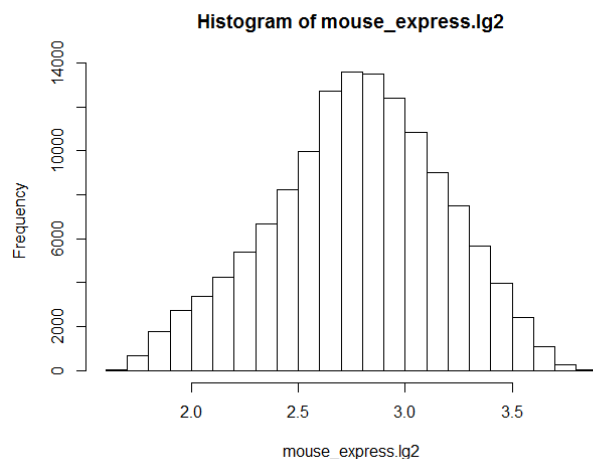


## HOMEWORK ASSIGNMENT 1

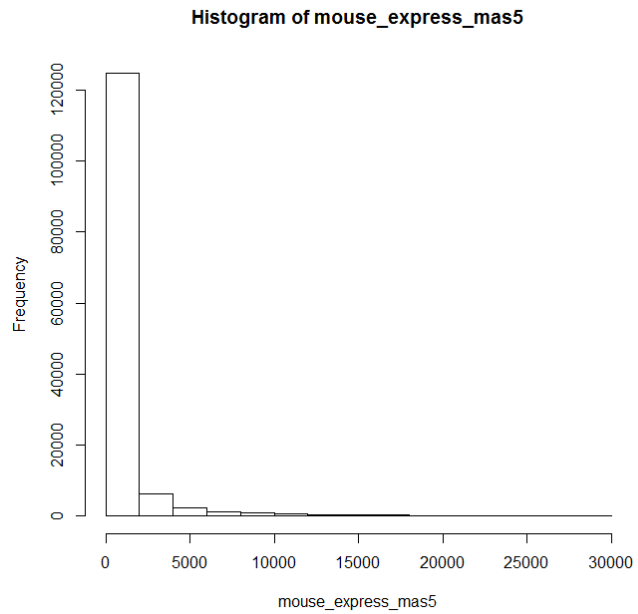
```
source("http://bioconductor.org/biocLite.R")  
biocLite("affy")  
getwd()  
setwd("E:/NYU_Courses/Applied Genomics/Affy_Files")  
library(affy)  
mousedata <- ReadAffy()  
mousedata.n <- rma(mousedata)  
mouse_express <- exprs(mousedata.n)  
mouse_express[1:10,]
```

	C42_CG1.ce1	C42_CG2.ce1	C42_CG3.ce1	CT6_CG1.ce1	CT6_CG2.ce1	CT6_CG3.ce1
1415670_at	8.430289	8.187219	8.360947	8.269767	8.362469	8.003444
1415671_at	10.812955	10.841856	10.581609	11.020599	10.629436	11.175956
1415672_at	10.036298	9.497218	10.124082	9.797085	8.970710	9.726272
1415673_at	7.049402	6.703319	6.892139	6.260740	5.622015	6.020518
1415674_a_at	9.955171	9.969085	9.836363	9.325984	9.850540	8.882297
1415675_at	9.156490	9.305600	9.029036	9.258452	8.959936	9.188322
1415676_a_at	11.497605	11.609315	11.621948	11.089580	11.658424	11.586485
1415677_at	8.738246	9.030087	8.996263	8.944964	9.054255	8.200982
1415678_at	10.563491	10.403000	10.693911	11.129190	10.395433	11.043122
1415679_at	10.744338	11.089143	11.138460	10.552351	10.734876	10.732911

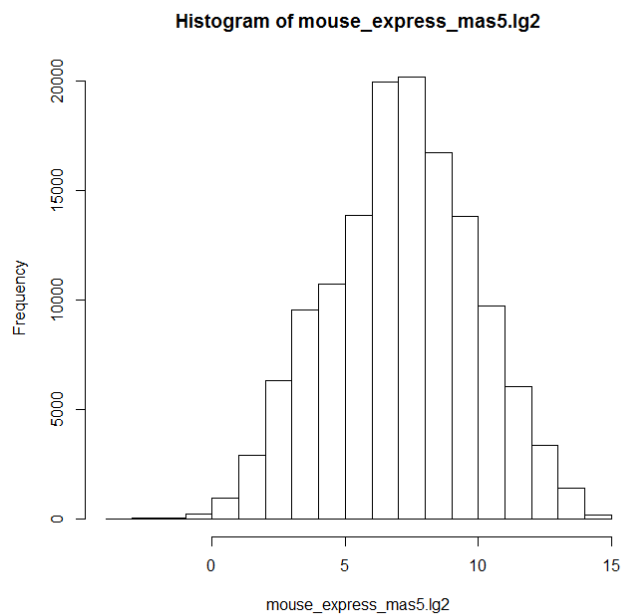
```
mousedata.m <- mas5(mousedata)  
mouse_express_mas5 <- exprs(mousedata.m)  
hist(mouse_express)
```



```
hist(mouse_express_mas5)
```



```
hist(mouse_express_mas5.lg2)
```

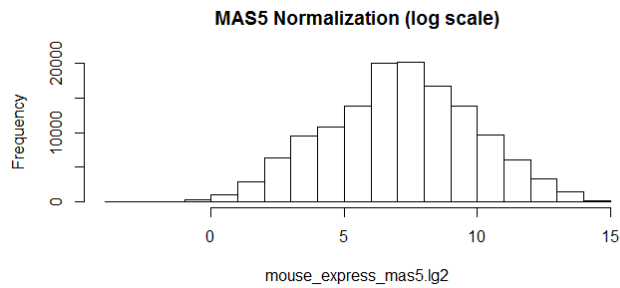
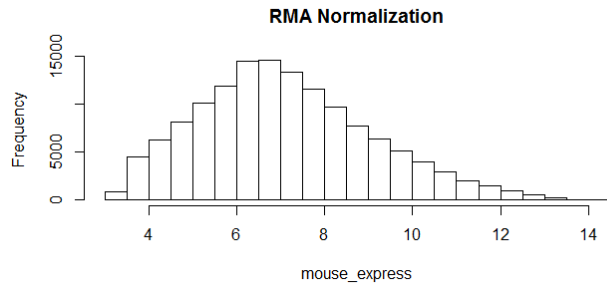


```
dev.off()
```

```
par(mfrow=c(2,1))
```

```
hist(mouse_express,main="RMA Normalization")
```

```
hist(mouse_express_mas5.lg2,main="MAS5 Normalization (log scale)")
```



```
mean_c1 <- mean(mouse_express[,1])
```

```
mean_c1
```

```
[1] 7.098912
```

```
mean(mouse_express[,2])
```

```
[1] 7.133301
```

```
mean(mouse_express[,3])
```

```
[1] 7.108277
```

```
mean(mouse_express_mas5.lg2[,1])
```

```
[1] 7.179056
```

```
mean(mouse_express_mas5.lg2[,2])
```

```
[1] 7.159718
```

```
mean(mouse_express_mas5.lg2[,3])
```

```
[1] 7.149023
```

```
var(mouse_express[,1])
```

```
[1] 3.834185
```

```
var(mouse_express[,2])
```

```
[1] 3.844447
```

```
var(mouse_express[,3])
```

```
[1] 3.887333
```

```
var(mouse_express_mas5.lg2[,1])
```

```
[1] 7.242537
```

```
var(mouse_express_mas5.lg2[,2])
```

```
[1] 7.373663
```

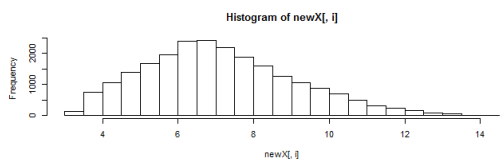
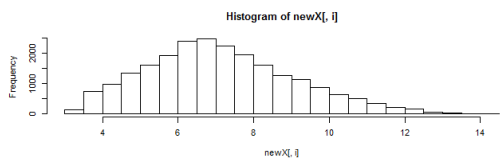
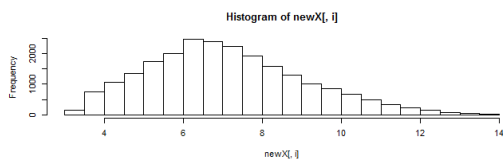
```
var(mouse_express_mas5.lg2[,3])
```

```
[1] 7.345885
```

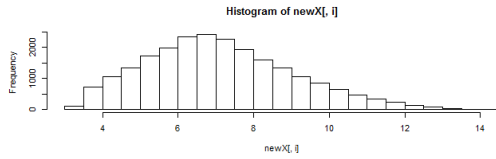
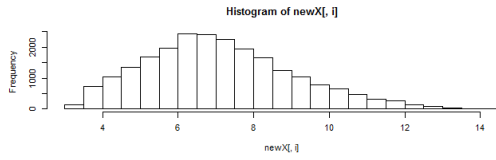
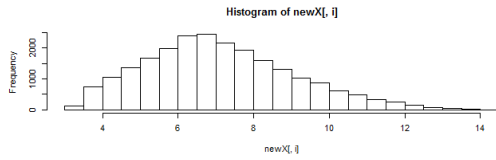
```
dev.off()
```

```
par(mfrow=c(3,1))
```

```
apply(mouse_express[,1:3], 2, hist);
```



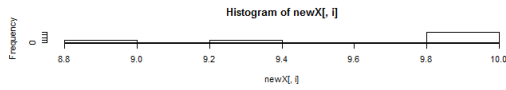
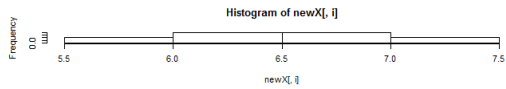
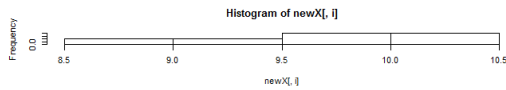
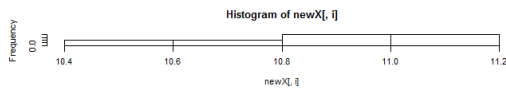
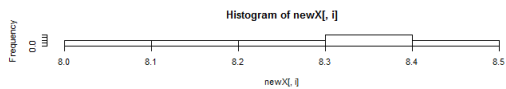
```
apply(mouse_express[,4:6], 2, hist);
```



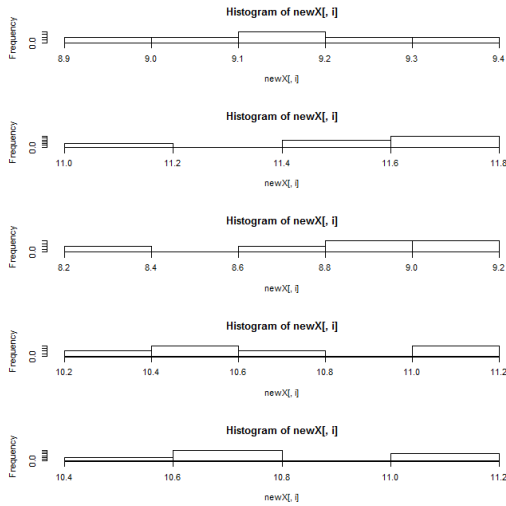
dev.off()

par(mfrow=c(5,1))

apply(mouse\_express[1:5,], 1, hist);



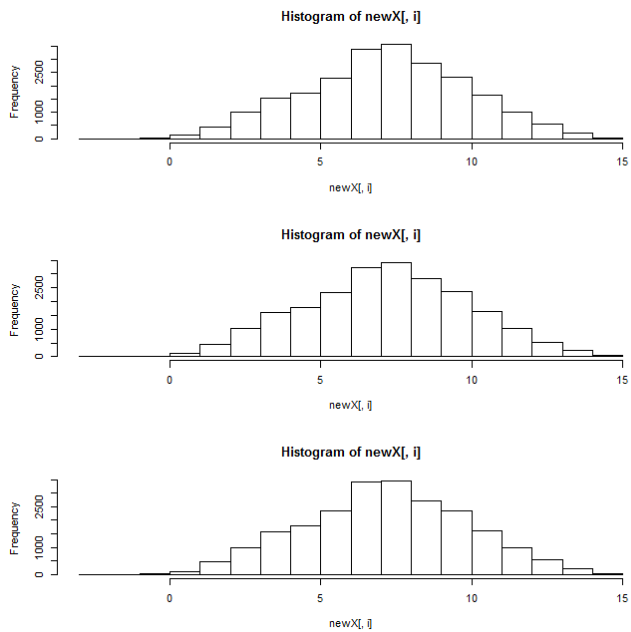
apply(mouse\_express[6:10,], 1, hist);



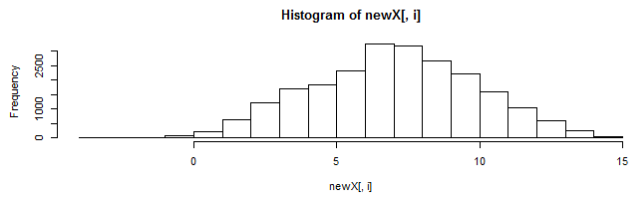
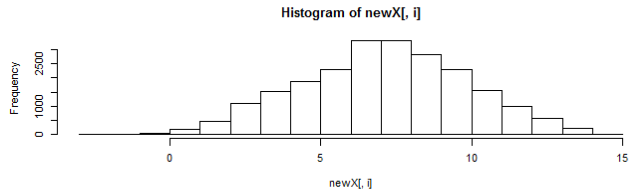
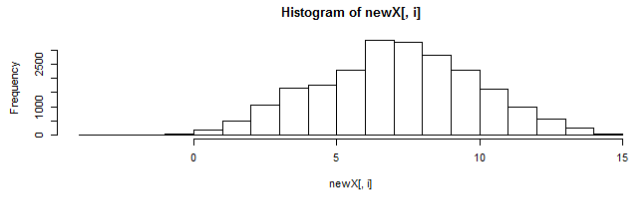
`dev.off()`

`par(mfrow=c(3,1))`

`apply(mouse_express_mas5.lg2[,1:3], 2, hist);`



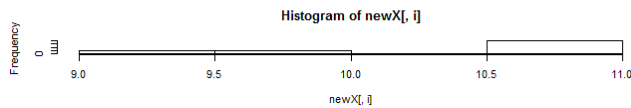
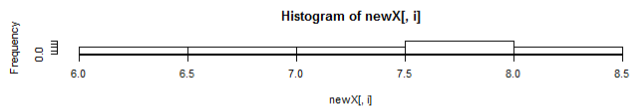
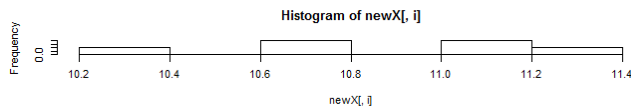
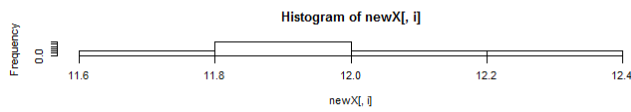
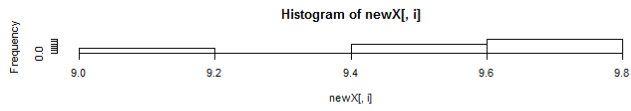
`apply(mouse_express_mas5.lg2[,4:6], 2, hist);`



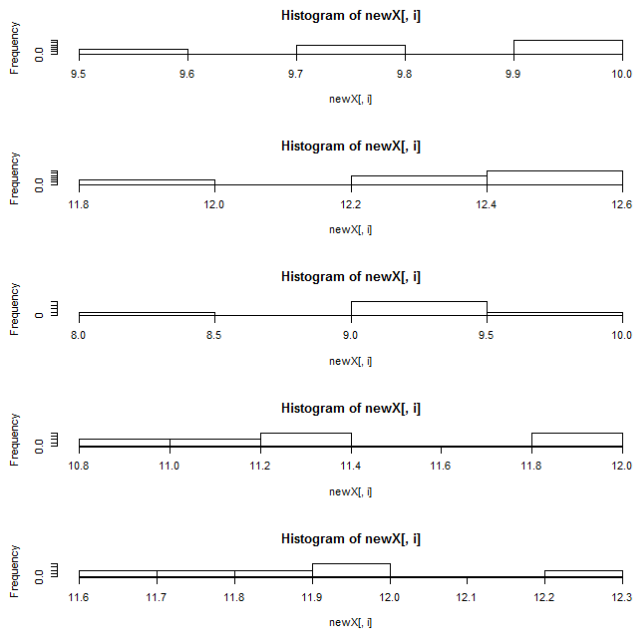
dev.off()

par(mfrow=c(5,1))

apply(mouse\_express\_mas5.lg2[1:5,], 1, hist);



```
apply(mouse_express_mas5.lg2[6:10,], 1, hist);
```



```
dev.off()
```

```
par(mfrow=c(5,2))
```

```
for(i in 1:5){
```

```
  hist(mouse_express[i,],main="RMA of Gene")
```

```
  hist(mouse_express_mas5.lg2[i,],main="MAS5 of Gene")
```

```
}
```

```
# First 5 Genes in Order with RMA Normalization on Left and MAS5 Normalization on right.
```



