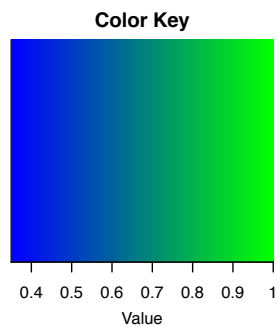


sharedsigeffects

Perform the analysis with separate analyses:

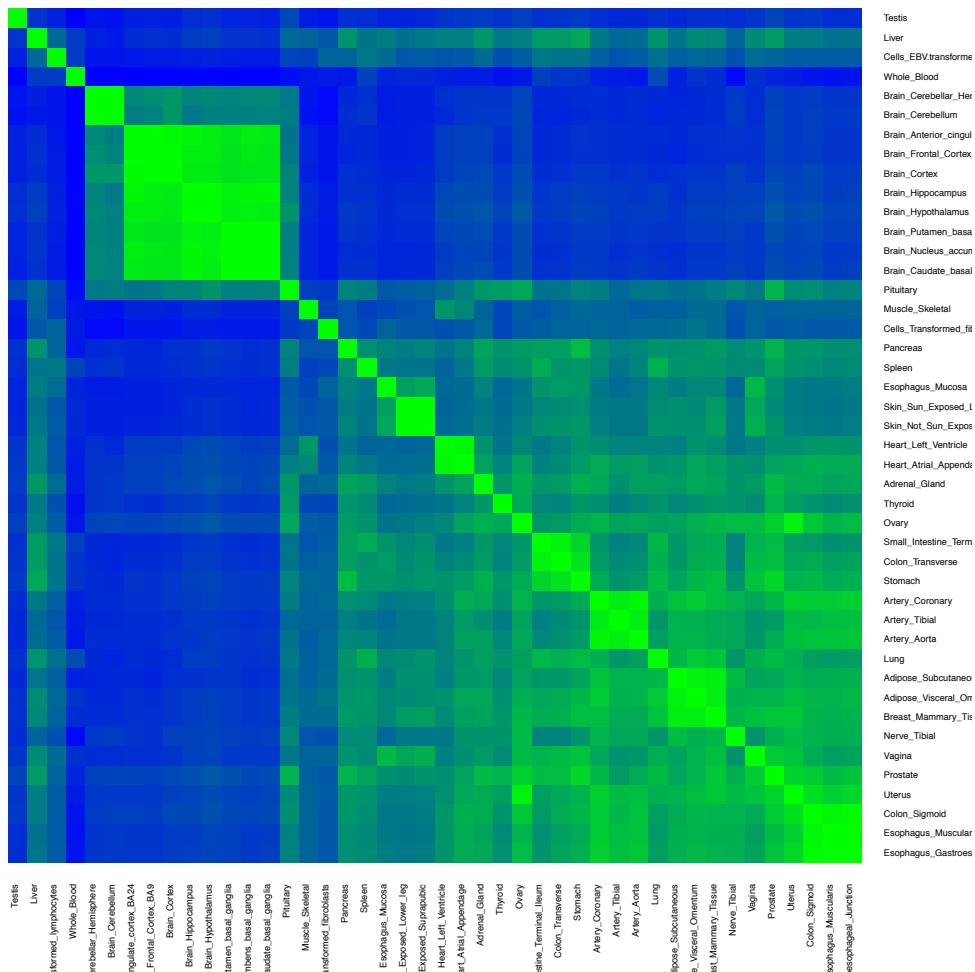
```
##  
## Attaching package: 'gplots'  
  
## The following object is masked from 'package:stats':  
##  
##      lowess
```

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

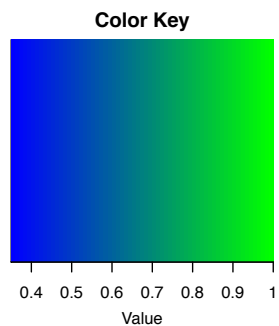


eQTL in either tissues and within 2-fold, SUB

Defined as QTL if LFSR<0.05

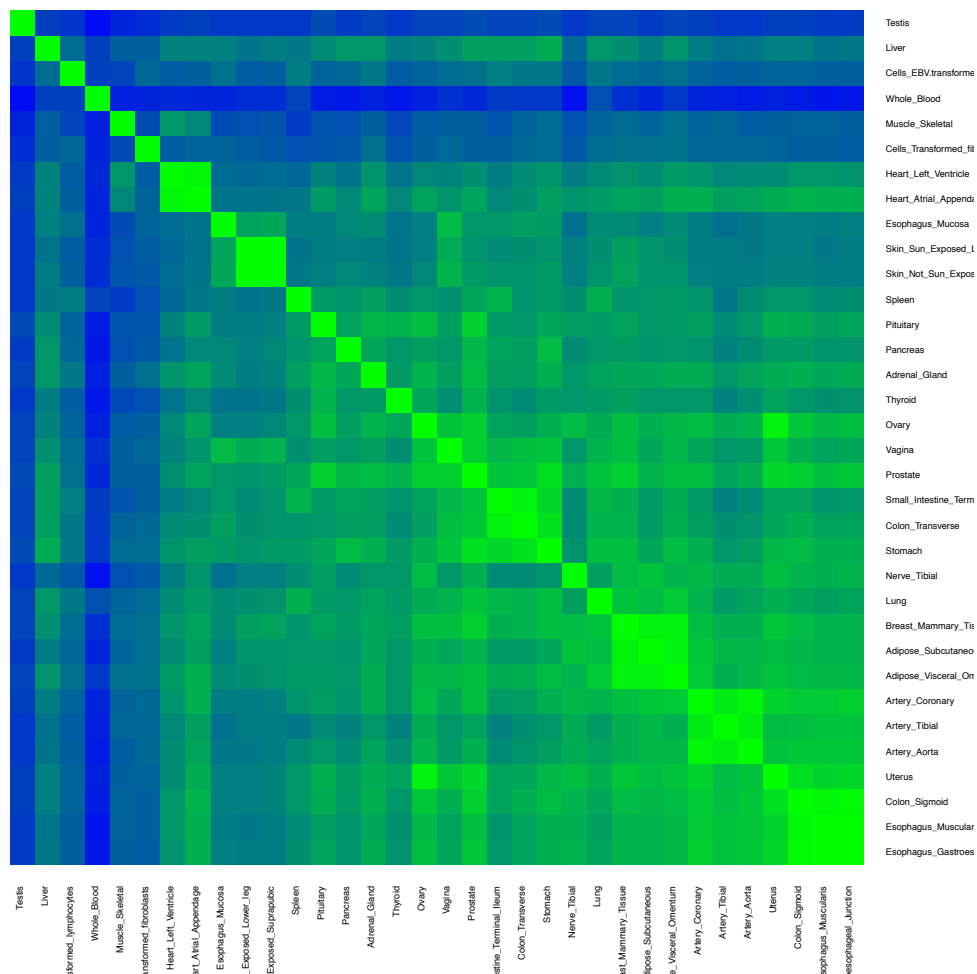


```
## [1] 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12
## [24] 11 10 9 8 7 6 5 4 3 2 1
```

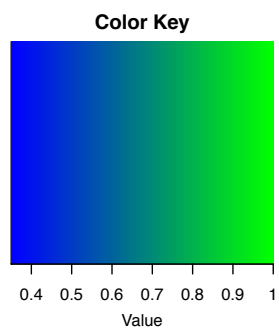


eQTL in either tissues and within 2-fold,SUB

Defined as QTL if LFSR<0.05

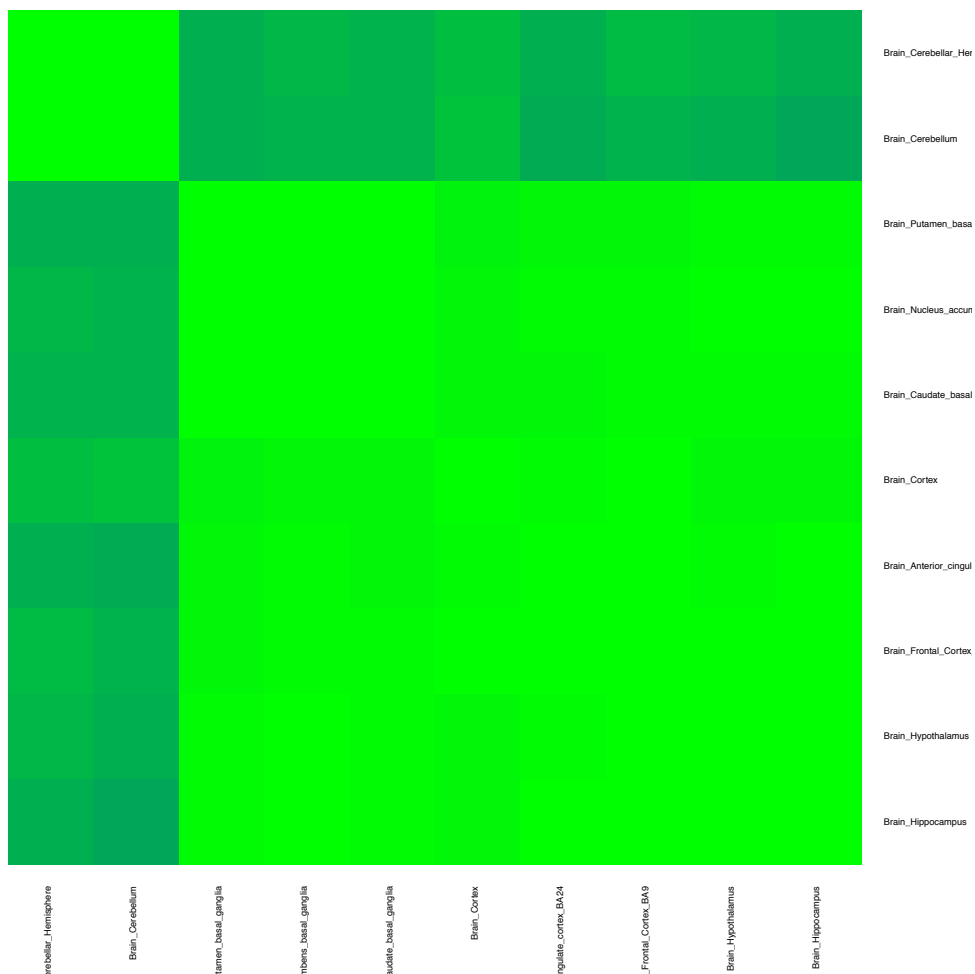


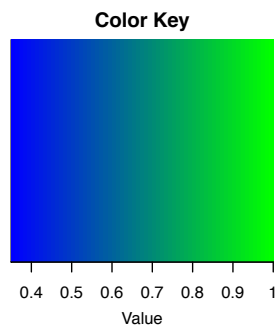
[1] 10 9 8 7 6 5 4 3 2 1



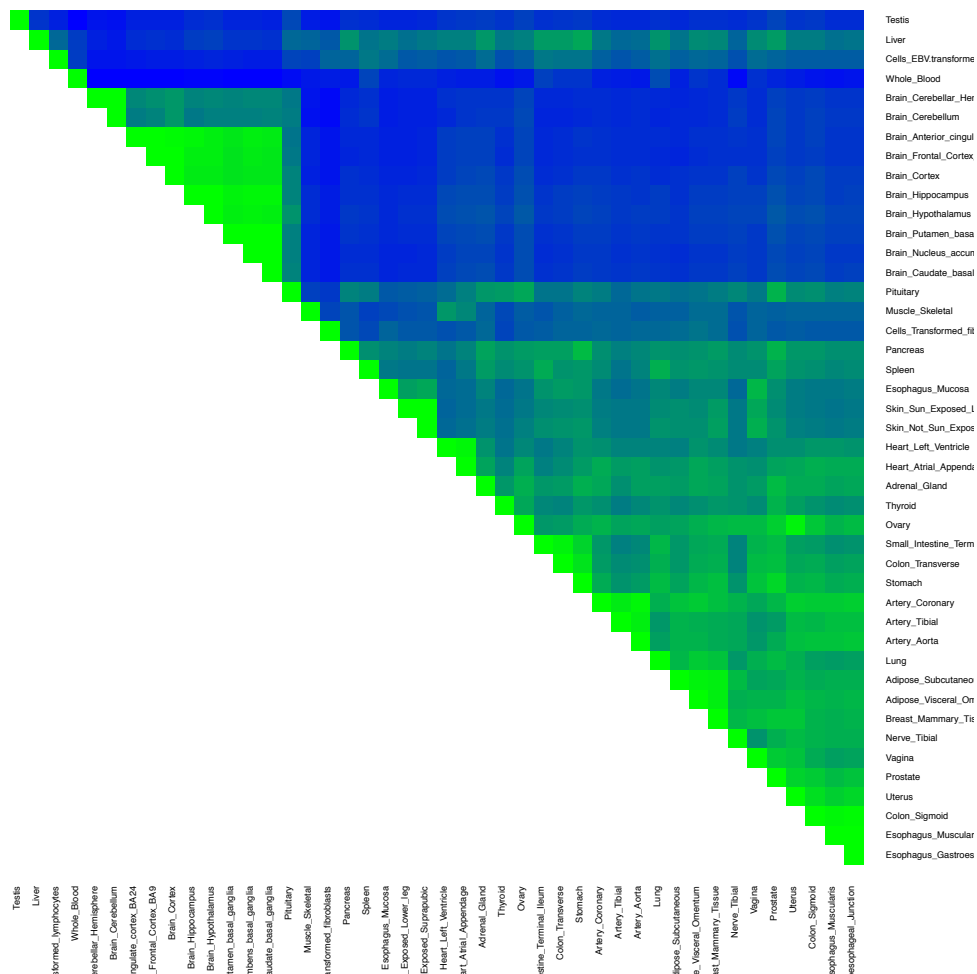
eQTL in either tissues and within 2-fold, SUB

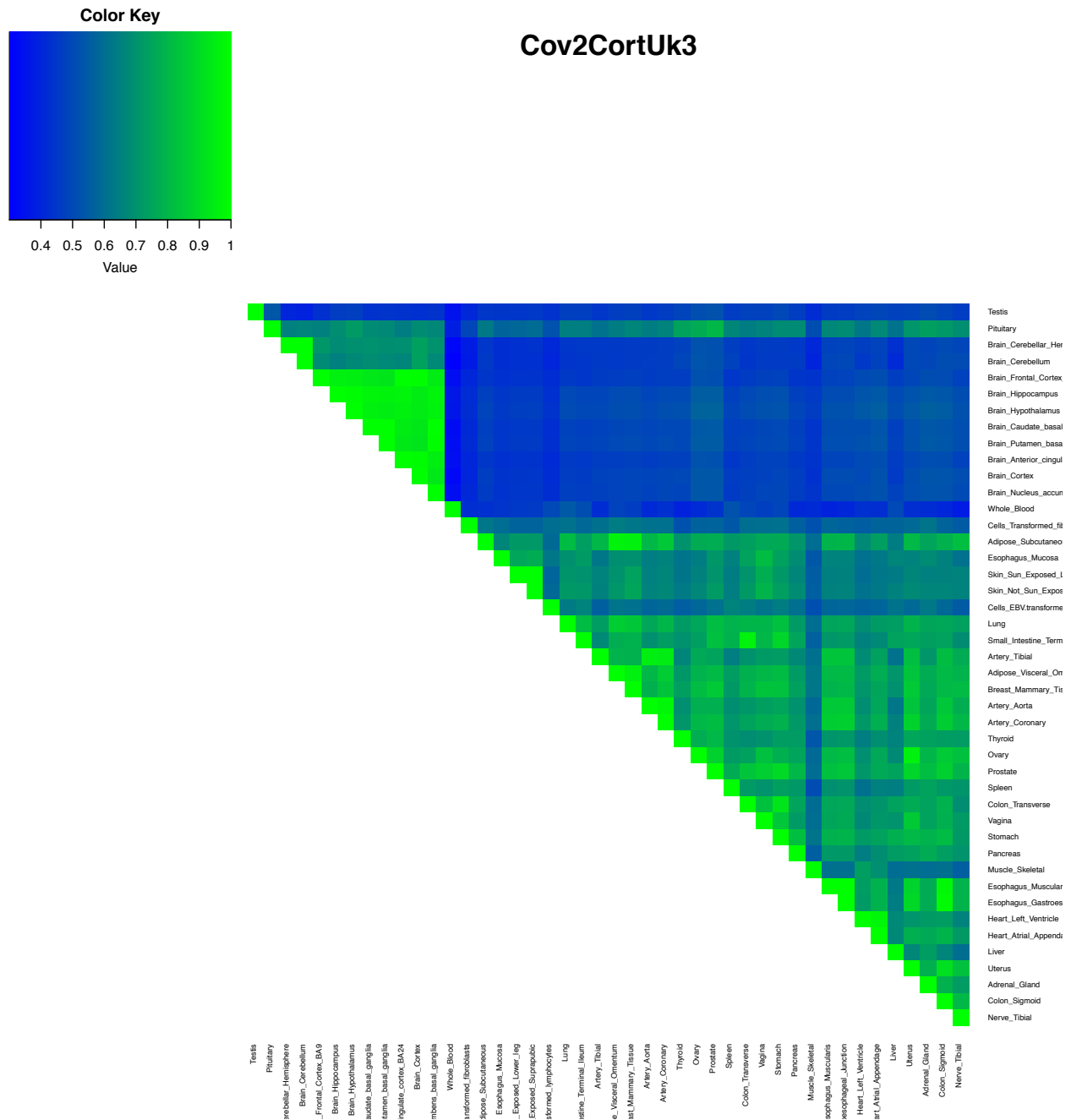
Defined as QTL if LFSR<0.05





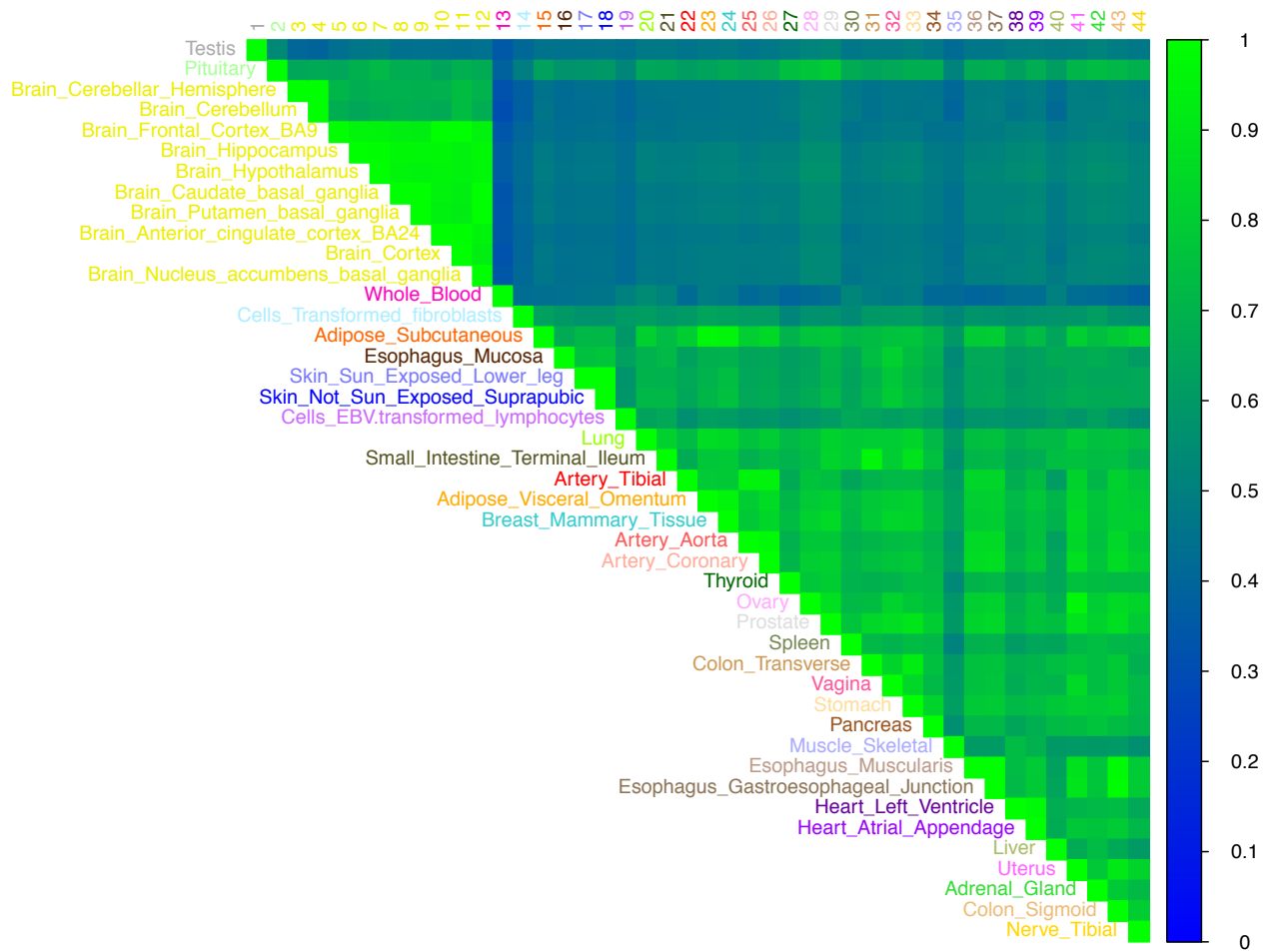
eQTL in either tissues and within 2-fold,SUB

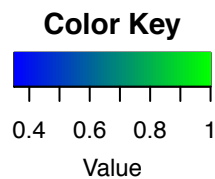




```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```

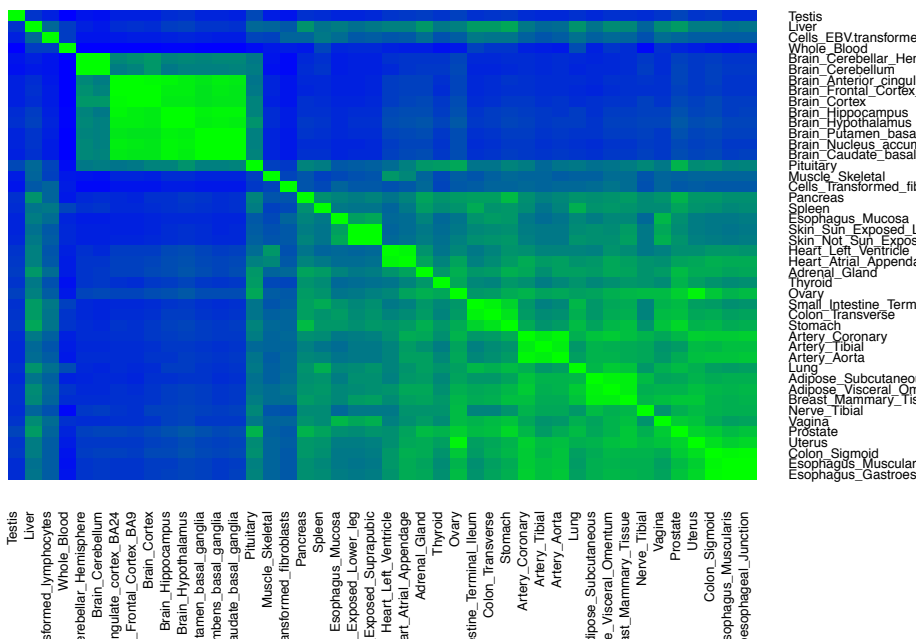
```
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
## used
```



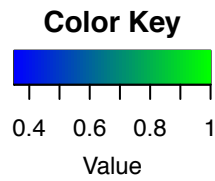


either tissues and within 2-fold, GLOBA

Defined as QTL if LFSR < 0.05

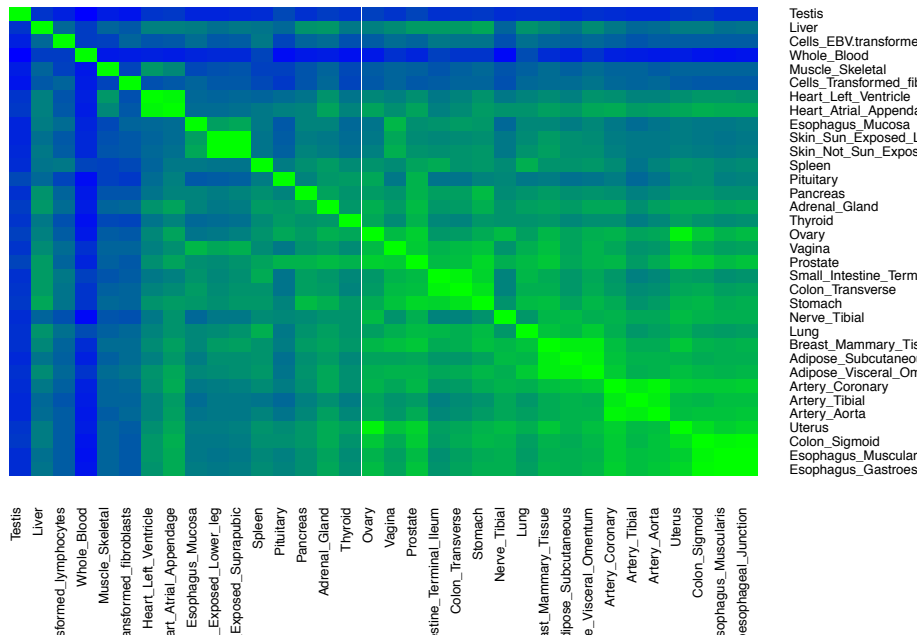


```
## [1] 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12
## [24] 11 10 9 8 7 6 5 4 3 2 1
```

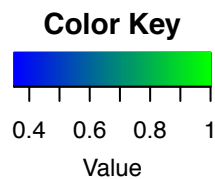



either tissues and within 2-fold, GLOBAL

Defined as QTL if LFSR<0.05

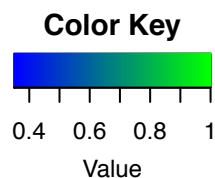
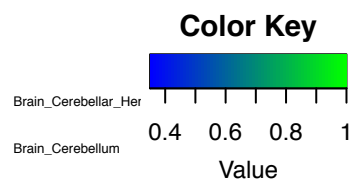
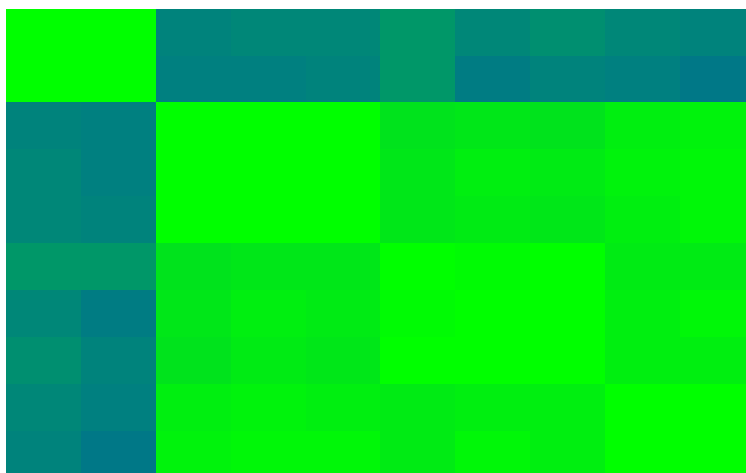


[1] 10 9 8 7 6 5 4 3 2 1

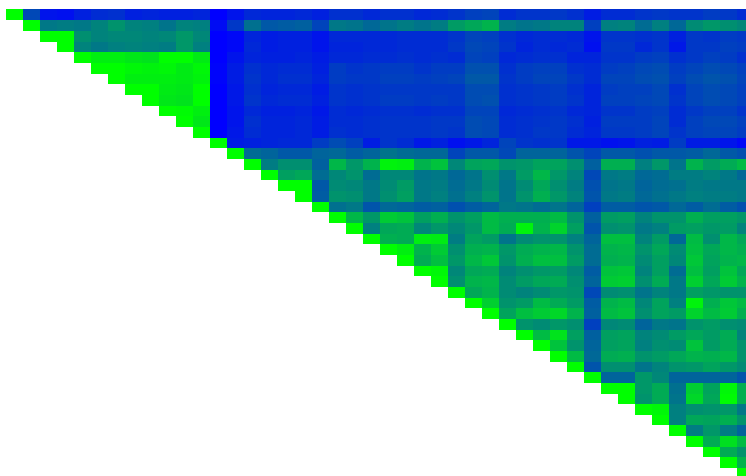


either tissues and within 2-fold, GLOBAL

Defined as QTL if LFSR<0.05



Pairwise Sharing by Magnitude



Tissuespecific by effect:

