

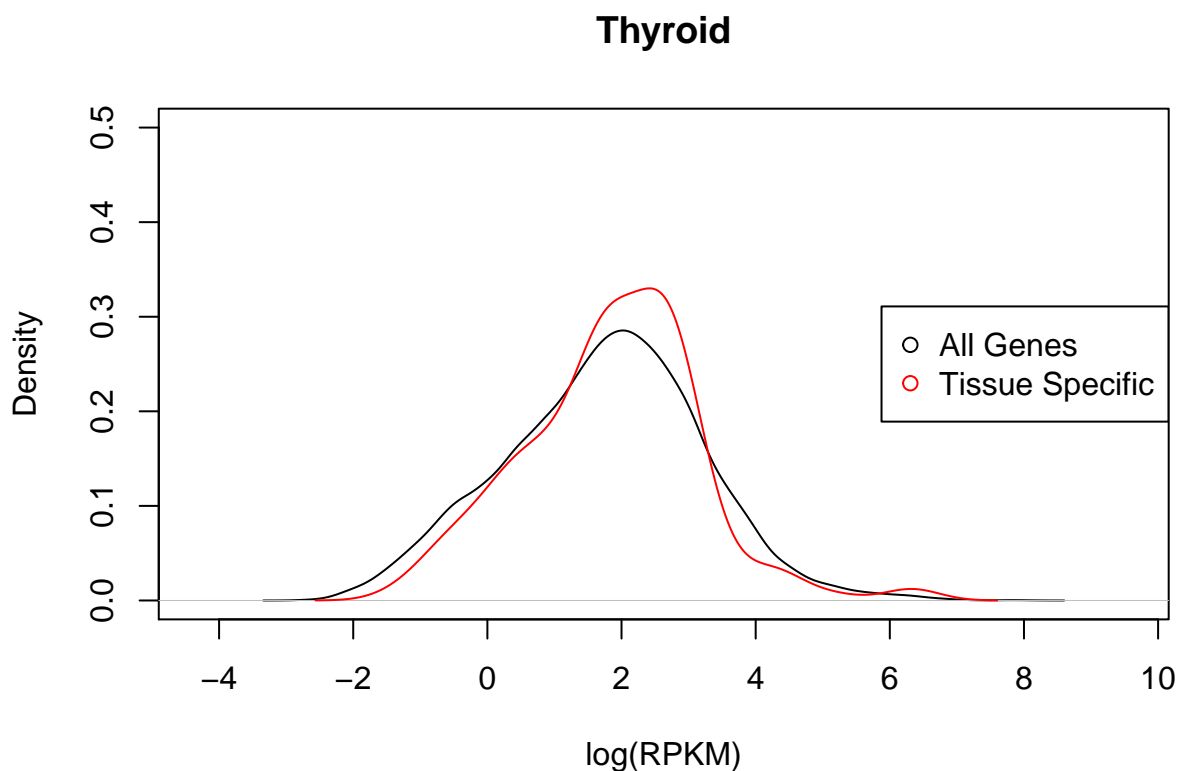
NormalQuantils

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

Here we compare quantiles and plot data:

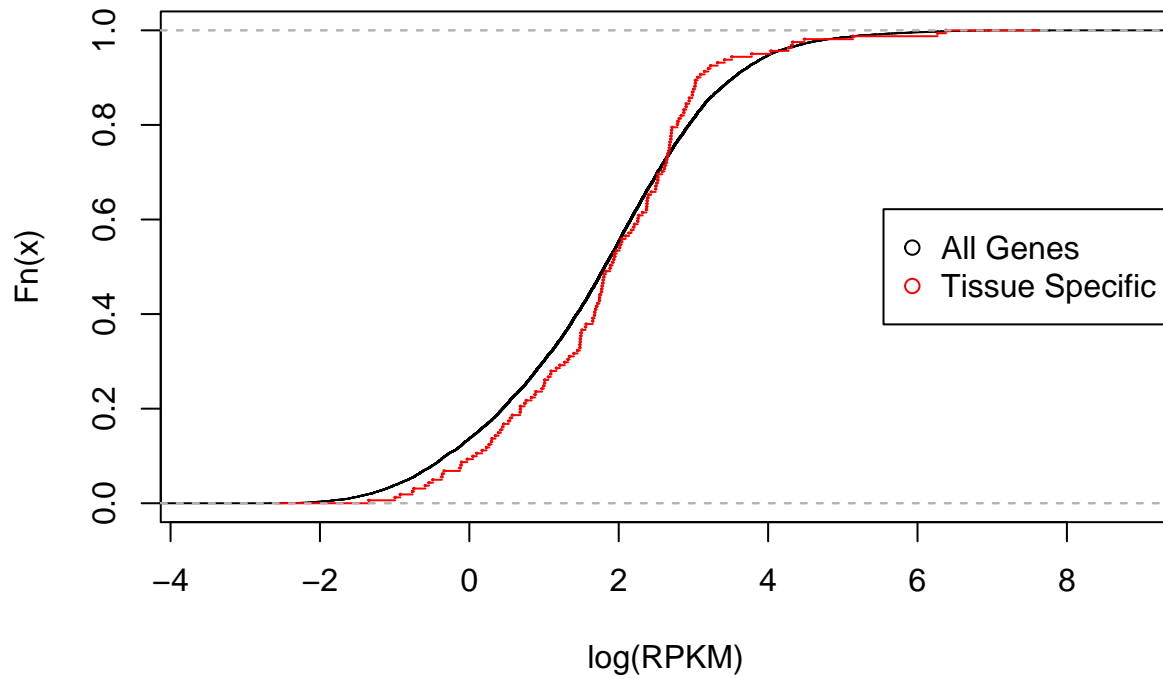
Thyroid:

```
#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",thresh = 0.05 )
```



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

Thyroid

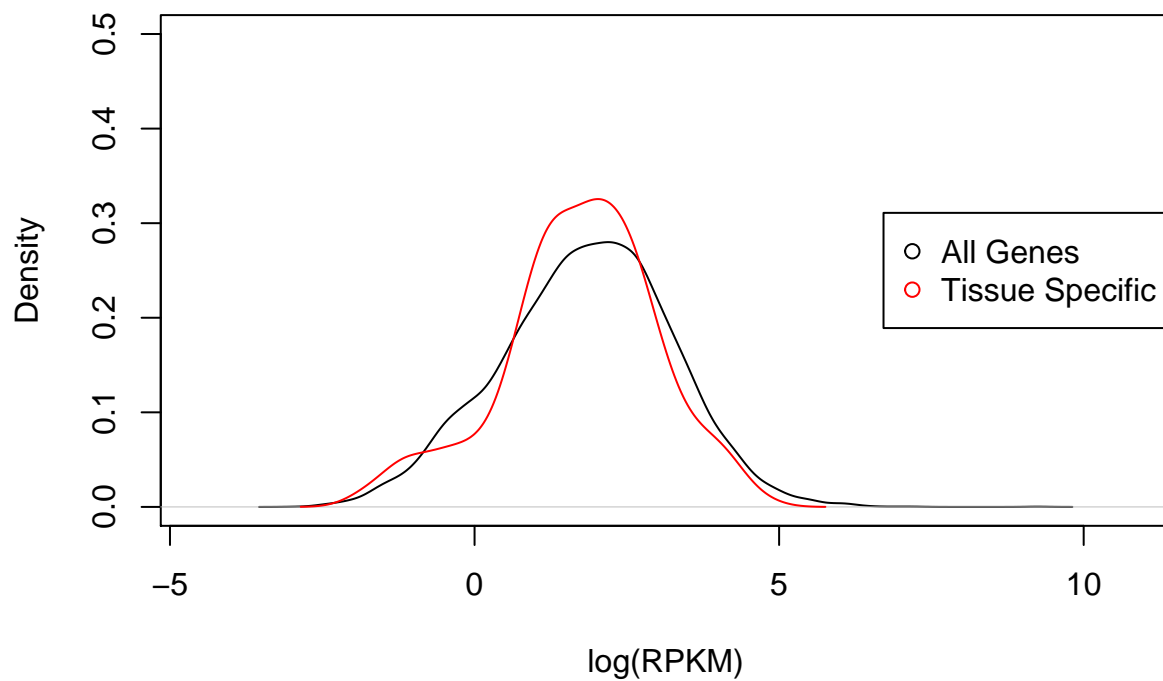


Testis:

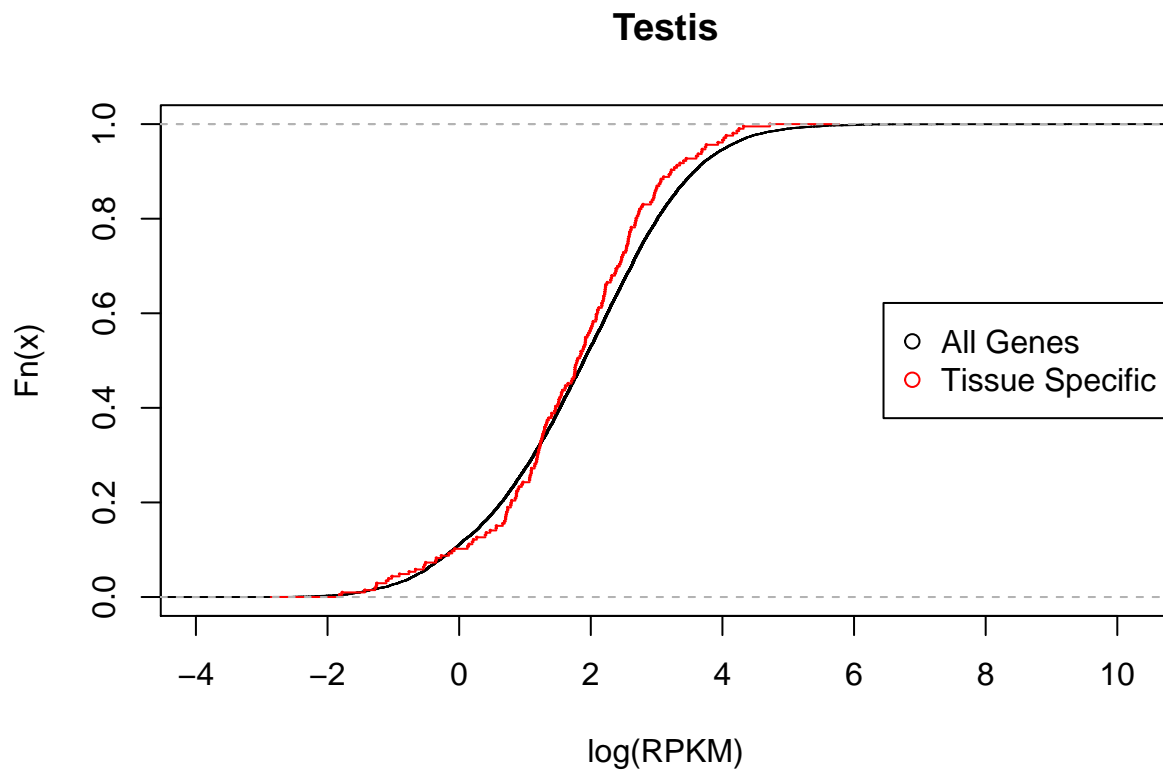
```
#compare.distribution(tissuename = "Testis",lfsr = lfsr,curvedata = log(exp.sort),thresh = 0.05)
```

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

Testis



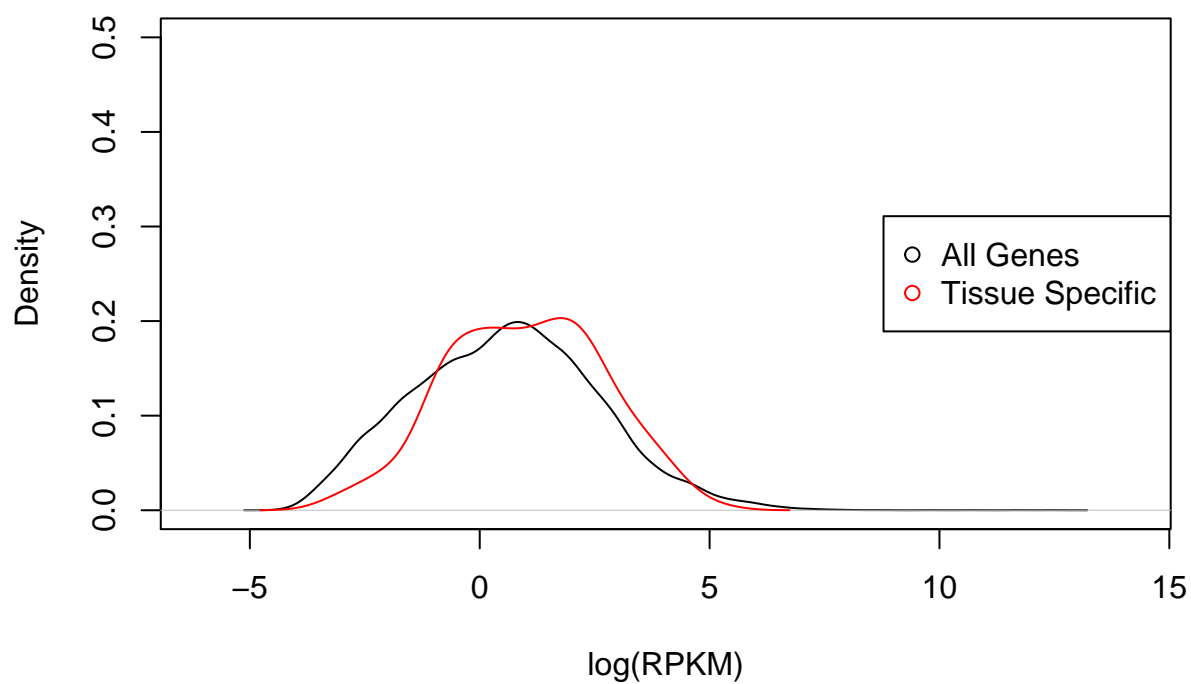
```
plot_tissuespecificthree(tissuename = "Testis",lfsr = lfsr,curvedata = log(exp.sort),title = "Test",thr
```



Whole Blood

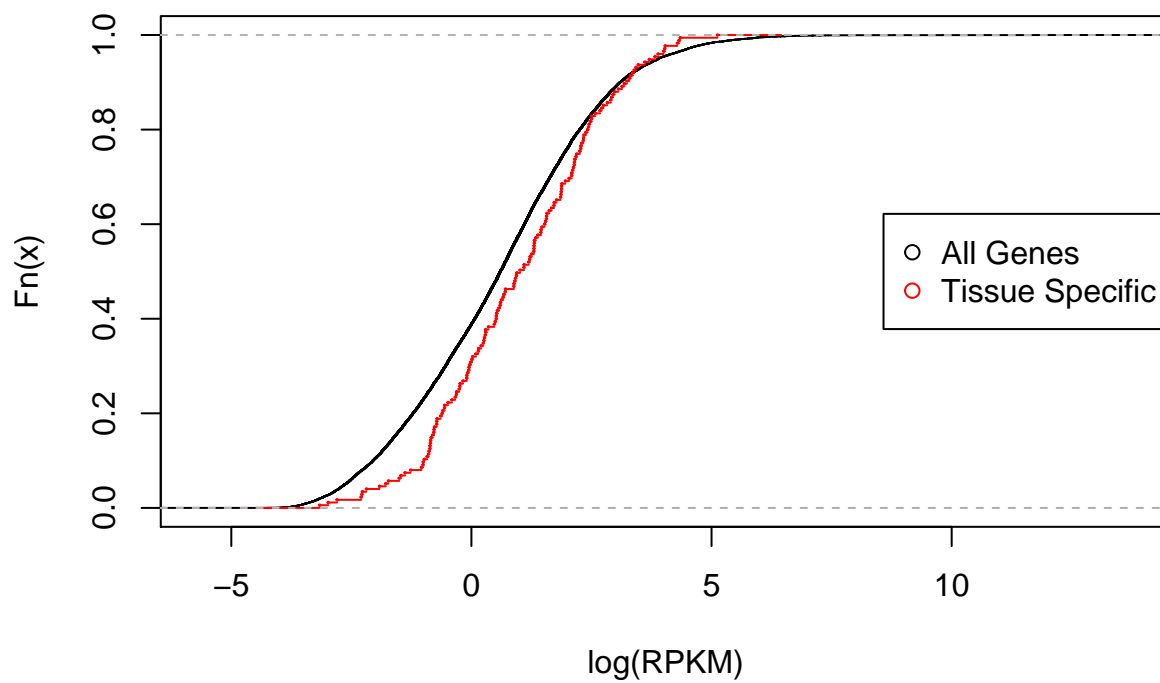
```
#compare.distribution(tissuename = "Whole_Blood",lfsr = lfsr,curvedata = log(exp.sort),thresh = 0.05 )
plot_tissuespecifictwo(tissuename = "Whole_Blood",lfsr = lfsr,curvedata = log(exp.sort),title = "Test",
```

Whole_Blood



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

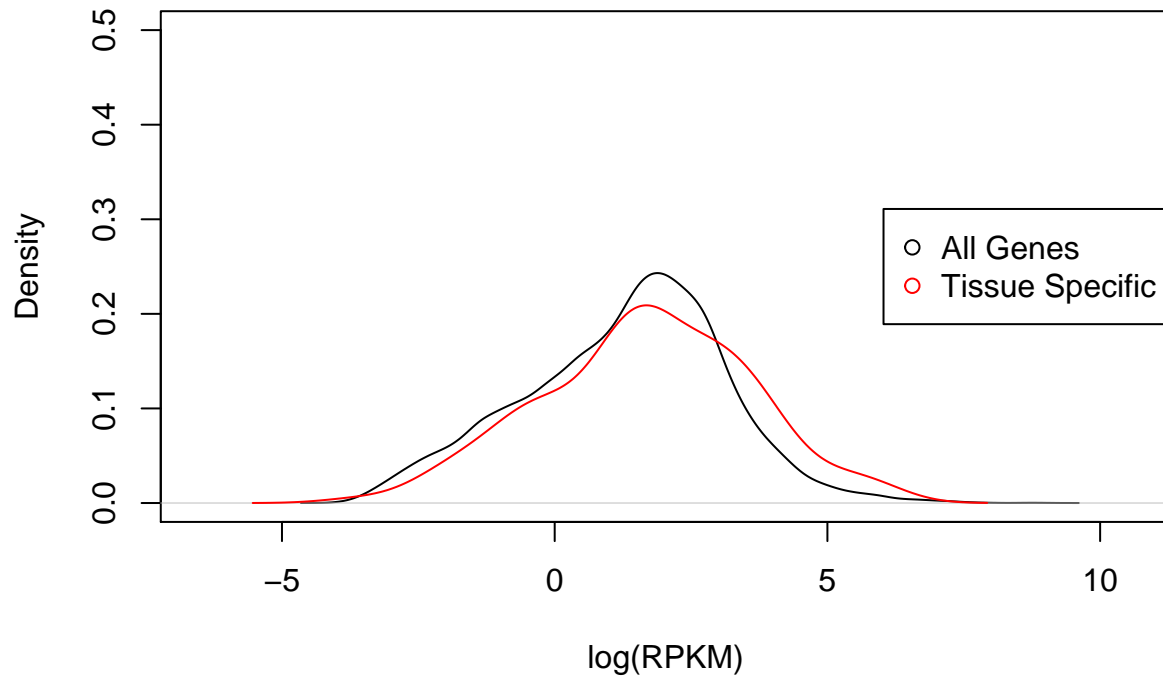
Whole_Blood



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

