

BalsamSugarExplr.R

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Sun Nov 27 19:20:30 2016

```
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:30      CC6-9 :10  Min.   : 1.00
## 2015-06-11:20 CH5   :16   H:56      CH5-6 : 7  1st Qu.:16.00
## 2015-06-03:17 CC6    :12              CHSR8-4: 7  Median :22.00
## 2015-06-06:12 EH4    : 9              CHSR8-6: 6  Mean   :21.57
## 2015-06-10: 8 WHSR9 : 8              EHSR1-2: 6  3rd Qu.:26.75
## 2015-06-02: 6 EHSR1 : 6              CH5-7  : 4  Max.   :48.00
## (Other)      : 3  (Other):18              (Other):46
##      mass
## Min.   :0.002182
## 1st Qu.:0.041771
## Median :0.079737
## Mean   :0.104480
## 3rd Qu.:0.142692
## 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:110 CC6-9 : 10 Min. : 1.00
## 2016-06-07:41 CC6 :31 H:127 EHSR1-2: 10 1st Qu.:18.00
## 2016-06-06:31 CHSR8 :30 CHSR8-4: 9 Median :24.00
## 2015-06-08:20 EH4 :24 CHSR8-6: 9 Mean :24.82
## 2015-06-11:20 EHSR1 :21 WSR10-1: 9 3rd Qu.:31.00
## 2015-06-03:17 WHSR9 :20 CC6-10 : 8 Max. :49.00
## (Other) :52 (Other):79 (Other):182
## mass
## Min. :0.0007309
## 1st Qu.:0.0256691
## Median :0.0513382
## Mean :0.0701392
## 3rd Qu.:0.0924000
## 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 16.56667 9.430996
## 2 H 24.25000 10.144860
```

```
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  23.0000 10.267969
## 2         H  26.3937  9.818316
```

```
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 0.09528345 0.06982932
## 2         H 0.10940649 0.09941259
```

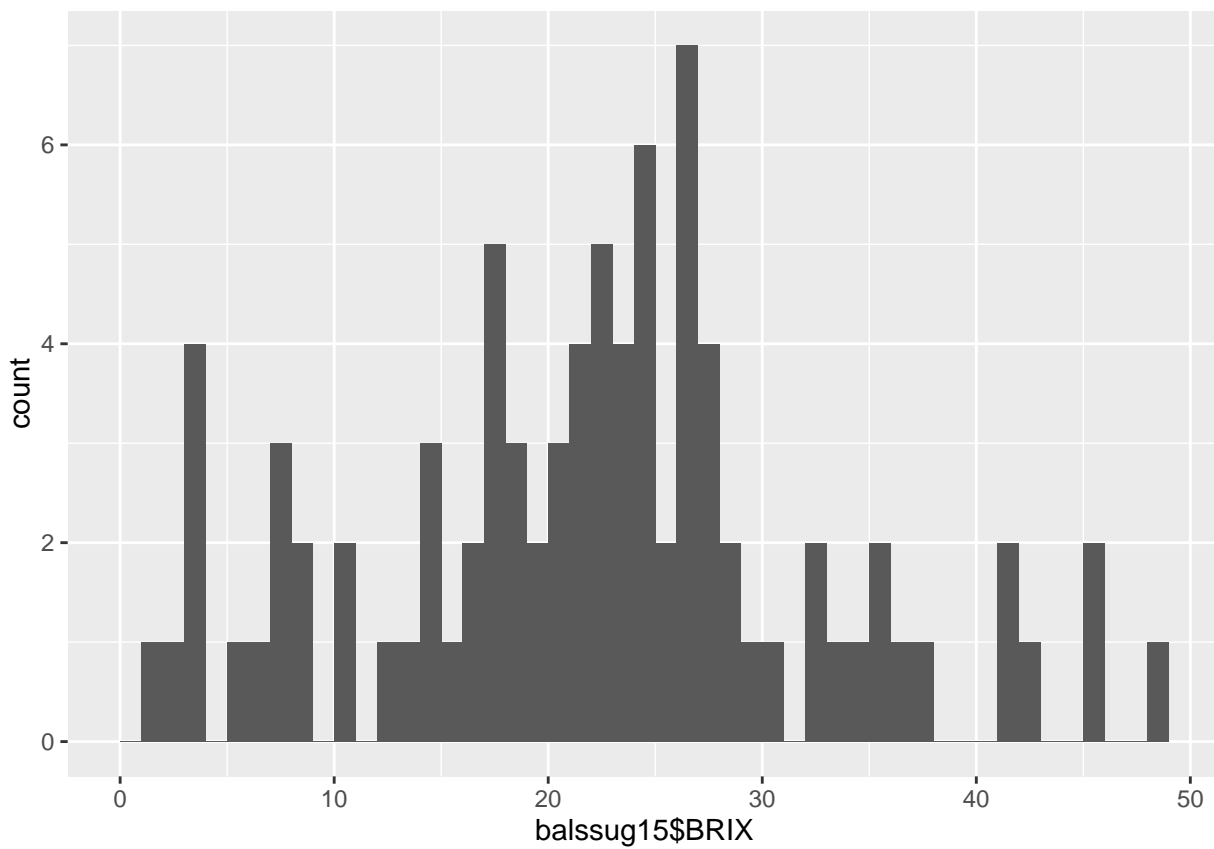
```
summarize(group_by(balssug16, treatment), meanmass = mean(mass), sdmass = sd(mass))
```

```
## 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
```

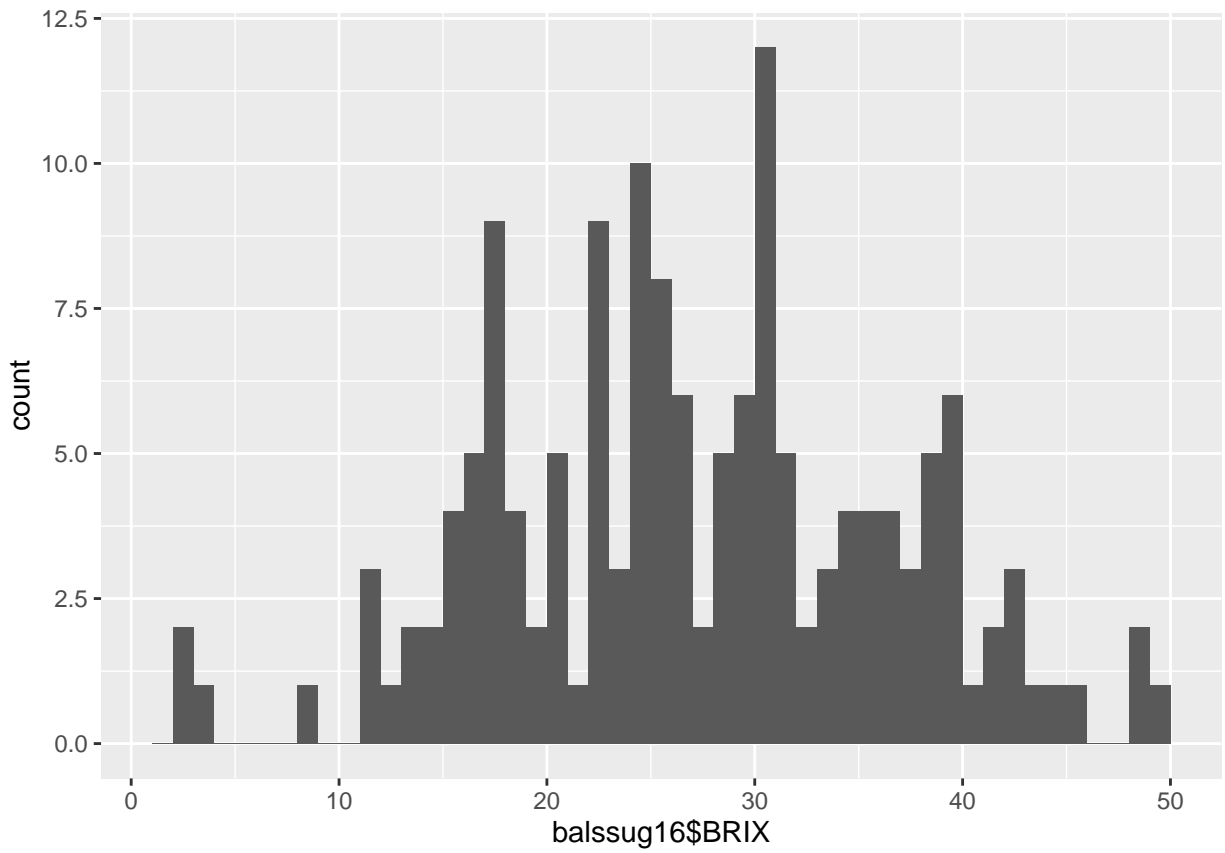
```
summarize(group_by(balssugboth, treatment), meanmass = mean(mass), sdmass = sd(mass))
```

```
## Source: local data frame [2 x 3]
##
##   treatment    meanmass    sdmass
##   (fctr)        (dbl)      (dbl)
## 1         C 0.06136855 0.05293235
## 2         H 0.07773579 0.07612578
```

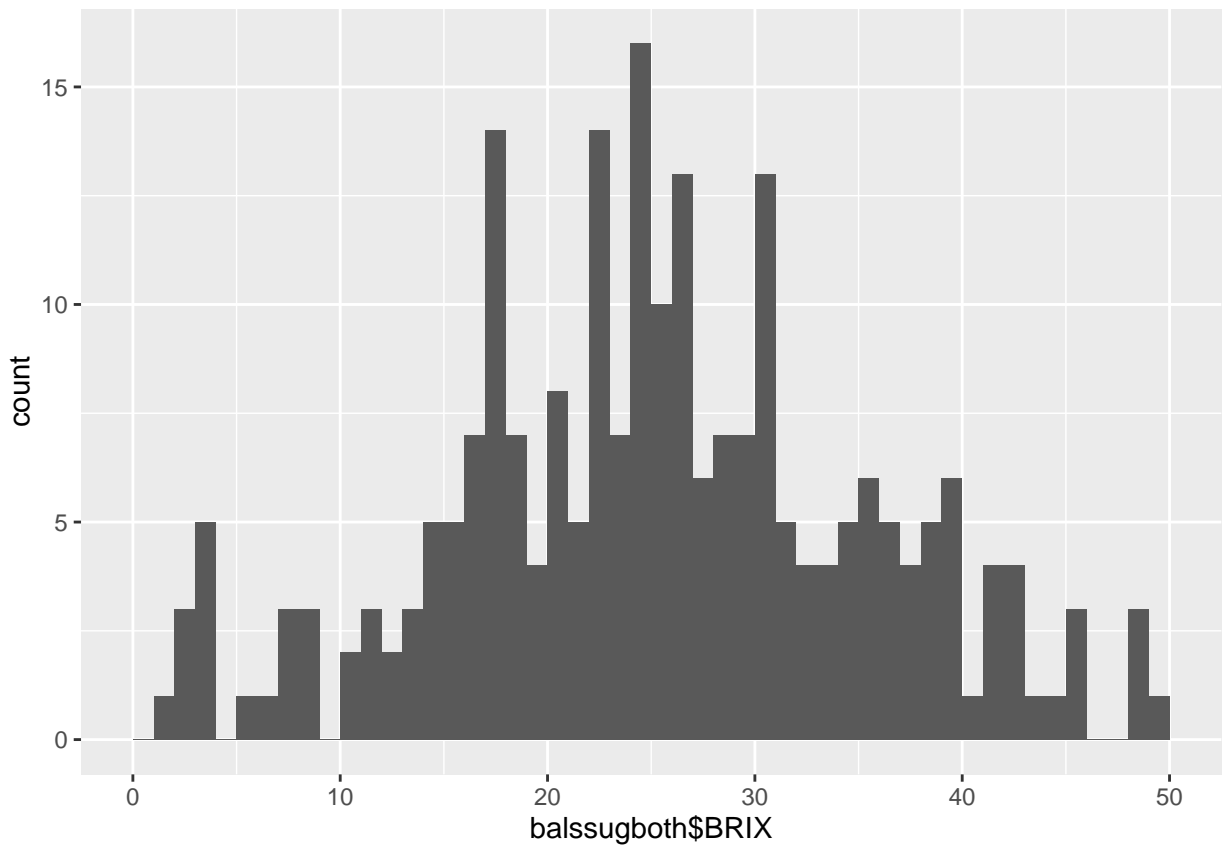
```
qplot(balssug15$BRIX, binwidth = 1)
```



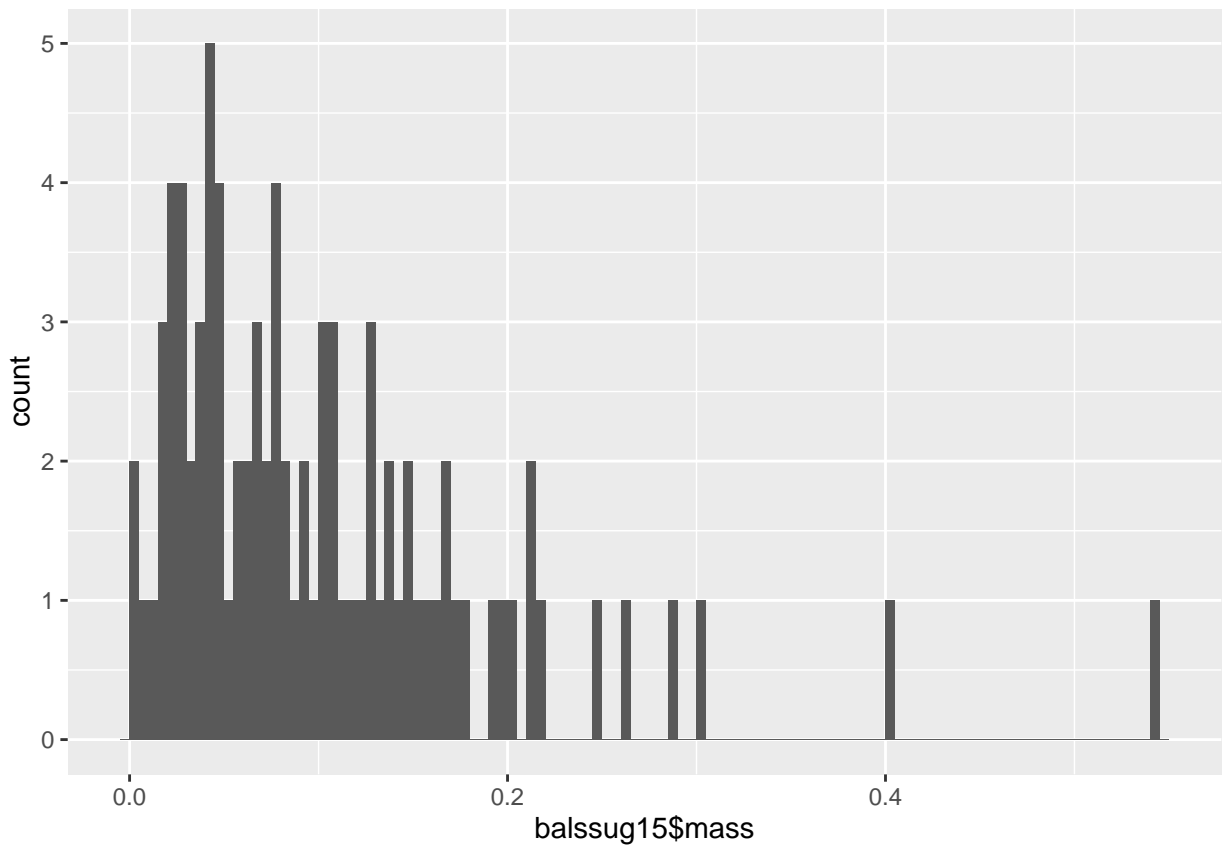
```
qplot(balssug16$BRIX, binwidth = 1)
```



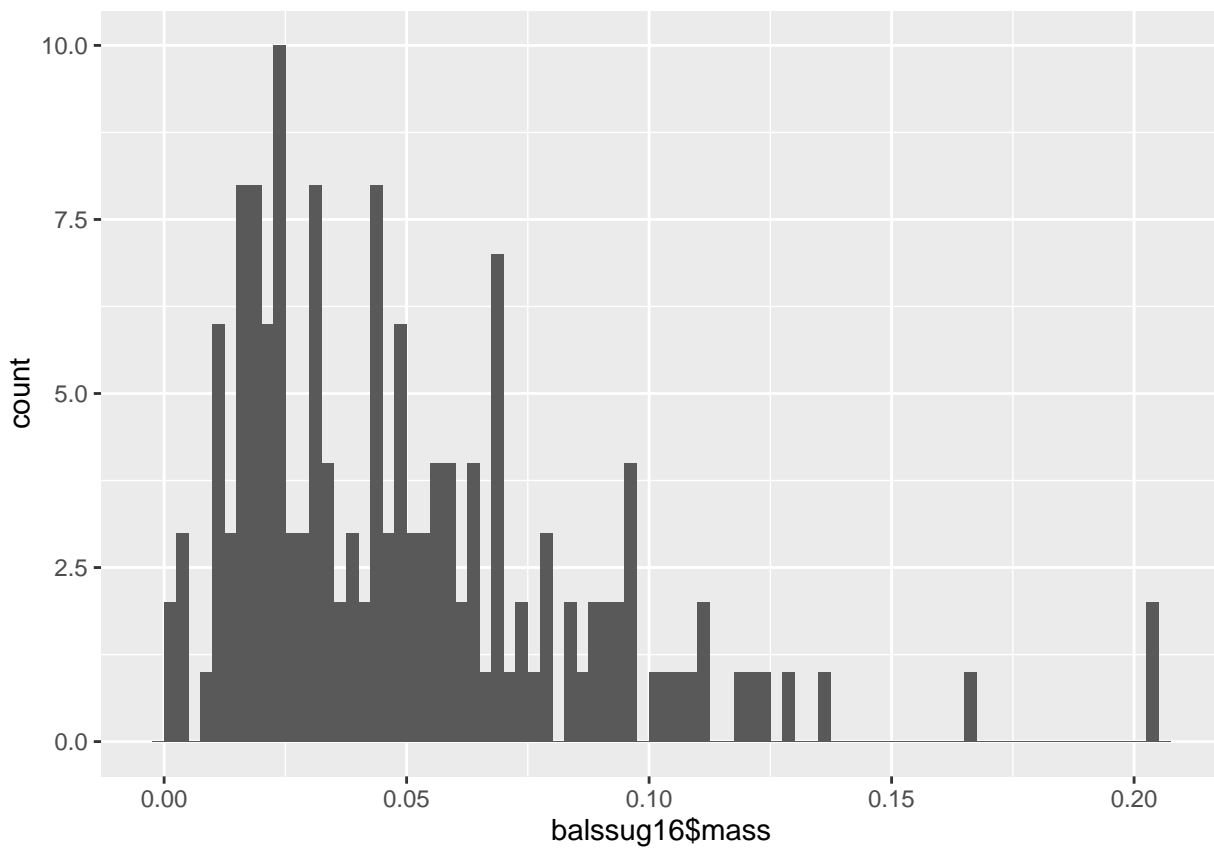
```
qplot(balssugboth$BRIX, binwidth = 1)
```



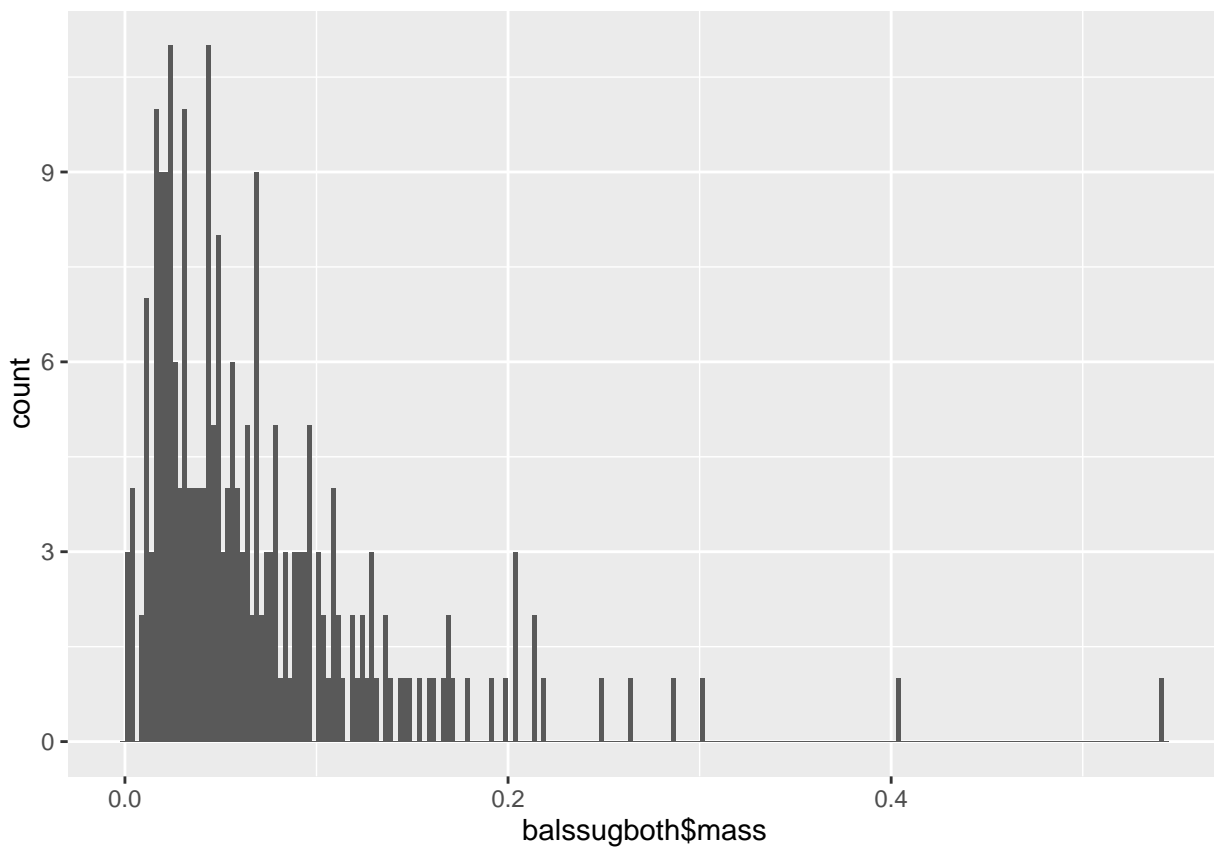
```
qplot(balssug15$mass, binwidth = 0.005)
```



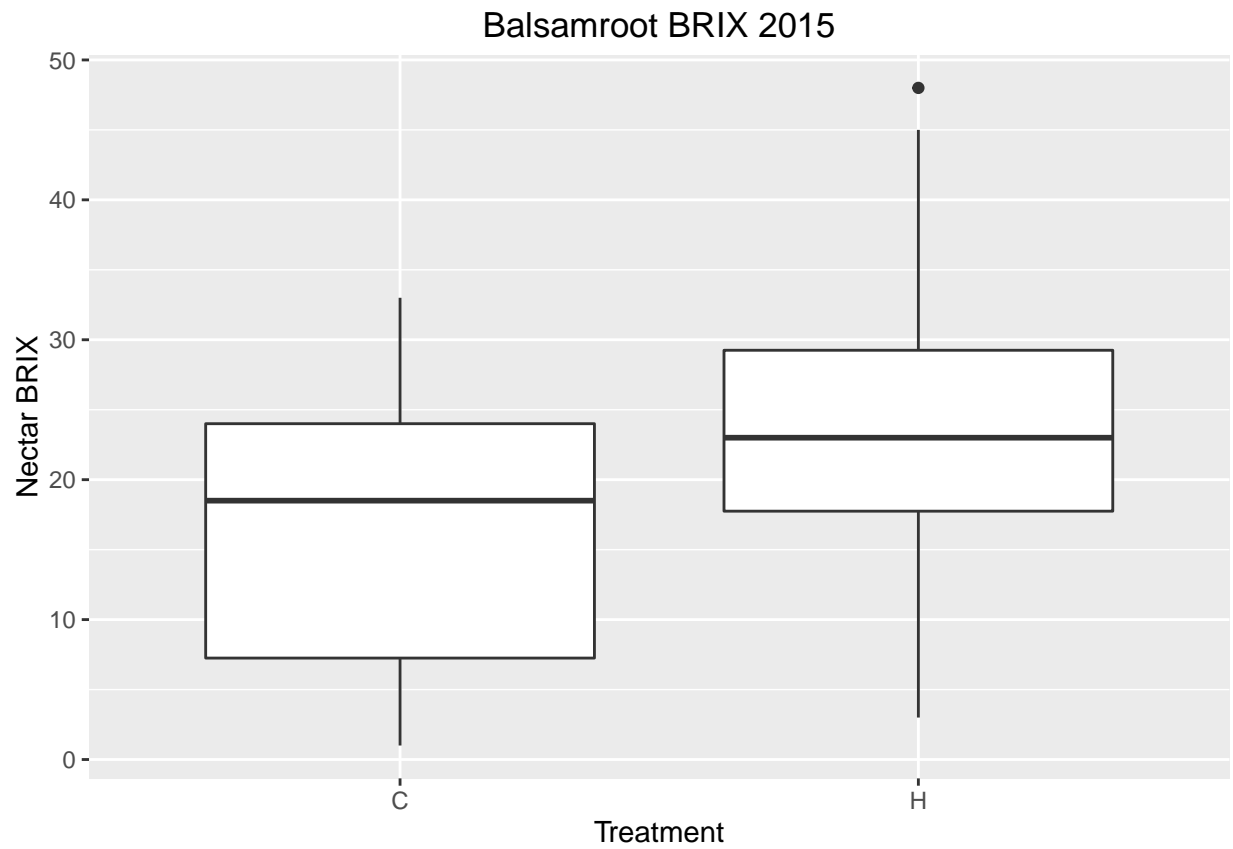
```
qplot(balssug16$mass, binwidth = .0025)
```



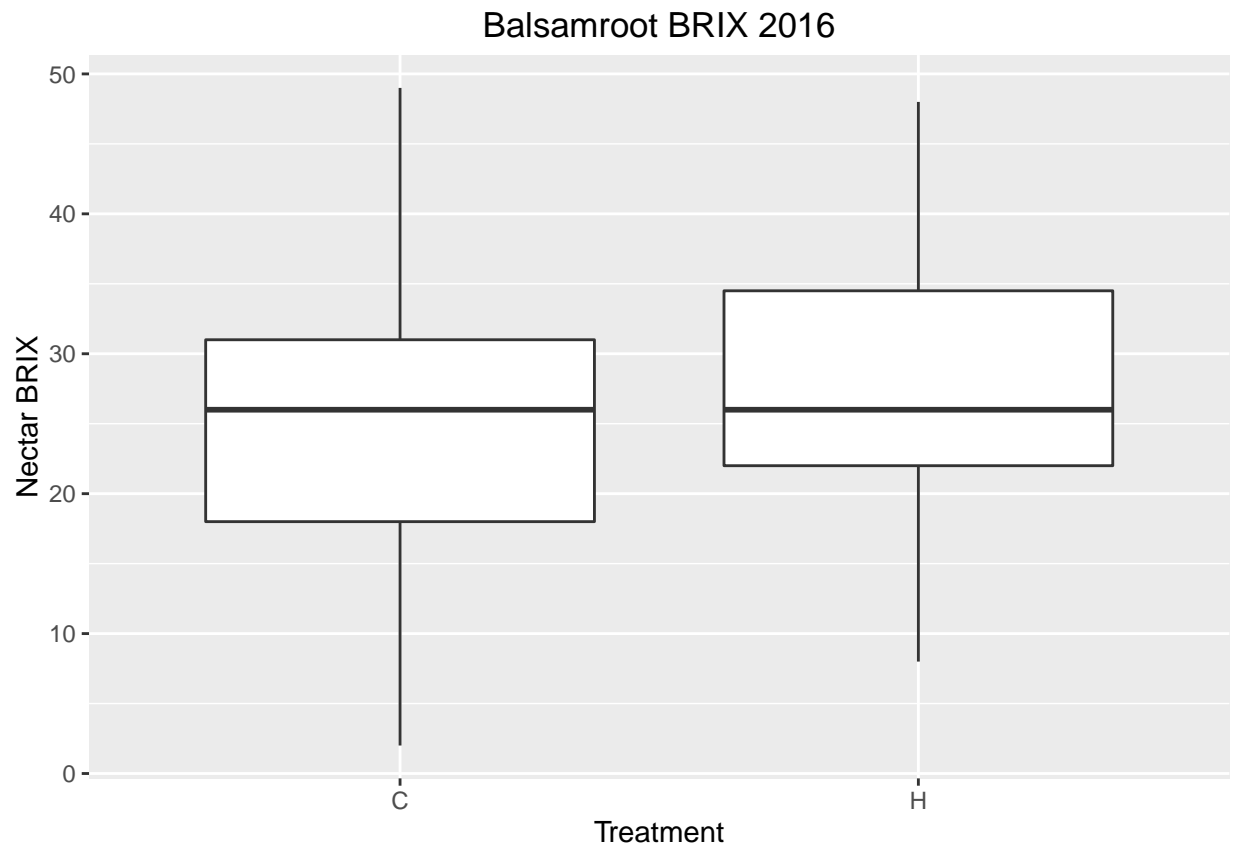
```
qplot(balssugboth$mass, binwidth = .0025)
```

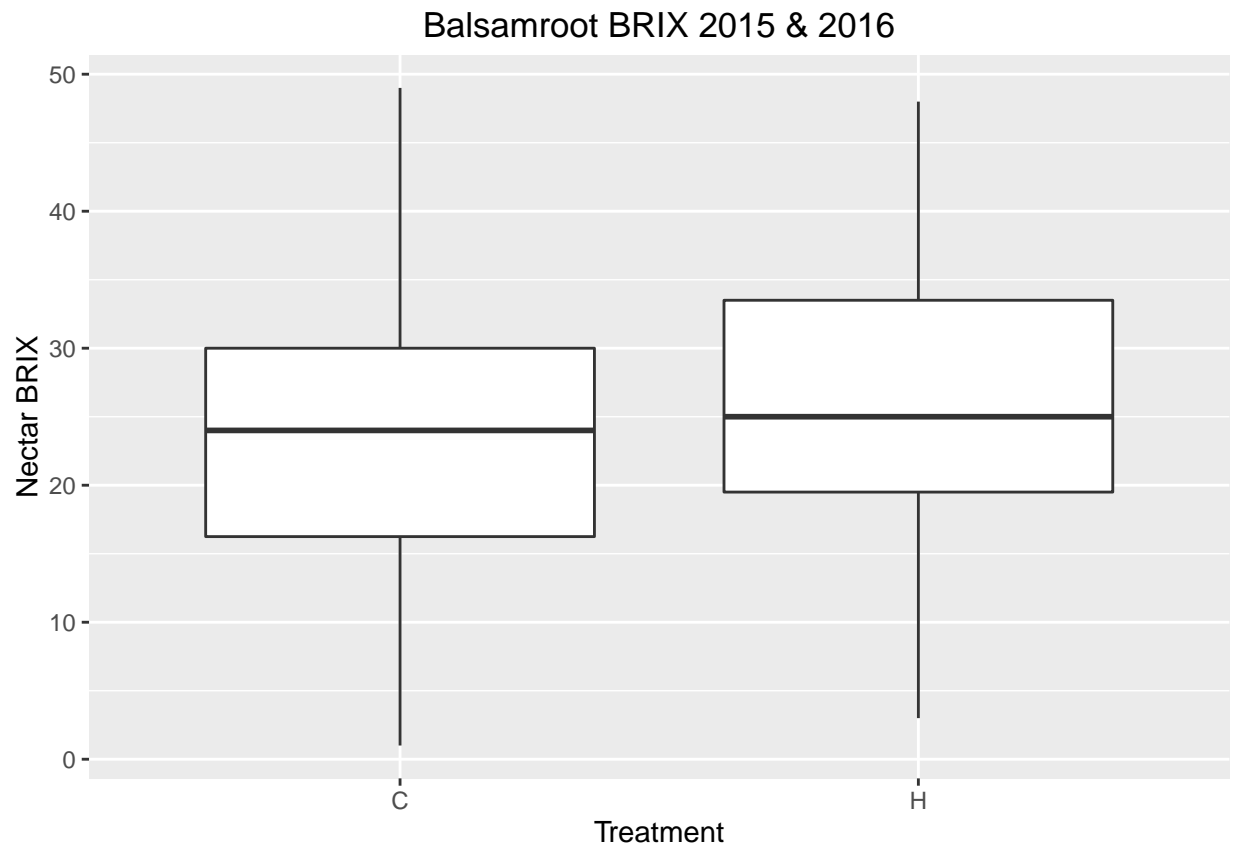
```
ggplot(balssug15, aes(x=treatment, y=BRIX)) + geom_boxplot() +
  xlab("Treatment") +
  ylab("Nectar BRIX") + ggtitle("Balsamroot BRIX 2015")
```



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



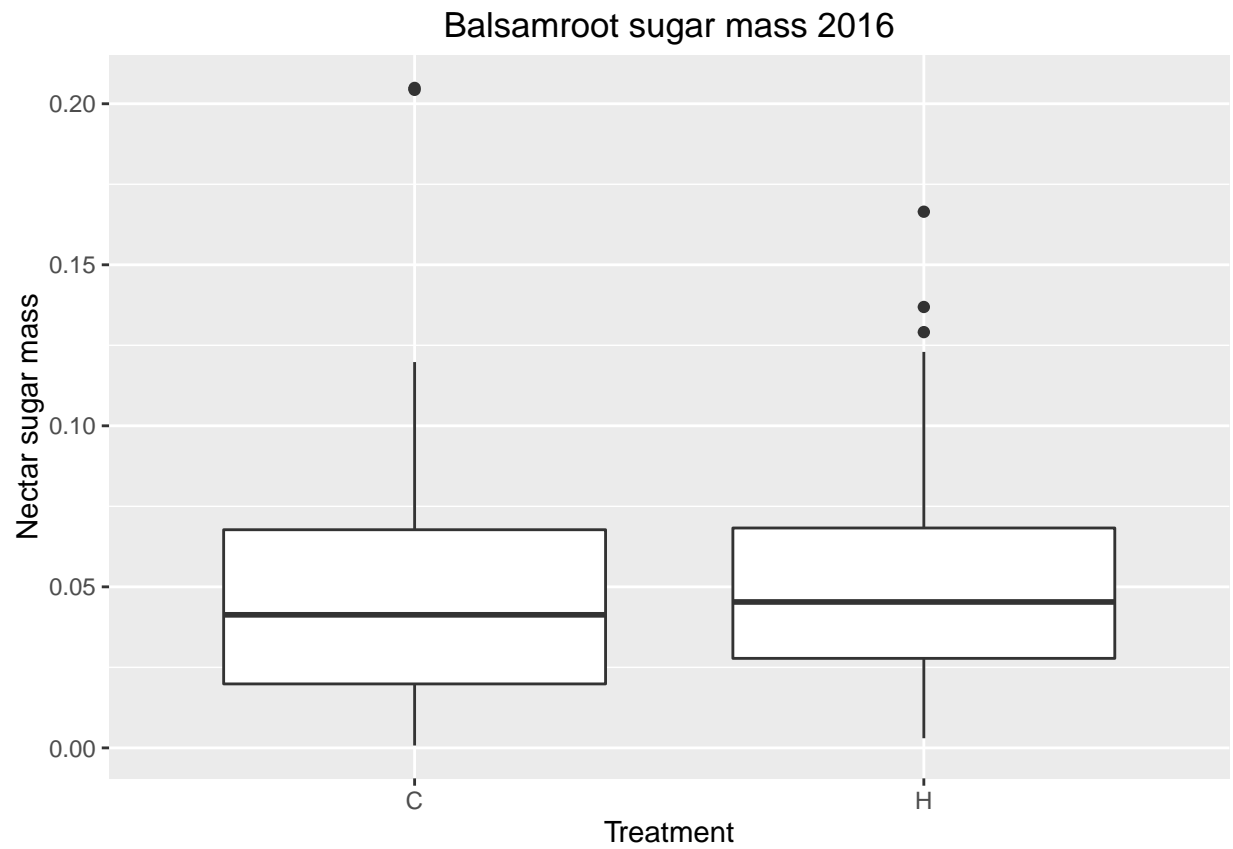
```
ggplot(balssugboth, aes(x=treatment, y=BRIX)) + geom_boxplot() +  
  xlab("Treatment") +  
  ylab("Nectar BRIX") + ggtitle("Balsamroot BRIX 2015 & 2016")
```



```
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] 1.157116
```

```
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] 1.093692
```

```

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

```

```
## [1] 2.026783
```

```

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

```

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

```

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

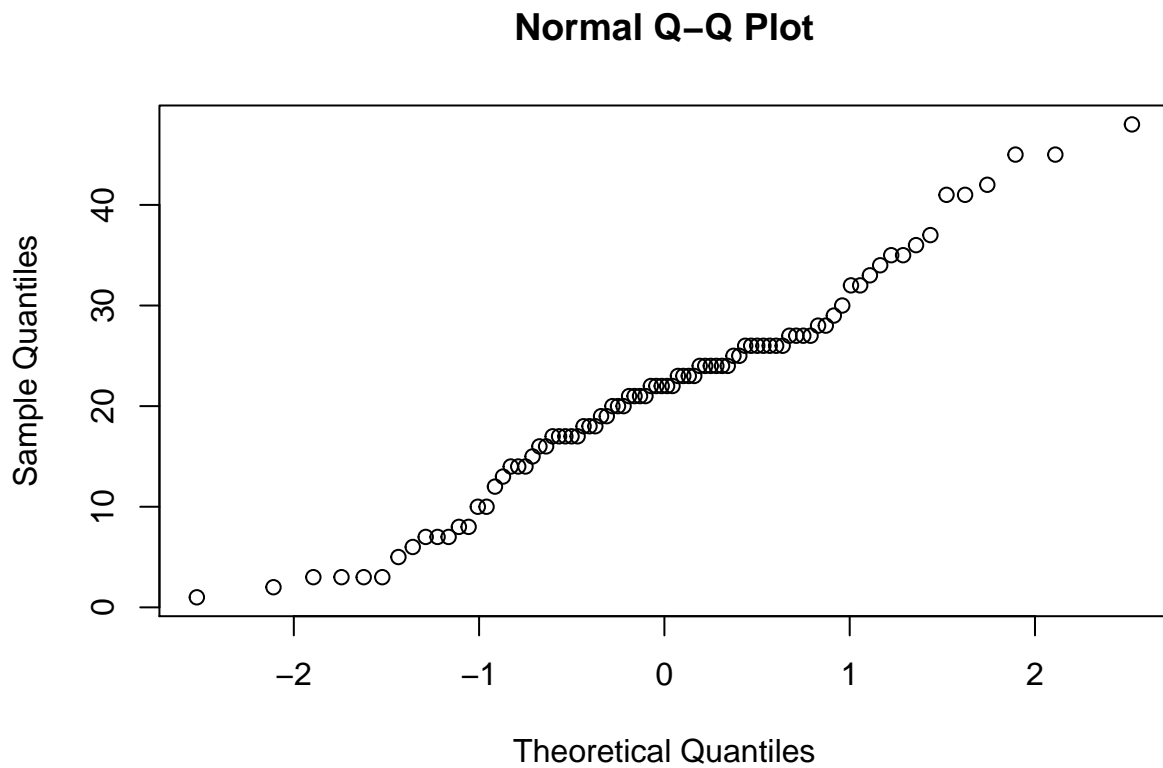
```

```
## [1] 2.068336
```

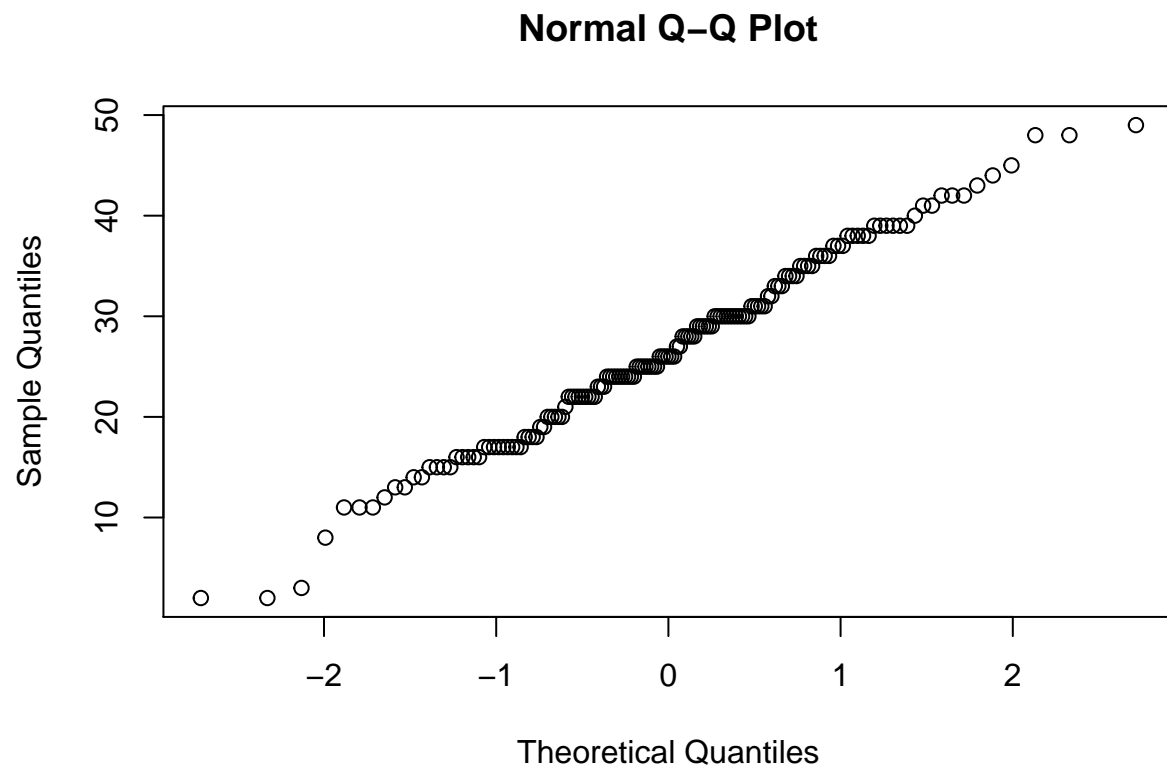
```

# Q-Q plots
qqnorm(balssug15$BRIX)

```

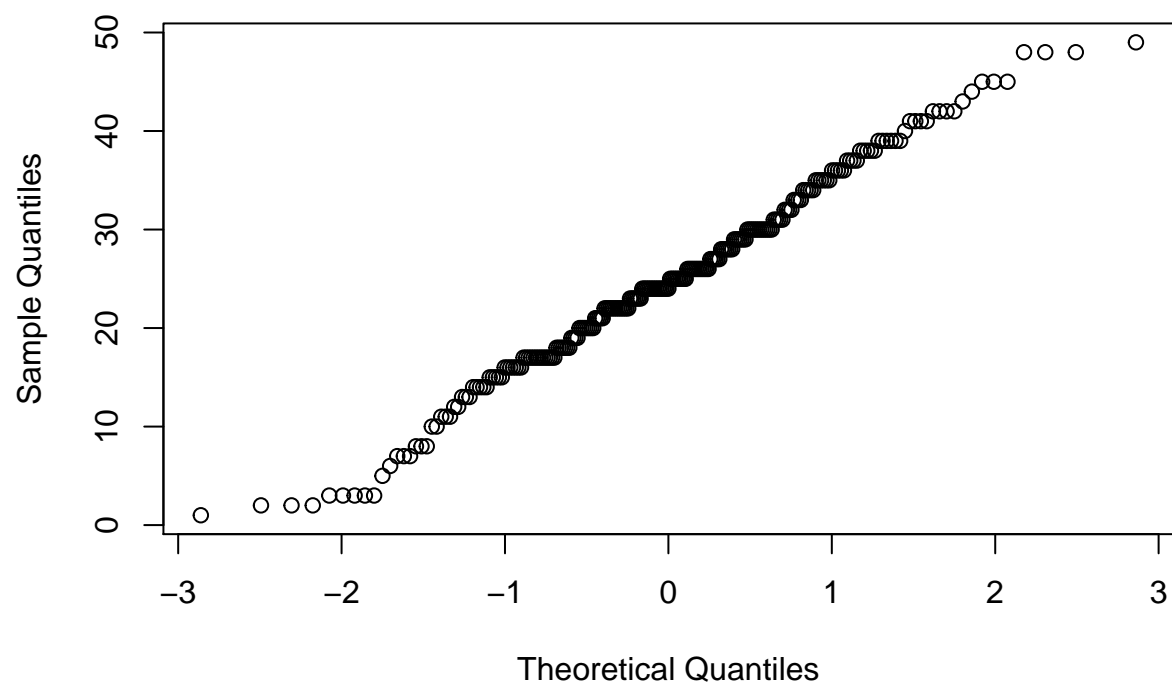



```
qqnorm(balssug16$BRIX)
```



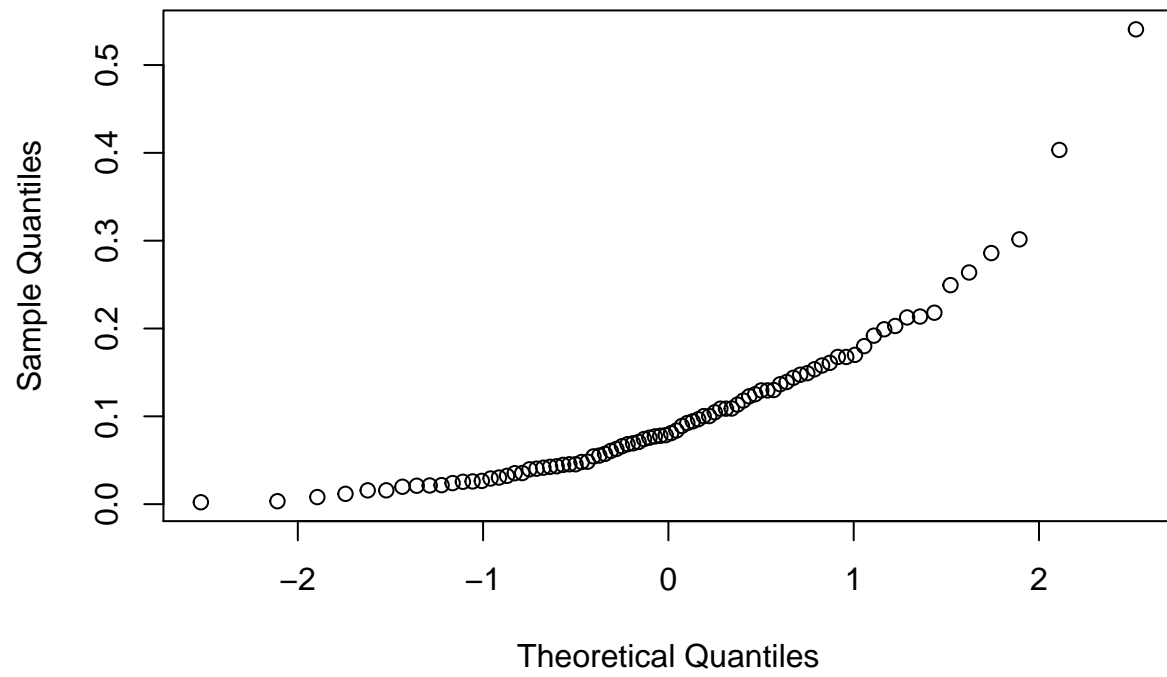
```
qqnorm(balssugboth$BRIX)
```

Normal Q-Q Plot



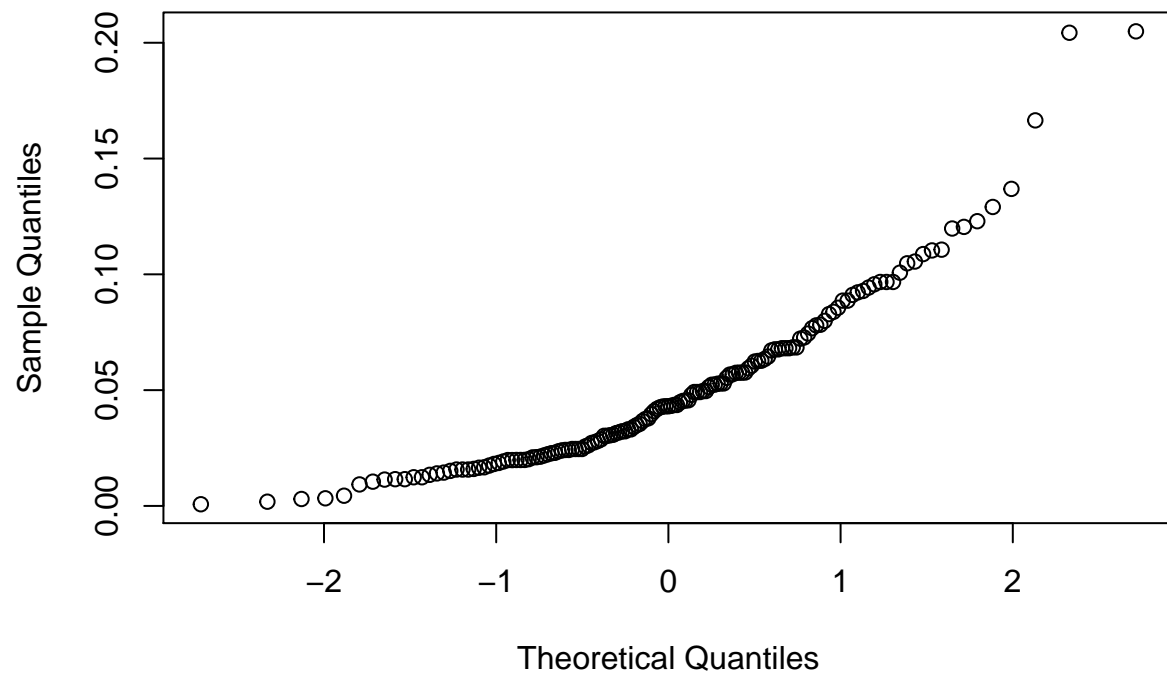
```
qqnorm(balssug15$mass)
```

Normal Q-Q Plot



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

Normal Q-Q Plot



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

Normal Q-Q Plot

