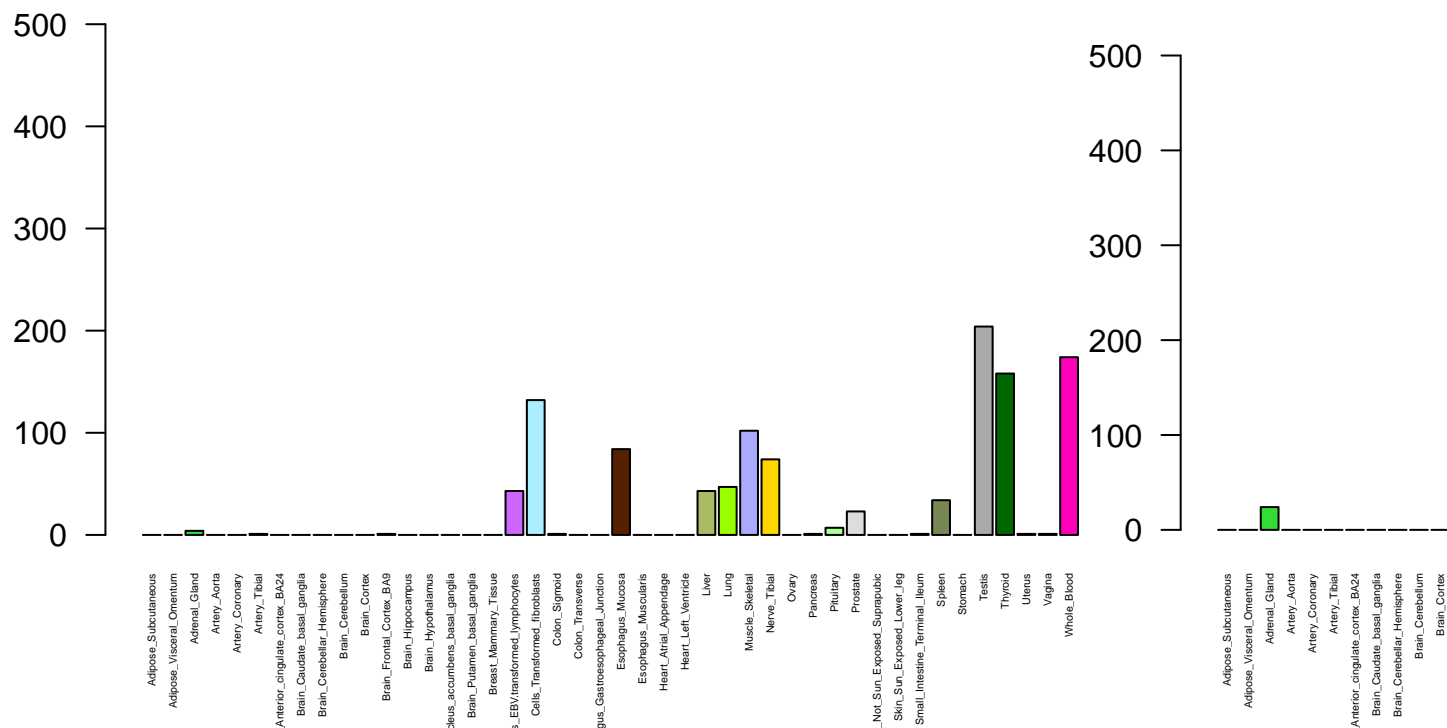# tspec

Tissuespecific by effect:

With pdf function:

```r
pdf("~/Dropbox/PaperEdits/Paper/Figures/tspecbynumber.pdf")

barplot(apply(lfsr.mash[which(rowSums(lfsr.mash<=thresh)==1),],2,function(x){sum(x<=thresh)}),las=2,cex
        ylim=c(0,500),col=col)

dev.off()
```

```
## pdf
##   2
```

```r
###Now plot the number of normalized effects greater than 0.5 for each tissue, given that those effects
#barplot(apply(pm.mash.beta.norm[which(rowSums(pm.mash.beta.norm>0.5)==1),],2,function(x){sum(x>0.5)}),
```

```r
###Now plot the number of normalized effects greater than 0.5 for each tissue, given that those effects

a=which(rowSums(pm.mash.beta.norm>0.5)==1)
lfsr.fold=as.matrix(lfsr.mash[a,])
pm=as.matrix(pm.mash.beta.norm[a,])
tspec=NULL
for(i in 1:ncol(pm)){
  #tspec[i]=sum(lfsr.fold[,i]<0.05&pm[,i]>0.5)
```

```
  tspec[i]=sum(pm[,i]>0.5)
  }##check to see that the effect is significant and greater than 0.5 max effect in only that tissue

tspec=as.matrix(tspec);rownames(tspec)=colnames(maxz)

pdf("~/Dropbox/PaperEdits/Paper/Figures/tspecbymag.pdf")

barplot(as.numeric(t(tspec)),#main=paste0("Number of eQTL with Bjnorm>0.5 in one Tissue"),
        las=2,cex.names=0.3,col=col,names=colnames(lfsr.fold))

dev.off()
```

```
## pdf
##   2
```