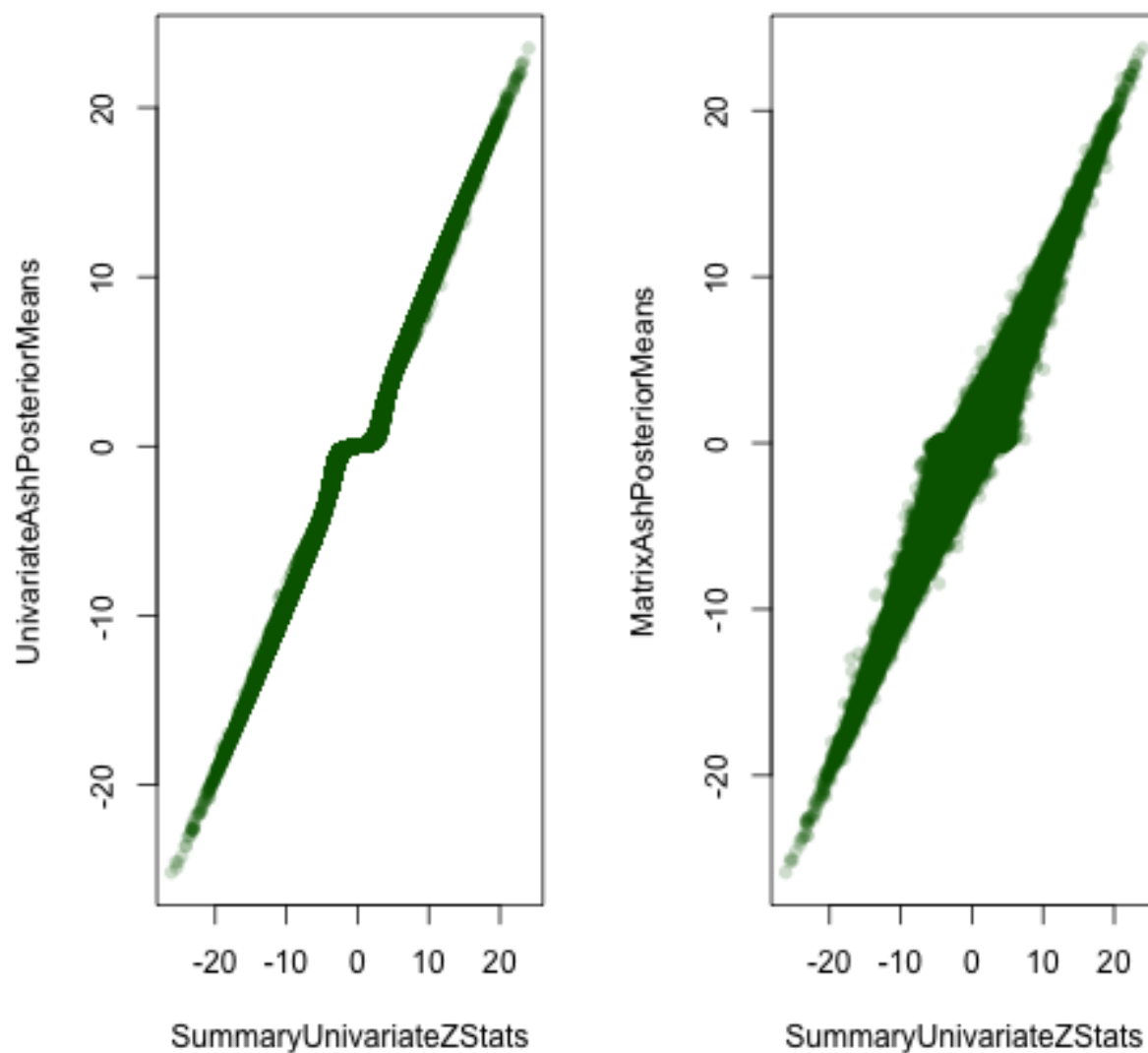


ComparingwithUnivariateAsh

In this document I compare with univariate ash

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

UnivariateAshAppliedtoAllTissuesixAshPosteriorMeansvsUnivariateS



```
## [1] "/Users/sarahurbut/Dropbox/UnivariateAsh"
```

We can consider the number of statistics at each threshold using both methods:

```
thresh=0.05  
sum(lfsr.mash<thresh)
```

```
## [1] 393414
```

```
sum(lfsr.ash<thresh)
```

```
## [1] 91755
```

We can see that Matrix ASH identifies 4.2876573 more associations than using univariate ash. Furthermore, if we consider the number of genes with at least one LFSR less than threshold, we also identify more using this multivariate method. Using

```
gene.func=function(lfsr,thresh){  
  sigmat=lfsr<thresh  
  sum(rowSums(sigmat)!=1)}  
  
gene.func(lfsr.mash,thresh=0.05)
```

```
## [1] 14887
```

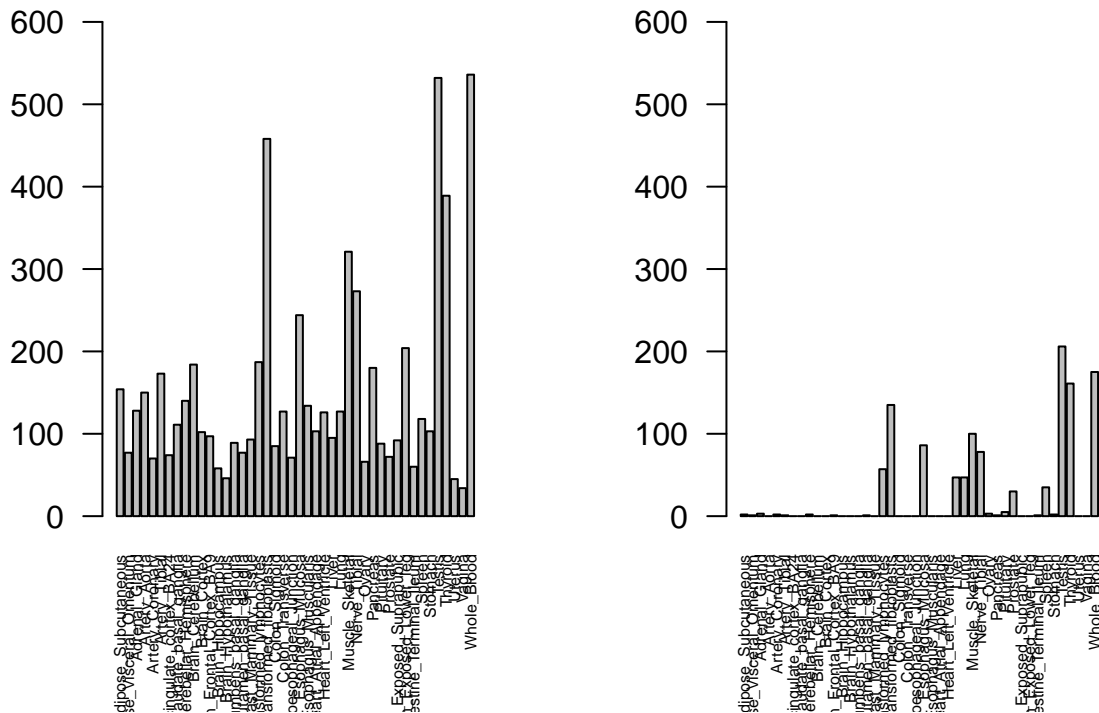
```
gene.func(lfsr.ash,thresh=0.05)
```

```
## [1] 9376
```

Let's consider how are bias towards or against tissue specificity changes:

```
par(mfrow=c(1,2))  
plot_singleontissues(lfsr.ash,thresh,method="ASH")  
plot_singleontissues(lfsr.mash,thresh,method="MATRIXASH")
```

Number of eQTL with $ASH < 0.05$ in Single of eQTL with $MATRIXASH < 0.05$ in S



Let's also count how many associations we might count as inconsistent by simply counting the number of times the signs differed in a vector of posterior means for a given gene snp pair:

```
inconsistent.func=function(posterior.means,lfsr,thresh=0.05){
h=apply(posterior.means,1,function(p){
  pos=sum(p>0);neg=sum(p<0);pos*neg!=0})
sum(h=="TRUE")}

inconsistent.func(pm.ash,lfsr.ash)
```

```
## [1] 14557
```

```
inconsistent.func(pm.mash,lfsr.mash)
```

```
## [1] 9597
```