

hettablewithst

Heterogeneity Analysis

First, we asked in how many tissues is a QTL significant.

```
## [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [12] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [23] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [34] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
sigmat=(lfsr<=thresh)
nsig= rowSums(sigmat)
(signall=mean(het.norm(pm.mash.beta[nsig>0,])>0))
```

```
## [1] 0.8494795
```

```
sigmat=(lfsr.nobrain<=thresh)
nsig= rowSums(sigmat)
(signnobrain=mean(het.norm(pm.mash.nobrain[nsig>0,])>0))
```

```
## [1] 0.8823972
```

```
sigmat=(lfsr.brain.only<=thresh)
nsig= rowSums(sigmat)
(signbrainonly=mean(het.norm(pm.mash.brain.only[nsig>0,])>0))
```

```
## [1] 0.9840876
```

```
#
##show that results are robust###
sigmat=(lfsr[, -c(7:16)]<=thresh)
nsig= rowSums(sigmat)
(signall.nobrain=mean(het.norm(pm.mash.beta[, -c(7:16)])>0))
```

```
## [1] 0.8621679
```

```
sigmat=(lfsr[, c(7:16)]<=thresh)
nsig= rowSums(sigmat)
(signall.brainonly=mean(het.norm(pm.mash.beta[nsig>0, c(7:16)])>0))
```

```
## [1] 0.9592103
```

```
####
sigmat=(lfsr<=thresh)
nsig= rowSums(sigmat)
(magall=mean(het.norm(pm.mash.beta[nsig>0,])>0.5))
```

```
## [1] 0.3669264
```

```

sigmat=(lfsr.nobrain<=thresh)
nsig= rowSums(sigmat)
(magnobrain=mean(het.norm(pm.mash.nobrain[nsig>0,])>0.5))

```

```
## [1] 0.4445148
```

```

sigmat=(lfsr.brain.only<=thresh)
nsig= rowSums(sigmat)
(magbrain=mean(het.norm(pm.mash.brain.only[nsig>0,])>0.5))

```

```
## [1] 0.8586027
```

```

##show that results are robust###
sigmat=(lfsr[, -c(7:16)]<=thresh)
nsig= rowSums(sigmat)
(magall.excludingbrain=mean(het.norm(pm.mash.beta[nsig>0, -c(7:16)])>0.5))

```

```
## [1] 0.4150936
```

```

sigmat=(lfsr[, c(7:16)]<=thresh)
nsig= rowSums(sigmat)
(magall.brainonly=mean(het.norm(pm.mash.beta[nsig>0, c(7:16)])>0.5))

```

```
## [1] 0.7755301
```