BalsamSugarExplr.R

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```
library(ggplot2)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
setwd("D:/Iowa State University/Debinski Lab/Nectar data/MAL")

balssug15 <- read.csv("nectar analysis/data files/balssugar15.csv", header = T)
balssug16 <- read.csv("nectar analysis/data files/balssugar16.csv", header = T)
balssugboth <- rbind(balssug15,balssug16)

#Data summaries

summary(balssug15)
```

```
##          date         plot    treatment     plant         BRIX
##  2015-06-08:20   CHSR8  :17   C:28      CC6-9  : 9   Min.   : 1.00
##  2015-06-11:18   CH5    :16   H:54      CH5-6  : 7   1st Qu.:17.00
##  2015-06-03:17   CC6    :11             CHSR8-4: 7   Median :22.00
##  2015-06-06:10   EH4    : 8             CHSR8-6: 6   Mean   :21.99
##  2015-06-10: 8   WHSR9  : 8             EHSR1-2: 5   3rd Qu.:27.00
##  2015-06-02: 6   WSR10  : 6             CH5-7  : 4   Max.   :48.00
##  (Other)   : 3   (Other):16             (Other):44
##       mass
##  Min.   :0.002182
##  1st Qu.:0.040685
##  Median :0.078226
##  Mean   :0.099705
##  3rd Qu.:0.134906
##  Max.   :0.540640
##
```

```
summary(balssug16)
```

```
##          date         plot    treatment     plant          BRIX
```

```
##  2016-06-05:17   CC6    :19   C:80      CC6-10 :  7   Min.   : 2.00
##  2016-06-06:31   CH5    :16   H:71      EC3-3  :  7   1st Qu.:20.00
##  2016-06-07:41   EH4    :15             WHSR9-2:  7   Median :26.00
##  2016-06-08:56   EHSR1  :15             EC3-1  :  6   Mean   :26.67
##  2016-06-16: 6   WC11   :14             EHSR1-1:  6   3rd Qu.:33.50
##                  CHSR8  :13             WC11-3 :  6   Max.   :49.00
##                  (Other):59             (Other):112
##       mass
##  Min.   :0.0007309
##  1st Qu.:0.0228482
##  Median :0.0430309
##  Mean   :0.0505809
##  3rd Qu.:0.0680964
##  Max.   :0.2049200
##
```

```
summary(balssugboth)
```

```
##          date         plot    treatment     plant          BRIX
##  2016-06-08:56   CH5    :32   C:108     CC6-9  :  9   Min.   : 1.00
##  2016-06-07:41   CC6    :30   H:125     CHSR8-4:  9   1st Qu.:18.00
##  2016-06-06:31   CHSR8  :30             CHSR8-6:  9   Median :25.00
##  2015-06-08:20   EH4    :23             EHSR1-2:  9   Mean   :25.02
##  2015-06-11:18   EHSR1  :20             WSR10-1:  9   3rd Qu.:31.00
##  2015-06-03:17   WHSR9  :20             CC6-10 :  8   Max.   :49.00
##  (Other)   :50   (Other):78             (Other):180
##       mass
##  Min.   :0.0007309
##  1st Qu.:0.0254691
##  Median :0.0496109
##  Mean   :0.0678692
##  3rd Qu.:0.0911309
##  Max.   :0.5406400
##
```

```
summarize(group_by(balssug15, treatment), meanBRIX = mean(BRIX), sdBRIX = sd(BRIX))
```

```
## Source: local data frame [2 x 3]
##
##   treatment meanBRIX    sdBRIX
##      (fctr)    (dbl)     (dbl)
## 1         C 17.32143  9.245834
## 2         H 24.40741 10.234088
```

```
summarize(group_by(balssug16, treatment), meanBRIX = mean(BRIX), sdBRIX = sd(BRIX))
```

```
## Source: local data frame [2 x 3]
##
##   treatment meanBRIX   sdBRIX
##      (fctr)    (dbl)    (dbl)
## 1         C 25.41250 9.550258
## 2         H 28.08451 9.277848
```

```
summarize(group_by(balssugboth, treatment), meanBRIX = mean(BRIX), sdBRIX = sd(BRIX))
```

```
## Source: local data frame [2 x 3]
##
##   treatment meanBRIX   sdBRIX
##      (fctr)    (dbl)    (dbl)
## 1         C 23.31481 10.07973
## 2         H 26.49600  9.83380
```

```
summarize(group_by(balssug15, treatment), meanmass = mean(mass), sdmass = sd(mass))
```

```
## Source: local data frame [2 x 3]
##
##   treatment   meanmass     sdmass
##      (fctr)      (dbl)      (dbl)
## 1         C 0.09401065 0.07152742
## 2         H 0.10265737 0.09211641
```

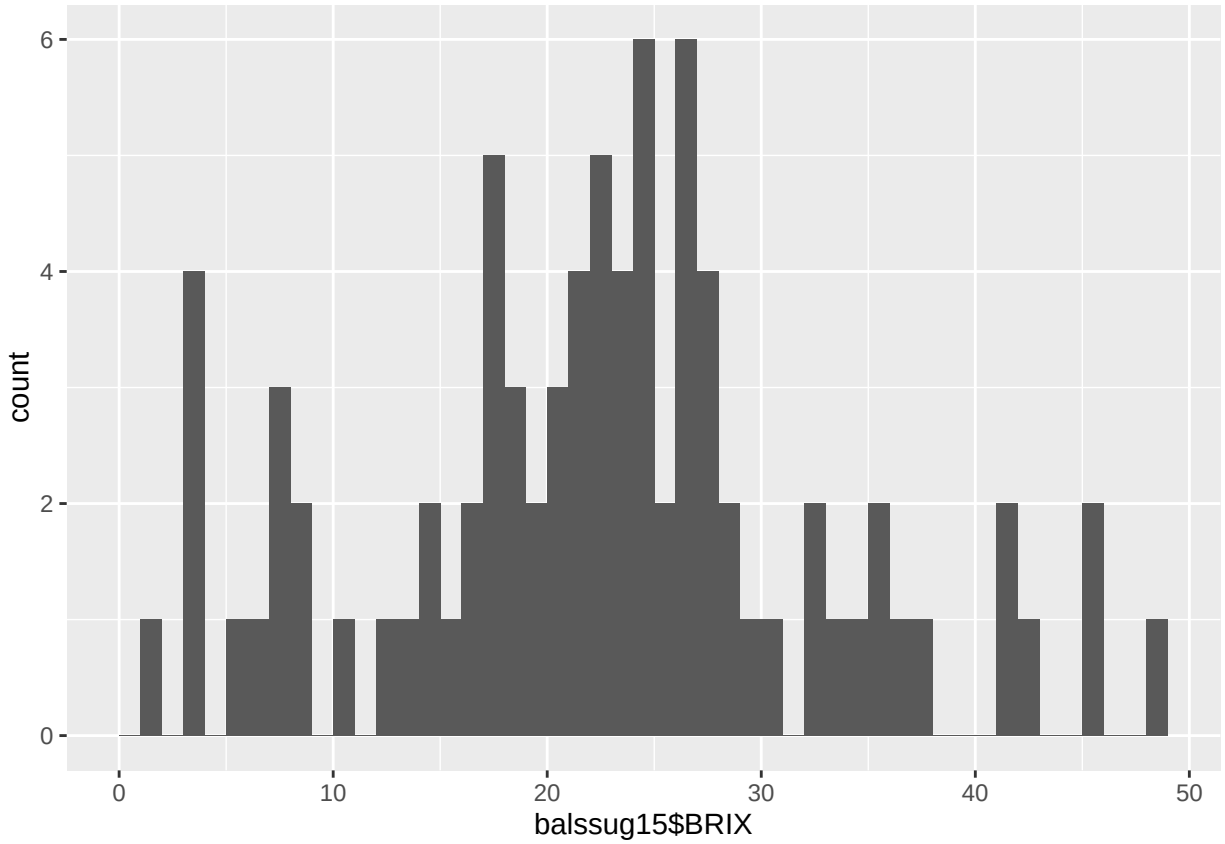
```
summarize(group_by(balssug16, treatment), meanmass = mean(mass), sdmass = sd(mass))
```

```
## Source: local data frame [2 x 3]
##
##   treatment   meanmass     sdmass
##      (fctr)      (dbl)      (dbl)
## 1         C 0.04865045 0.03840909
## 2         H 0.05275608 0.03508288
```

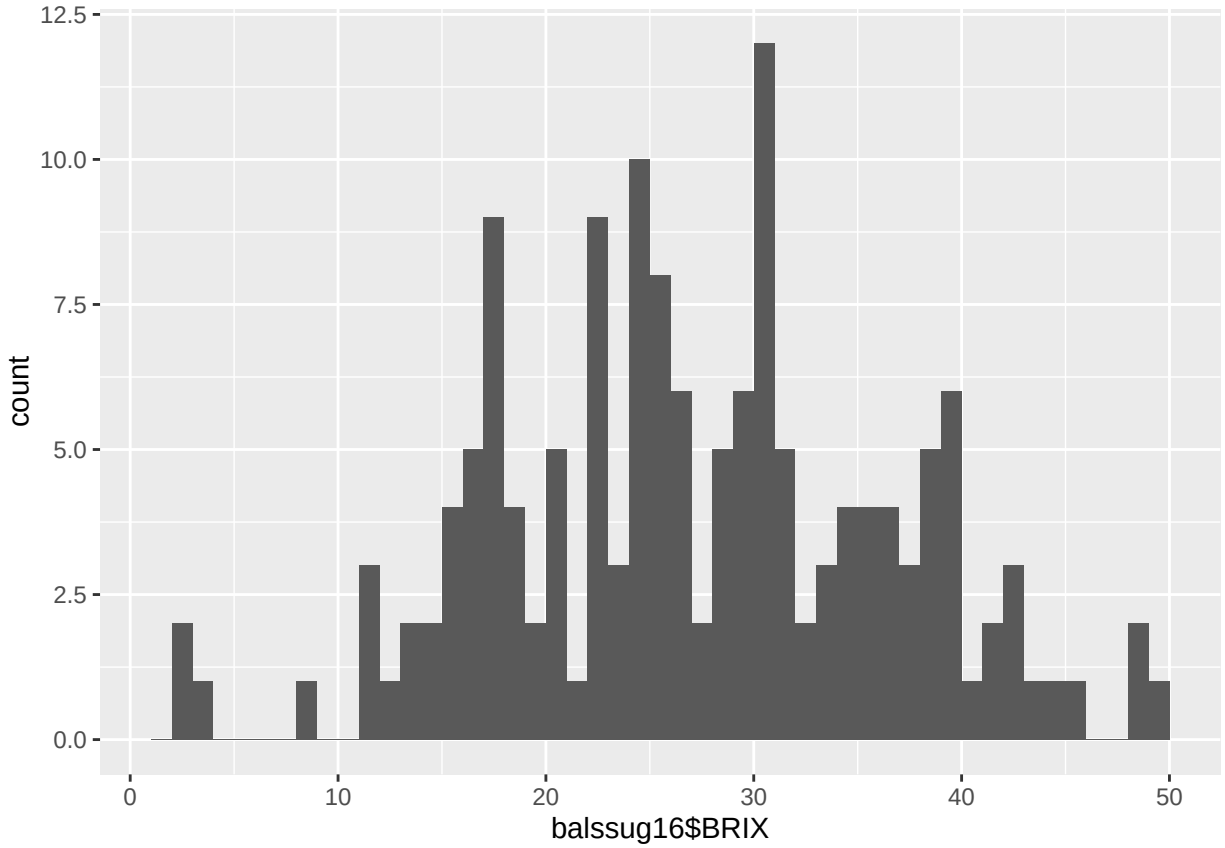
```
summarize(group_by(balssugboth, treatment), meanmass = mean(mass), sdmass = sd(mass))
```

```
## Source: local data frame [2 x 3]
##
##   treatment   meanmass     sdmass
##      (fctr)      (dbl)      (dbl)
## 1         C 0.06041051 0.05271659
## 2         H 0.07431344 0.07026804
```

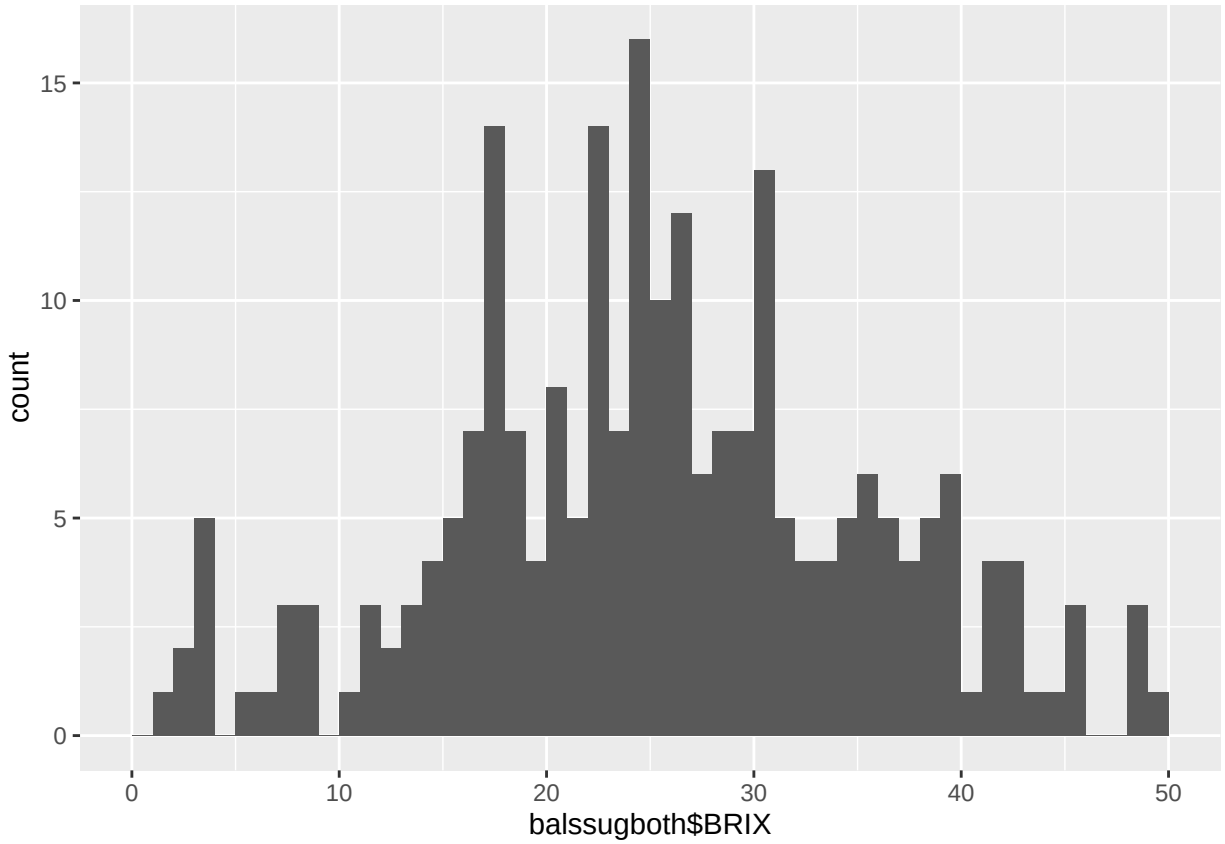
```
qplot(balssug15$BRIX, binwidth = 1)
```



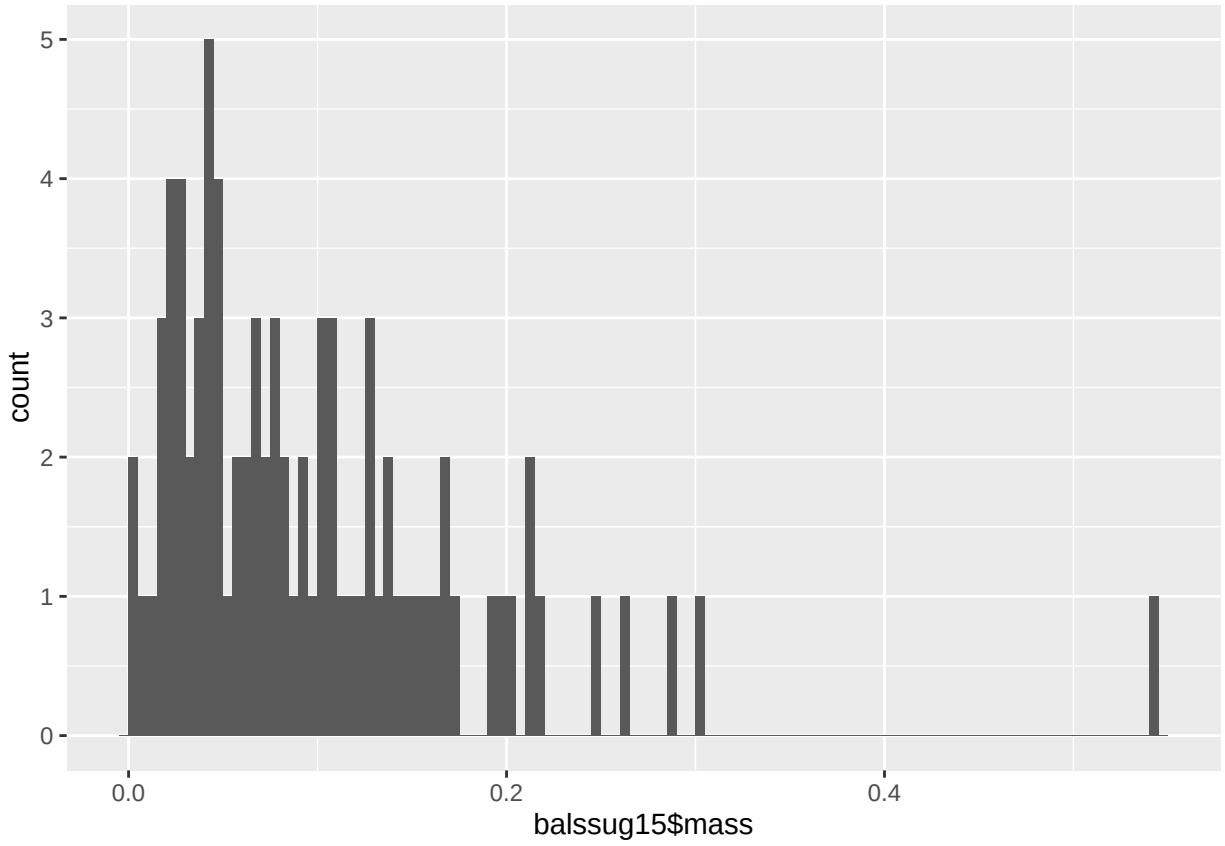

```
qplot(balssug16$BRIX, binwidth = 1)
```



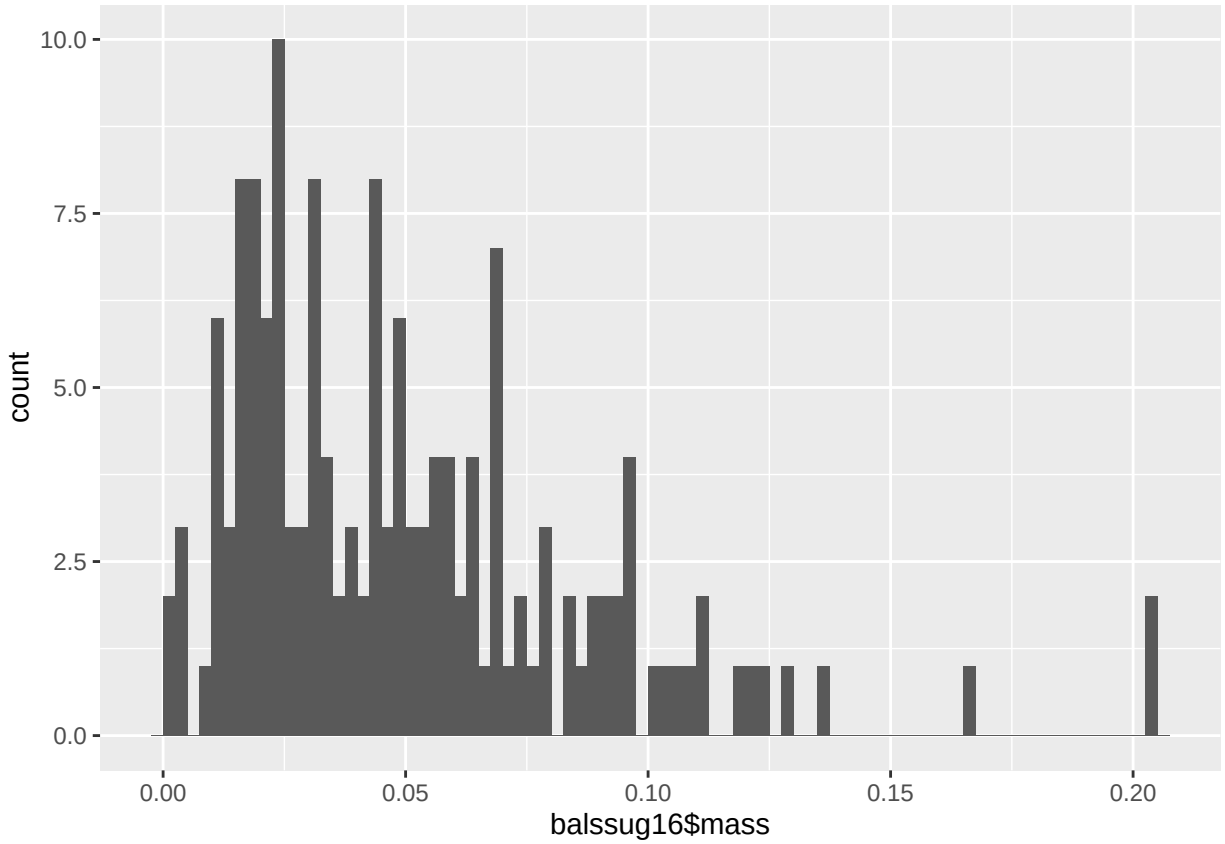

```
qplot(balssugboth$BRIX, binwidth = 1)
```



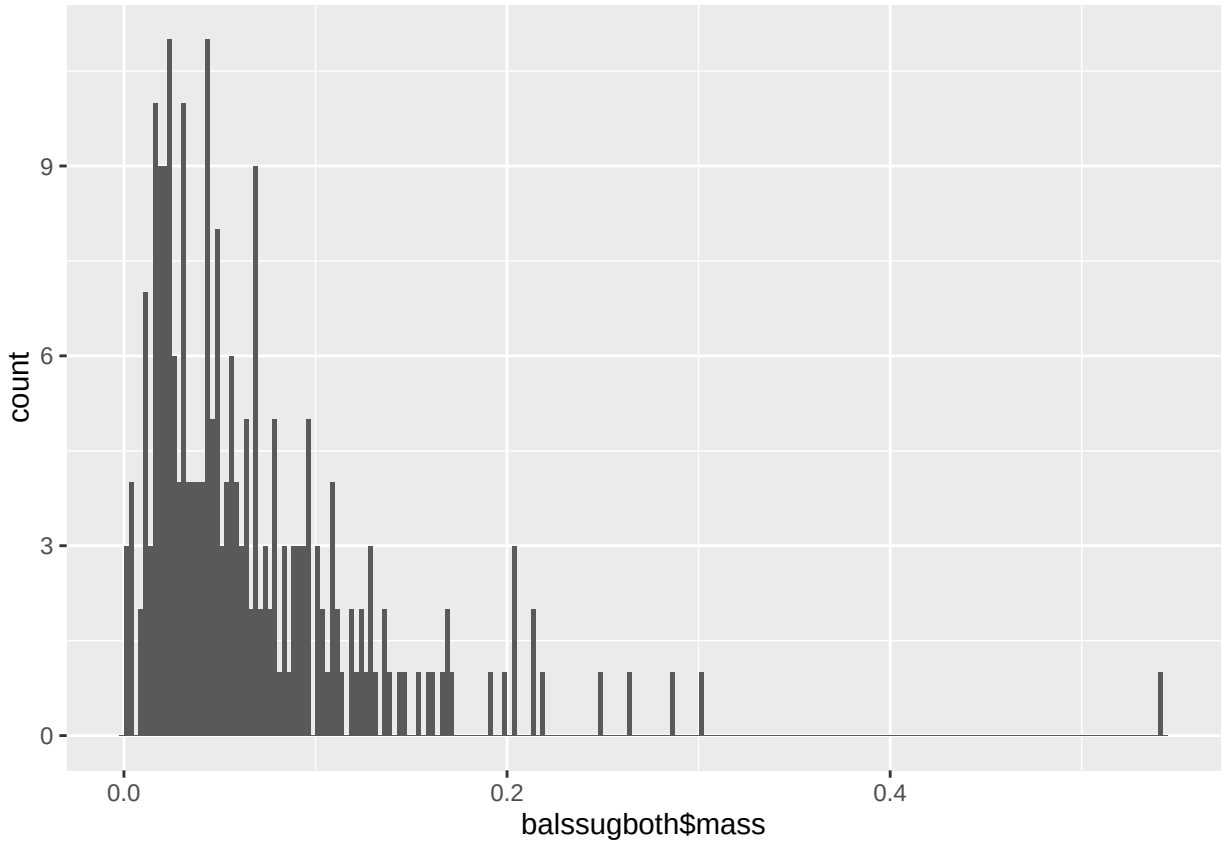

```
qplot(balssug15$mass, binwidth = 0.005)
```



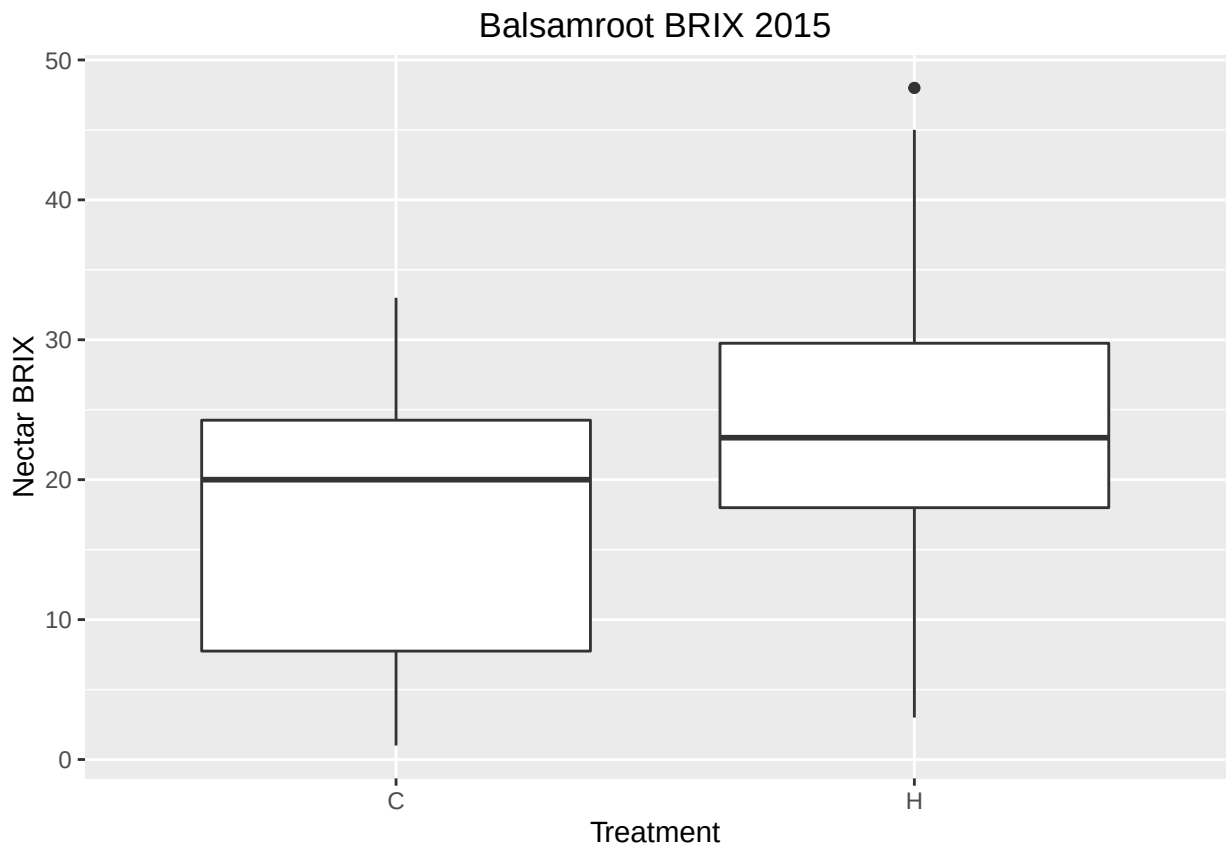

```
qplot(balssug16$mass, binwidth = .0025)
```



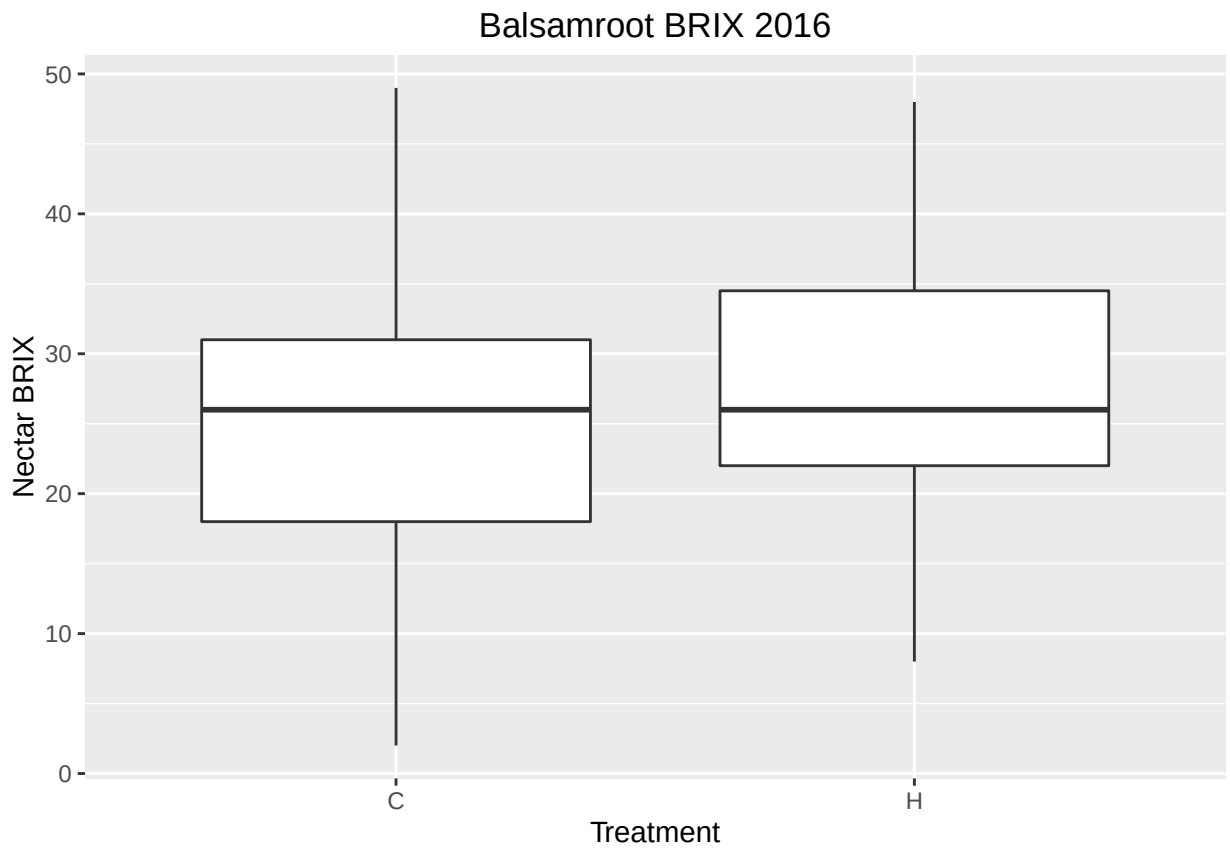

```
qplot(balssugboth$mass, binwidth = .0025)
```



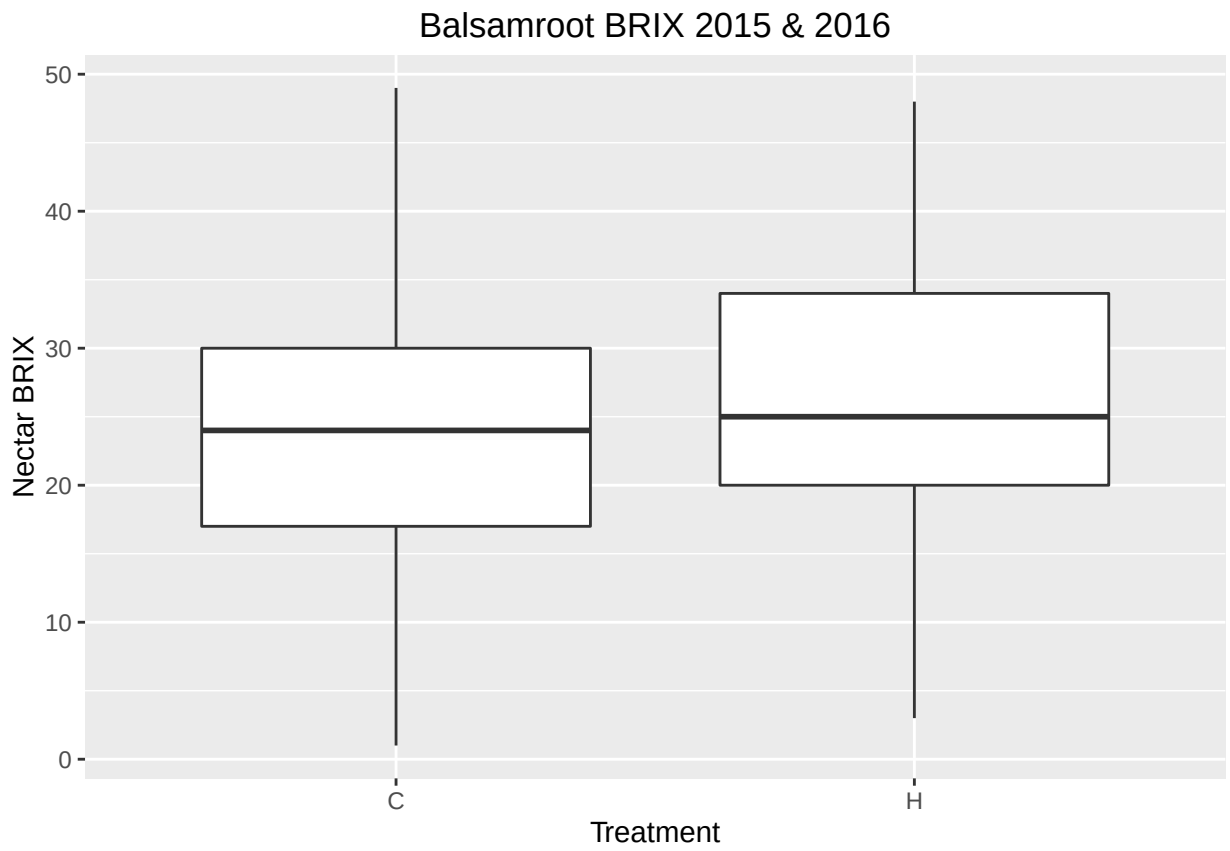

```
ggplot(balssug15, aes(x=treatment, y=BRIX)) + geom_boxplot() +
  xlab("Treatment") +
  ylab("Nectar BRIX") + ggtitle("Balsamroot BRIX 2015")
```



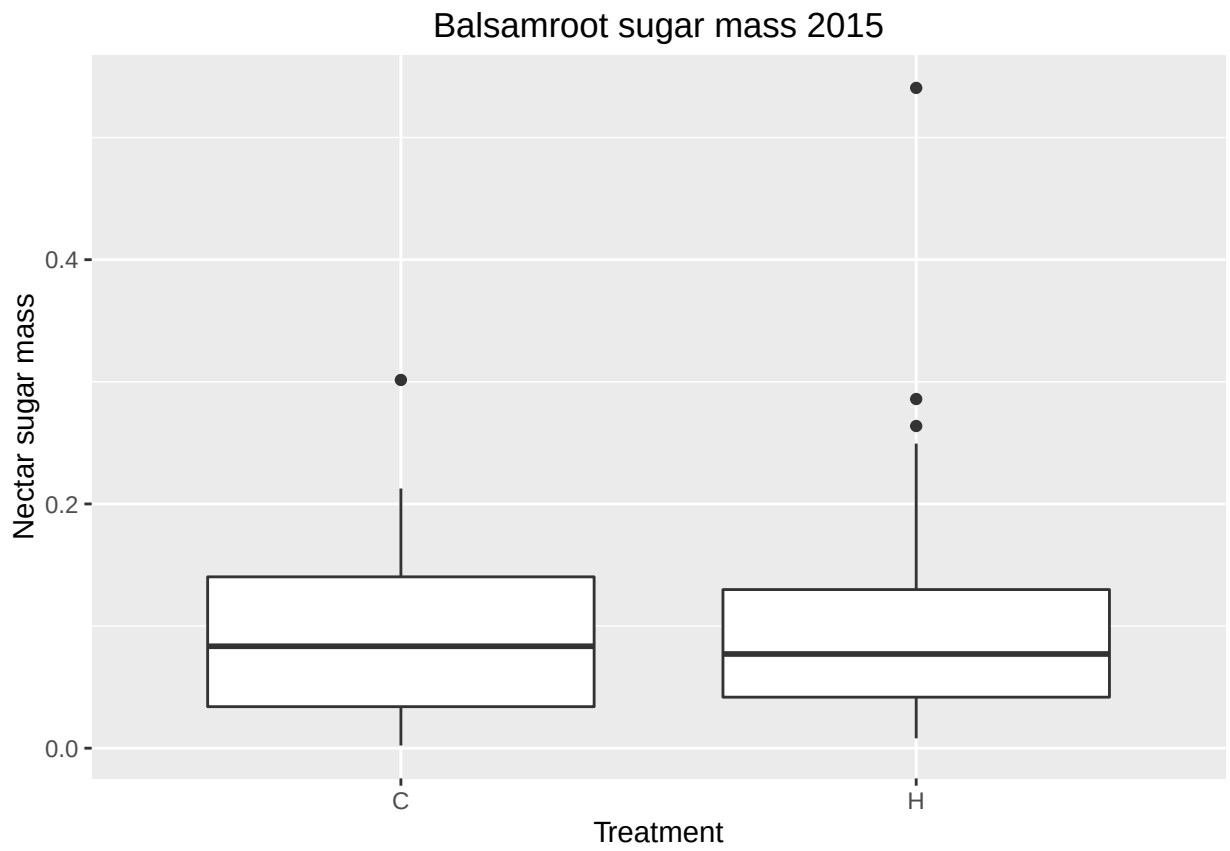

```
ggplot(balssug16, aes(x=treatment, y=BRIX)) + geom_boxplot() +
  xlab("Treatment") +
  ylab("Nectar BRIX") + ggtitle("Balsamroot BRIX 2016")
```



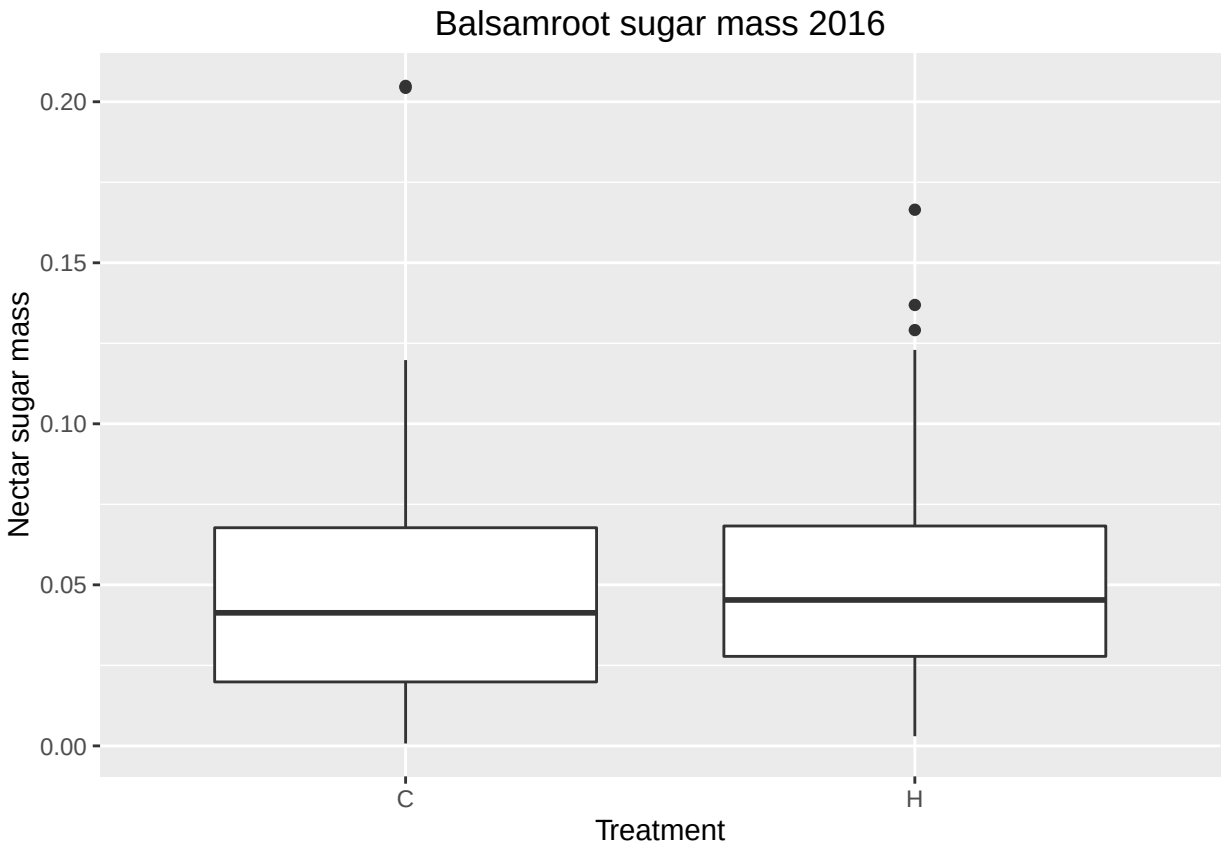

```
ggplot(balssugboth, aes(x=treatment, y=BRIX)) + geom_boxplot() +
  xlab("Treatment") +
  ylab("Nectar BRIX") + ggtitle("Balsamroot BRIX 2015 & 2016")
```



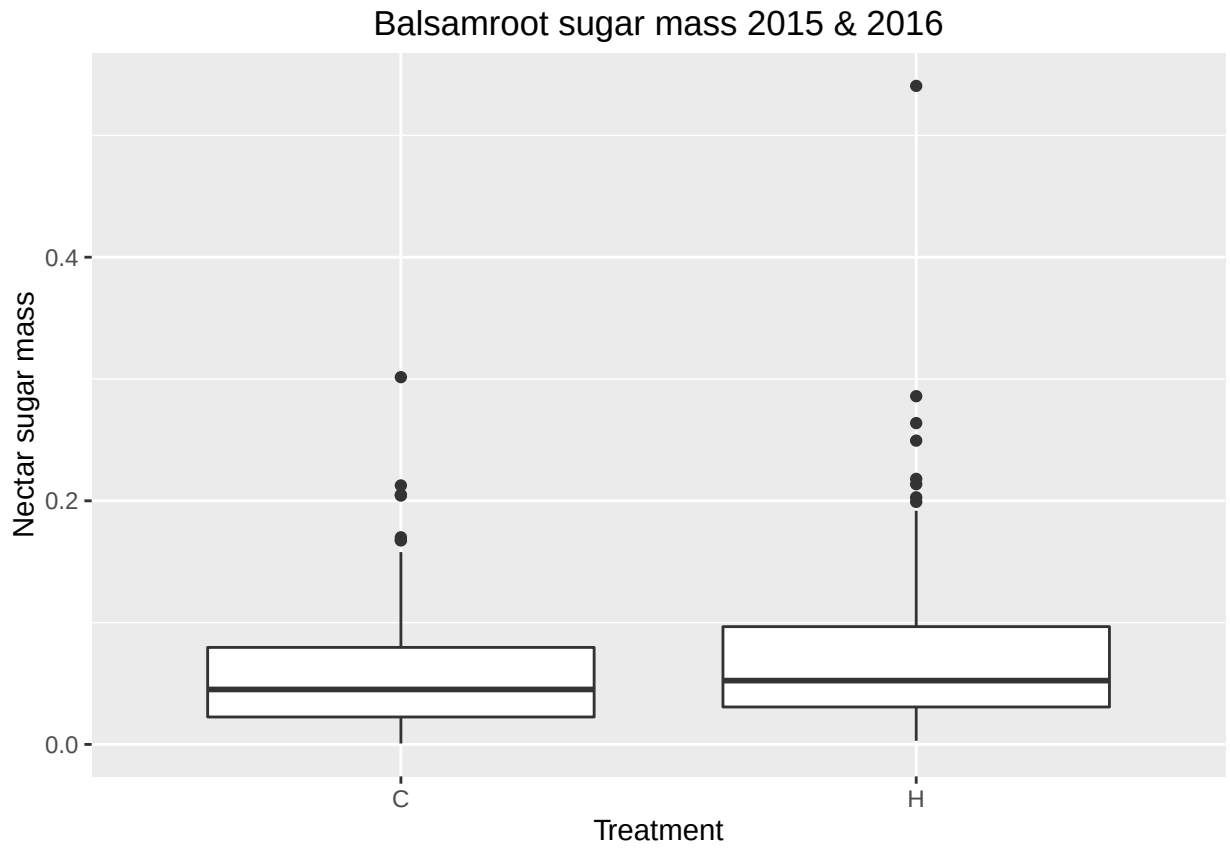

```
ggplot(balssug15, aes(x=treatment, y=mass)) + geom_boxplot() +
  xlab("Treatment") +
  ylab("Nectar sugar mass") + ggtitle("Balsamroot sugar mass 2015")
```




```
ggplot(balssug16, aes(x=treatment, y=mass)) + geom_boxplot() +
  xlab("Treatment") +
  ylab("Nectar sugar mass") + ggtitle("Balsamroot sugar mass 2016")
```




```
ggplot(balssugboth, aes(x=treatment, y=mass)) + geom_boxplot() +
  xlab("Treatment") +
  ylab("Nectar sugar mass") + ggtitle("Balsamroot sugar mass 2015 & 2016")
```




```
# Homoscedastic?

var15C <- sd(balssug15$BRIX[balssug15$treatment=="C"])^2
var15H <- sd(balssug15$BRIX[balssug15$treatment=="H"])^2
ratio15 <- var15H/var15C
ratio15
```

```
## [1] 1.225197
```

```
var16C <- sd(balssug16$BRIX[balssug16$treatment=="C"])^2
var16H <- sd(balssug16$BRIX[balssug16$treatment=="H"])^2
ratio16 <- var16C/var16H
ratio16
```

```
## [1] 1.059585
```

```
varbothC <- sd(balssugboth$BRIX[balssugboth$treatment=="C"])^2
varbothH <- sd(balssugboth$BRIX[balssugboth$treatment=="H"])^2
ratioboth <- varbothC/varbothH
ratioboth
```

```
## [1] 1.050642
```

```r
var15C <- sd(balssug15$mass[balssug15$treatment=="C"])^2
var15H <- sd(balssug15$mass[balssug15$treatment=="H"])^2
ratio15 <- var15H/var15C
ratio15
```

```
## [1] 1.658551
```

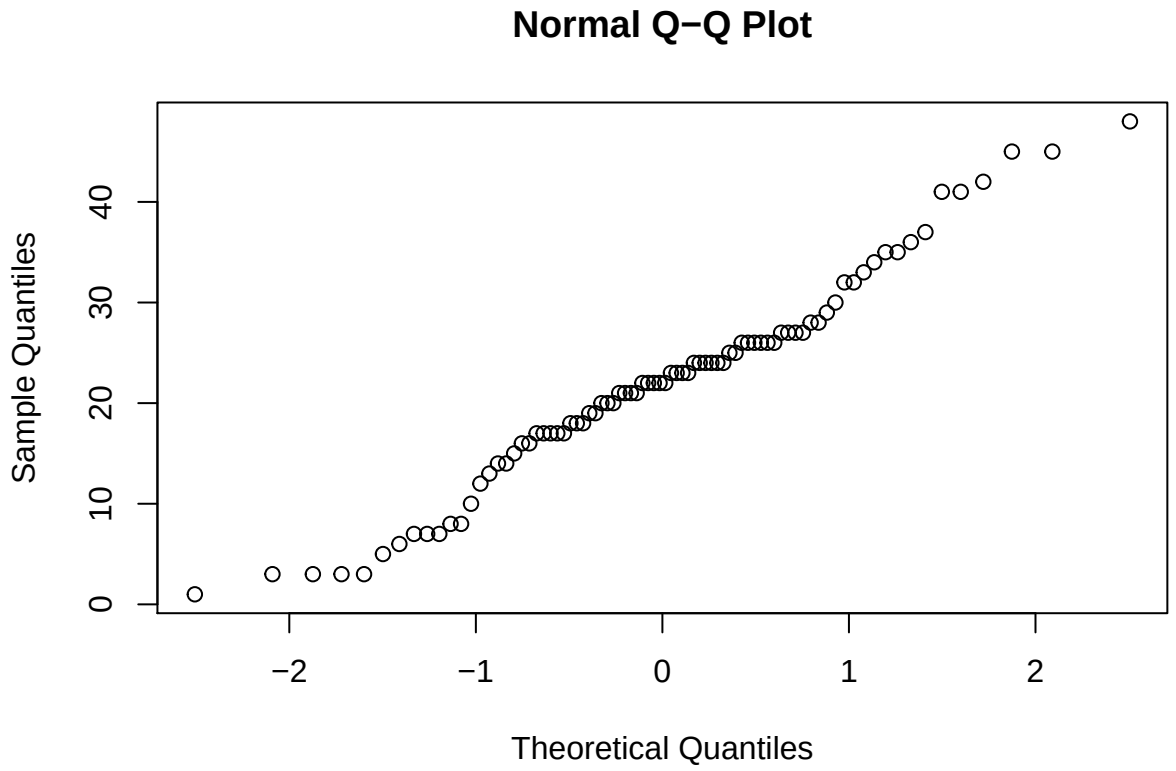
```r
var16C <- sd(balssug16$mass[balssug16$treatment=="C"])^2
var16H <- sd(balssug16$mass[balssug16$treatment=="H"])^2
ratio16 <- var16C/var16H
ratio16
```

```
## [1] 1.198609
```

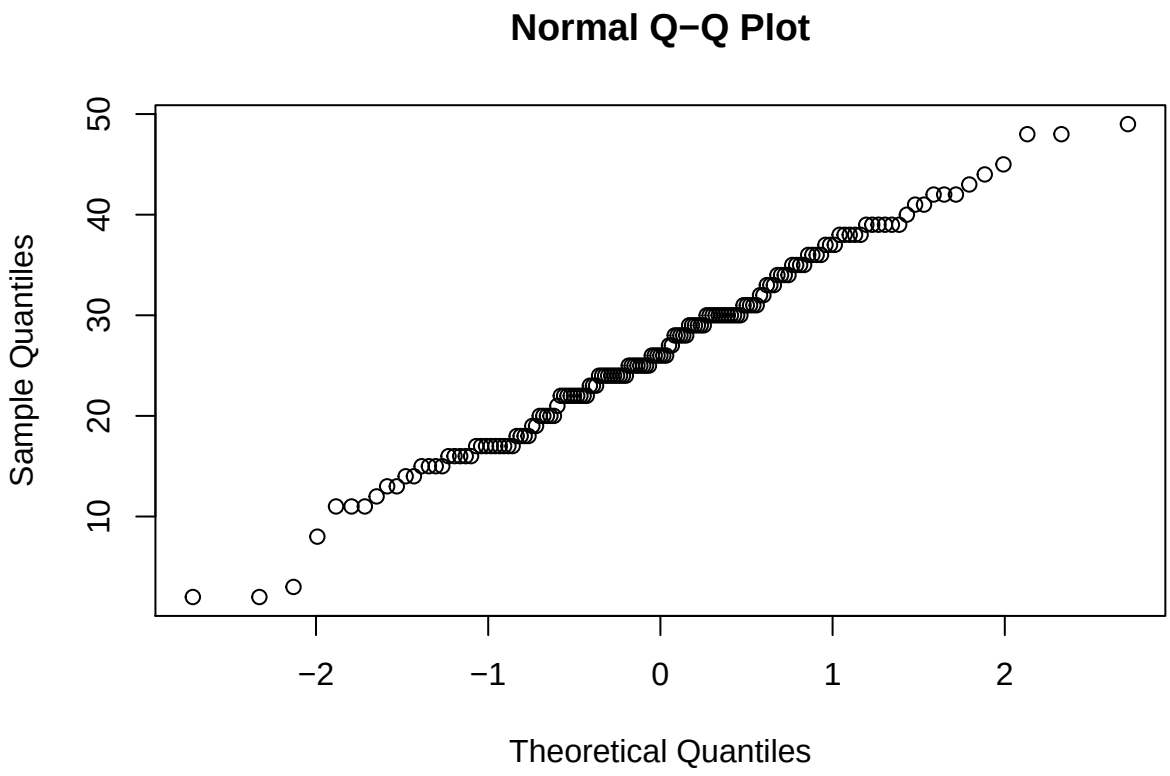
```r
varbothC <- sd(balssugboth$mass[balssugboth$treatment=="C"])^2
varbothH <- sd(balssugboth$mass[balssugboth$treatment=="H"])^2
ratioboth <- varbothH/varbothC
ratioboth
```

```
## [1] 1.776729
```

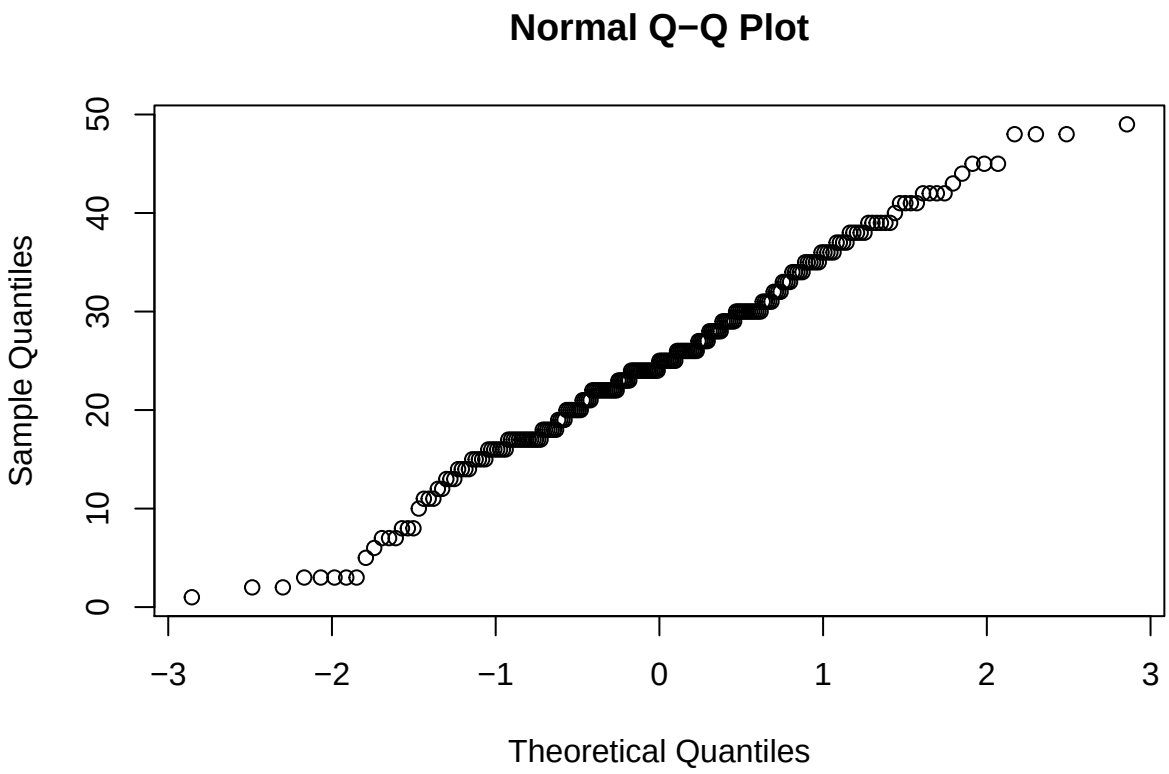
```r
# Q-Q plots
qqnorm(balssug15$BRIX)
```



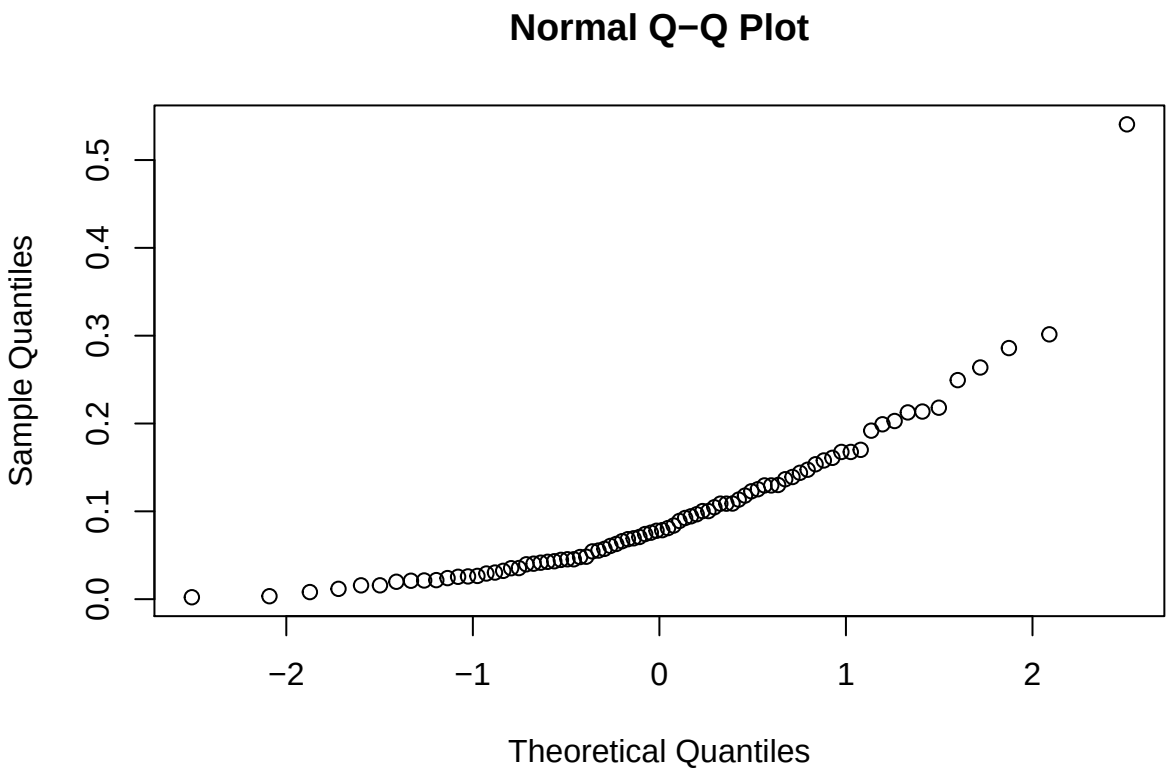
```
qqnorm(balssug16$BRIX)
```



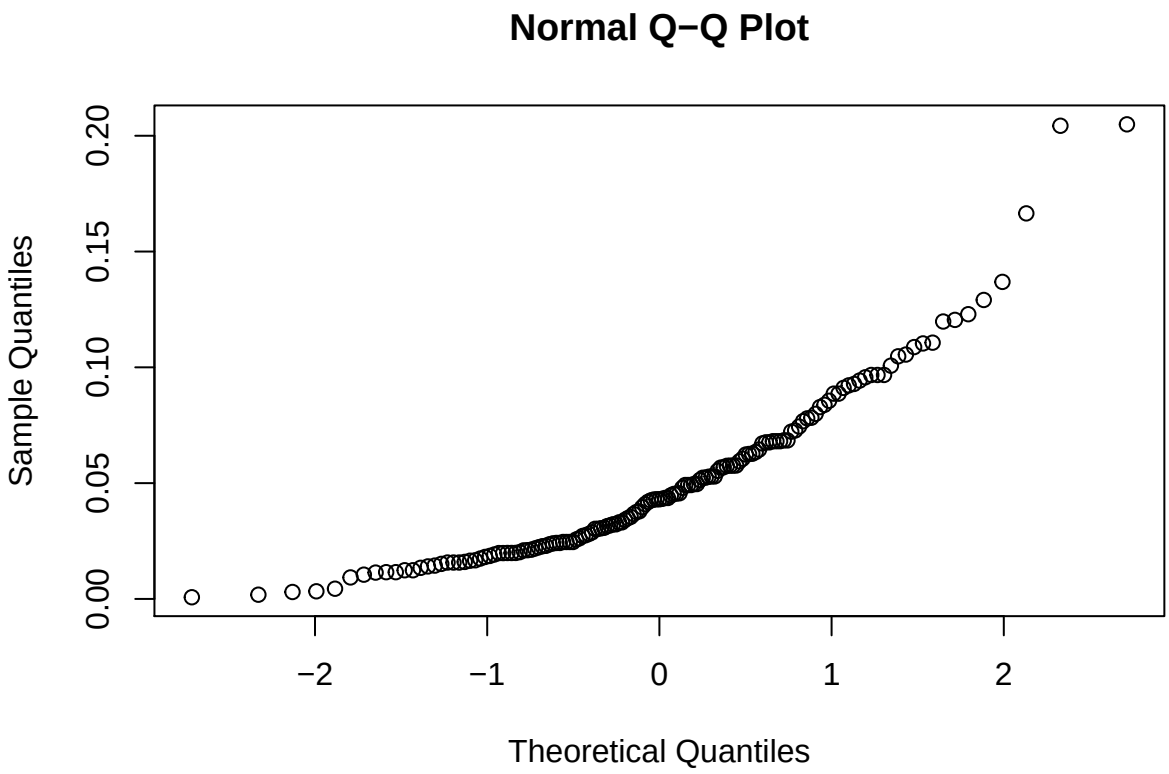

```
qqnorm(balssugboth$BRIX)
```



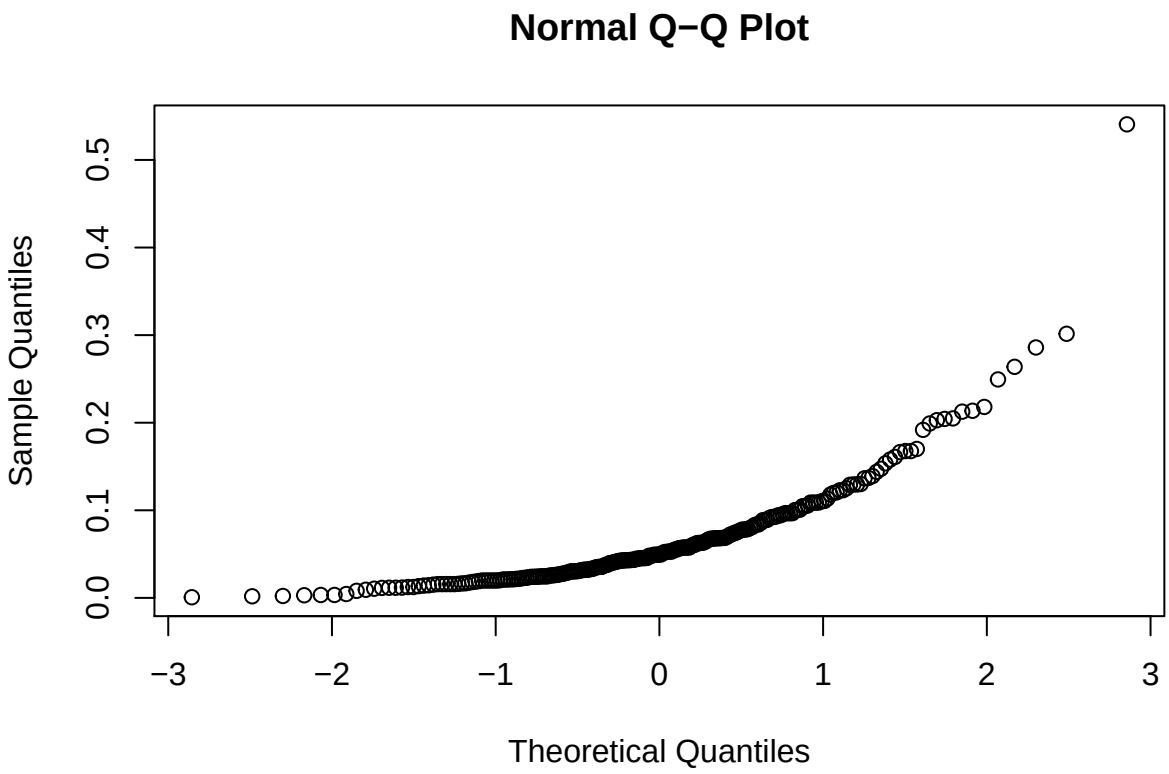

```
qqnorm(balssug15$mass)
```




```
qqnorm(balssug16$mass)
```




```
qqnorm(balssugboth$mass)
```


Normal Q−Q Plot
Sample Quantiles
0.0
0.1
0.2
0.3
0.4
0.5
−3
−2
−1
0
1
2
3
Theoretical Quantiles