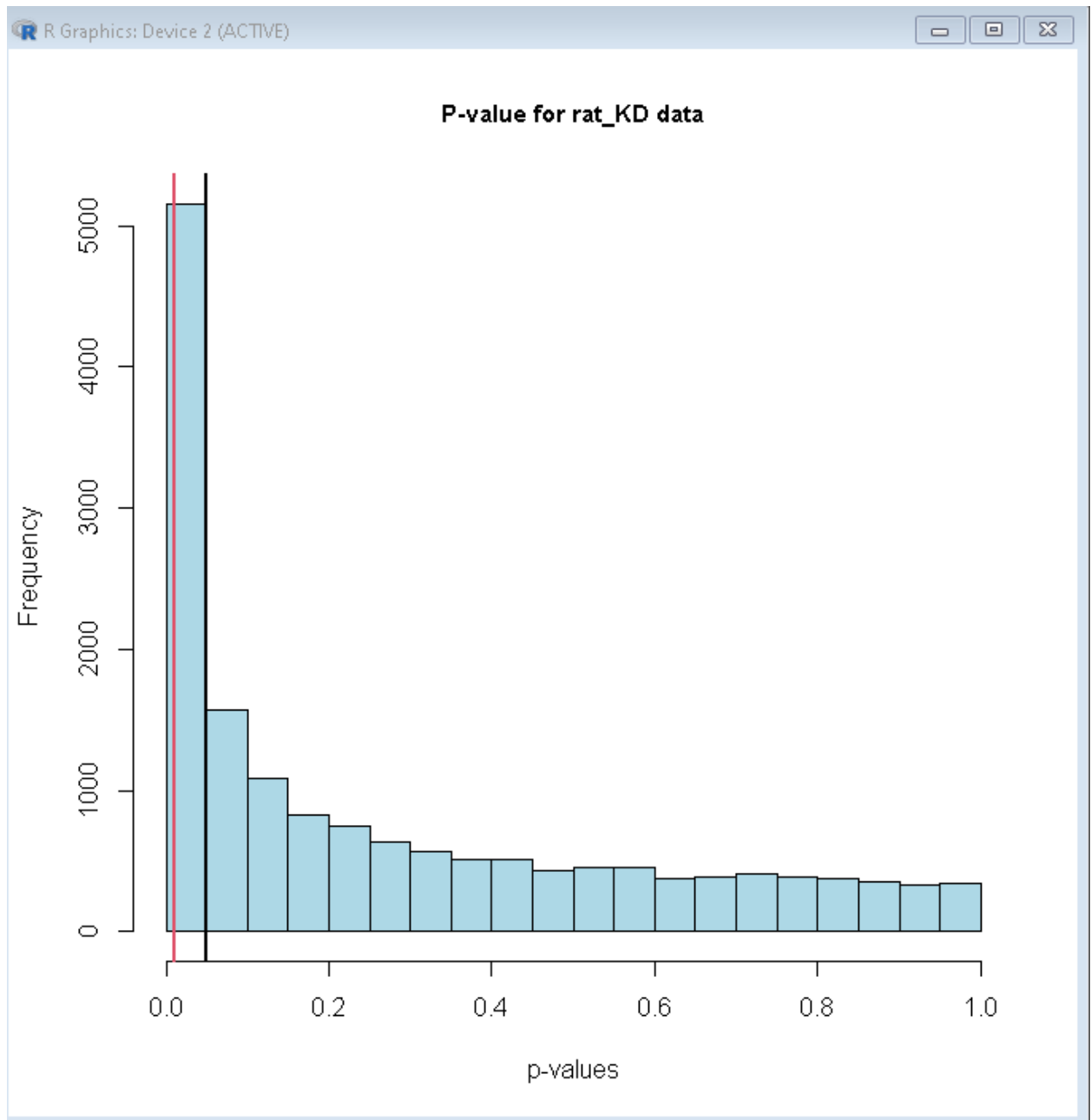


Lab 5

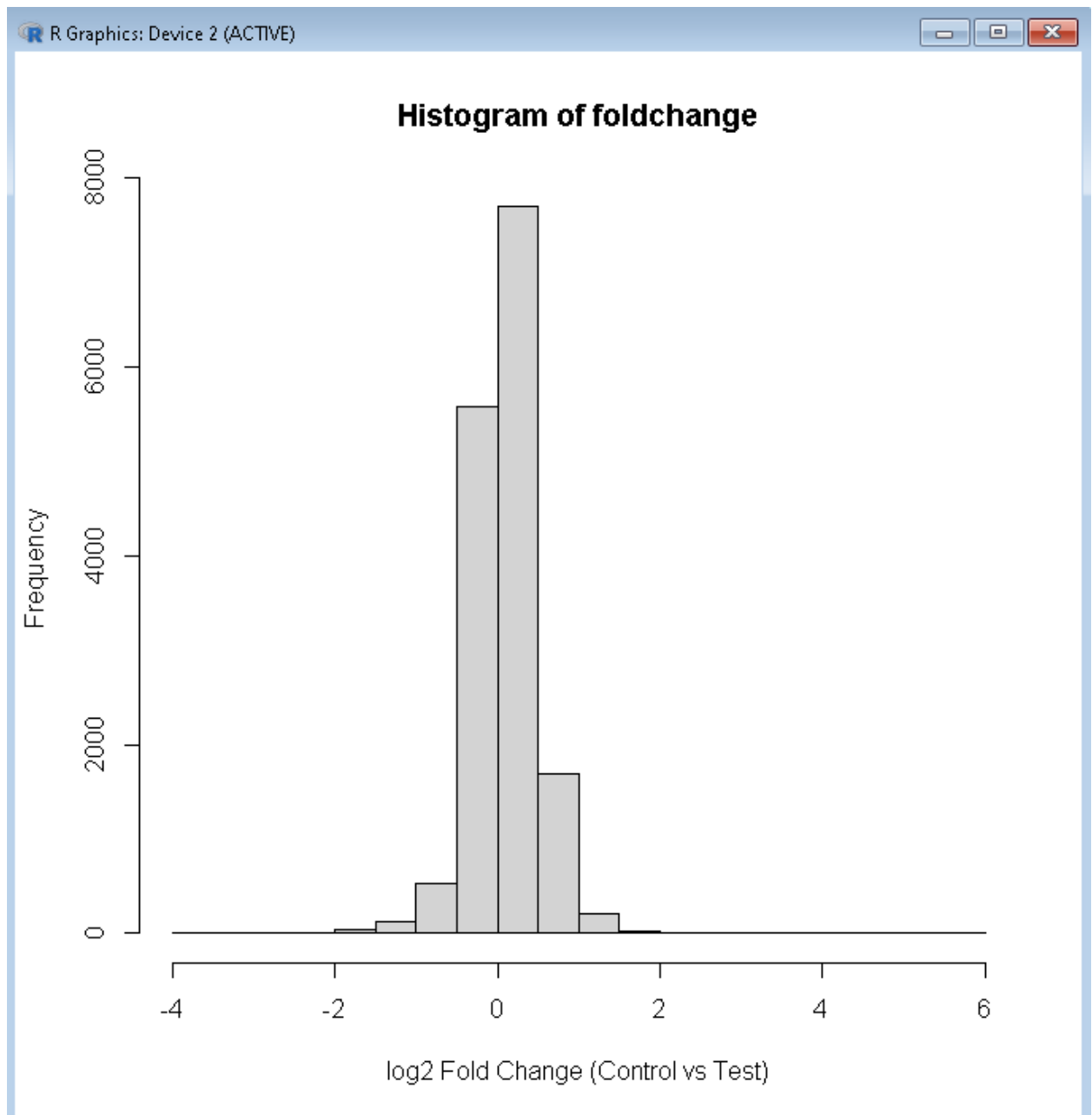
- 1.
2. `rat <- read.table("rat_KD.txt", header=T, row.names = 1)`
3.

```
lograt <- log2(rat)
t.test.all.genes <- function(x,s1,s2) {
  x1 <- x[s1]
  x2 <- x[s2]
  x1 <- as.numeric(x1)
  x2 <- as.numeric(x2)
  t.out <- t.test(x1,x2, alternative="two.sided",var.equal=T)
  out <- as.numeric(t.out$p.value)
  return(out)}
pv <- apply(lograt,1, t.test.all.genes,s1=c(1:6),s2=c(7:11))
```
4.

```
hist(pv,col="lightblue",xlab="p-values",main="P-value for rat_KD data",cex.main=0.9)
abline(v=.05,col=1,lwd=2)
abline(v=.01,col=2,lwd=2)
length(pv[pv<.05])
length(pv[pv<.01])
5160 are less than .05 and 2414 are less than .01
length(pv[pv<3.140112e-06]) = 12 prob sets less than the adjusted p-value.
When you divide an alpha of .05 by the total number of the probesets that have a value less than this are
about 12 of these probesets.
Value = 3.140112e-06
```



- 5.
- ```
keto = apply(lograt[, 7:11], 1, mean)
control = apply(lograt[,1:6], 1, mean)
foldchange <- control - keto
hist(foldchange, xlab = "log2 Fold Change (Control vs Test)")
```



6.

```
keto = apply(lograt[, 7:11], 1, mean)
control = apply(lograt[, 1:6], 1, mean)
```

```
linear2 <- 2^(foldchange)
max(linear2)
[1] 55.15521
> min(linear2)
[1] 0.08240443
```

```
pv[pv < 3.140112e-06 & linear2 > 2]
```

```
1367553_x_at 1370239_at 1370240_x_at 1371102_x_at 1371245_a_at
1.224053e-08 5.280180e-08 1.622293e-09 2.583221e-08 6.370531e-09
1388608_x_at
1.743055e-07
```

```
1367553_x_at 1370239_at 1370240_x_at 1371102_x_at 1371245_a_at
1.224053e-08 5.280180e-08 1.622293e-09 2.583221e-08 6.370531e-09
1388608_x_at
1.743055e-07
```

7. 1367553\_x\_at -involved in the hemoglobin subunit beta.  
 1370239\_at – Hba-a2 which is the hemoglobin alpha 2. Molecular function is oxygen binding, heme binding, metal ion binding, and organic acid binding.  
 1370240\_x\_at – also involved in the hemoglobin alpha same as the probset 1370239\_at  
 1371102\_x\_at – involved in hemoglobin beta adult s chain which is Hbb-bs. Molecular functions involve oxygen carrier activity, oxygen binding, heme binding, and metal ion binding. Biological process is oxygen transport and cellular oxidant detoxification.  
 1371245\_a\_at – exact same use the 1371102\_x\_at involved in the Hbb-bs hemoglobin.  
 1388608\_x\_at – involved in the hemoglobin alpha adult chain 1  
 General biological function associated with these probesets is that they are all involved in the hemoglobin which has the function of oxygen transport and oxygen binding in the molecular level.

8.

```
ttestRat <- function(g, s1, s2) {
 x = g[s1]
 y = g[s2]
 x = as.numeric(x)
 y = as.numeric(y)
 results = t.test(x, y)
 results$p.value
}
rawpvalue = apply(rat, 1, ttestRat, s1 = c(1:6), s2 = c(7:11))

p.trans <- -1 * log10(rawpvalue)

plot(range(p.trans), range(foldchange), type='n', xlab='-1*log10(p-value)', ylab='fold change', main='Volcano
Plot\nControl and Keto group
differences')
points(p.trans, foldchange, col='black', pch=21, bg=1)
points(p.trans[(p.trans > -log10(.05)&foldchange > log2(2))], foldchange[(p.trans > -
log10(.05)&foldchange > log2(2))], col=1, bg=2, pch=21)
points(p.trans[(p.trans > -log10(.05)&foldchange < -log2(2))], foldchange[(p.trans > -
log10(.05)&foldchange < -log2(2))], col=1, bg=3, pch=21)
abline(v = -log10(.05))
abline(h = -log2(2))
abline(h = log2(2))
```

### Volcano Plot Control and Keto group differences

