

expressionconfirm

Here, we simply plot the density of the average expression for all genes

```
## Warning: package 'knitr' was built under R version 3.2.5
```

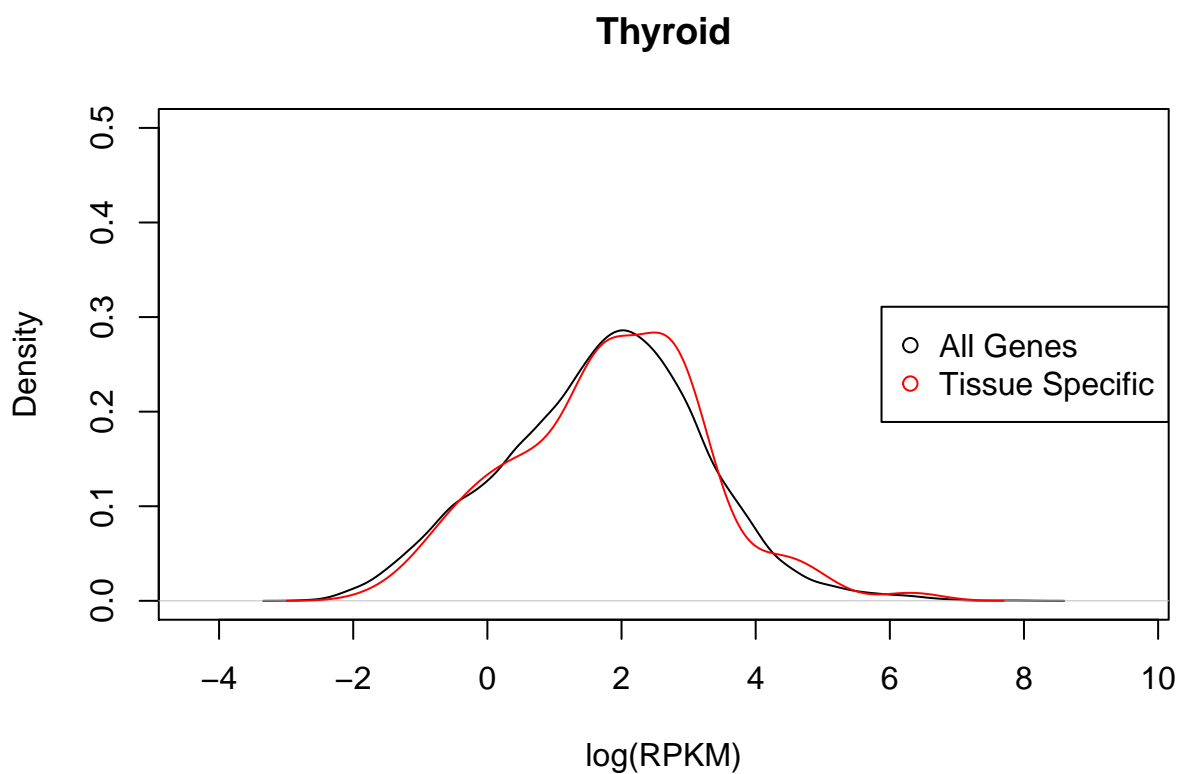
```
## Warning: package 'qtlcharts' was built under R version 3.2.5
```

Here we compare quantiles and plot data:

Thyroid:

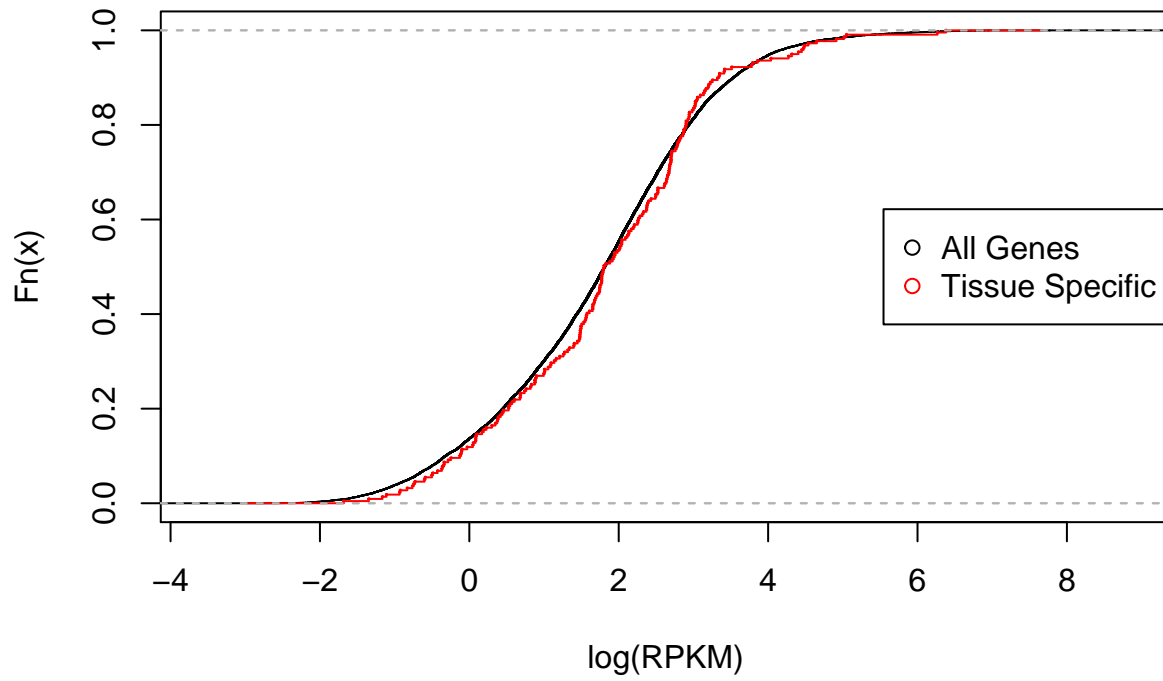
```
#compare.distribution(tissuename = "Thyroid",lfsr = lfsr,curvedata = log(exp.sort),thresh = 0.05 )
```

```
plot_tissuespecifictwo(tissuename = "Thyroid",lfsr = lfsr,curvedata = log(exp.sort),title = "Test",thre
```



```
plot_tissuespecificthree(tissuename = "Thyroid",lfsr = lfsr,curvedata = log(exp.sort),title = "Test",th
```

Thyroid

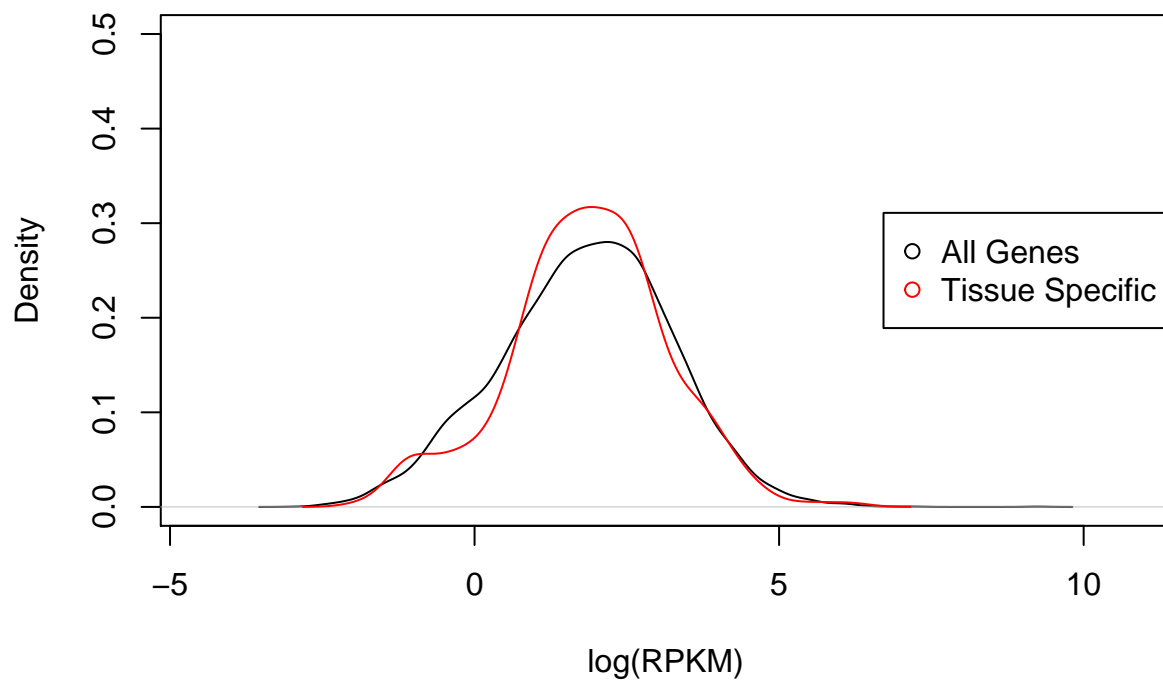


Testis:

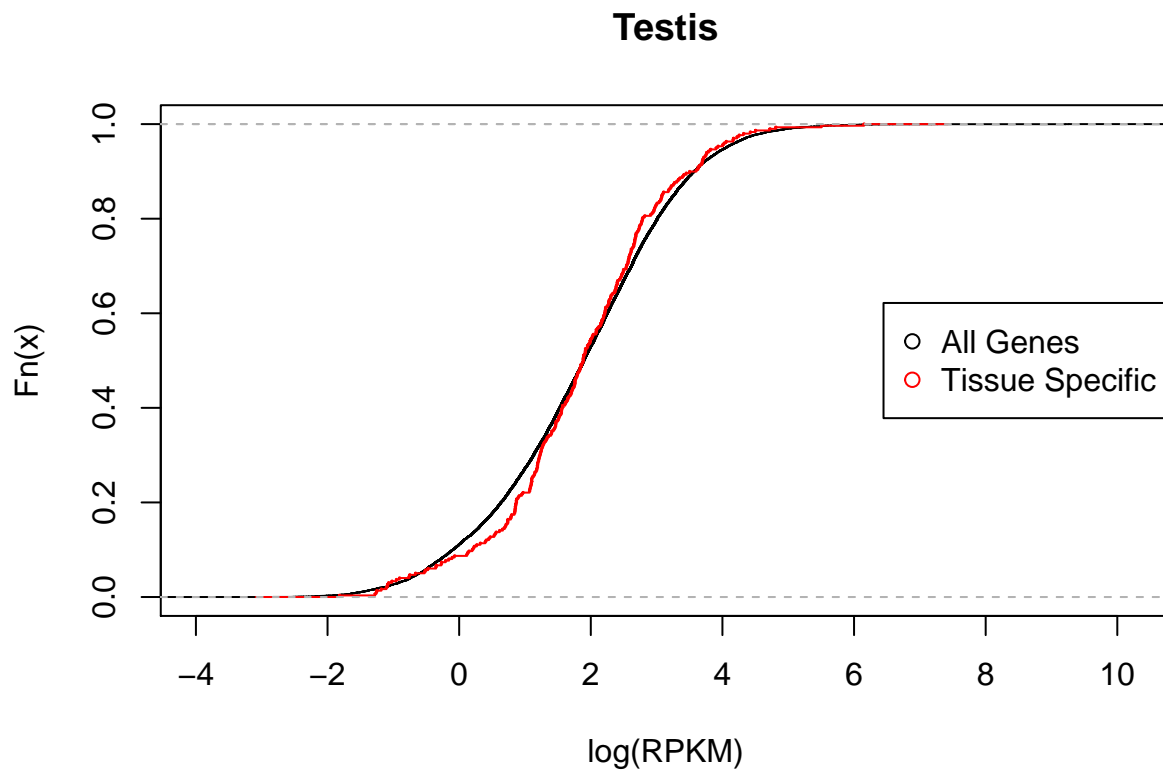
```
#compare.distribution(tissuename = "Testis",lfsr = lfsr,curvedata = log(exp.sort),thresh = 0.05)
```

```
plot_tissuespecifictwo(tissuename = "Testis",lfsr = lfsr,curvedata = log(exp.sort),title = "Test",thresh = 0.05)
```

Testis



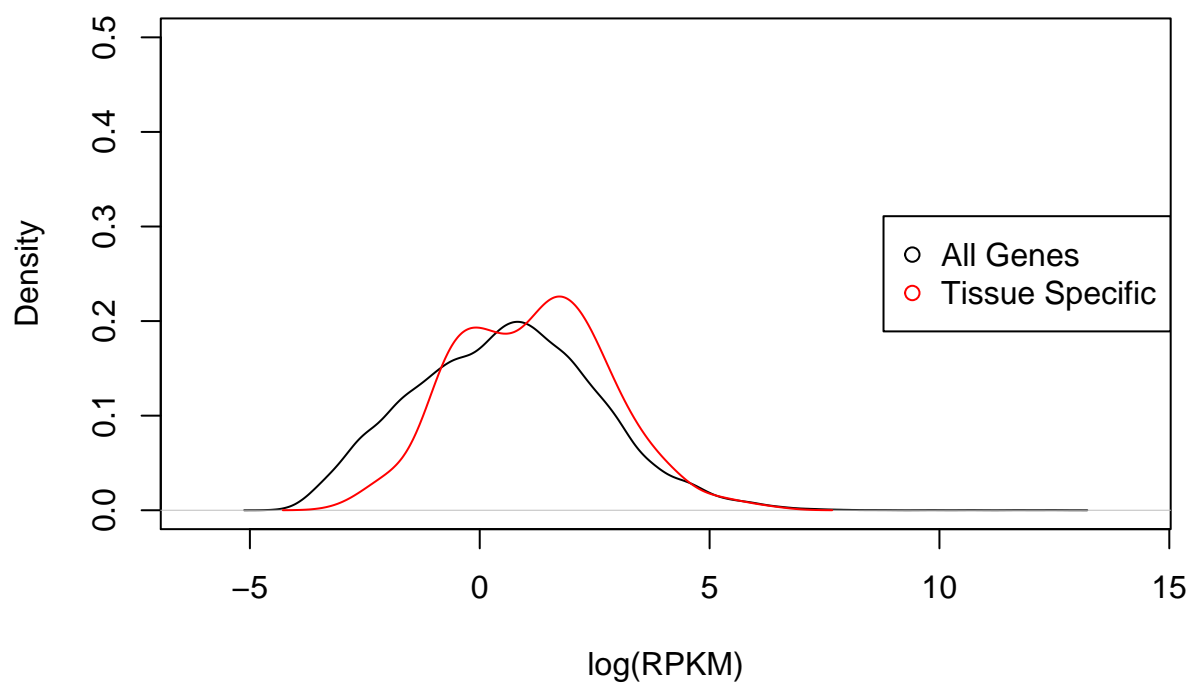
```
plot_tissuespecificthree(tissuename = "Testis",lfsr = lfsr,curvedata = log(exp.sort),title = "Test",thr
```



Whole Blood

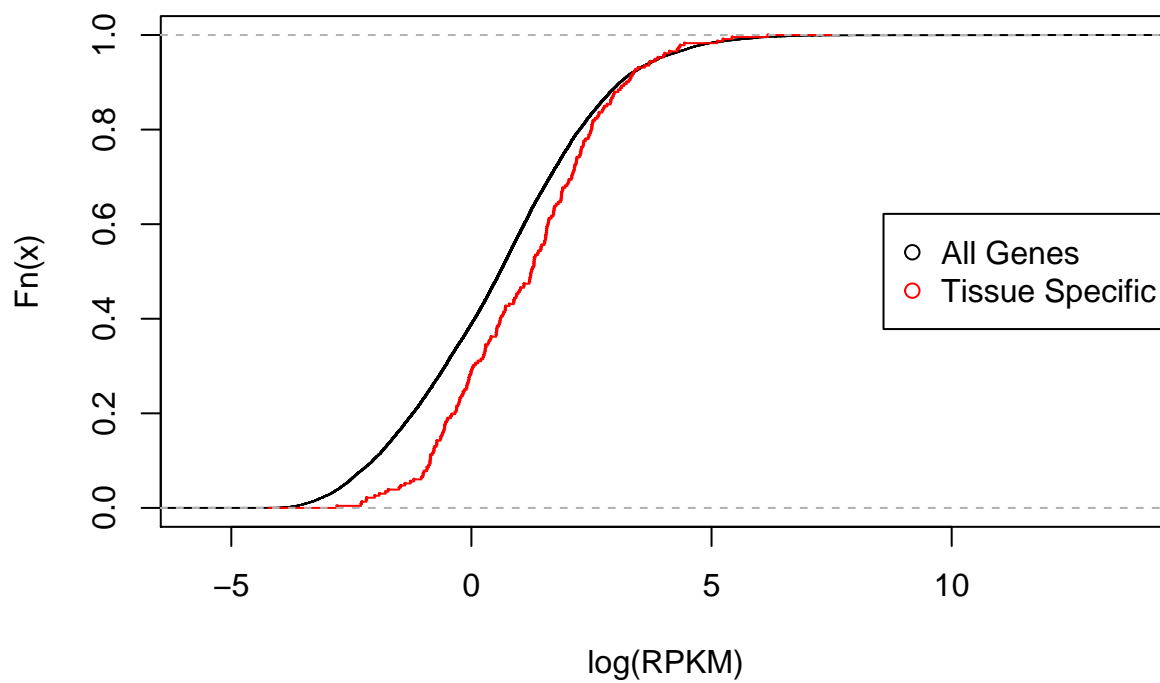
```
#compare.distribution(tissuename = "Whole_Blood",lfsr = lfsr,curvedata = log(exp.sort),thresh = 0.05 )
plot_tissuespecifictwo(tissuename = "Whole_Blood",lfsr = lfsr,curvedata = log(exp.sort),title = "Test",
```

Whole_Blood



```
plot_tissuespecificthree(tissuename = "Whole_Blood",lfsr = lfsr,curvedata = log(exp.sort),title = "Test
```

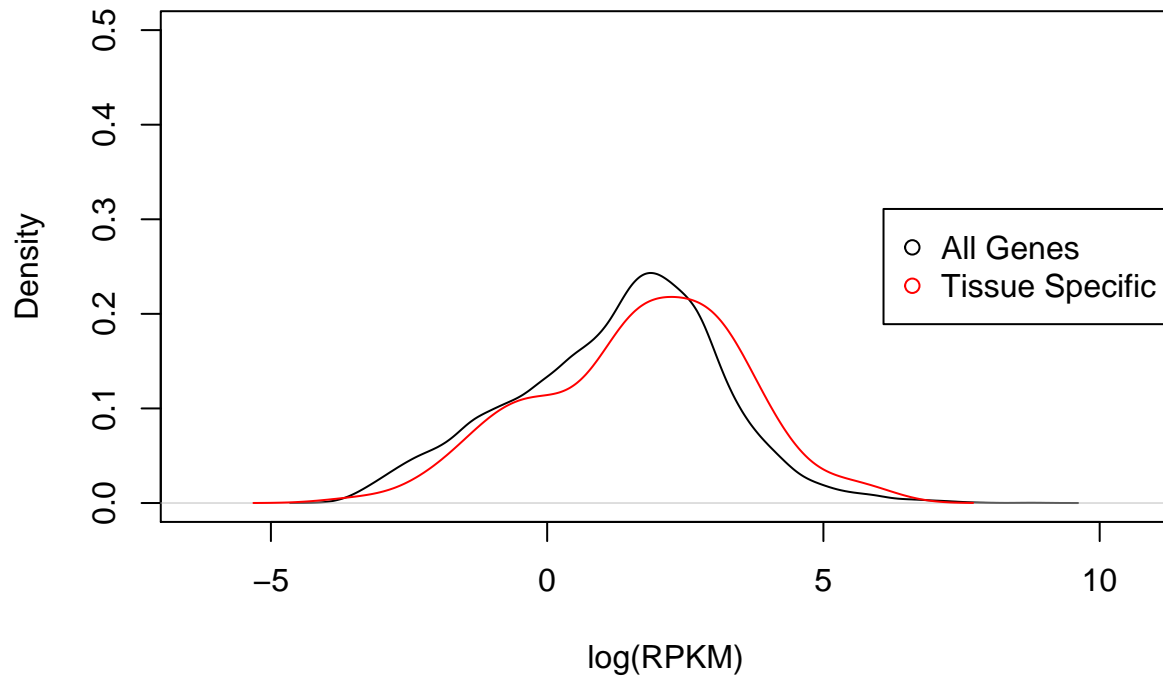
Whole_Blood



Muscle_Skeletal

```
plot_tissuespecifictwo(tissuename = "Cells_Transformed_fibroblasts",lfsr = lfsr,curvedata = log(exp.sor
```

Cells_Transformed_fibroblasts



```
plot_tissuespecifictthree(tissuename = "Cells_Transformed_fibroblasts",lfsr = lfsr,curvedata = log(exp.s
```

Cells_Transformed_fibroblasts

