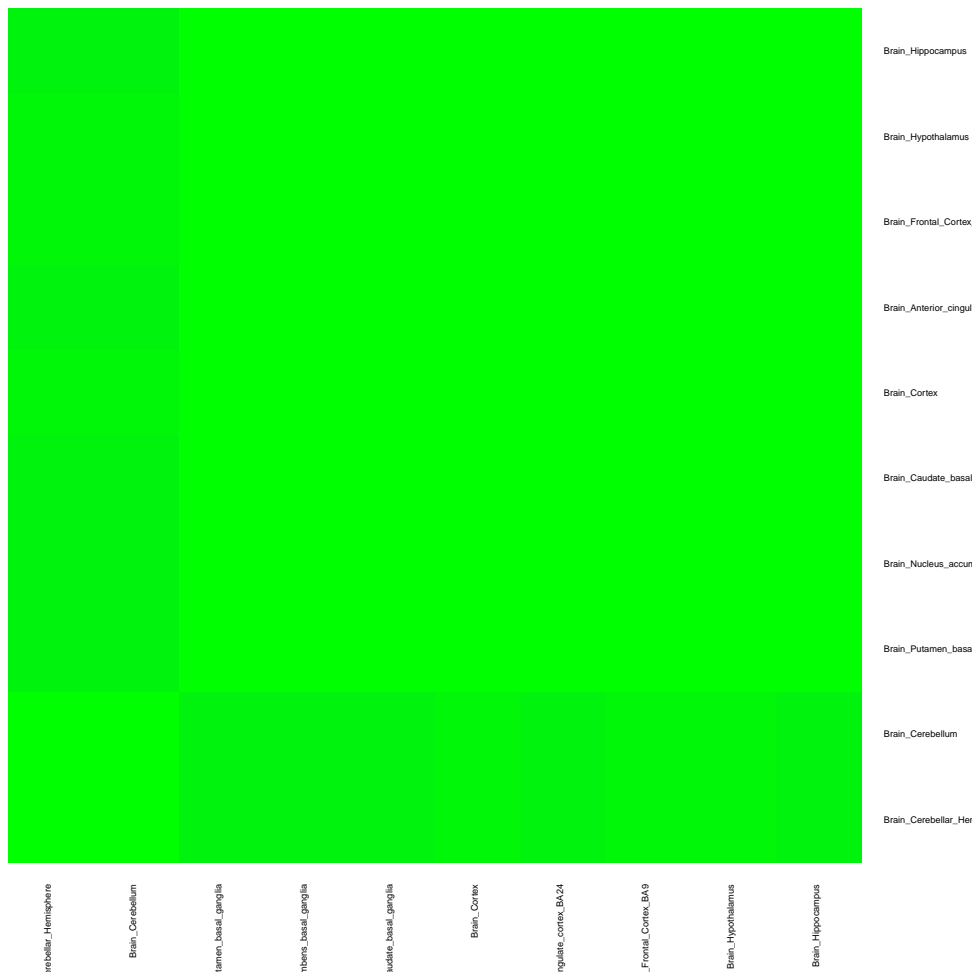


## [1] 10 9 8 7 6 5 4 3 2 1



## eQTL in either tissues and Same Sign,SUB

Defined as QTL if LFSR<0.05

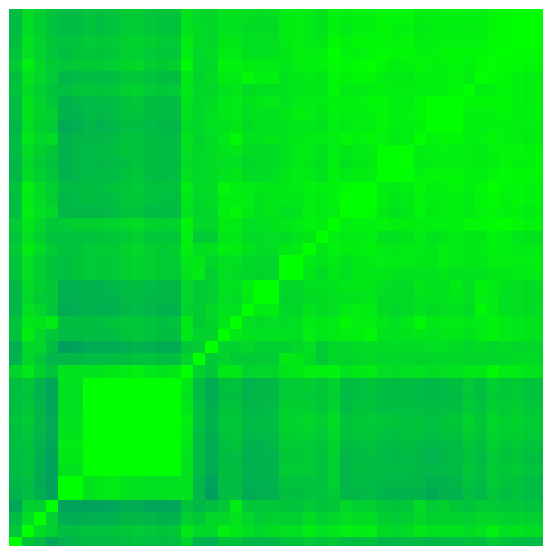


Repeat with all

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



Defined as QTL if LFSR $\leq$ 0.05

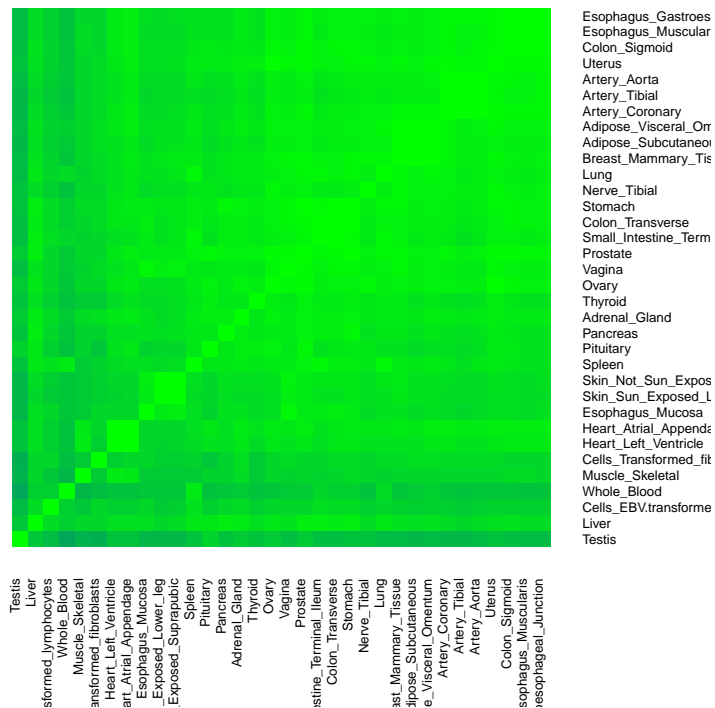


Esophagus\_Gastroes  
Esophagus\_Muscular  
Colon\_Sigmoid  
Uterus  
Prostate  
Vagina  
Nerve\_Tibial  
Breast\_Mammary\_Tis  
Adipose\_Visceral\_O  
Esophagus\_Subcutane  
Lung  
Artery\_Aorta  
Artery\_Tibial  
Artery\_Pulmonary  
Stomach  
Colon\_Transverse  
Small\_Intestine\_Ter  
Thyroid  
Adrenal\_Gland  
Heart\_Atrial\_Append  
Heart\_Left\_Ventricle  
Heart\_Right\_Ventricle  
Skin\_Sun\_Exposed  
Skin\_Sun\_Exposed\_I  
Esophagus\_Mucosa  
Spleen  
Pancreas  
Cells\_Transformed\_F  
Muscle\_Skeletal  
Pituitary  
Brain\_Caudate\_basal  
Brain\_Nucleus\_accu  
Brain\_Putamen\_basal  
Brain\_Hypothalamus  
Brain\_Hippocampus  
Brain\_Cortex  
Brain\_Frontal\_Cortex  
Brain\_Anterior\_cing  
Brain\_Cerebellum  
Brain\_Cerebellar\_her  
Whole\_Blood  
Cells\_EBVtransforme  
Liver

[illegible]

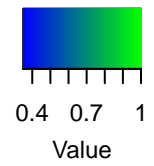
```
## [1] 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12
## [24] 11 10 9 8 7 6 5 4 3 2 1
```

Defined as QTL if LFSR<0.05



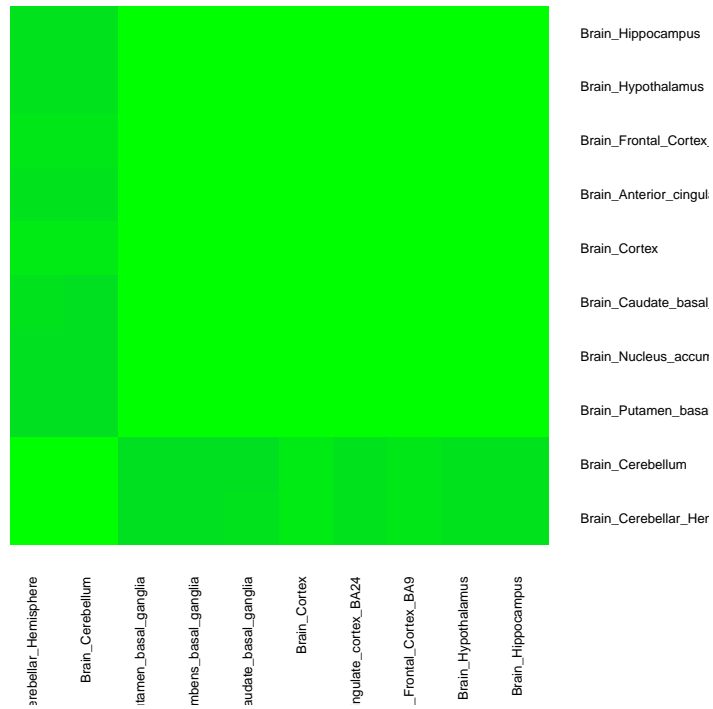
```
##      [1] 10  9  8  7  6  5  4  3  2  1
```

## Color Key



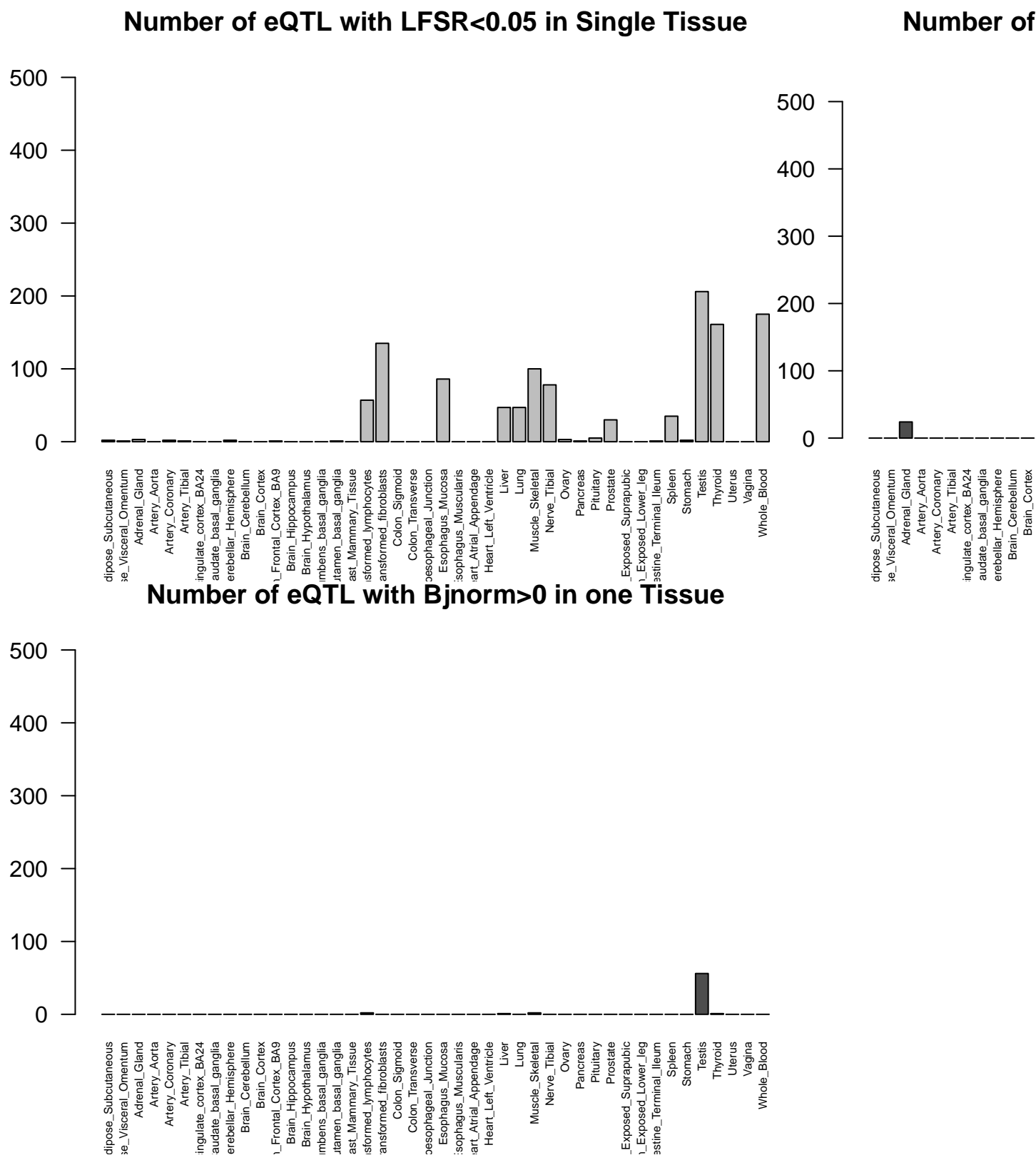
across tissues and within 2-fold, GL

Defined as QTL if LFSR<0.05



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))

```

