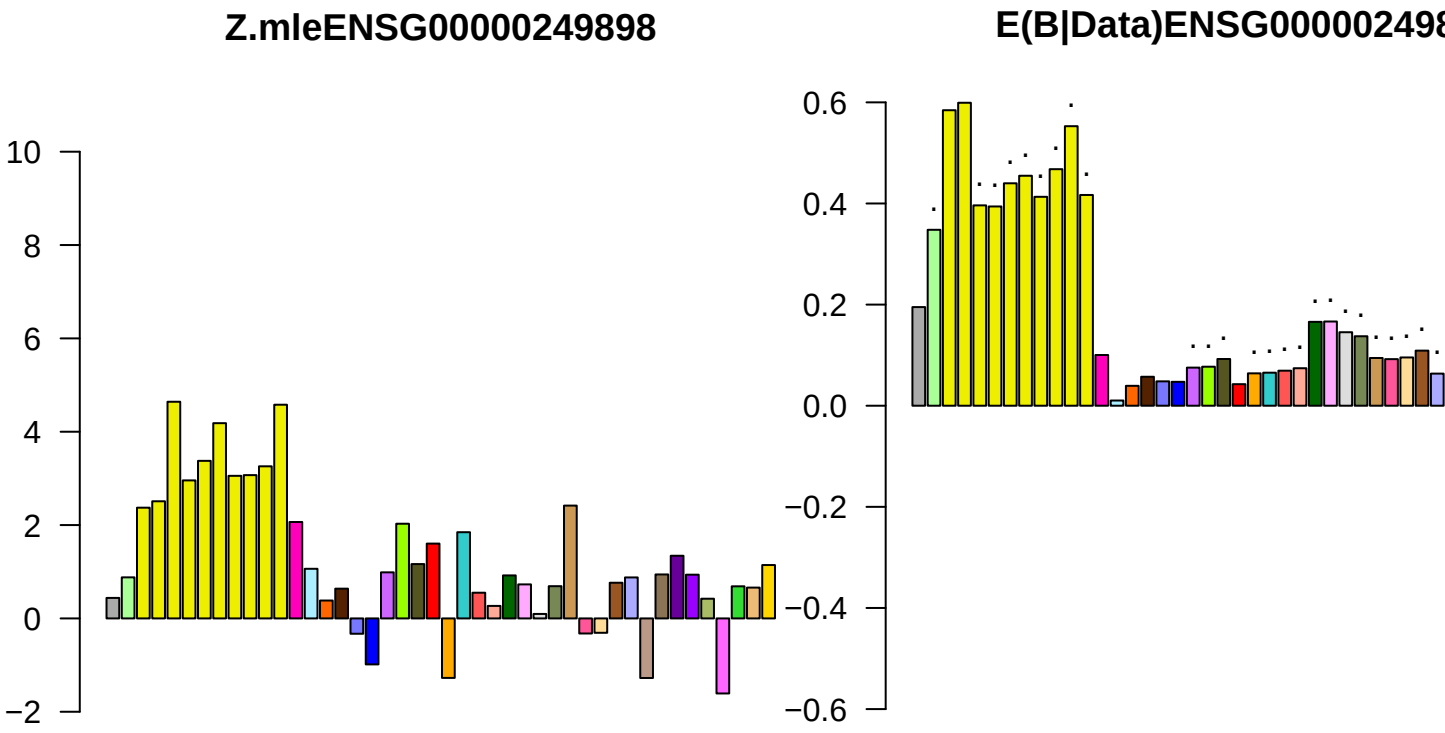
ExampleFinals

```
library('knitr')
knitr::opts_chunk$set(cache=TRUE)
opts_chunk$set(fig.path = "/Users/sarahurbut/Dropbox/PaperEdits/Paper/Figures/")
```

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

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

```
three.ex.3=which(rownames(z.stat)=="ENSG00000249898.3_8_6521432_T_C_b37")
newfunc.2(three.ex.3)
```

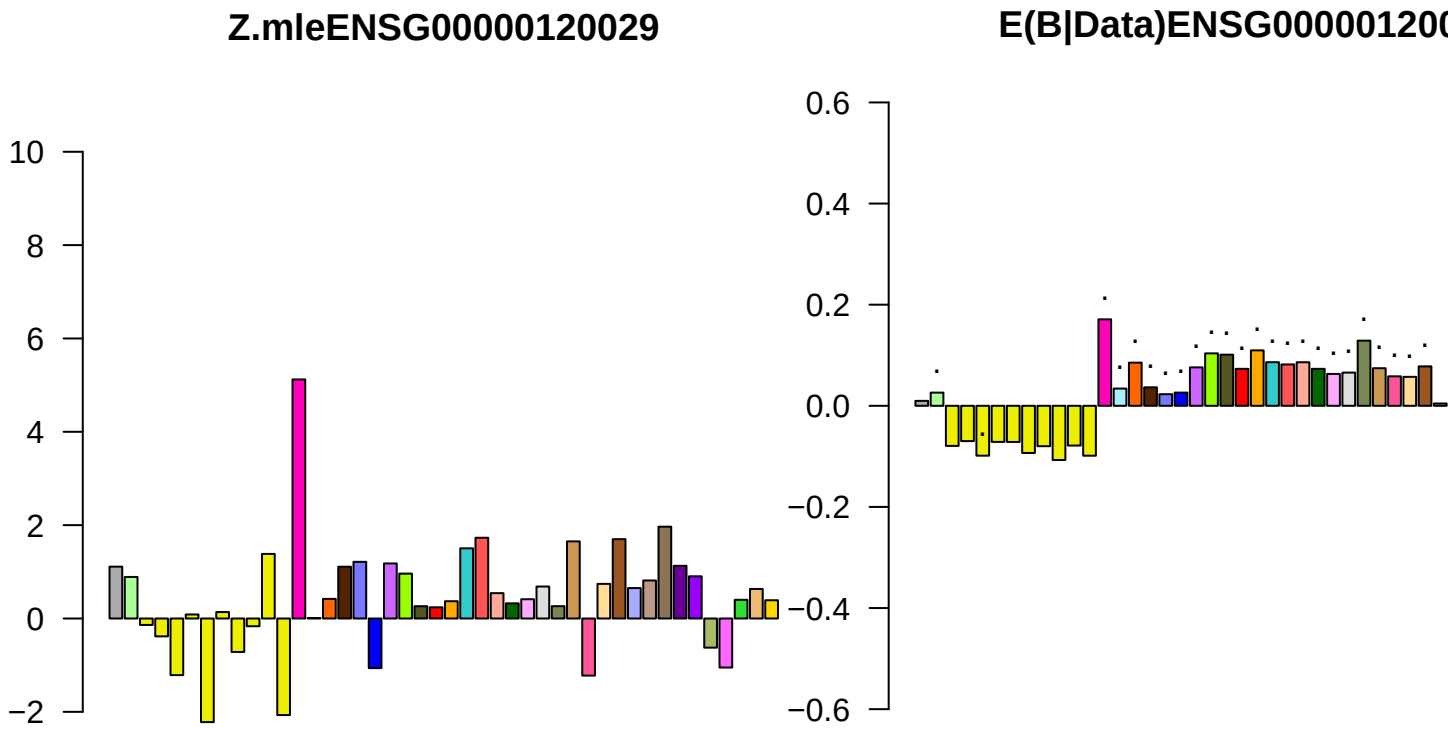



```
whole.blood.spec=which(rowSums(pm.beta.norm[,-44]<0.5)==43&(rowSums(lfsr[,1:44]<0.05)>=40))
```

Here are examples of uk5

Old example:

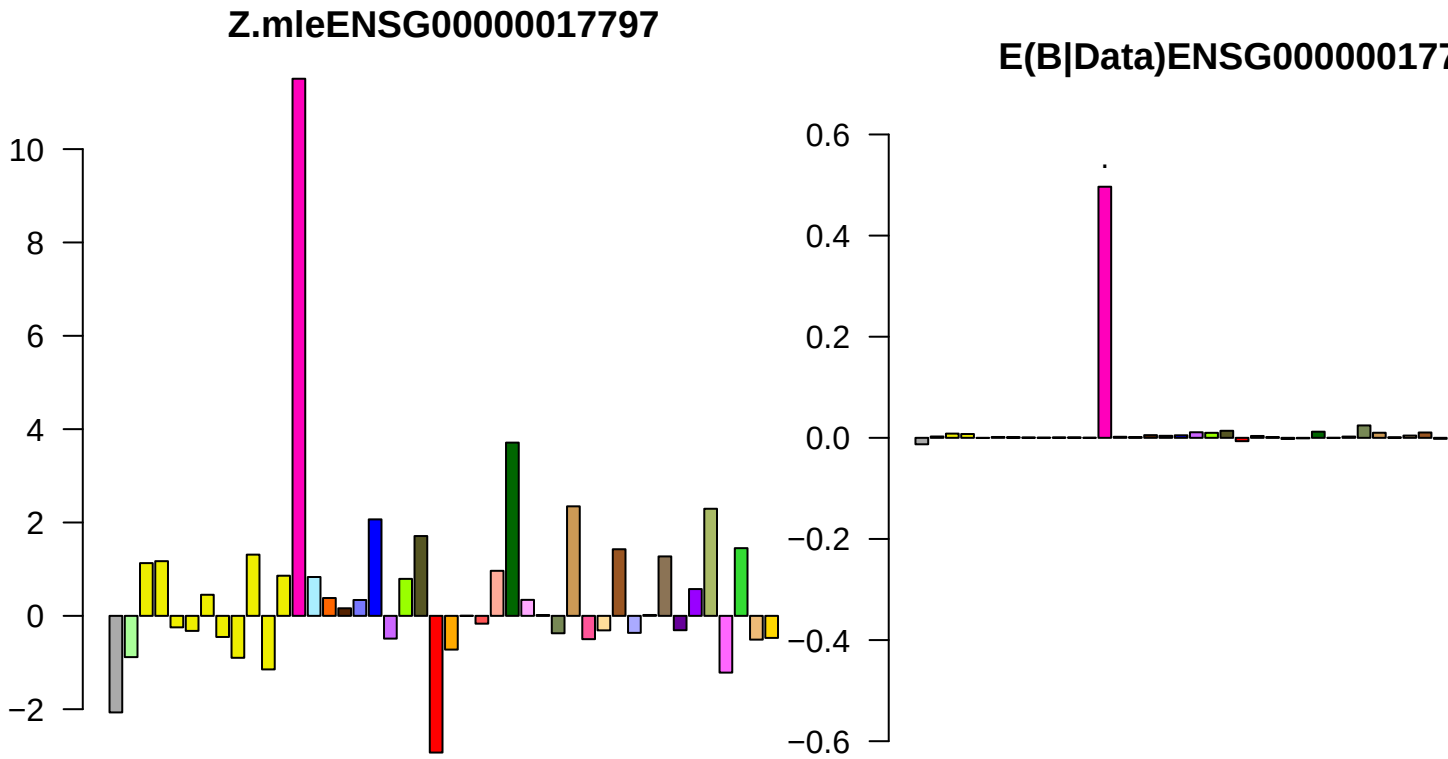
```
five.ex=which(rownames(z.stat)=="ENSG00000120029.8_10_103924251_G_A_b37")
testes.spec=which(rowSums(pm.beta.norm[,-40]<0.5)==43&(rowSums(lfsr[,1:44]<0.05)>=40))[1:10]

newfunc.2(five.ex)
```



Lastly, the inclusion of the eQTLBMA lite configurations (in which the SNP has a non-zero effect in only one tissue) coupled with the learned patterns of tissue specificity evident in matrices Uk 5 through 9 serve to allow the preservation of qualitatively specific effects. Here, we show a gene-snp pair demonstrating strong posterior probability from arising from one of the eQTL-bma lite configs. Accordingly we reject the significance of the effect size estimates in all tissues but testes, a pattern consistent with the presence of tissue-specificity described below. Together, these results cement the resolution afforded by methods which can distinguish among tissues in which a QTL is called active, beyond reducing genetic effects to binary 'on' or 'off' conclusions.

Good example for whole bllood with decent rpkm across the board:

```
wholebloodfour=(which(rownames(z.stat)=="ENSG00000017797.7_18_9488704_C_T_b37"))
newfunc.2(wholebloodfour)
```



To plot the PC:

```
# pi.mash=readRDS("~/gtexresults_matrixash//Data/pisAug13withED.rds")$pihat
# abr.names=read.table("~/gtexresults_matrixash/Data/abbreviate.names.txt")
# #pi.mash=readRDS("~/Dropbox/withzero/piswithzero.rds")$pihat[-1189]
# pi.mat.mash=matrix(data = pi.mash,nrow = 22,ncol =54,byrow = TRUE)
# par(mfrow=c(3,3))
# par(mar=c(4,3,2,1))
# for(i in 2:9){
#
# v=svd(covmat[[i]])$v
#   colnames(v)=rownames(v)=abr.names[,2]
# max.effect=sign(v[,1][which.max(abs(v[,1]))])
# barplot(max.effect*v[,1],las=2,main=paste0("EigenVector1ofUk=",i),#main=ifelse(i!=5,paste0("EigenVect
#         col=i-1,axisnames=ifelse(i==2,TRUE,FALSE),cex.names=ifelse(i==2,0.4,NULL))
# #if(i==5) { mtext(paste0("EigenVector1ofUk=",i))}
# }
#
# barplot(rep(1,44),main="Consistent Config, mash.lite")
#
# significantUK=order(colSums(pi.mat.mash),decreasing = T)[1:6]
#
# par(mfrow=c(1,1))
# #par(mfrow=c(2,3))
# #par(mar=c(4,3,2,1))
# for(i in significantUK){
#
# v=svd(covmat[[i]])$v
#   colnames(v)=rownames(v)=abr.names[,2]
# max.effect=sign(v[,1][which.max(abs(v[,1]))])
```

```
# barplot(max.effect*v[,1],las=2,main=paste0("EigenVector1ofUk=",i,",pihat=",round(colSums(pi.mat.mash)
#         col=i-1,axisnames=ifelse(i==2,TRUE,FALSE),cex.names=ifelse(i==2,0.4,NULL))
# #if(i==5) { mtext(paste0("EigenVector1ofUk=",i))}
# }
#
# #barplot(rep(1,44),main="Consistent Config, mash.lite")
```