

BalsamrootDataExplore_v1.R

Audrey McCombs

Tue Sep 27 18:44:17 2016

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

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

## The following object is masked from 'package:GGally':
##
##      nasa

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

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

```
library(mvnormtest)
library(HH)
```

```
## Loading required package: lattice

## Loading required package: grid

## Loading required package: latticeExtra

## Loading required package: RColorBrewer

##
## Attaching package: 'latticeExtra'

## The following object is masked from 'package:ggplot2':
##
##      layer

## Loading required package: multcomp

## Loading required package: mvtnorm

## Loading required package: survival
```

```

## Loading required package: TH.data

## Loading required package: MASS

##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##      select

##
## Attaching package: 'TH.data'

## The following object is masked from 'package:MASS':
##
##      geyser

## Loading required package: gridExtra

```

```
library(Rcmdr)
```

```

## Warning: package 'Rcmdr' was built under R version 3.2.5

## Loading required package: splines

## Loading required package: RcmdrMisc

## Warning: package 'RcmdrMisc' was built under R version 3.2.5

## Loading required package: car

## Warning: package 'car' was built under R version 3.2.5

##
## Attaching package: 'car'

## The following objects are masked from 'package:HH':
##
##      logit, vif

## Loading required package: sandwich

## The Commander GUI is launched only in interactive sessions

```

```
library(nlme)
```

```

##
## Attaching package: 'nlme'

## The following object is masked from 'package:dplyr':
##
##      collapse

```

```
#####
### 2015-2016 data ###
#####

# Create the data frames

##Read in the data

setwd("D:/Iowa State University/Debinski Lab/Nectar data/Nectar analysis for manuscript")

# Balsamroot volume, 2015-2016

volume.balsam <- read.csv("Nectar_Vol_Balsam.csv", header = T, col.names = c("Date", "Date.Factor", "Year.Factor", "Plot", "Heat", "Plant", "Volume", "log.vol"))
volume.balsam <- data.frame(volume.balsam[,1:7])
volume.balsam$Date.Factor <- as.factor(volume.balsam$Date.Factor)
volume.balsam$Year.Factor <- as.factor(volume.balsam$Year.Factor) # 1 = 2015, 2 = 2016
volume.balsam$Heat <- as.factor(volume.balsam$Heat) # 0 = control, 1 = heat
volume.balsam$Plant <- as.factor(paste(volume.balsam$Plot, volume.balsam$Plant, sep="-"))
volume.balsam$Plot <- as.factor(volume.balsam$Plot)
volume.balsam$log.vol <- log(volume.balsam$Volume)
head(volume.balsam)
```

```
##      Date Date.Factor Year.Factor Plot Heat Plant Volume log.vol
## 1 6/2/2015          1          1 WHSR9  1 WHSR9-2 0.4363636 -0.8292794
## 2 6/2/2015          1          1 WHSR9  1 WHSR9-1 0.7272727 -0.3184537
## 3 6/2/2015          1          1 WSR10  0 WSR10-9 0.3636364 -1.0116009
## 4 6/2/2015          1          1 WSR10  0 WSR10-1 0.4909091 -0.7114963
## 5 6/2/2015          1          1 WSR10  0 WSR10-1 0.5272727 -0.6400374
## 6 6/2/2015          1          1 WSR10  0 WSR10-9 1.8909091  0.6370577
```

```
# Balsamroot sugar, 2015-2016

sugar.balsam <- read.csv("Nectar_BRIX_Balsam.csv", header = T, col.names = c("Date", "Date.Factor", "Year.Factor", "Plot", "Heat", "Plant", "BRIX", "Mass"))
sugar.balsam <- data.frame(sugar.balsam[,1:8])
sugar.balsam$Date.Factor <- as.factor(sugar.balsam$Date.Factor)
sugar.balsam$Year.Factor <- as.factor(sugar.balsam$Year.Factor)
sugar.balsam$Heat <- as.factor(sugar.balsam$Heat)
sugar.balsam$Plant <- as.factor(paste(sugar.balsam$Plot, sugar.balsam$Plant, sep="-"))
sugar.balsam$Plot <- as.factor(sugar.balsam$Plot)
sugar.balsam$log.mass <- log(sugar.balsam$Mass)
head(sugar.balsam)
```

```
##      Date Date.Factor Year.Factor Plot Heat Plant BRIX Mass
## 1 6/2/2015          1          1 WSR10  0 WSR10-6 12 0.07079273
## 2 6/2/2015          1          1 WSR10  0 WSR10-4 22 0.10028000
## 3 6/2/2015          1          1 WSR10  0 WSR10-6 42 0.10874182
## 4 6/2/2015          1          1 WHSR9  1 WHSR9-4 18 0.12281818
## 5 6/2/2015          1          1 WHSR9  1 WHSR9-4 27 0.19911818
## 6 6/2/2015          1          1 WSR10  0 WSR10-2 29 0.20286000
##      log.mass
## 1 -2.647999
## 2 -2.299789
## 3 -2.218779
```

```
## 4 -2.097050
## 5 -1.613857
## 6 -1.595239
```

#Data summaries

```
summary(volume.balsam)
```

```
##      Date      Date.Factor Year.Factor      Plot      Heat
## 6/8/2016 :60      12       :60      1: 92      CHSR8 :38      0:116
## 6/7/2016 :45      11       :45      2:168      CH5   :34      1:144
## 6/6/2016 :34      10       :34              CC6    :31
## 6/8/2015 :21       4        :21              EH4    :26
## 6/11/2015:20       6        :20              WHSR9 :24
## 6/5/2016 :19       9        :19              EHSR1 :22
## (Other)  :61      (Other):61              (Other):85
##      Plant      Volume      log.vol
## CHSR8-4: 12      Min.    :0.01818      Min.    : -4.007
## CC6-9   : 10      1st Qu.:0.09091      1st Qu.: -2.398
## CHSR8-6: 10      Median :0.16364      Median : -1.810
## EHSR1-2: 10      Mean    :0.29413      Mean    : -1.794
## CHSR8-2: 9       3rd Qu.:0.33182      3rd Qu.: -1.103
## EC3-3   : 9       Max.    :3.98182      Max.    : 1.382
## (Other):200
```

```
summarize(group_by(volume.balsam, Heat), meanVol = mean(Volume), sdVolume = sd(Volume))
```

```
## Source: local data frame [2 x 3]
##
##      Heat meanVol sdVolume
##      (fctr)      (dbl)      (dbl)
## 1         0 0.292790 0.4350334
## 2         1 0.295202 0.4400984
```

```
summary(sugar.balsam)
```

```
##      Date      Date.Factor Year.Factor      Plot      Heat
## 6/8/2016 :56      12       :56      1: 86      CC6    :31      0:108
## 6/7/2016 :41      11       :41      2:151      CH5    :31      1:129
## 6/6/2016 :31      10       :31              CHSR8 :31
## 6/11/2015:18       4        :18              EH4    :26
## 6/8/2015 :18       6        :18              EHSR1 :21
## 6/3/2015 :17       2        :17              WHSR9 :20
## (Other)  :56      (Other):56              (Other):77
##      Plant      BRIX      Mass      log.mass
## WHSR9-2: 10      Min.    : 1.00      Min.    :0.0007309      Min.    : -7.2212
## CH5-2   : 9       1st Qu.:18.00      1st Qu.:0.0256691      1st Qu.: -3.6625
## EHSR1-1: 9       Median :24.00      Median :0.0513382      Median : -2.9693
## CC6-1   : 8       Mean    :24.83      Mean    :0.0704628      Mean    : -3.0449
## CC6-10  : 7       3rd Qu.:31.00      3rd Qu.:0.0922091      3rd Qu.: -2.3837
## CC6-7   : 7       Max.    :49.00      Max.    :0.5947491      Max.    : -0.5196
## (Other):187
```

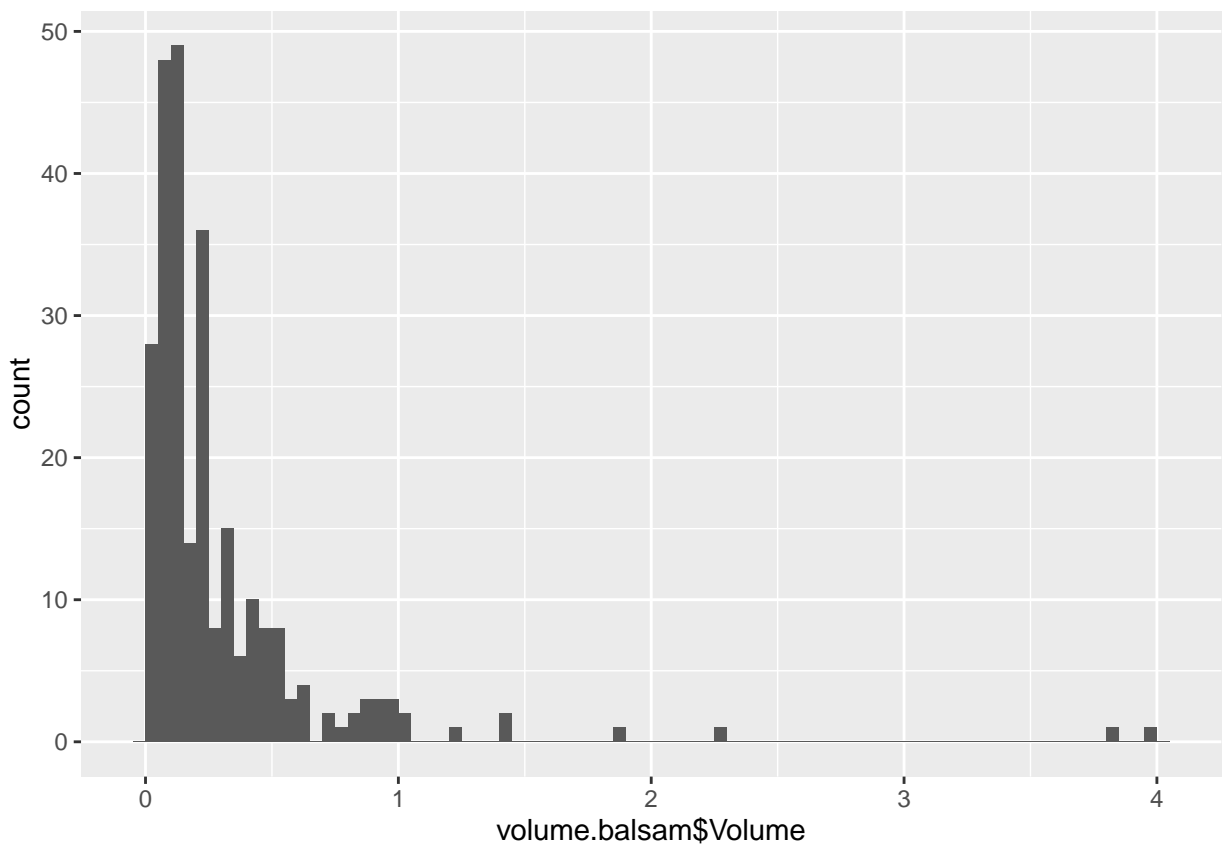
```
summarize(group_by(sugar.balsam, Heat), meanBRIX = mean(BRIX), meanMass = mean(Mass), sdBRIX = sd(BRIX))
```

```
## Source: local data frame [2 x 5]
```

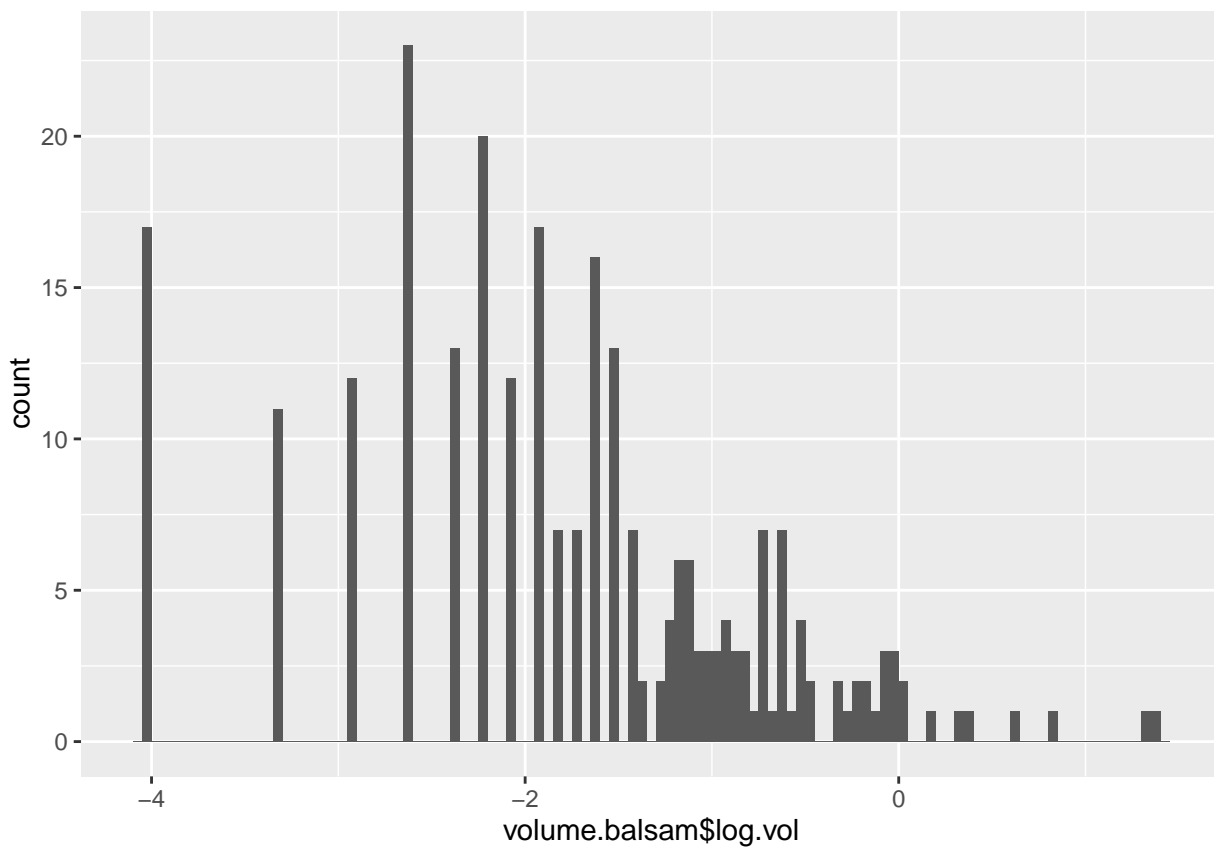
```
##
```

```
##      Heat meanBRIX  meanMass  sdBRIX  sdMass  
##   (fctr)   (dbl)    (dbl)    (dbl)   (dbl)  
## 1      0 24.54630 0.06284670 9.839254 0.05150040  
## 2      1 25.06202 0.07683914 10.487159 0.08190646
```

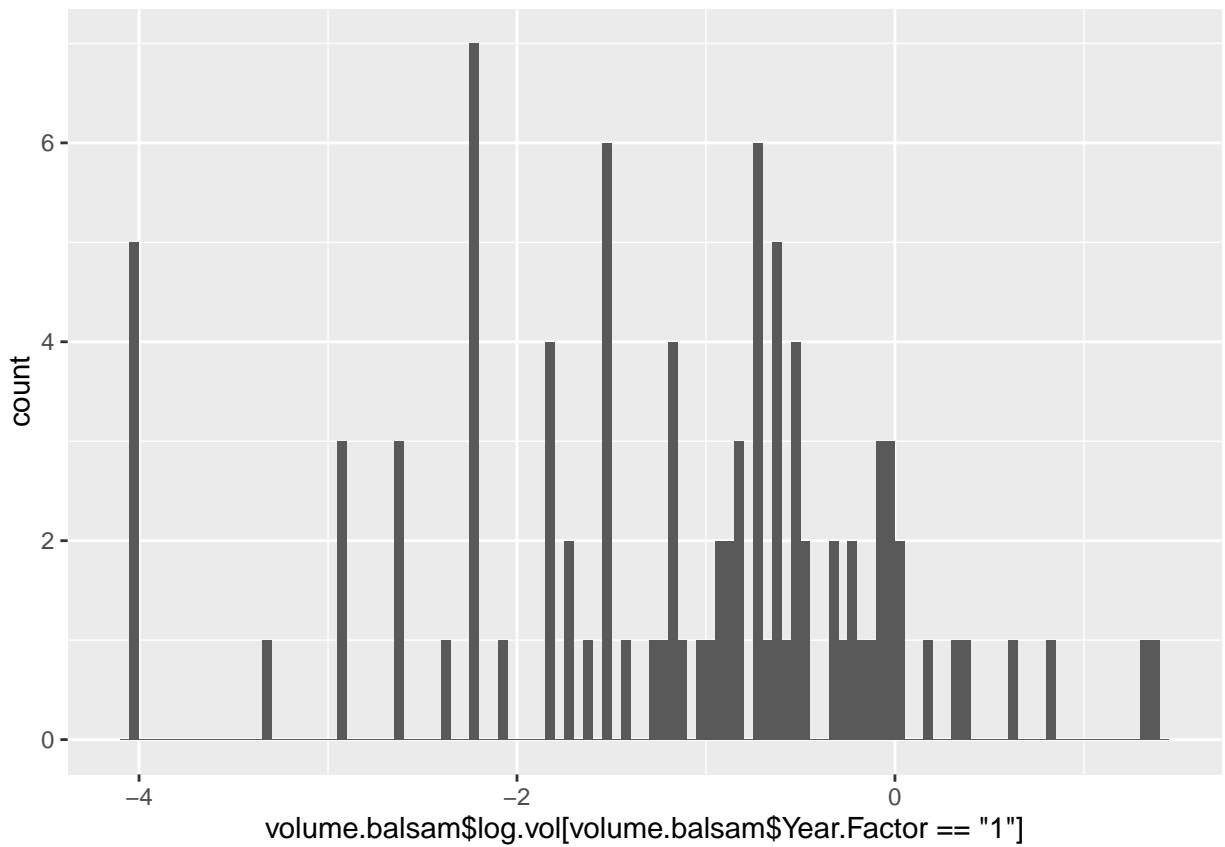
```
qplot(volume.balsam$Volume, binwidth = 0.05)
```



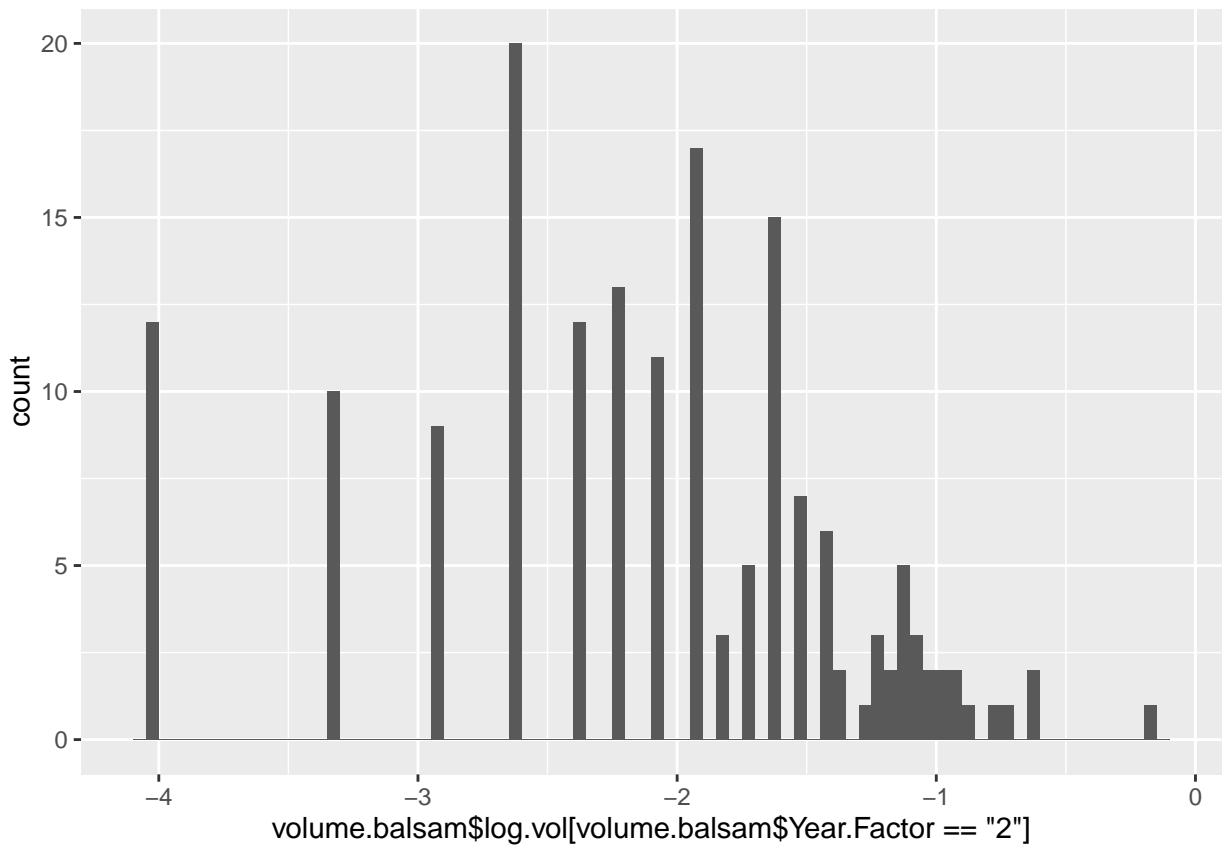
```
qplot(volume.balsam$log.vol, binwidth = .05)
```



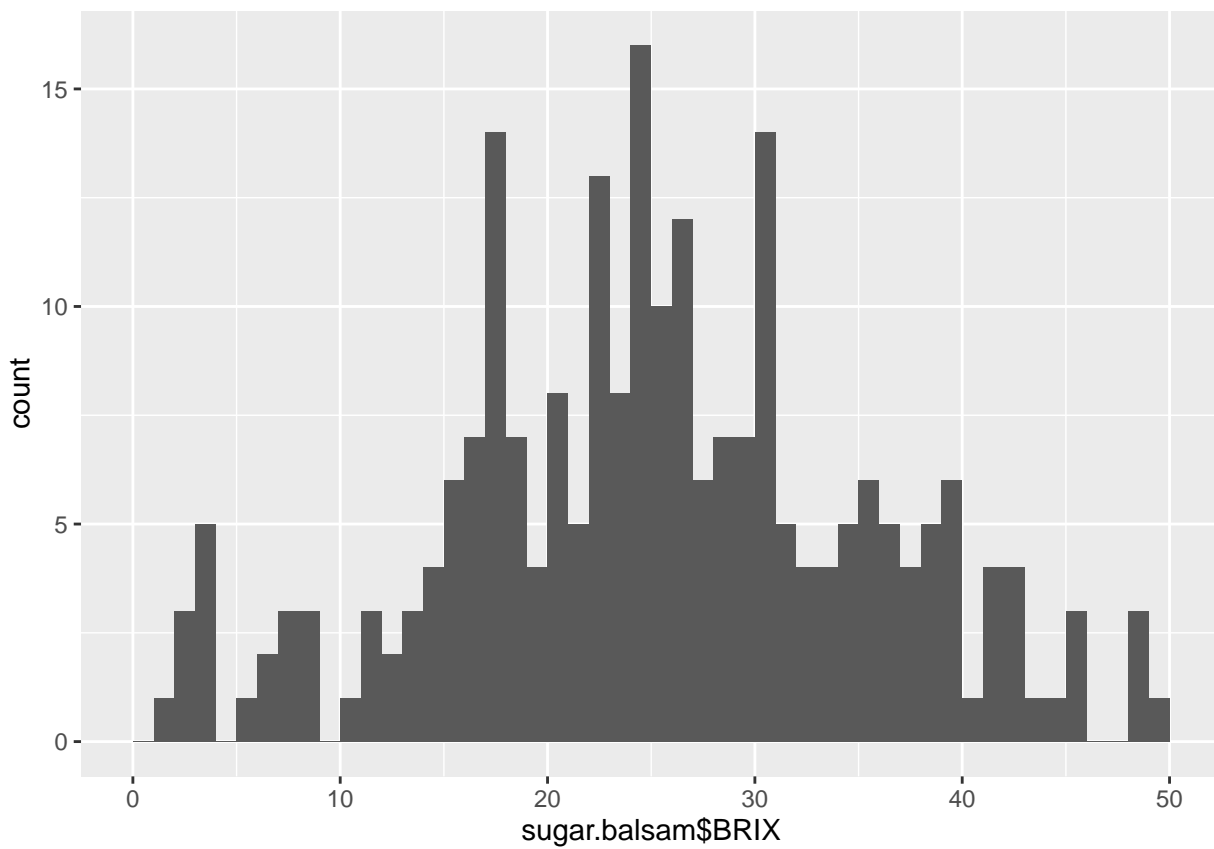
```
qplot(volume.balsam$log.vol[volume.balsam$Year.Factor == "1"], binwidth = .05)
```



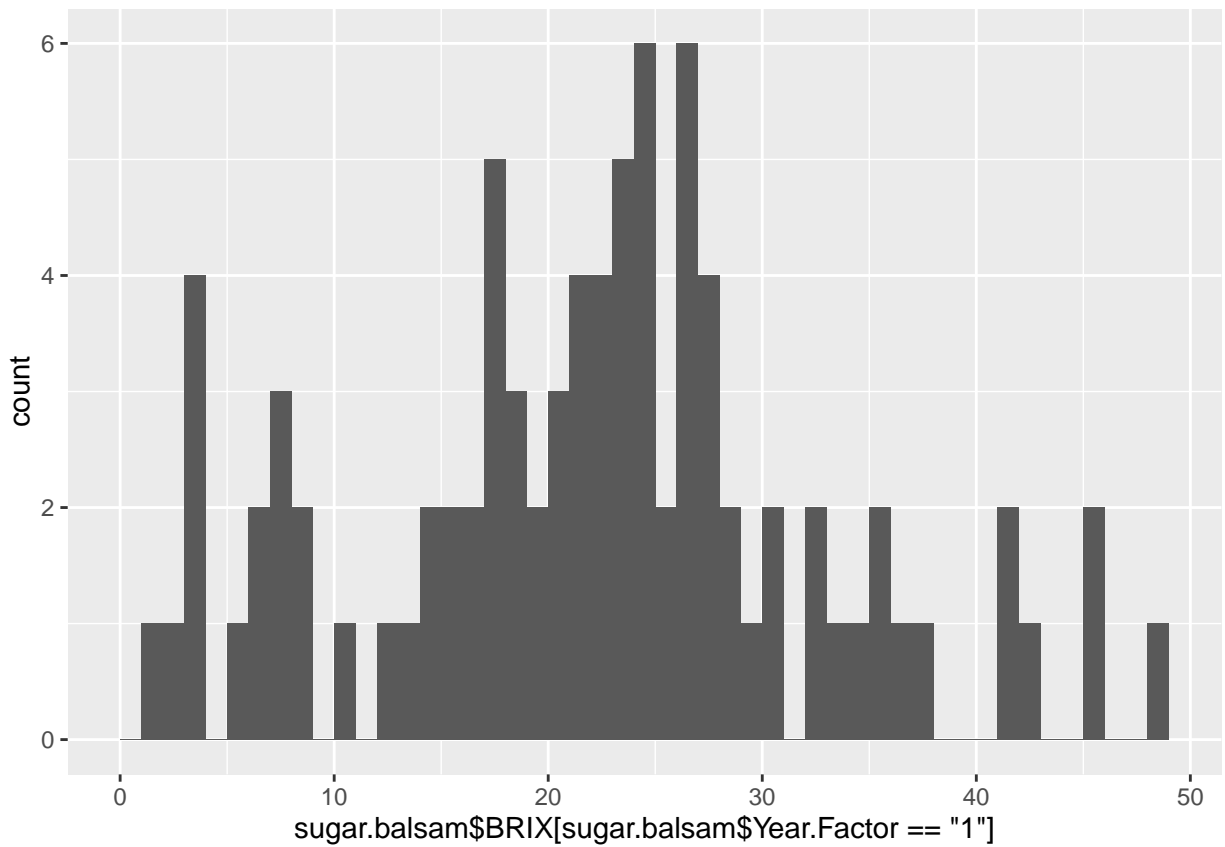
```
qplot(volume.balsam$log.vol[volume.balsam$Year.Factor == "2"], binwidth = .05)
```



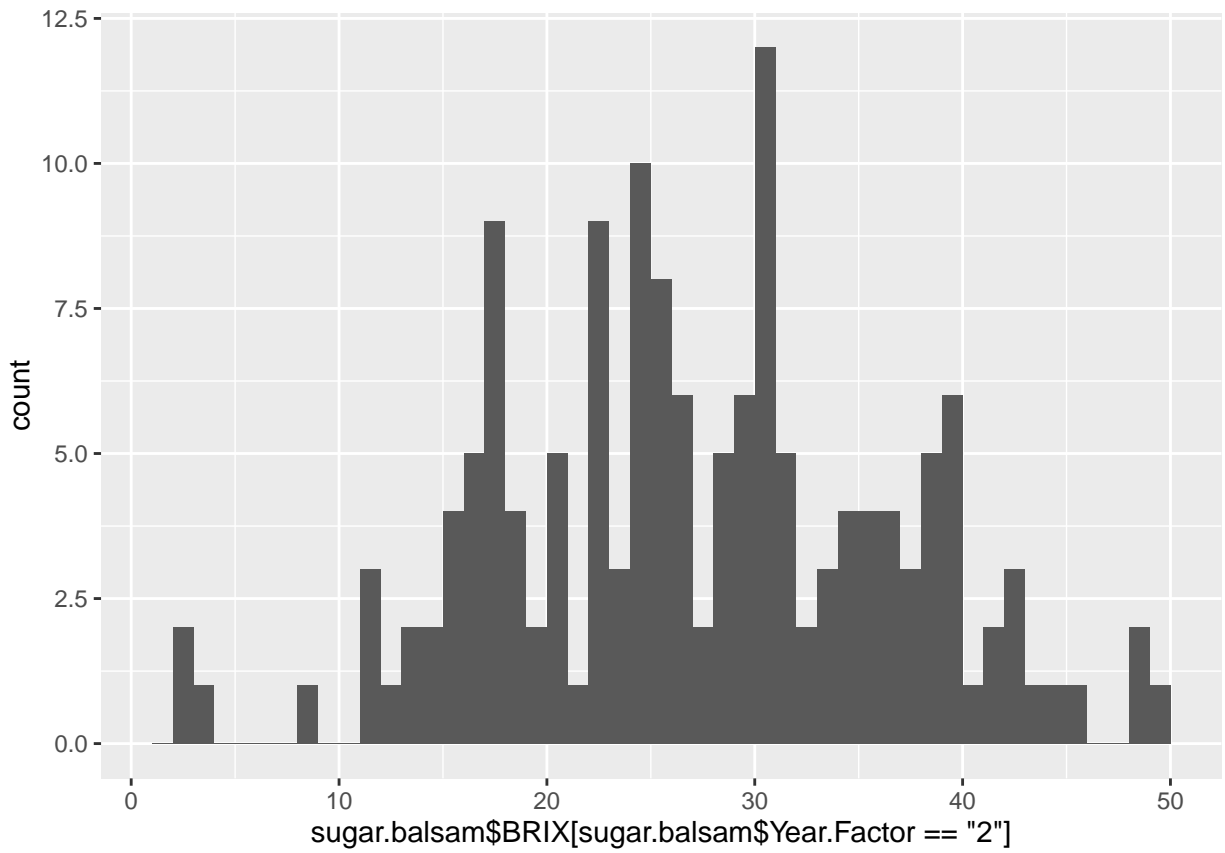
```
qplot(sugar.balsam$BRIX, binwidth = 1)
```

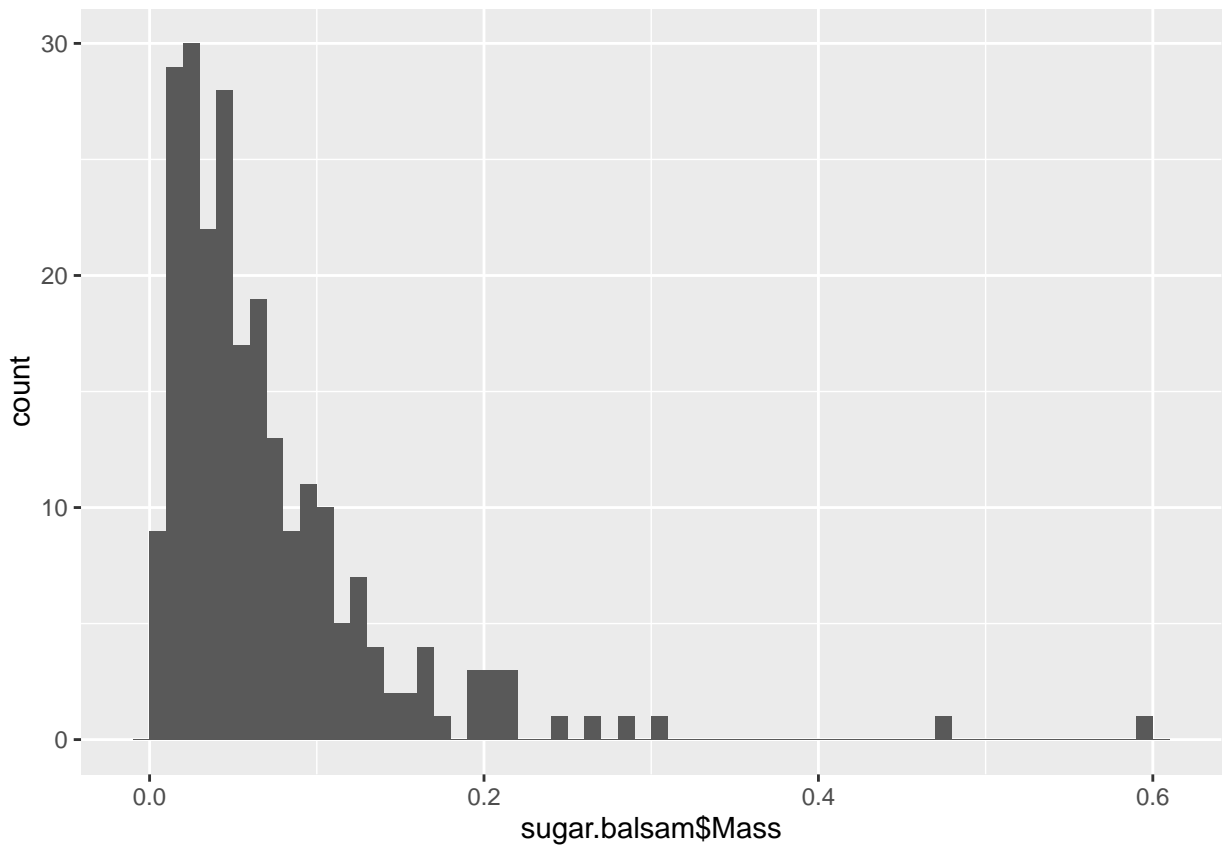
```
qplot(sugar.balsam$BRIX[sugar.balsam$Year.Factor == "1"], binwidth = 1)
```



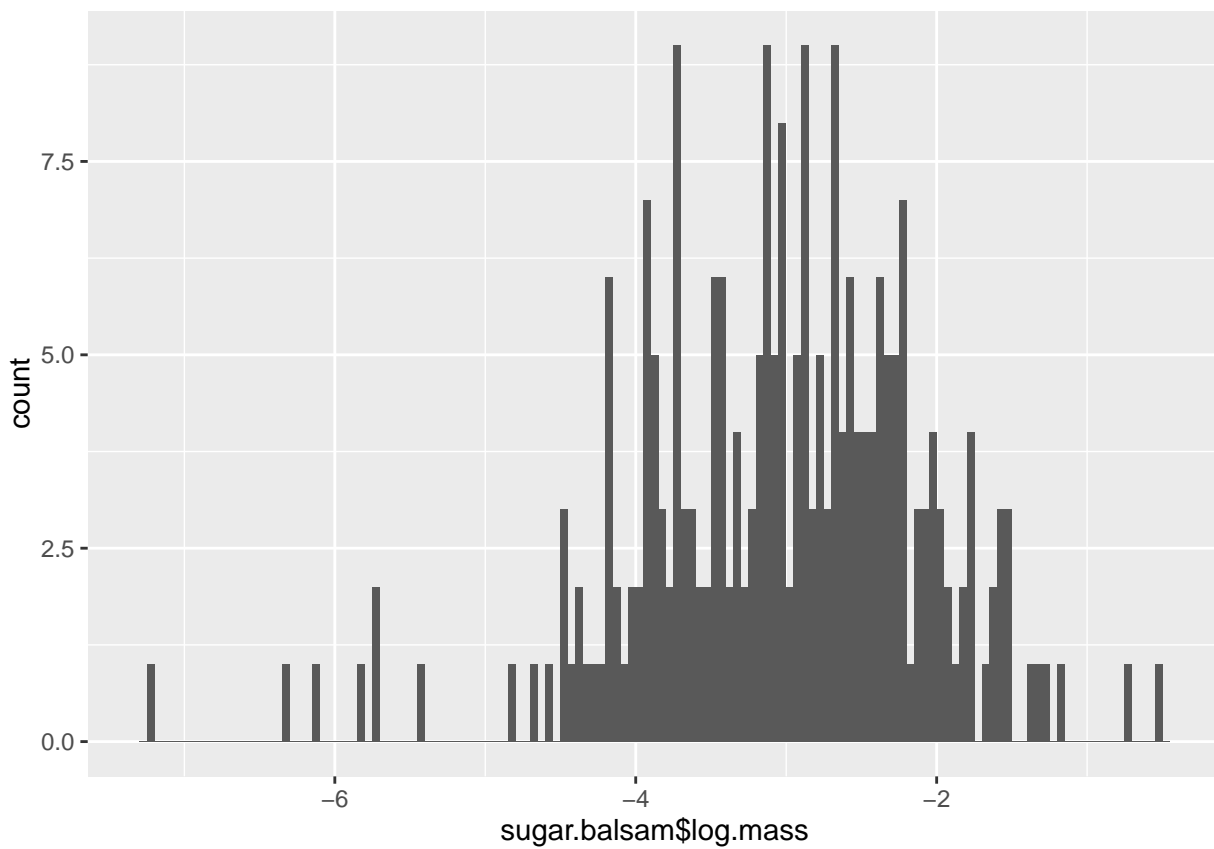
```
qplot(sugar.balsam$BRIX[sugar.balsam$Year.Factor == "2"], binwidth = 1)
```



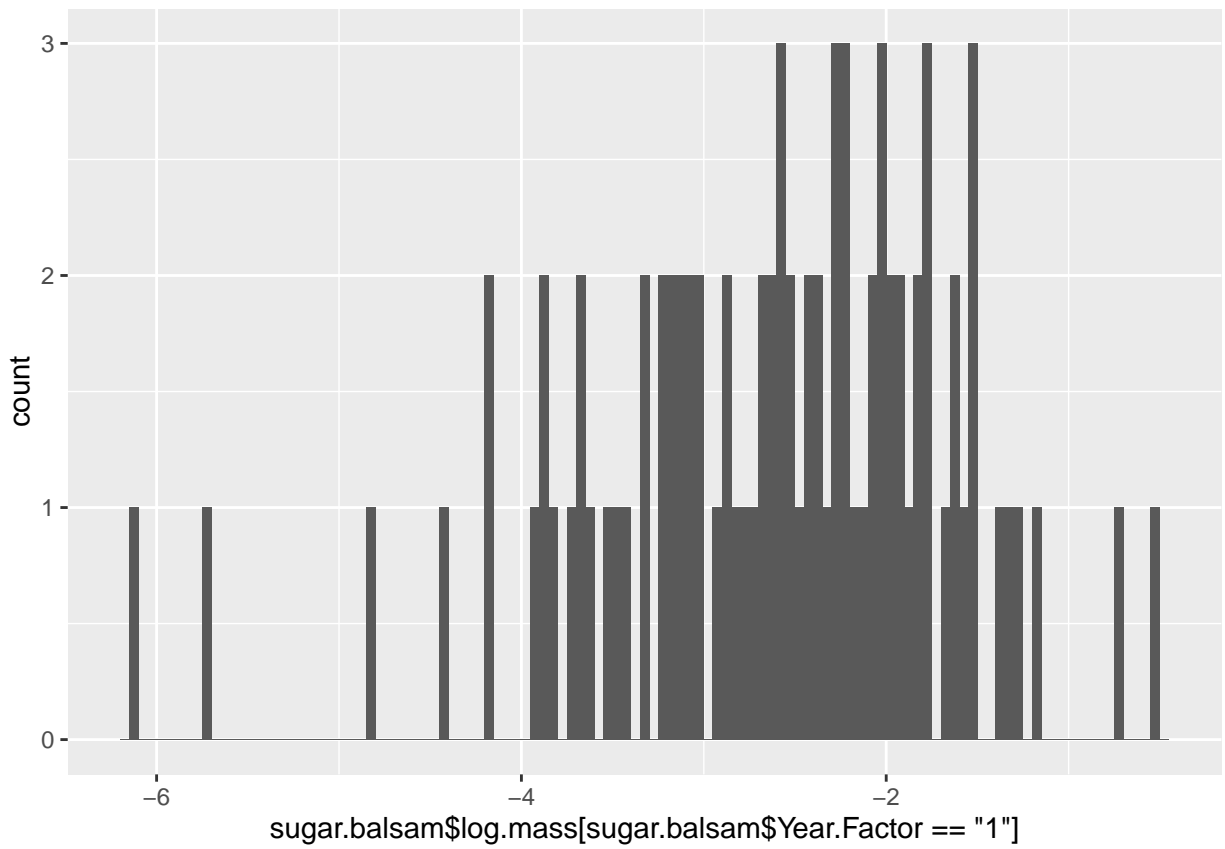
```
qplot(sugar.balsam$Mass, binwidth = 0.01)
```



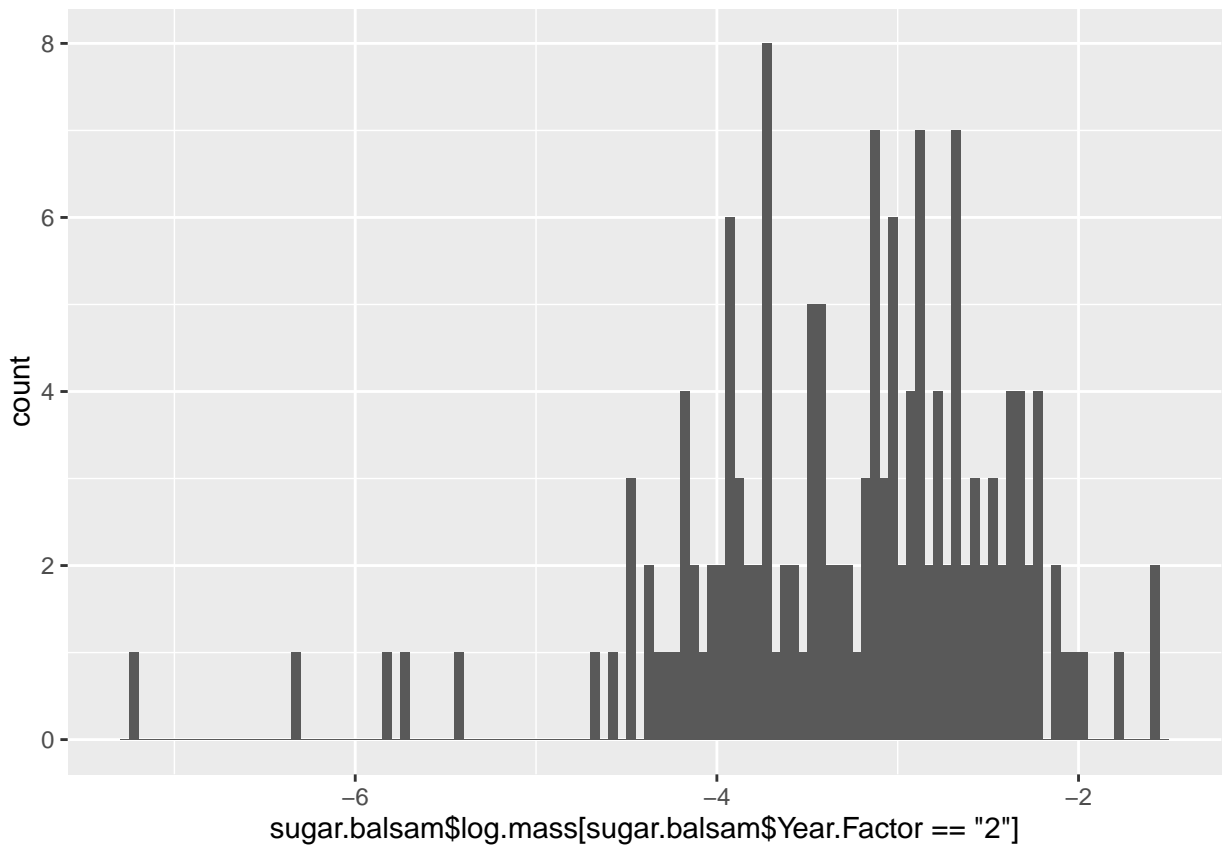
```
qplot(sugar.balsam$log.mass, binwidth = .05)
```



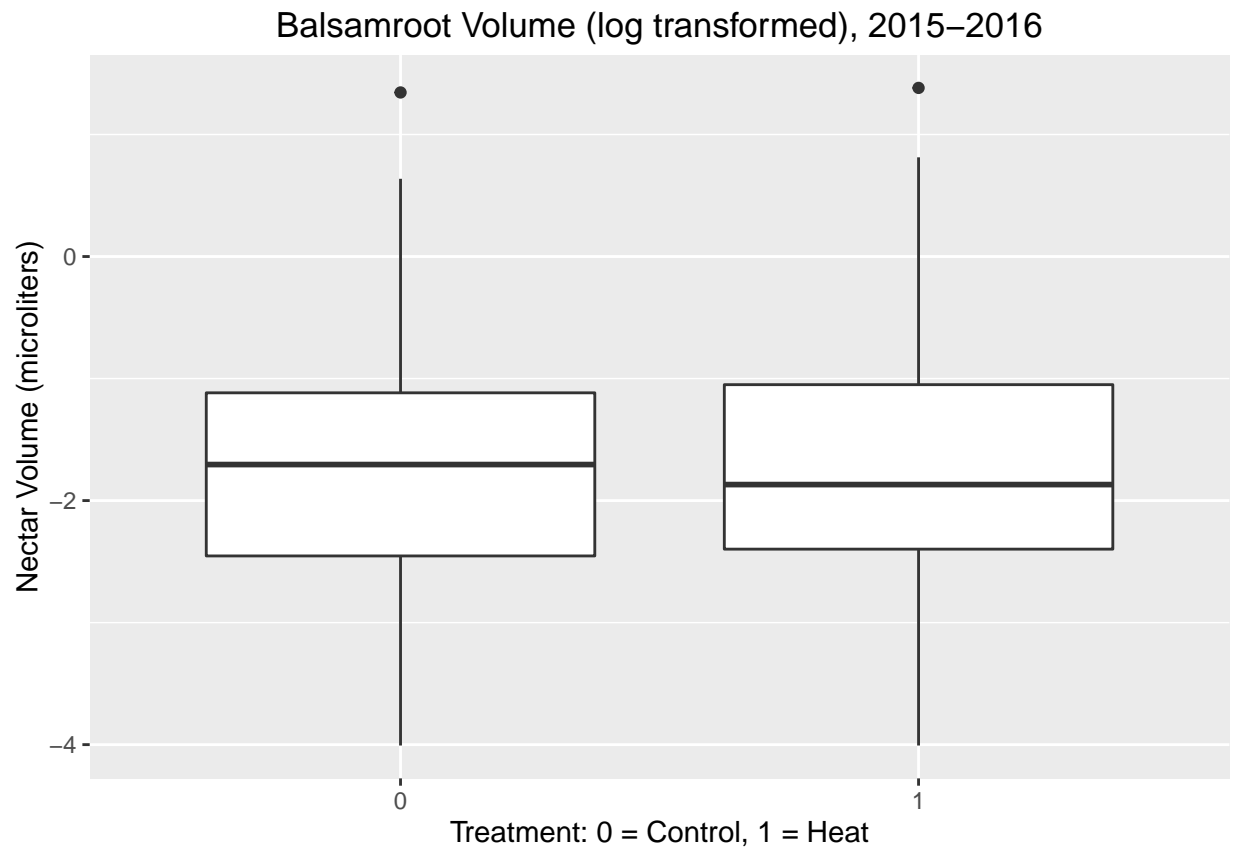
```
qplot(sugar.balsam$log.mass[sugar.balsam$Year.Factor == "1"], binwidth = .05)
```



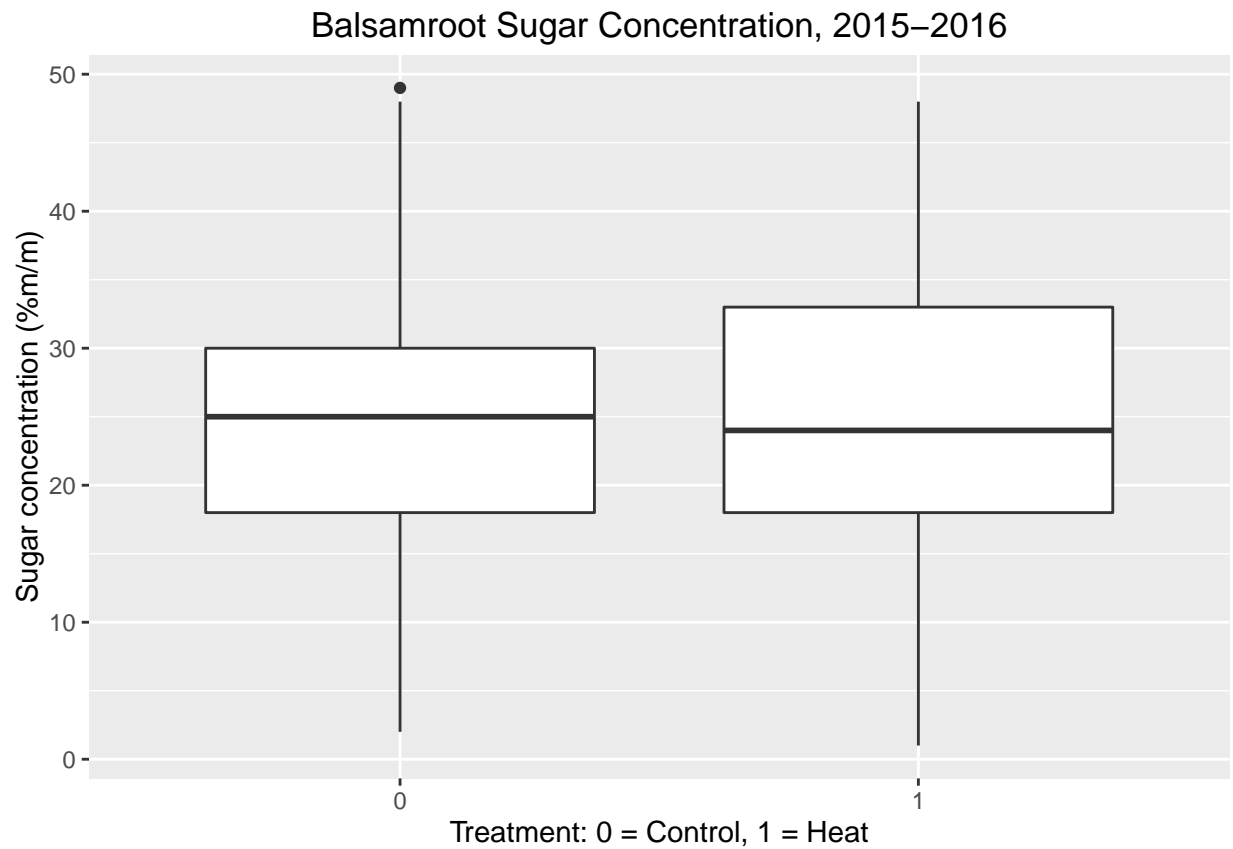
```
qplot(sugar.balsam$log.mass[sugar.balsam$Year.Factor == "2"], binwidth = .05)
```



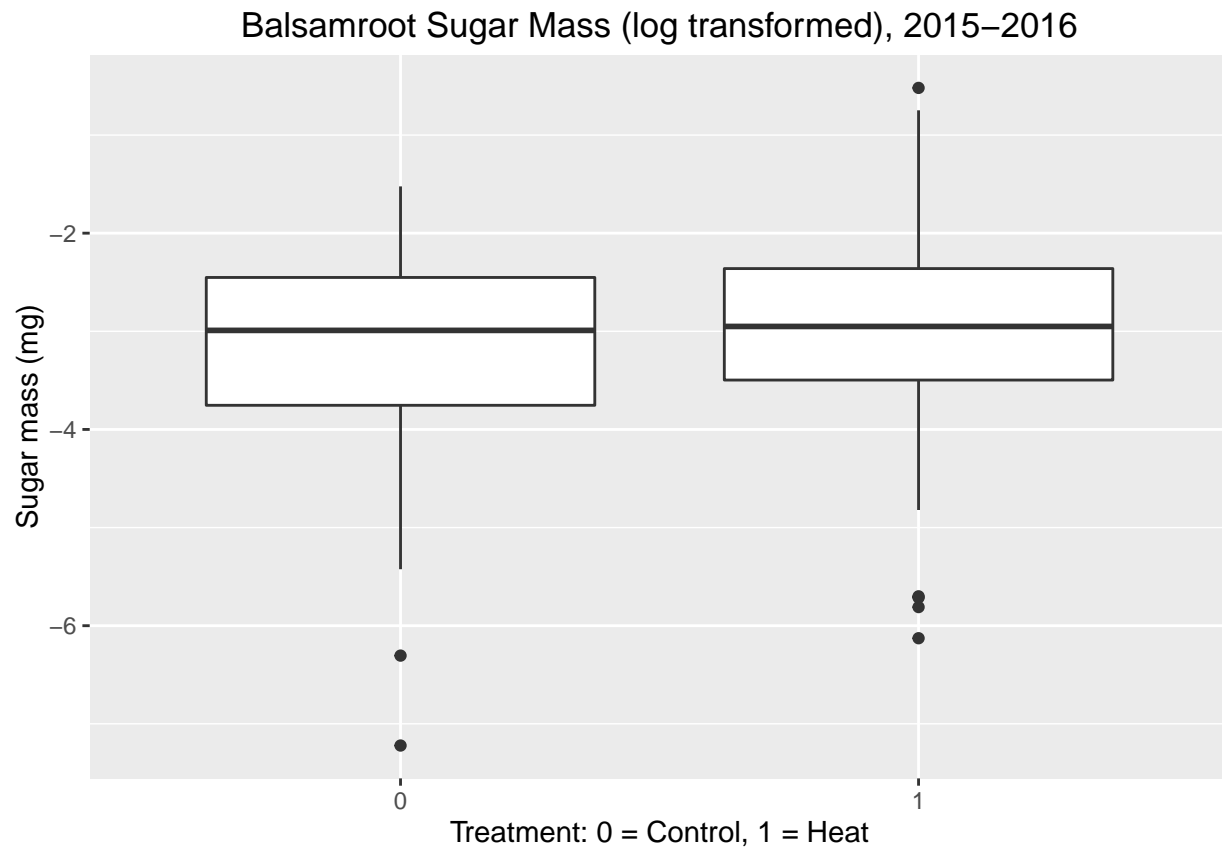
```
ggplot(volume.balsam, aes(x=Heat, y=log.vol)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Nectar Volume (microliters)") + ggtitle("Balsamroot Volume (log transformed), 2015-2016")
```



```
ggplot(sugar.balsam, aes(x=Heat, y=BR1X)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Sugar concentration (%m/m)") + ggtitle("Balsamroot Sugar Concentration, 2015-2016")
```

```
ggplot(sugar.balsam, aes(x=Heat, y=log.mass)) + geom_boxplot() +  
  xlab("Treatment: 0 = Control, 1 = Heat") +  
  ylab("Sugar mass (mg)") + ggtitle("Balsamroot Sugar Mass (log transformed), 2015-2016")
```



```
#Normality tests
```

```
# Test normality for volume by treatment, 2015-2016
```

```
shapiro.test(as.matrix(volume.balsam[volume.balsam[,5] == "0", 8])) #control
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: as.matrix(volume.balsam[volume.balsam[, 5] == "0", 8])
```

```
## W = 0.98849, p-value = 0.4343
```

```
shapiro.test(as.matrix(volume.balsam[volume.balsam[,5] == "1", 8])) #heat treatment
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: as.matrix(volume.balsam[volume.balsam[, 5] == "1", 8])
```

```
## W = 0.9773, p-value = 0.01709
```

```
# Test normality for sugar concentration by treatment, 2015-2016
```

```
shapiro.test(as.matrix(sugar.balsam[sugar.balsam[,5] == "0", 7])) #control
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: as.matrix(sugar.balsam[sugar.balsam[, 5] == "0", 7])
## W = 0.98782, p-value = 0.4381
```

```
shapiro.test(as.matrix(sugar.balsam[sugar.balsam[,5] == "1", 7])) #heat treatment
```

```
##
## Shapiro-Wilk normality test
##
## data: as.matrix(sugar.balsam[sugar.balsam[, 5] == "1", 7])
## W = 0.9859, p-value = 0.2049
```

```
# Test normality for sugar mass by treatment, 2015-2016
shapiro.test(as.matrix(sugar.balsam[sugar.balsam[,5] == "0", 9])) #control
```

```
##
## Shapiro-Wilk normality test
##
## data: as.matrix(sugar.balsam[sugar.balsam[, 5] == "0", 9])
## W = 0.9391, p-value = 9.147e-05
```

```
shapiro.test(as.matrix(sugar.balsam[sugar.balsam[,5] == "1", 9])) #heat treatment
```

```
##
## Shapiro-Wilk normality test
##
## data: as.matrix(sugar.balsam[sugar.balsam[, 5] == "1", 9])
## W = 0.9724, p-value = 0.009781
```

```
#Homoscedasticity tests
```

```
#Levene test for Homogeneity of variances
leveneTest(volume.balsam[,8],volume.balsam[,5]) #Volume
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1  1.3198 0.2517
##      258
```

```
leveneTest(sugar.balsam[,7],sugar.balsam[,5]) #Concentration
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1  0.3848 0.5356
##      235
```

```
leveneTest(sugar.balsam[,9],sugar.balsam[,5]) #Mass
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1  0.0923 0.7616
##      235
```

```
#Fligner test for homogeneity of variances  
fligner.test(volume.balsam[,8],volume.balsam[,5]) #Volume
```

```
##  
## Fligner-Killeen test of homogeneity of variances  
##  
## data: volume.balsam[, 8] and volume.balsam[, 5]  
## Fligner-Killeen:med chi-squared = 0.738, df = 1, p-value = 0.3903
```

```
fligner.test(sugar.balsam[,7],sugar.balsam[,5]) #Concentration
```

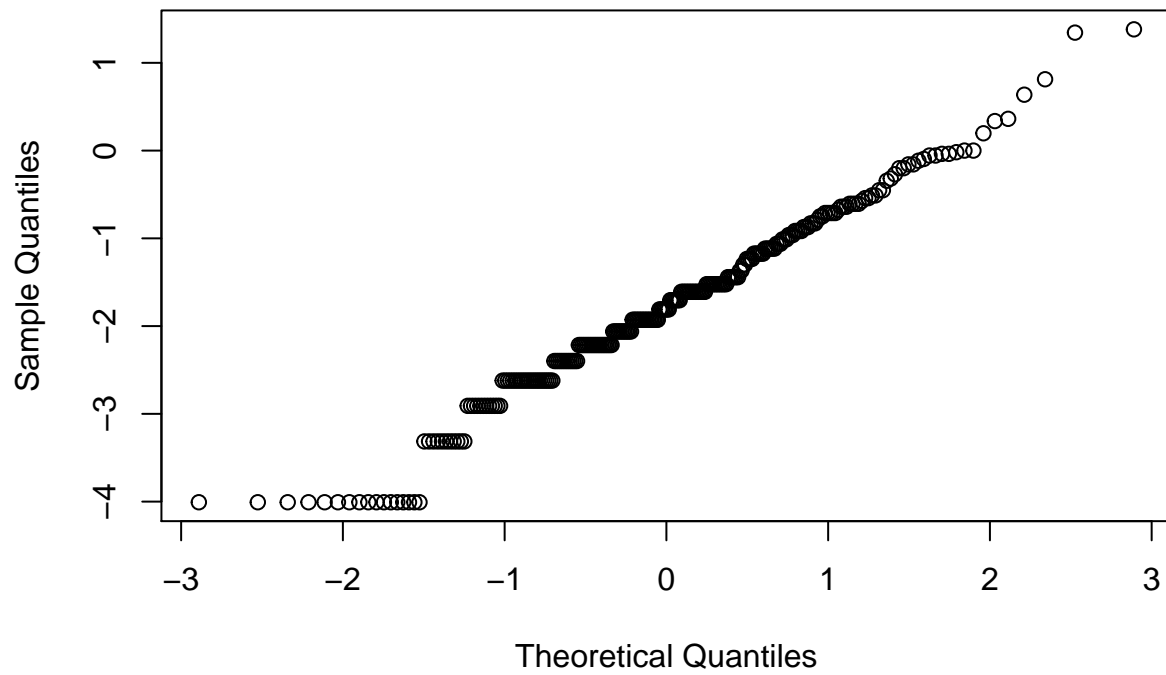
```
##  
## Fligner-Killeen test of homogeneity of variances  
##  
## data: sugar.balsam[, 7] and sugar.balsam[, 5]  
## Fligner-Killeen:med chi-squared = 0.27962, df = 1, p-value =  
## 0.5969
```

```
fligner.test(sugar.balsam[,9],sugar.balsam[,5]) #Mass
```

```
##  
## Fligner-Killeen test of homogeneity of variances  
##  
## data: sugar.balsam[, 9] and sugar.balsam[, 5]  
## Fligner-Killeen:med chi-squared = 0.23879, df = 1, p-value =  
## 0.6251
```

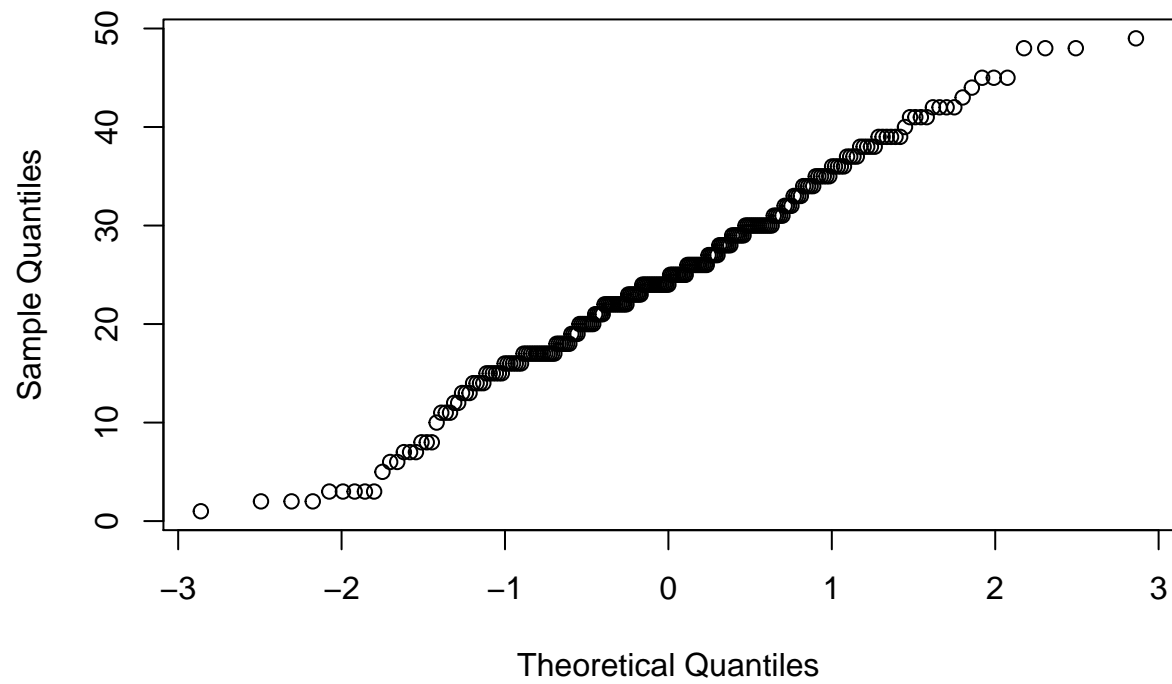
```
qqnorm(volume.balsam$log.vol)
```

Normal Q-Q Plot



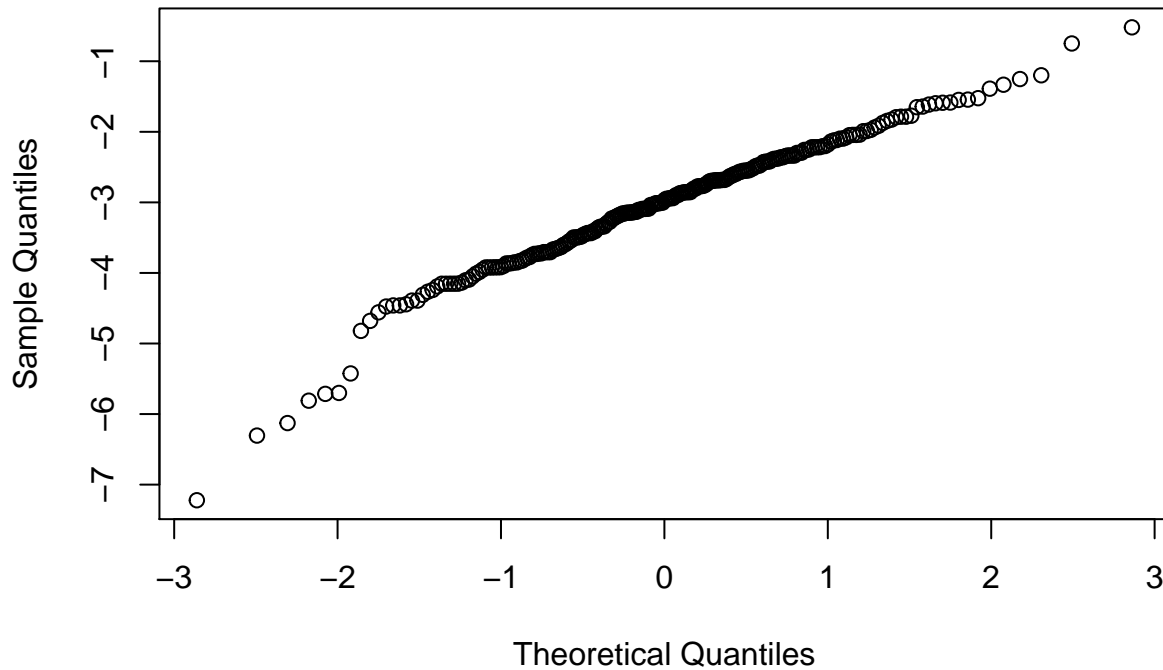
```
qqnorm(sugar.balsam$BRIX)
```

Normal Q-Q Plot



```
qqnorm(sugar.balsam$log.mass)
```

Normal Q-Q Plot



```
#####
### 2016 only data ###
#####

#Data summaries

volume.balsam2016 <- as.data.frame(volume.balsam[volume.balsam$Year.Factor == "2",])
summary(volume.balsam2016)
```

```
##      Date      Date.Factor Year.Factor      Plot      Heat      Plant
## 6/8/2016 :60    12      :60    1: 0      CC6      :19    0:85    EC3-3 : 8
## 6/7/2016 :45    11      :45    2:168    CHSR8     :19    1:83    WHSR9-2: 8
## 6/6/2016 :34    10      :34          CH5       :18          CC6-10 : 7
## 6/5/2016 :19     9       :19          EHSR1      :16          CH5-2 : 6
## 6/16/2016:10    13      :10          CSR7       :15          EC3-1 : 6
## 6/10/2015: 0     1       : 0          EH4        :15          EHSR1-1: 6
## (0ther) : 0     (0ther): 0          (Other):66          (Other):127
##      Volume      log.vol
## Min.   :0.01818   Min.   :-4.0073
## 1st Qu.:0.07273   1st Qu.: -2.6210
## Median :0.12727   Median : -2.0614
## Mean   :0.15942   Mean    : -2.1350
## 3rd Qu.:0.20000   3rd Qu.: -1.6094
## Max.   :0.85455   Max.    : -0.1572
##
```

```
summarize(group_by(volume.balsam2016, Heat), meanVol = mean(Volume), sdVolume = sd(Volume))
```

```
## Source: local data frame [2 x 3]
##
##      Heat  meanVol  sdVolume
##   (fctr)    (dbl)    (dbl)
## 1      0 0.1659893 0.1328342
## 2      1 0.1526835 0.1127952
```

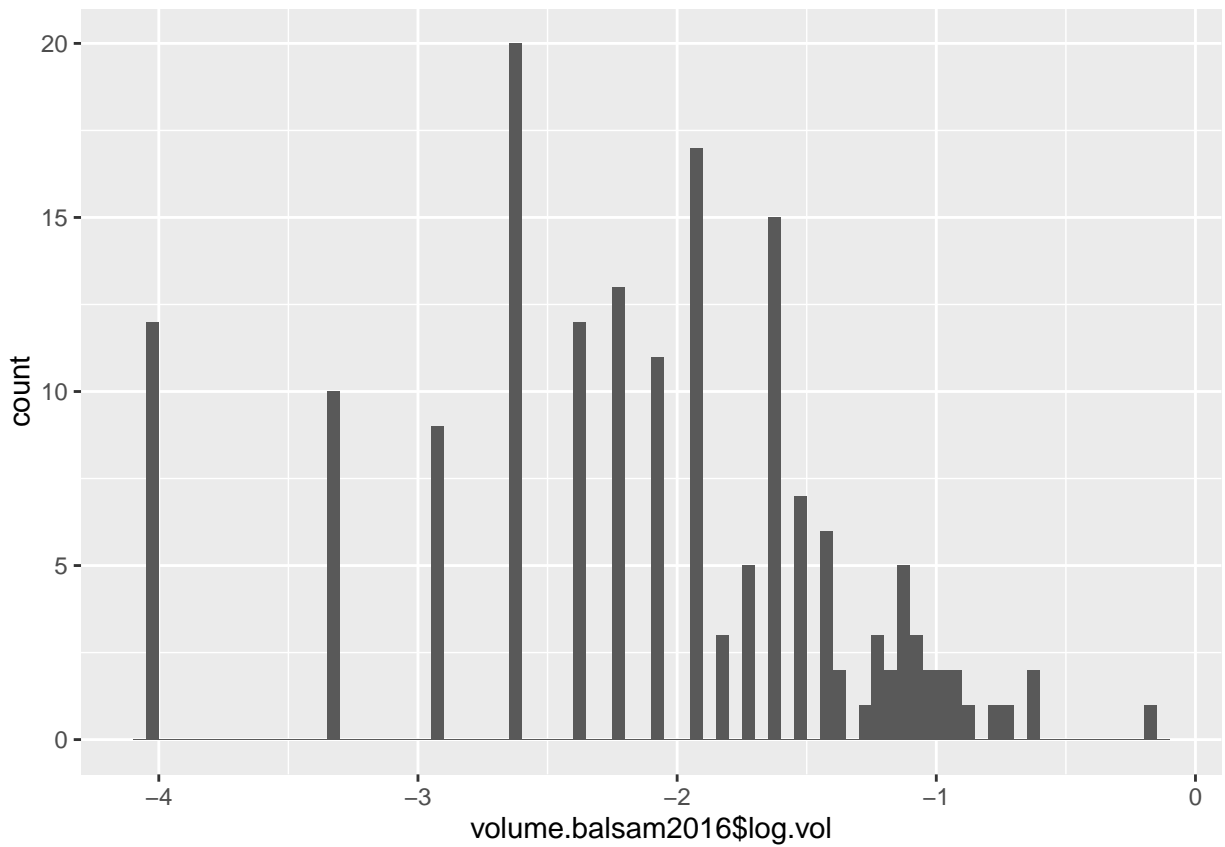
```
sugar.balsam2016 <- as.data.frame((sugar.balsam[sugar.balsam$Year.Factor == "2",]))
summary(sugar.balsam2016)
```

```
##      Date      Date.Factor Year.Factor      Plot      Heat      Plant
## 6/8/2016 :56      12      :56      1: 0      CC6      :19      0:80      CC6-10 : 7
## 6/7/2016 :41      11      :41      2:151     CH5      :16      1:71      EC3-3  : 7
## 6/6/2016 :31      10      :31              EH4      :15              WHSR9-2: 7
## 6/5/2016 :17      9       :17              EHSR1     :15              EC3-1  : 6
## 6/16/2016: 6      13      : 6              WC11      :14              EHSR1-1: 6
## 6/10/2015: 0      1       : 0              CHSR8     :13              WC11-3 : 6
## (Other)  : 0      (Other): 0              (Other):59              (Other):112
##      BRIX      Mass      log.mass
## Min.   : 2.00      Min.   :0.0007309      Min.   : -7.221
## 1st Qu.:20.00      1st Qu.:0.0228482      1st Qu.: -3.779
## Median :26.00      Median :0.0430309      Median : -3.146
## Mean   :26.67      Mean   :0.0505809      Mean   : -3.275
## 3rd Qu.:33.50      3rd Qu.:0.0680964      3rd Qu.: -2.687
## Max.   :49.00      Max.   :0.2049200      Max.   : -1.585
##
```

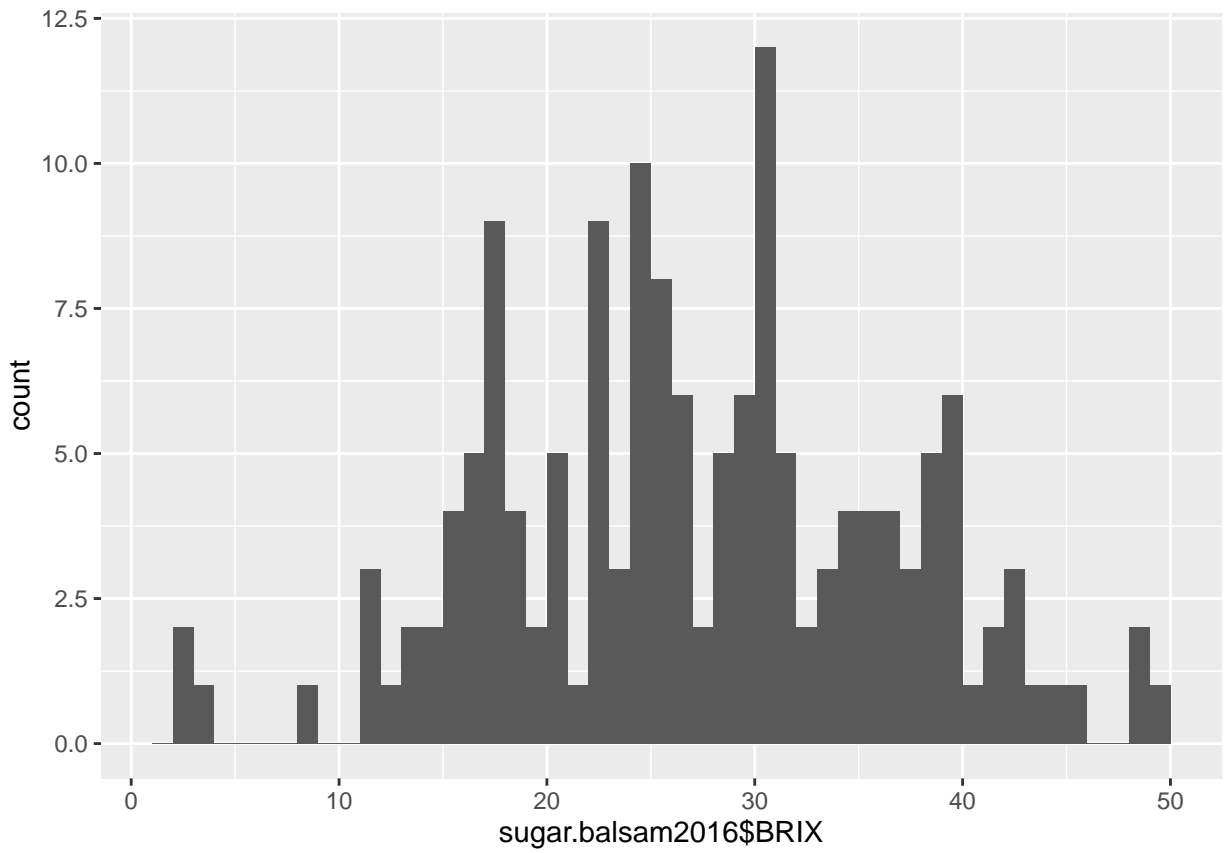
```
summarize(group_by(sugar.balsam2016, Heat), meanBRIX = mean(BRIX), meanMass = mean(Mass), sdBRIX = sd(B
```

```
## Source: local data frame [2 x 5]
##
##      Heat meanBRIX  meanMass  sdBRIX  sdMass
##   (fctr)    (dbl)    (dbl)    (dbl)    (dbl)
## 1      0 25.41250 0.04865045 9.550258 0.03840909
## 2      1 28.08451 0.05275608 9.277848 0.03508288
```

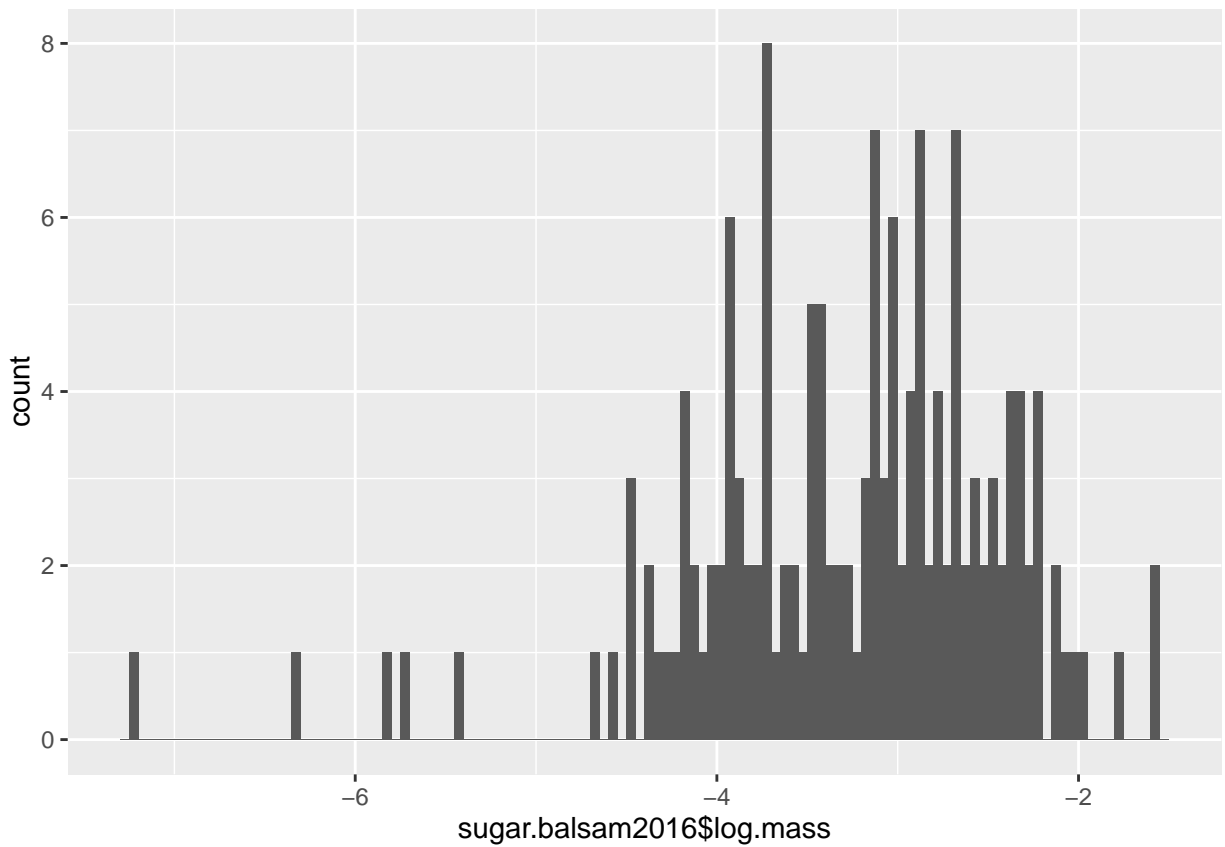
```
qplot(volume.balsam2016$log.vol, binwidth = .05)
```

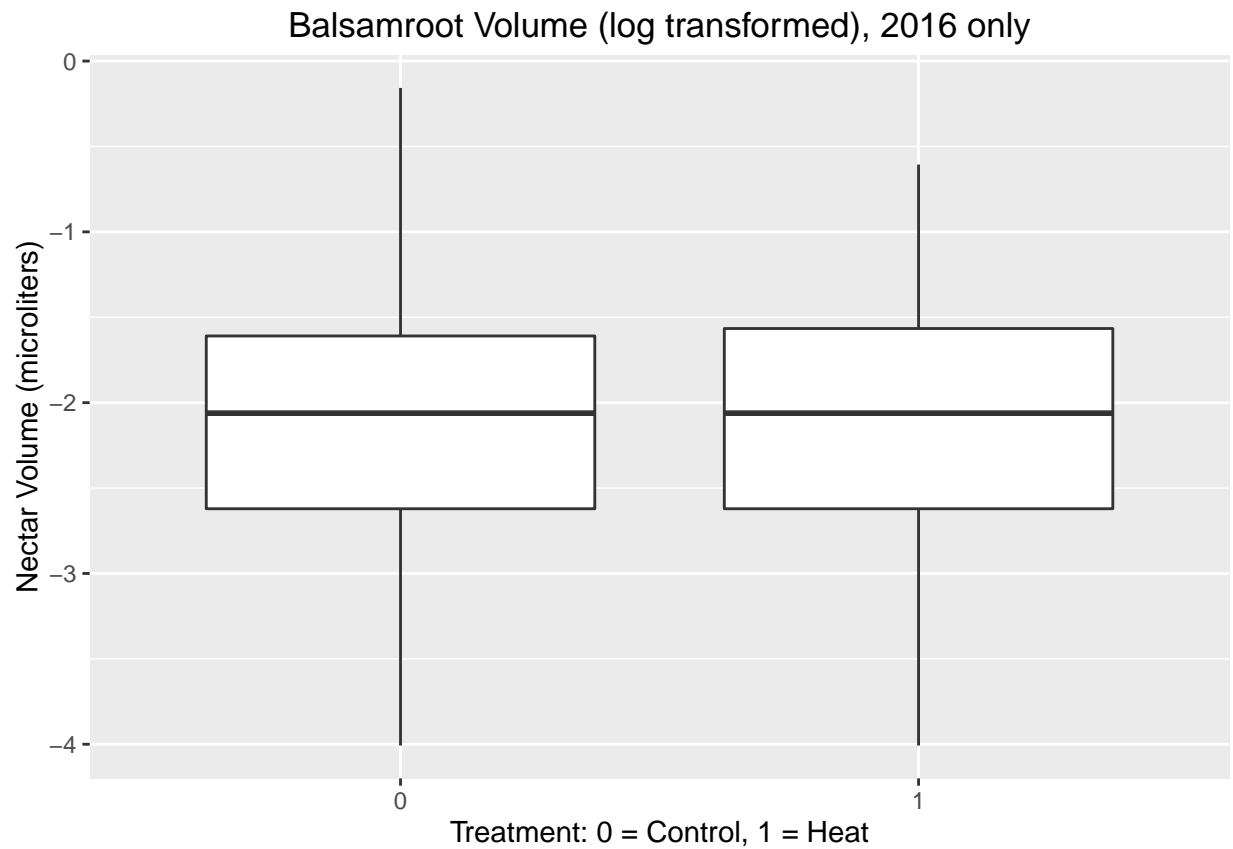
```
qplot(sugar.balsam2016$BRIX, binwidth = 1)
```



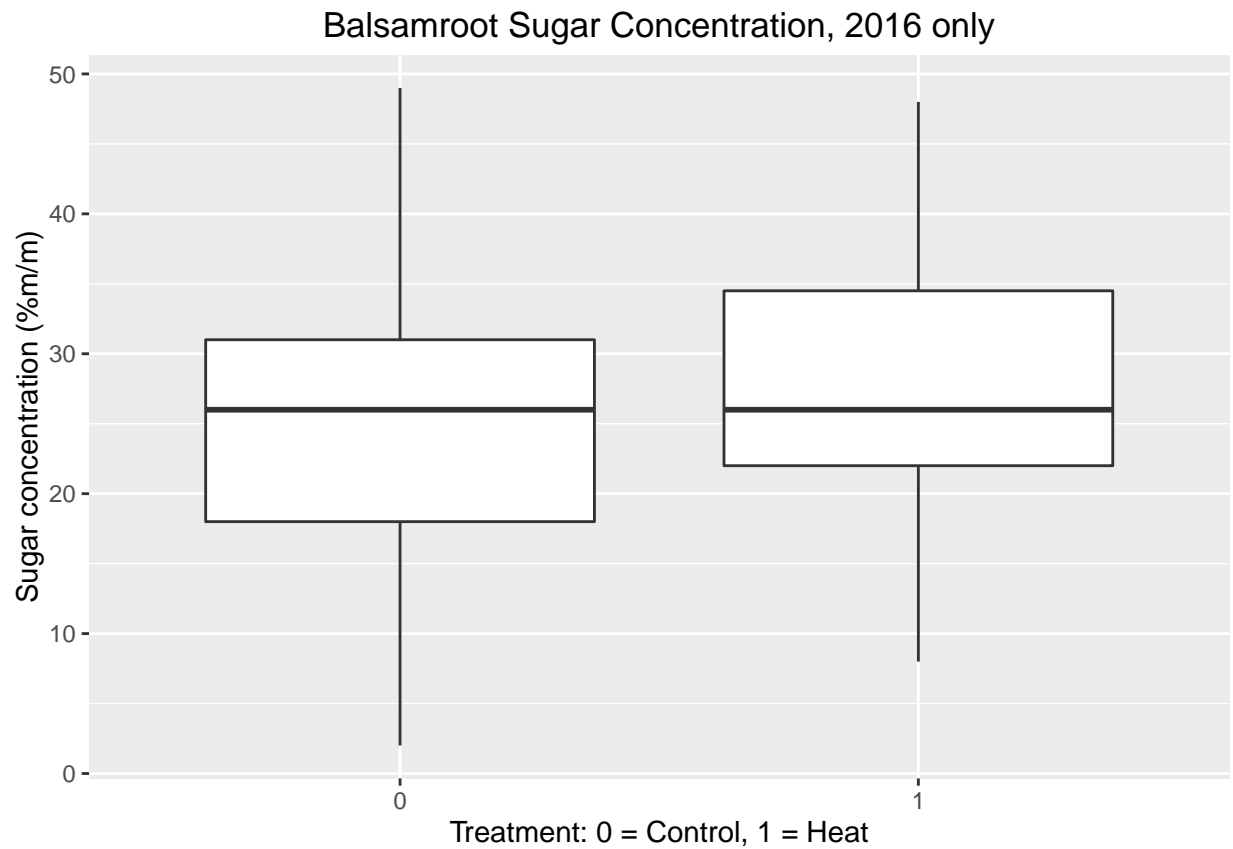
```
qplot(sugar.balsam2016$log.mass, binwidth = .05)
```



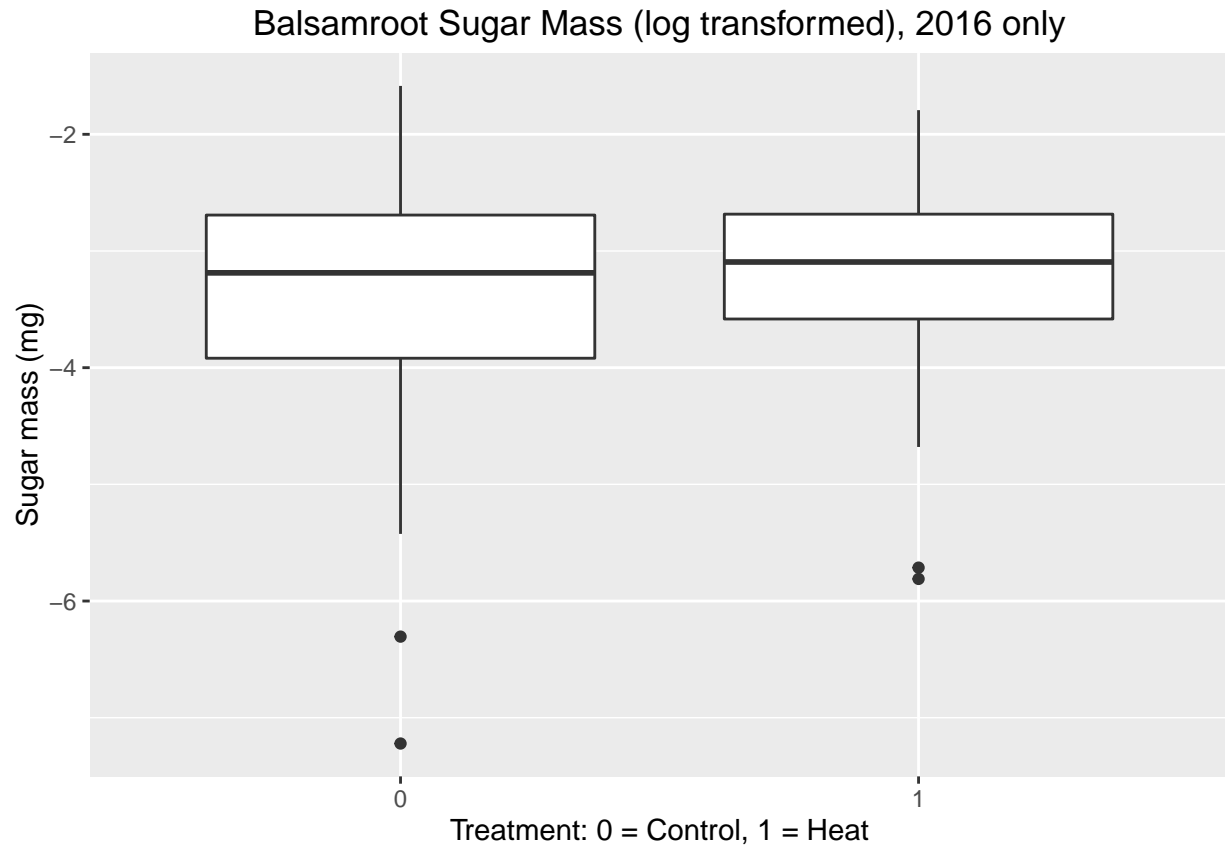
```
ggplot(volume.balsam2016, aes(x=Heat, y=log.vol)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Nectar Volume (microliters)") + ggtitle("Balsamroot Volume (log transformed), 2016 only")
```



```
ggplot(sugar.balsam2016, aes(x=Heat, y=BRIX)) + geom_boxplot() +  
  xlab("Treatment: 0 = Control, 1 = Heat") +  
  ylab("Sugar concentration (%m/m)") + ggtitle("Balsamroot Sugar Concentration, 2016 only")
```



```
ggplot(sugar.balsam2016, aes(x=Heat, y=log.mass)) + geom_boxplot() +  
  xlab("Treatment: 0 = Control, 1 = Heat") +  
  ylab("Sugar mass (mg)") + ggtitle("Balsamroot Sugar Mass (log transformed), 2016 only")
```



```
#Normality tests
```

```
# Test normality for volume by treatment, 2016 only
```

```
shapiro.test(as.matrix(volume.balsam2016[volume.balsam2016[,5] == "0", 8])) #control
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: as.matrix(volume.balsam2016[volume.balsam2016[, 5] == "0", 8])
```

```
## W = 0.98005, p-value = 0.2117
```

```
shapiro.test(as.matrix(volume.balsam2016[volume.balsam2016[,5] == "1", 8])) #heat treatment
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: as.matrix(volume.balsam2016[volume.balsam2016[, 5] == "1", 8])
```

```
## W = 0.93421, p-value = 0.000367
```

```
# Test normality for sugar concentration by treatment, 2016 only
```

```
shapiro.test(as.matrix(sugar.balsam2016[sugar.balsam2016[,5] == "0", 7])) #control
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
## data: as.matrix(sugar.balsam2016[sugar.balsam2016[, 5] == "0", 7])
## W = 0.98475, p-value = 0.4602

shapiro.test(as.matrix(sugar.balsam2016[sugar.balsam2016[,5] == "1", 7])) #heat treatment

##
## Shapiro-Wilk normality test
##
## data: as.matrix(sugar.balsam2016[sugar.balsam2016[, 5] == "1", 7])
## W = 0.97857, p-value = 0.265

# Test normality for sugar mass by treatment, 2016
shapiro.test(as.matrix(sugar.balsam2016[sugar.balsam2016[,5] == "0", 9])) #control

##
## Shapiro-Wilk normality test
##
## data: as.matrix(sugar.balsam2016[sugar.balsam2016[, 5] == "0", 9])
## W = 0.91748, p-value = 7.243e-05

shapiro.test(as.matrix(sugar.balsam2016[sugar.balsam2016[,5] == "1", 9])) #heat treatment

##
## Shapiro-Wilk normality test
##
## data: as.matrix(sugar.balsam2016[sugar.balsam2016[, 5] == "1", 9])
## W = 0.94605, p-value = 0.004178

#Homoscedasticity tests

#Levene test for Homogeneity of variances
leveneTest(volume.balsam2016[,8],volume.balsam2016[,5]) #Volume

## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1  0.6048 0.4379
##      166

leveneTest(sugar.balsam2016[,7],sugar.balsam2016[,5]) #Concentration

## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1  0.0203 0.887
##      149

leveneTest(sugar.balsam2016[,9],sugar.balsam2016[,5]) #Mass

## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1  1.7758 0.1847
##      149
```

```
#Fligner test for homogeneity of variances  
fligner.test(volume.balsam2016[,8],volume.balsam2016[,5]) #Volume
```

```
##  
## Fligner-Killeen test of homogeneity of variances  
##  
## data: volume.balsam2016[, 8] and volume.balsam2016[, 5]  
## Fligner-Killeen:med chi-squared = 0.36589, df = 1, p-value =  
## 0.5453
```

```
fligner.test(sugar.balsam2016[,7],sugar.balsam2016[,5]) #Concentration
```

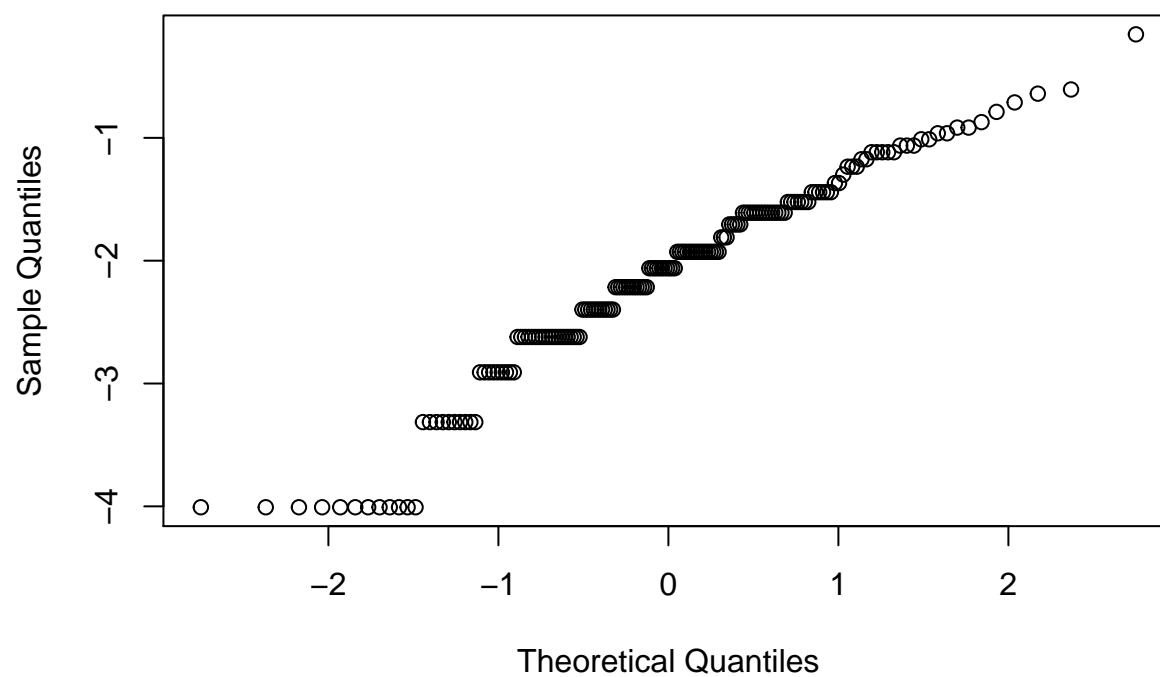
```
##  
## Fligner-Killeen test of homogeneity of variances  
##  
## data: sugar.balsam2016[, 7] and sugar.balsam2016[, 5]  
## Fligner-Killeen:med chi-squared = 0.0021787, df = 1, p-value =  
## 0.9628
```

```
fligner.test(sugar.balsam2016[,9],sugar.balsam2016[,5]) #Mass
```

```
##  
## Fligner-Killeen test of homogeneity of variances  
##  
## data: sugar.balsam2016[, 9] and sugar.balsam2016[, 5]  
## Fligner-Killeen:med chi-squared = 2.0309, df = 1, p-value = 0.1541
```

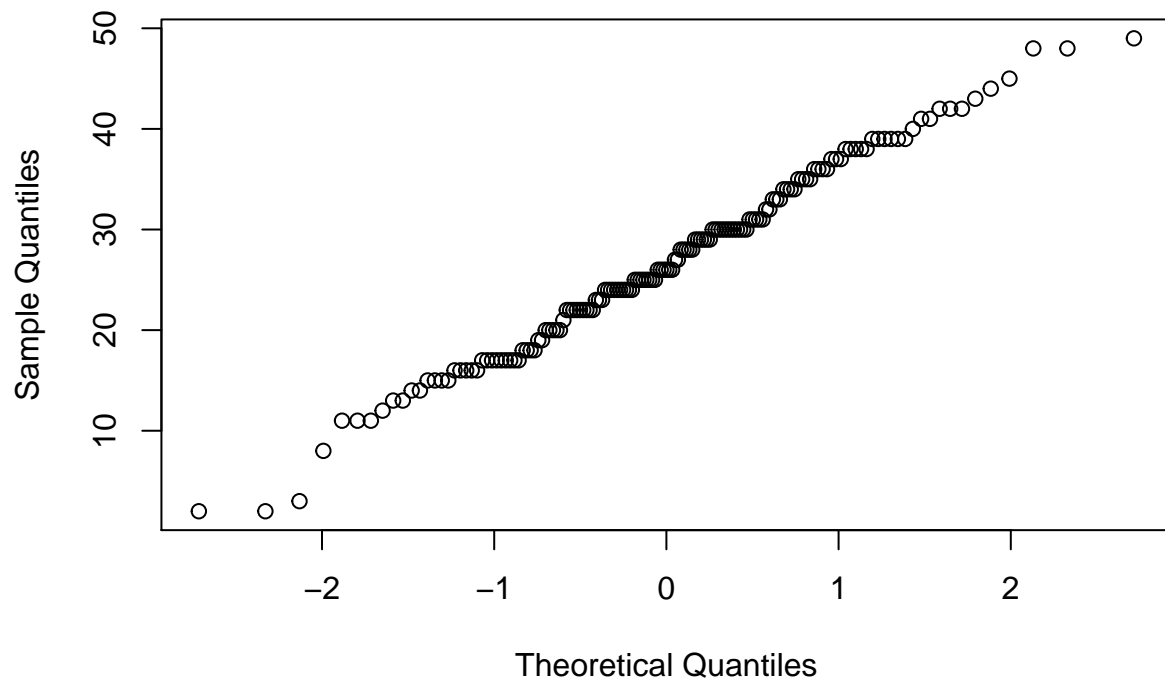
```
qqnorm(volume.balsam2016$log.vol)
```


Normal Q-Q Plot



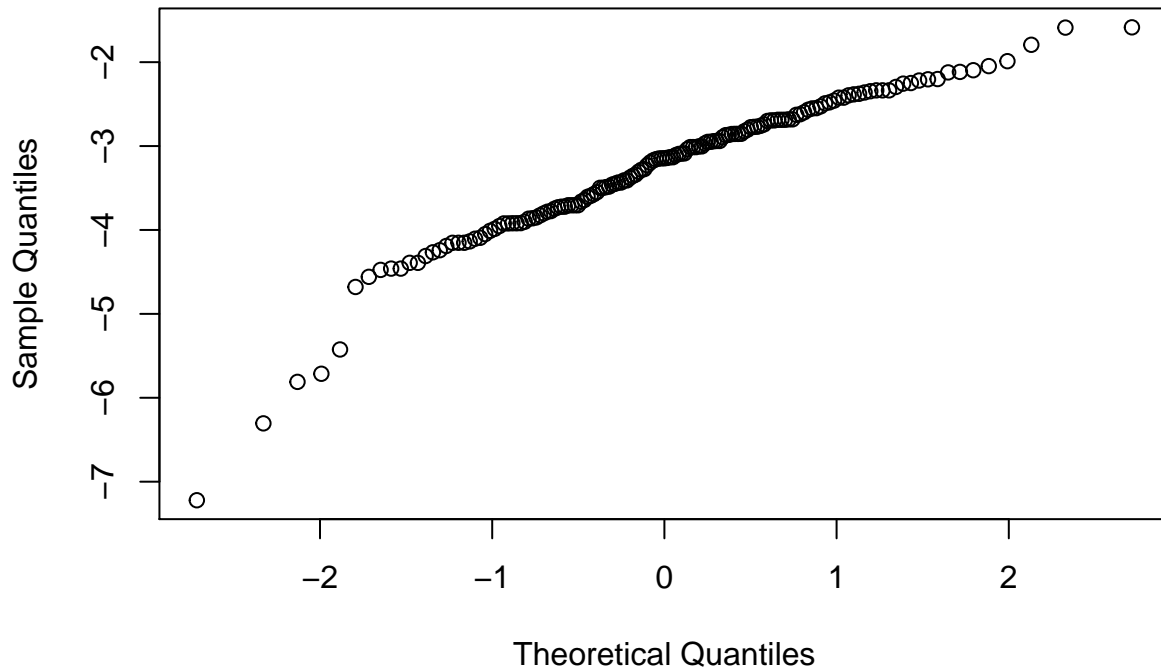
```
qqnorm(sugar.balsam2016$BRIX)
```

Normal Q-Q Plot



```
qqnorm(sugar.balsam2016$log.mass)
```

Normal Q-Q Plot



```
#####
### 2015 only data ###
#####

#Data summaries

volume.balsam2015 <- as.data.frame(volume.balsam[volume.balsam$Year.Factor == "1",])
summary(volume.balsam2015)
```

```
##      Date      Date.Factor Year.Factor      Plot      Heat      Plant
## 6/8/2015 :21      4      :21      1:92      CHSR8 :19      0:31      CC6-9 :10
## 6/11/2015:20      6      :20      2: 0      CH5   :16      1:61      CHSR8-4: 9
## 6/3/2015 :17      2      :17              CC6    :12              CH5-6  : 7
## 6/6/2015 :12      3      :12              EH4    :11              CHSR8-6: 6
## 6/10/2015:10      5      :10              WHSR9   : 9              EHSR1-2: 6
## 6/2/2015 : 6      1      : 6              EHSR1   : 6              CH5-7  : 4
## (0ther)  : 6      (0ther): 6              (Other):19              (Other):50
##      Volume      log.vol
## Min.      :0.01818  Min.      :-4.0073
## 1st Qu.:0.16364    1st Qu.: -1.8101
## Median :0.40909    Median : -0.8941
## Mean      :0.54012    Mean      :-1.1703
## 3rd Qu.:0.63636    3rd Qu.: -0.4520
## Max.      :3.98182    Max.      : 1.3817
##
```

```
summarize(group_by(volume.balsam2015, Heat), meanVol = mean(Volume), sdVolume = sd(Volume))
```

```
## Source: local data frame [2 x 3]
##
##      Heat  meanVol  sdVolume
##   (fctr)    (dbl)    (dbl)
## 1      0 0.6404692 0.7110573
## 2      1 0.4891207 0.6147382
```

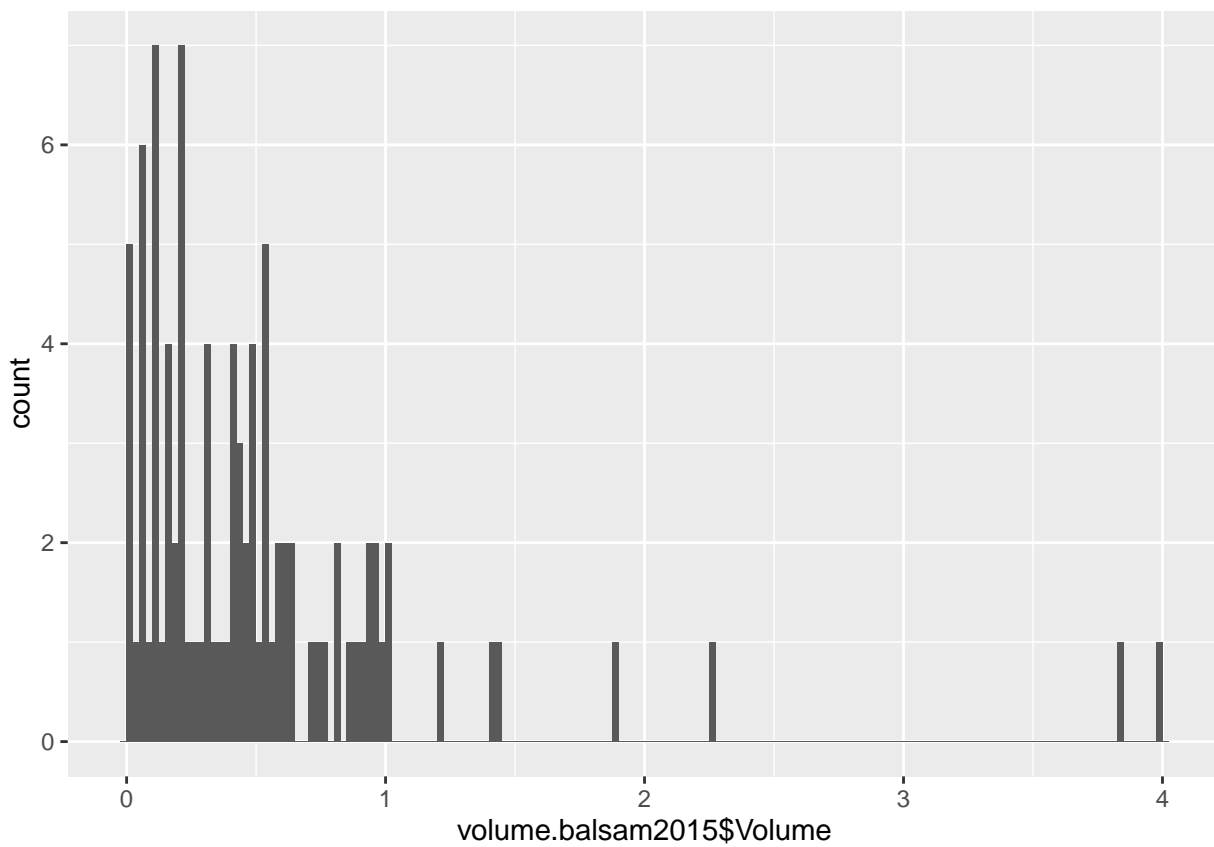
```
sugar.balsam2015 <- as.data.frame((sugar.balsam[sugar.balsam$Year.Factor == "1",]))
summary(sugar.balsam2015)
```

```
##      Date      Date.Factor Year.Factor      Plot      Heat      Plant
## 6/11/2015:18  4          :18  1:86      CHSR8  :18  0:28  CH5-6   : 6
## 6/8/2015 :18  6          :18  2: 0      CH5    :15  1:58  CH5-2   : 4
## 6/3/2015 :17  2          :17          CC6     :12          CHSR8-5: 4
## 6/6/2015 :12  3          :12          EH4     :11          CHSR8-9: 4
## 6/10/2015: 9  5          : 9          WHSR9    : 8          CC6-1   : 3
## 6/2/2015 : 6  1          : 6          EHSR1    : 6          CC6-7   : 3
## (Other) : 6  (Other): 6          (Other):16          (Other):62
##      BRIX      Mass      log.mass
## Min.   : 1.00  Min.   :0.002182  Min.   :-6.1276
## 1st Qu.:16.00  1st Qu.:0.041771  1st Qu.: -3.1756
## Median :22.00  Median :0.079737  Median : -2.5291
## Mean   :21.59  Mean   :0.105372  Mean   : -2.6407
## 3rd Qu.:27.00  3rd Qu.:0.138456  3rd Qu.: -1.9772
## Max.   :48.00  Max.   :0.594749  Max.   : -0.5196
##
```

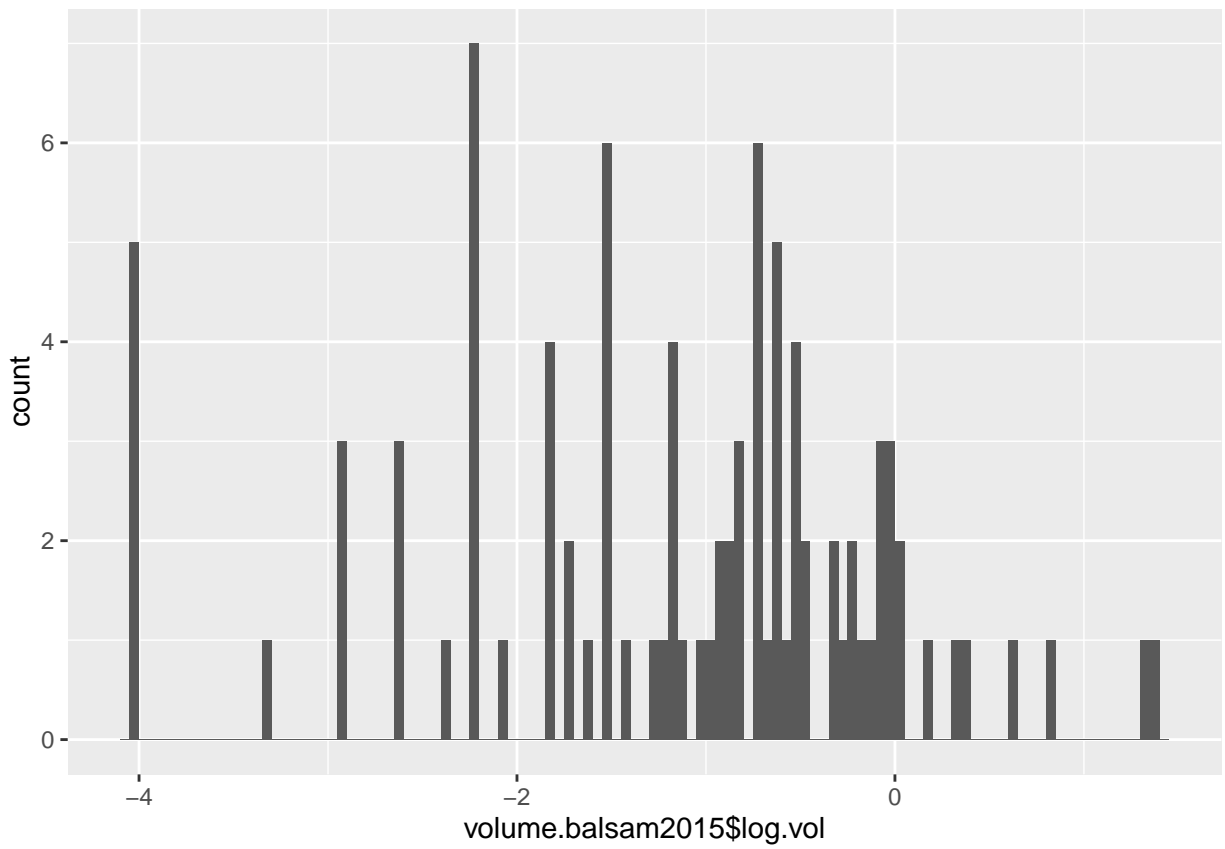
```
summarize(group_by(sugar.balsam2015, Heat), meanBRIX = mean(BRIX), meanMass = mean(Mass), sdBRIX = sd(B
```

```
## Source: local data frame [2 x 5]
##
##      Heat meanBRIX meanMass  sdBRIX  sdMass
##   (fctr)    (dbl)    (dbl)    (dbl)    (dbl)
## 1      0 22.07143 0.1034074 10.40274 0.06237946
## 2      1 21.36207 0.1063201 10.76821 0.10930112
```

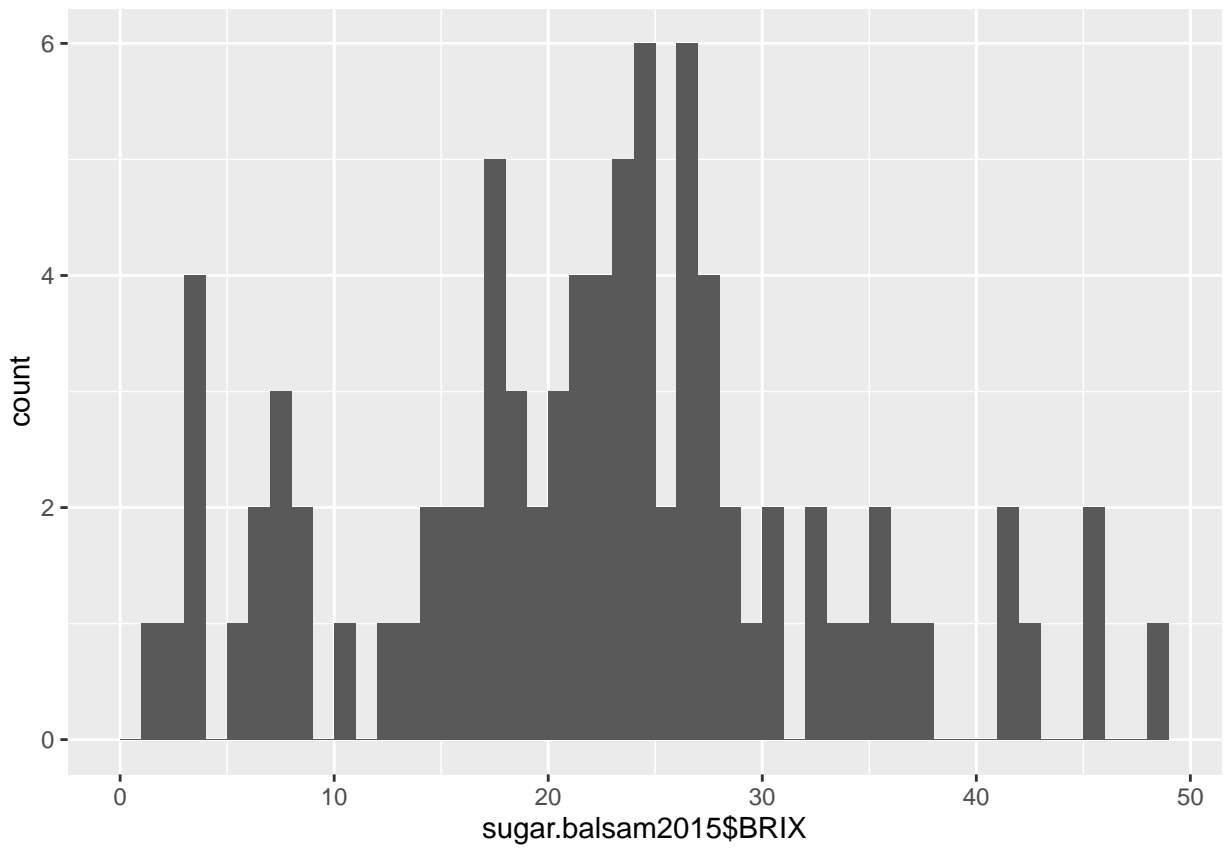
```
qplot(volume.balsam2015$Volume, binwidth = .025)
```



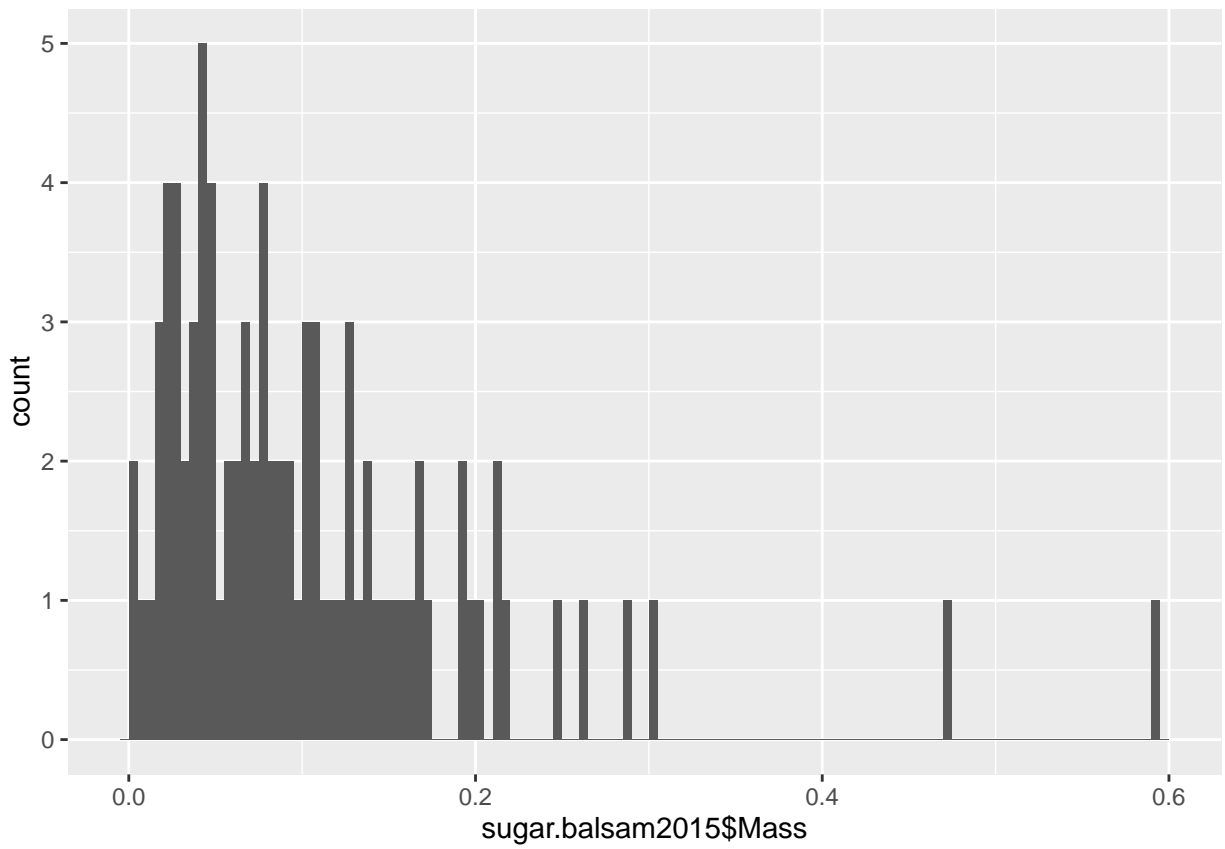
```
qplot(volume.balsam2015$log.vol, binwidth = .05)
```



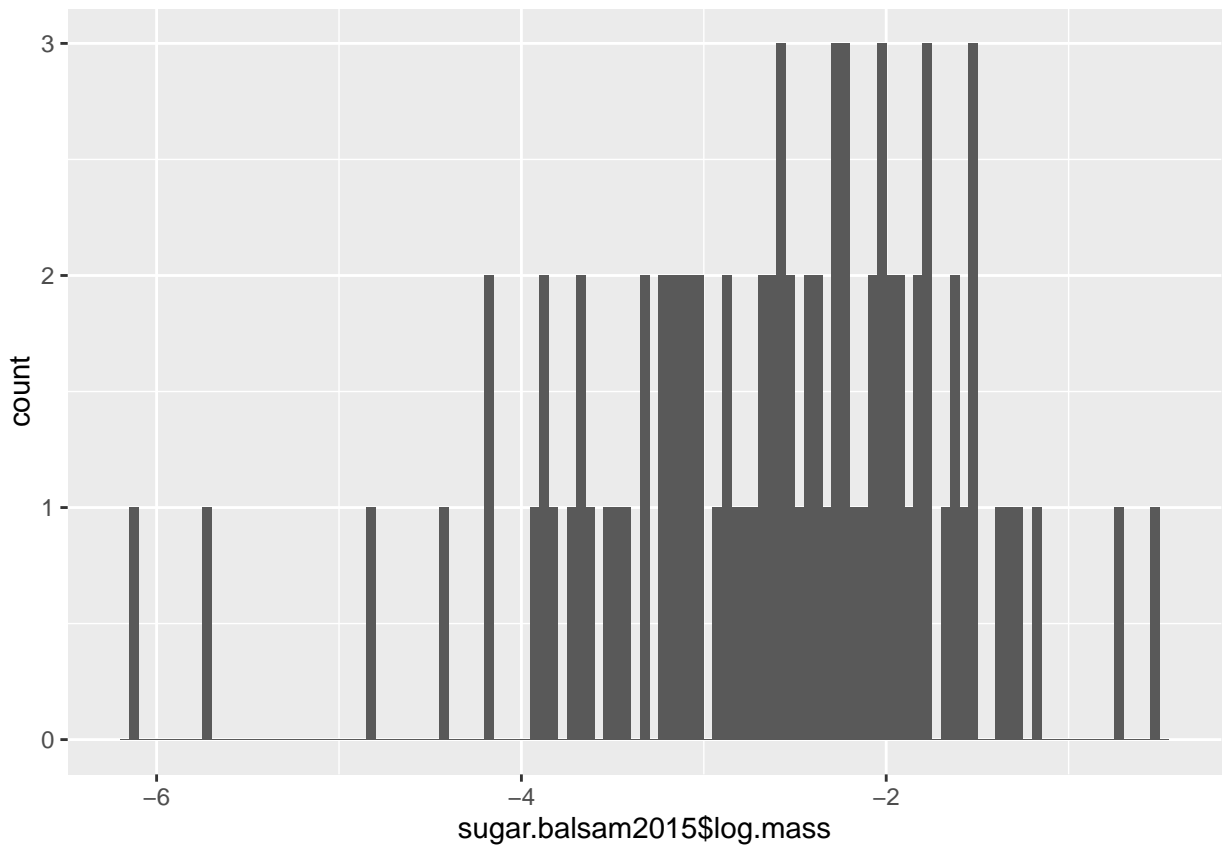
```
qplot(sugar.balsam2015$BRIX, binwidth = 1)
```



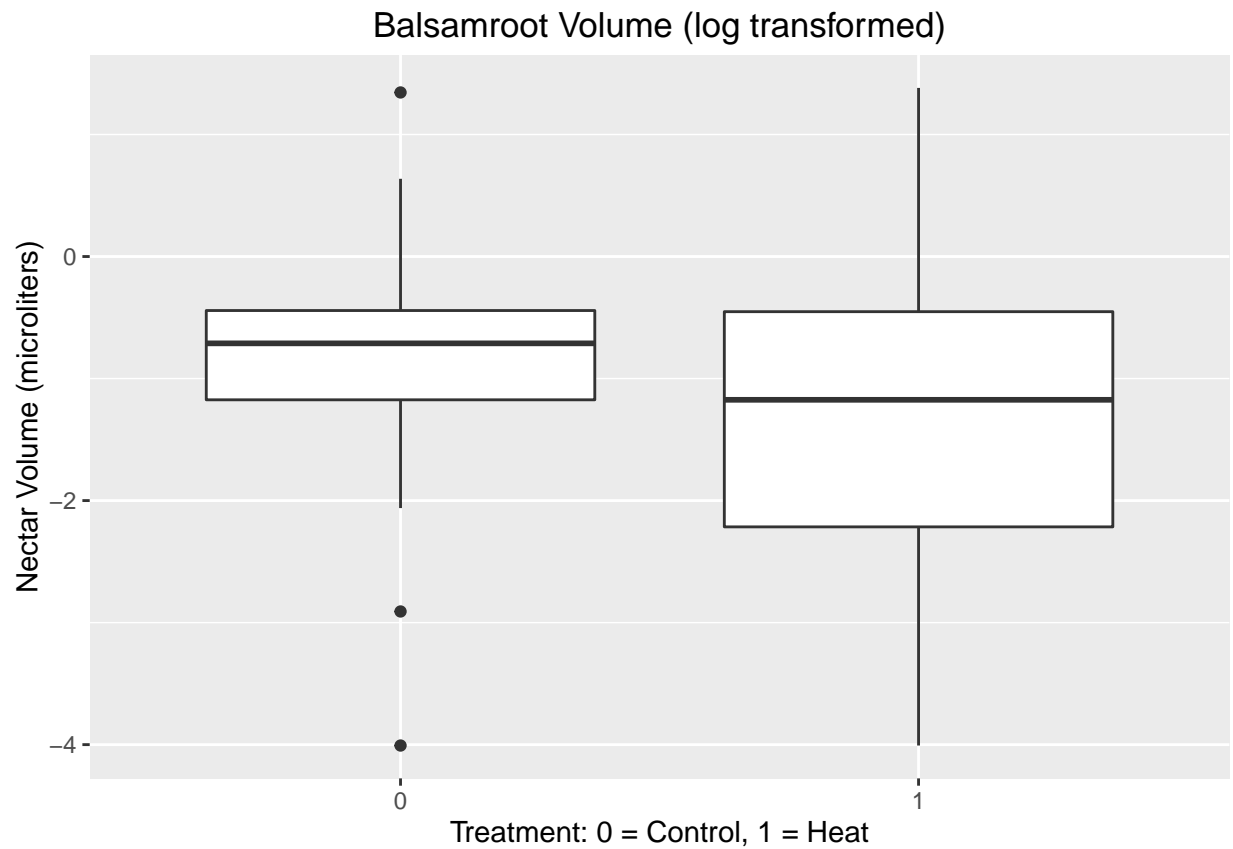
```
qplot(sugar.balsam2015$Mass, binwidth = .005)
```



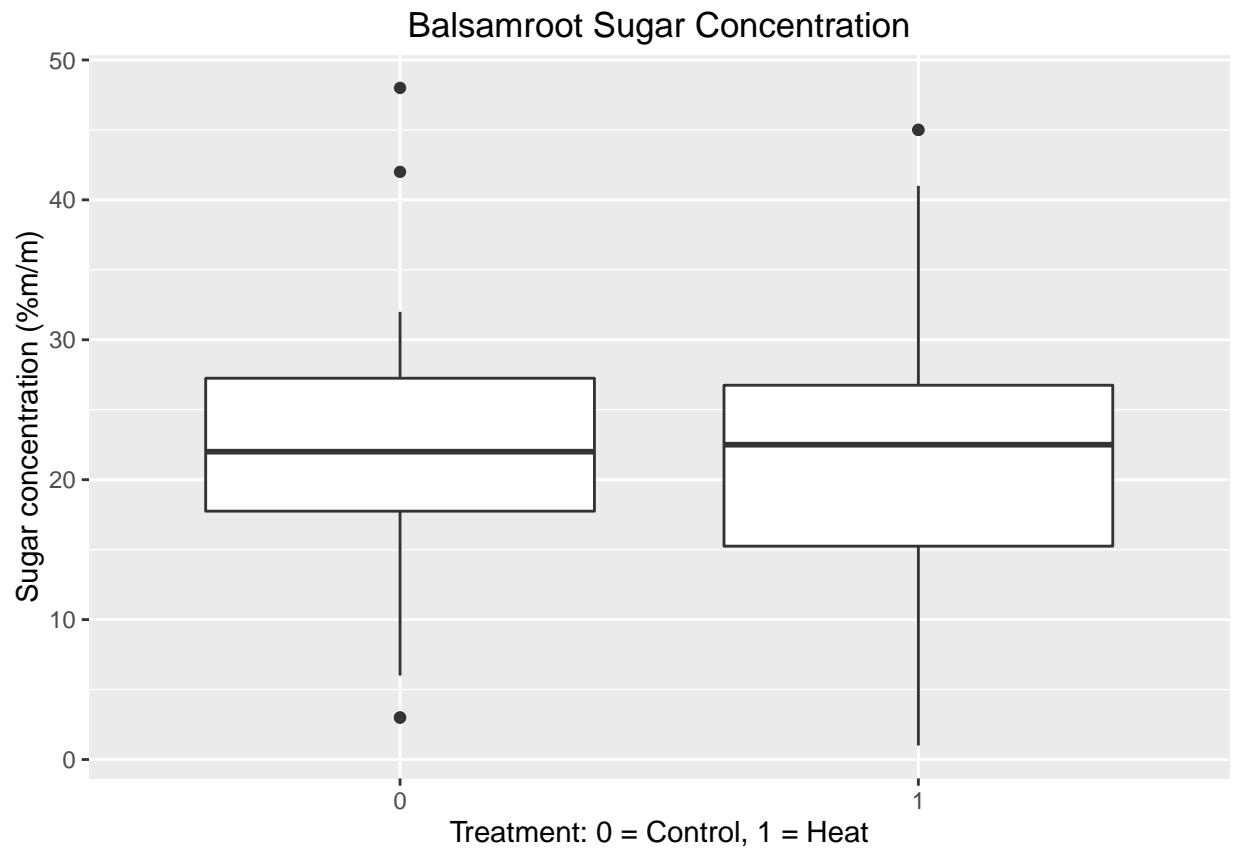
```
qplot(sugar.balsam2015$log.mass, binwidth = .05)
```

```
ggplot(volume.balsam2015, aes(x=Heat, y=log.vol)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Nectar Volume (microliters)") + ggtitle("Balsamroot Volume (log transformed)")
```



```
ggplot(sugar.balsam2015, aes(x=Heat, y=BRIX)) + geom_boxplot() +
  xlab("Treatment: 0 = Control, 1 = Heat") +
  ylab("Sugar concentration (%m/m)") + ggtitle("Balsamroot Sugar Concentration")
```



```
ggplot(sugar.balsam2015, aes(x=Heat, y=log.mass)) + geom_boxplot() +  
  xlab("Treatment: 0 = Control, 1 = Heat") +  
  ylab("Sugar mass (mg)") + ggtitle("Balsamroot Sugar Mass (log transformed)")
```



```
#Normality tests
```

```
# Test normality for volume by treatment, 2016 only
```

```
shapiro.test(as.matrix(volume.balsam2015[volume.balsam2015[,5] == "0", 8])) #control
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: as.matrix(volume.balsam2015[volume.balsam2015[, 5] == "0", 8])
```

```
## W = 0.92861, p-value = 0.04019
```

```
shapiro.test(as.matrix(volume.balsam2015[volume.balsam2015[,5] == "1", 8])) #heat treatment
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: as.matrix(volume.balsam2015[volume.balsam2015[, 5] == "1", 8])
```

```
## W = 0.96722, p-value = 0.1012
```

```
# Test normality for sugar concentration by treatment, 2016 only
```

```
shapiro.test(as.matrix(sugar.balsam2015[sugar.balsam2015[,5] == "0", 7])) #control
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
## data:  as.matrix(sugar.balsam2015[sugar.balsam2015[, 5] == "0", 7])
## W = 0.96026, p-value = 0.3536

shapiro.test(as.matrix(sugar.balsam2015[sugar.balsam2015[,5] == "1", 7])) #heat treatment

##
## Shapiro-Wilk normality test
##
## data:  as.matrix(sugar.balsam2015[sugar.balsam2015[, 5] == "1", 7])
## W = 0.97529, p-value = 0.2823

# Test normality for sugar mass by treatment, 2016
shapiro.test(as.matrix(sugar.balsam2015[sugar.balsam2015[,5] == "0", 9])) #control

##
## Shapiro-Wilk normality test
##
## data:  as.matrix(sugar.balsam2015[sugar.balsam2015[, 5] == "0", 9])
## W = 0.9251, p-value = 0.04644

shapiro.test(as.matrix(sugar.balsam2015[sugar.balsam2015[,5] == "1", 9])) #heat treatment

##
## Shapiro-Wilk normality test
##
## data:  as.matrix(sugar.balsam2015[sugar.balsam2015[, 5] == "1", 9])
## W = 0.96255, p-value = 0.07063

#Homoscedasticity tests

#Levene test for Homogeneity of variances
leveneTest(volume.balsam2015[,8],volume.balsam2015[,5]) #Volume

## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1  3.7279 0.05666 .
##      90
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

leveneTest(sugar.balsam2015[,7],sugar.balsam2015[,5]) #Concentration

## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1  0.2965 0.5875
##      84
```

```
leveneTest(sugar.balsam2015[,9],sugar.balsam2015[,5]) #Mass
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1  1.8755 0.1745
##      84
```

```
#Fligner test for homogeneity of variances
```

```
fligner.test(volume.balsam2015[,8],volume.balsam2015[,5]) #Volume
```

```
##
## Fligner-Killeen test of homogeneity of variances
##
## data:  volume.balsam2015[, 8] and volume.balsam2015[, 5]
## Fligner-Killeen:med chi-squared = 4.2479, df = 1, p-value = 0.0393
```

```
fligner.test(sugar.balsam2015[,7],sugar.balsam2015[,5]) #Concentration
```

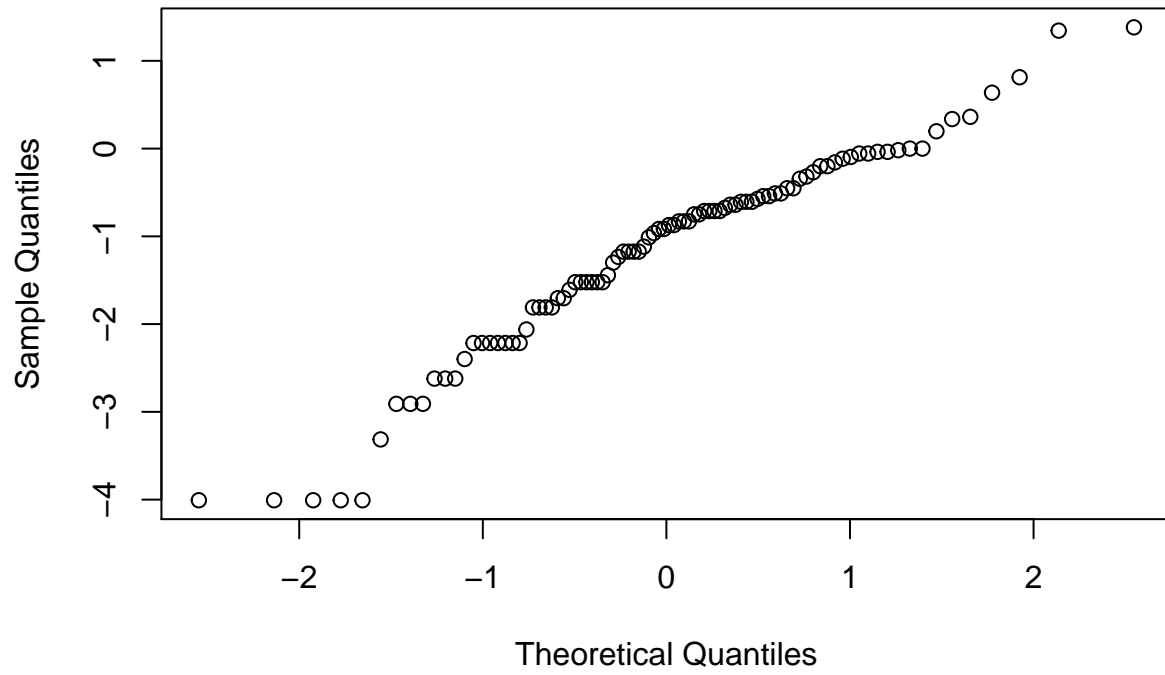
```
##
## Fligner-Killeen test of homogeneity of variances
##
## data:  sugar.balsam2015[, 7] and sugar.balsam2015[, 5]
## Fligner-Killeen:med chi-squared = 0.216, df = 1, p-value = 0.6421
```

```
fligner.test(sugar.balsam2015[,9],sugar.balsam2015[,5]) #Mass
```

```
##
## Fligner-Killeen test of homogeneity of variances
##
## data:  sugar.balsam2015[, 9] and sugar.balsam2015[, 5]
## Fligner-Killeen:med chi-squared = 1.5403, df = 1, p-value = 0.2146
```

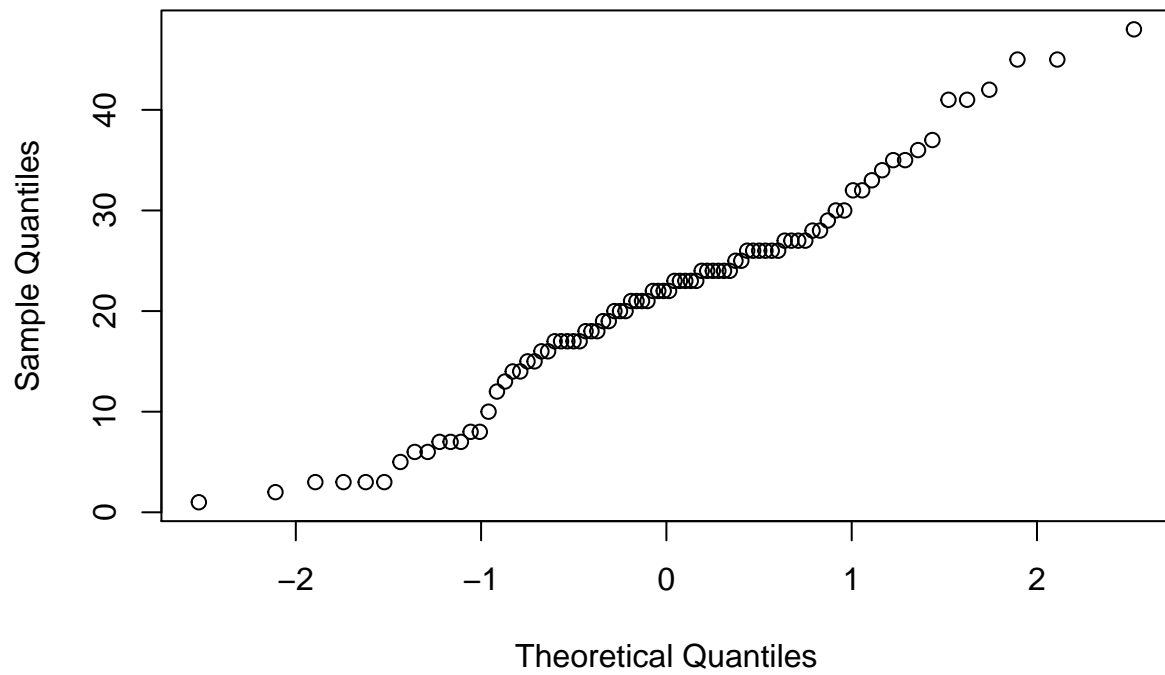
```
qqnorm(volume.balsam2015$log.vol)
```

Normal Q-Q Plot



```
qqnorm(sugar.balsam2015$BRIX)
```

Normal Q-Q Plot



```
qqnorm(sugar.balsam2015$log.mass)
```


Normal Q-Q Plot

