mice2

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8/14/2017

```r
mice <- read.csv("/Users/micheldelange/Documents/mice/data/mice.csv",header=TRUE)[1:40,]
tail(mice$Data.Set)
```

```
## [1] met 4#3 PLT2      met 2#2 female fat met 2#3 female WT
## [4] met 2#4 female WT  met 3#4 female WT  met 4#4 PLT2
## 40 Levels: M PLT2 female2 (13)-19 ... Pound male WT2 (11)-16-2016-09-07
```

```r
table(mice$Animal_type)
```

```
##
##  PLT2_female    PLT2_male Pound_female   Pound_male    WT_female
##            5            9            9            7            6
##      WT_male
##            4
```

```r
mice$CD19pos_B220pos_0_prop <-  mice$CD19pos_B220pos_0 / mice$Live_cells_0
mice$CD19pos_B220pos_3_prop <-  mice$CD19pos_B220pos_3 / mice$Live_cells_3
mice$CD19pos_B220pos_10_prop <-  mice$CD19pos_B220pos_10 / mice$Live_cells_10
mice$CD19pos_B220pos_17_prop <-  mice$CD19pos_B220pos_17/ mice$Live_cells_17
mice$CD19pos_B220pos_24_prop <-  mice$CD19pos_B220pos_24 / mice$Live_cells_24
mice$CD19pos_B220pos_31_prop <-  mice$CD19pos_B220pos_31 / mice$Live_cells_31
```

```r
par(mfrow=c(1,1))
#boxplot(mice$Animal_type,mice$CD19pos_B220pos_0_perc)

female <- mice[grepl('female',mice$Animal_type),]
male   <- mice[grepl('_male',mice$Animal_type),]

female$Animal_type = factor(female$Animal_type)
male$Animal_type = factor(male$Animal_type)

par(mfrow=c(1,2))


plot(' ',xlim=c(0,31),ylim=c(0,1),main='proportion CD19posB22, male mice 1 to 10 ',ylab='CD19pos_B220',
for (mouse in 1:10) {

  lines(c(0,3,10,17,24,31),
  c(male$CD19pos_B220pos_0_prop[mouse],
  male$CD19pos_B220pos_3_prop[mouse],
  male$CD19pos_B220pos_10_prop[mouse],
  male$CD19pos_B220pos_17_prop[mouse],
  male$CD19pos_B220pos_24_prop[mouse],
  male$CD19pos_B220pos_31_prop[mouse]
  ),
  pch='.',col=rainbow(20)[mouse])
```
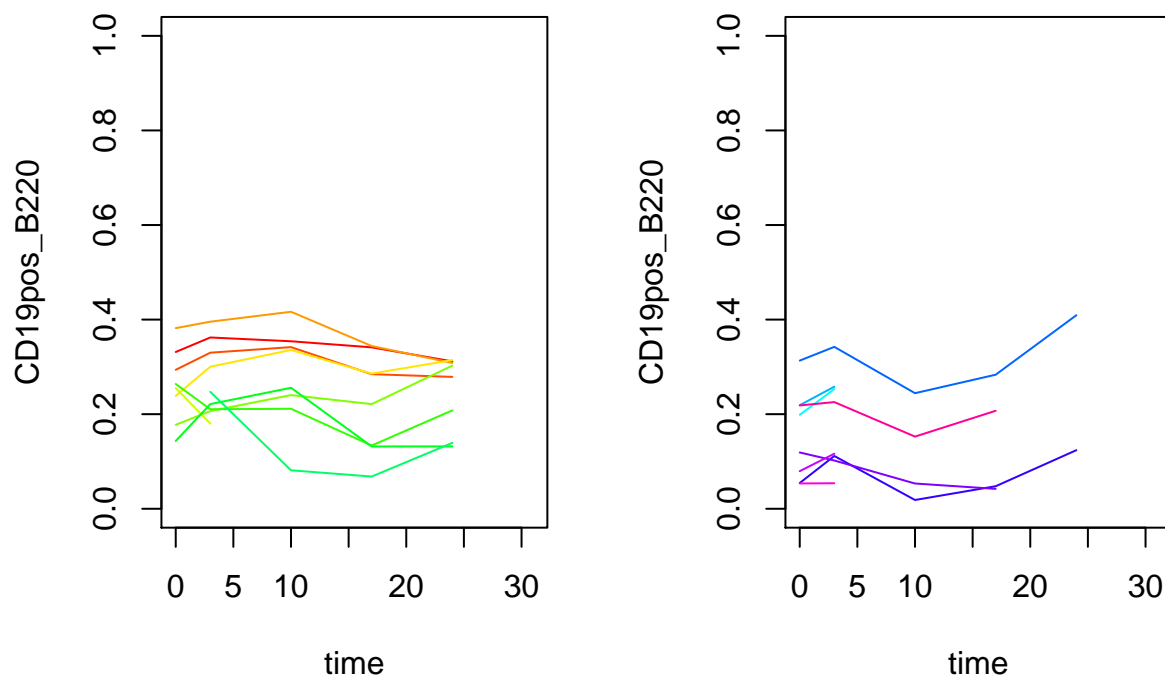
```
}
plot(' ',xlim=c(0,31),ylim=c(0,1),main='proportion CD19posB22, male mice 11 to 20  ',ylab='CD19pos_B220
for (mouse in 11:20) {
  lines(c(0,3,10,17,24,31),
        c(male$CD19pos_B220pos_0_prop[mouse],
          male$CD19pos_B220pos_3_prop[mouse],
          male$CD19pos_B220pos_10_prop[mouse],
          male$CD19pos_B220pos_17_prop[mouse],
          male$CD19pos_B220pos_24_prop[mouse],
          male$CD19pos_B220pos_31_prop[mouse]),
        pch='.',col=rainbow(20)[mouse])
}
```

roportion CD19posB22, male mice 1)portion CD19posB22, male mice 11


```
## same thing, by animal type
male_wt <- mice[grepl('WT_male',mice$Animal_type),]
male_pound <- mice[grepl('Pound_male',mice$Animal_type),]
male_plt2 <- mice[grepl('PLT2_male',mice$Animal_type),]

par(mfrow=c(1,3))


plot(' ',xlim=c(0,31),ylim=c(0,1),main='proportion CD19posB22, WT_male mice 1 to 4 ',ylab='CD19pos_B220
for (mouse in seq(1:4)) {

  lines(c(0,3,10,17,24,31),
        c(male_wt$CD19pos_B220pos_0_prop[mouse],
          male_wt$CD19pos_B220pos_3_prop[mouse],
          male_wt$CD19pos_B220pos_10_prop[mouse],
          male_wt$CD19pos_B220pos_17_prop[mouse],
          male_wt$CD19pos_B220pos_24_prop[mouse],
```
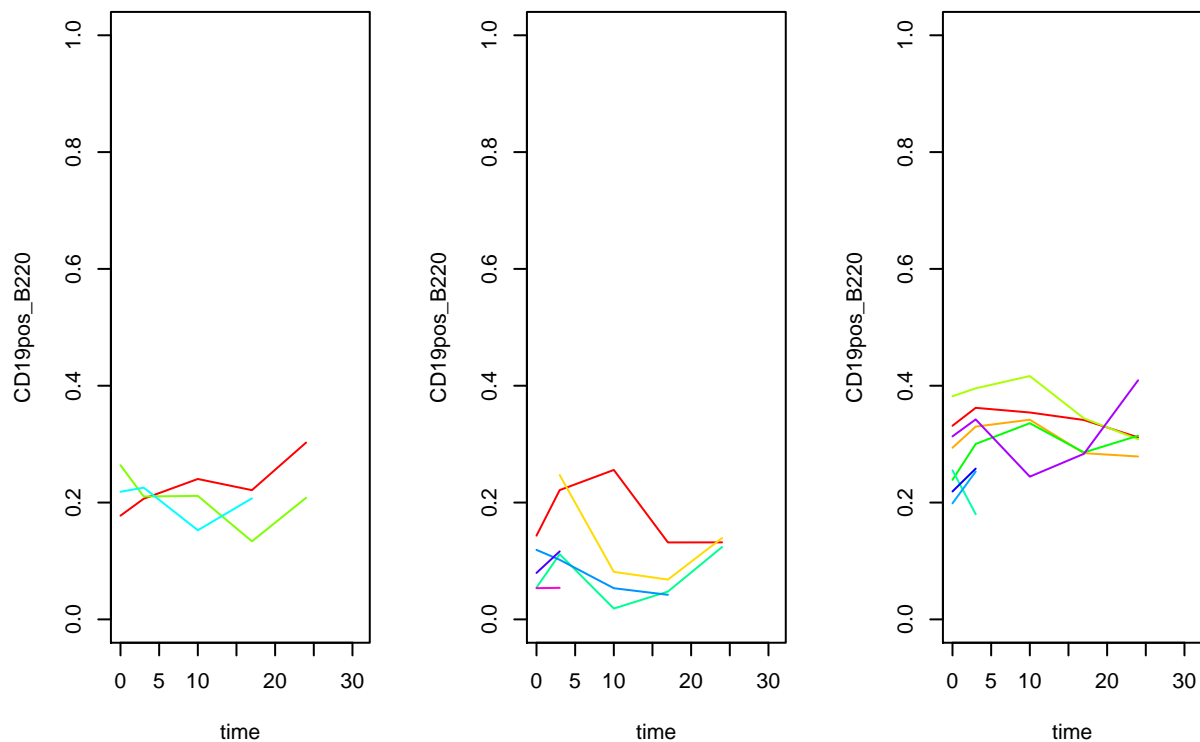
```r
          male_wt$CD19pos_B220pos_31_prop[mouse]
        ),
        pch='.',col=rainbow(4)[mouse])
}

plot(' ',xlim=c(0,31),ylim=c(0,1),main='proportion CD19posB22, Pound_male mice 1 to 7 ',ylab='CD19pos_B2
for (mouse in seq(1:7)) {
  lines(c(0,3,10,17,24,31),
        c(male_pound$CD19pos_B220pos_0_prop[mouse],
          male_pound$CD19pos_B220pos_3_prop[mouse],
          male_pound$CD19pos_B220pos_10_prop[mouse],
          male_pound$CD19pos_B220pos_17_prop[mouse],
          male_pound$CD19pos_B220pos_24_prop[mouse],
          male_pound$CD19pos_B220pos_31_prop[mouse]
        ),
        pch='.',col=rainbow(7)[mouse])
}

plot(' ',xlim=c(0,31),ylim=c(0,1),main='proportion CD19posB22, Pound_plt2 mice 1 to 9 ',ylab='CD19pos_B2
for (mouse in seq(1:9)) {
  lines(c(0,3,10,17,24,31),
        c(male_plt2$CD19pos_B220pos_0_prop[mouse],
          male_plt2$CD19pos_B220pos_3_prop[mouse],
          male_plt2$CD19pos_B220pos_10_prop[mouse],
          male_plt2$CD19pos_B220pos_17_prop[mouse],
          male_plt2$CD19pos_B220pos_24_prop[mouse],
          male_plt2$CD19pos_B220pos_31_prop[mouse]
        ),
        pch='.',col=rainbow(9)[mouse])
}
```

```r
table(female$Animal_type)
```

```
##
##  PLT2_female Pound_female    WT_female
##           5            9            6
```

```r
table(male$Animal_type)
```

```
##
##   PLT2_male  Pound_male     WT_male
##           9           7           4
```

```r
female$plt2 <- grepl('PLT2',female$Animal_type)
female$pound <- grepl('Pound_',female$Animal_type)
male$plt2 <- grepl('PLT2',male$Animal_type)
male$pound <- grepl('Pound_',male$Animal_type)
```

```r
table(female$Animal_type)
```
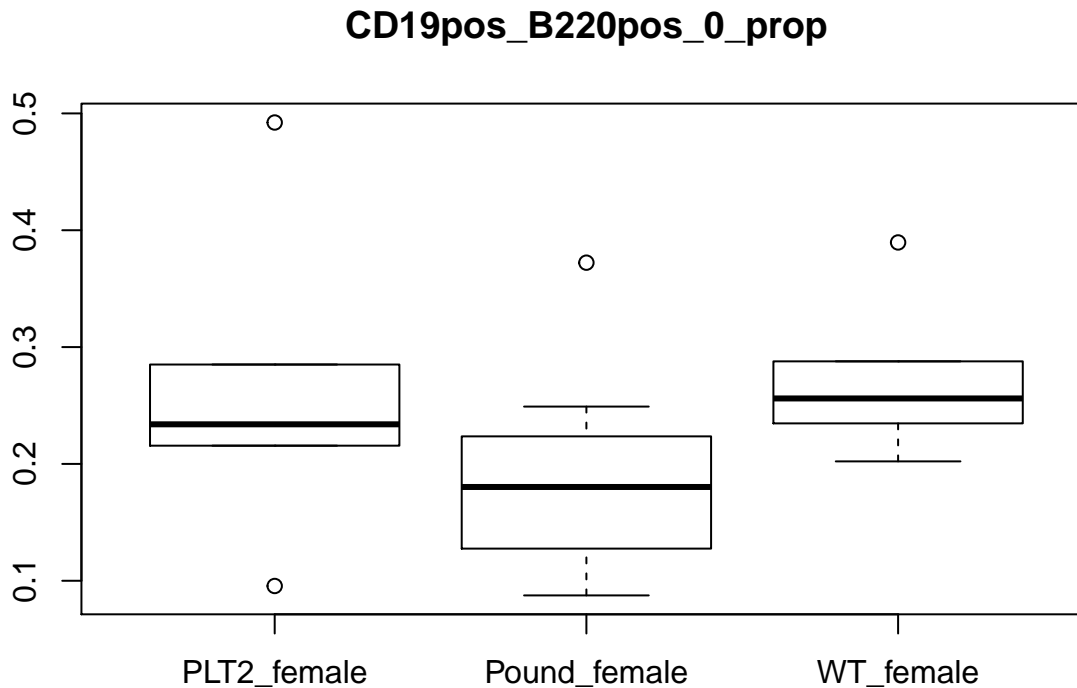
```
##
##  PLT2_female Pound_female    WT_female
##           5            9            6
```

```r
table(male$Animal_type)
```

```
##
##   PLT2_male  Pound_male     WT_male
##           9           7           4
```

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

```r
plot(female$Animal_type,female$CD19pos_B220pos_0_prop,main="CD19pos_B220pos_0_prop")
```
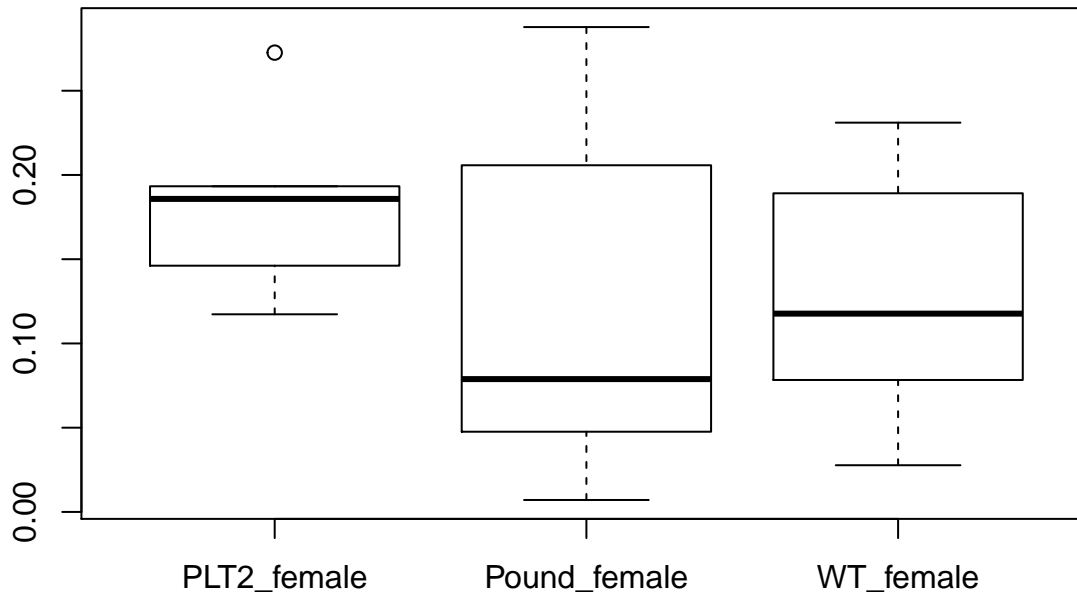
CD19pos_B220pos_0_prop


```r
m <- glm(female$CD19pos_B220pos_0_prop ~ 1 + female$plt2 + female$pound, weights = female$Live_cells_0,
         family='quasibinomial')
summary(m)
```

```
##
## Call:
## glm(formula = female$CD19pos_B220pos_0_prop ~ 1 + female$plt2 +
##     female$pound, family = "quasibinomial", weights = female$Live_cells_0)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -219.299   -40.426   -22.041     5.459   199.214
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -1.00550    0.19073  -5.272 6.23e-05 ***
## female$plt2TRUE -0.05814    0.26940  -0.216    0.832
## female$poundTRUE 0.02191    0.30080   0.073    0.943
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 7699.671)
##
##     Null deviance: 136340  on 19  degrees of freedom
## Residual deviance: 135703  on 17  degrees of freedom
## AIC: NA
##
```

```
## Number of Fisher Scoring iterations: 4
```

```r
plot(female$Animal_type,female$CD19pos_B220pos_3_prop)
```
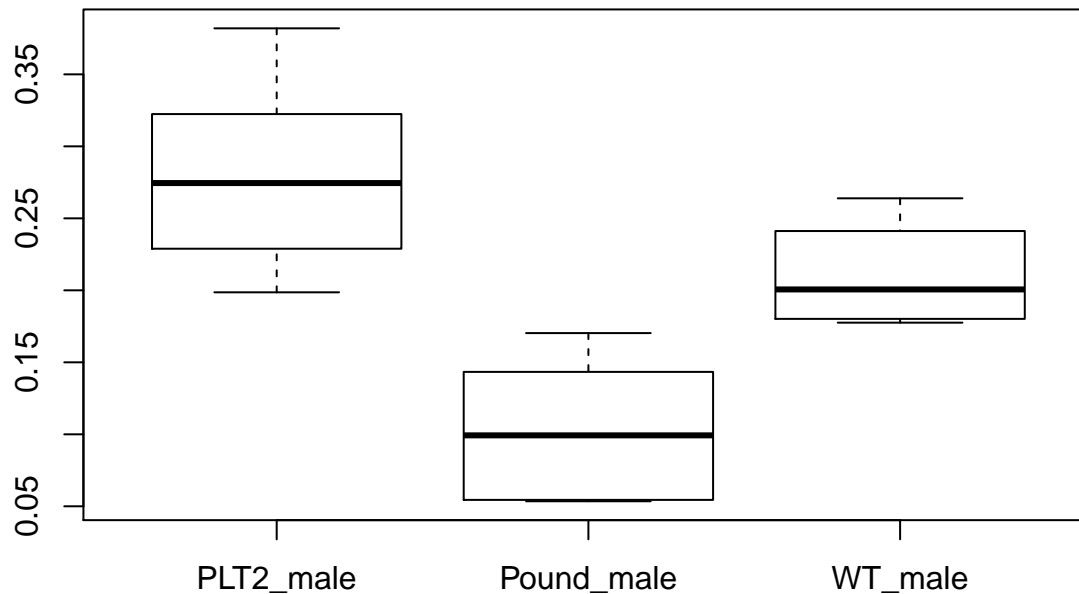


```r
m <- glm(female$CD19pos_B220pos_3_prop ~ 1 + female$plt2 + female$pound, weights = female$Live_cells_3,
         family='quasibinomial')
summary(m)
```

```
##
## Call:
## glm(formula = female$CD19pos_B220pos_3_prop ~ 1 + female$plt2 +
##     female$pound, family = "quasibinomial", weights = female$Live_cells_3)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -162.219   -52.912     4.925    57.367   190.557
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -2.3038     0.3989  -5.776 2.24e-05 ***
## female$plt2TRUE   0.6276     0.5312   1.181    0.254
## female$poundTRUE  0.3565     0.4971   0.717    0.483
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 9172.837)
##
##     Null deviance: 164606  on 19  degrees of freedom
## Residual deviance: 151504  on 17  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
#### male
```

```r
plot(male$Animal_type,male$CD19pos_B220pos_0_prop,main="CD19pos_B220pos_0_prop")
```

CD19pos_B220pos_0_prop


```
m <- glm(male$CD19pos_B220pos_0_prop ~ 1 + male$plt2 + male$pound, weights = male$Live_cells_0,
         family='quasibinomial')
summary(m)
```
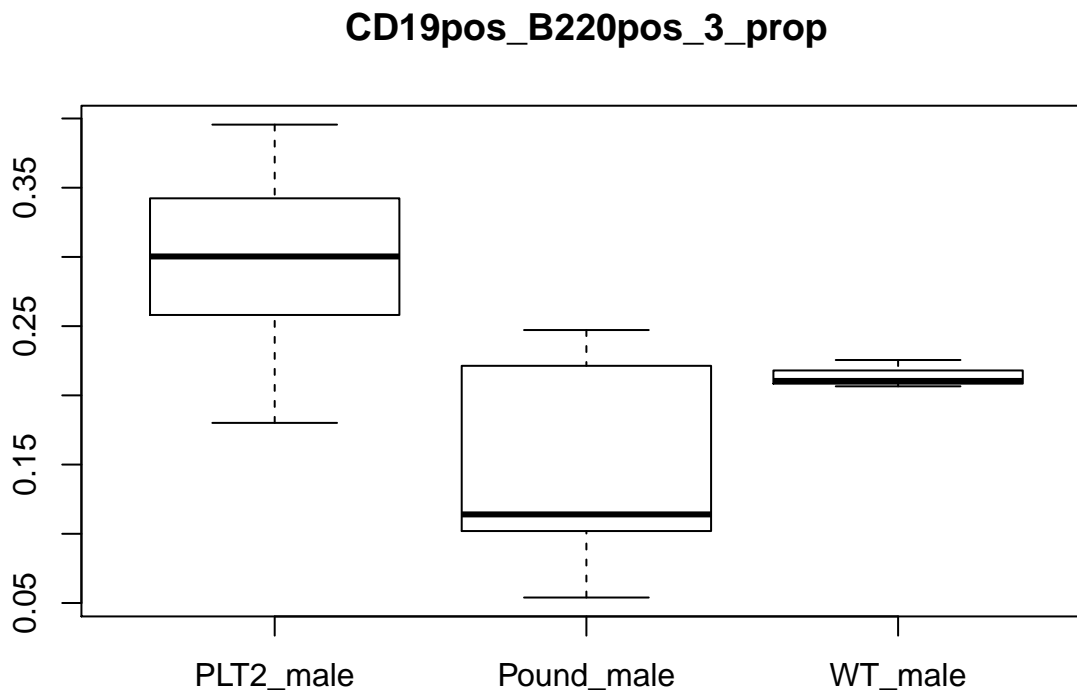
```
##
## Call:
## glm(formula = male$CD19pos_B220pos_0_prop ~ 1 + male$plt2 + male$pound,
##     family = "quasibinomial", weights = male$Live_cells_0)
##
## Deviance Residuals:
##     Min      1Q  Median      3Q     Max
## -34.227  -22.044  -2.987   16.583  48.556
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1.3804     0.1857  -7.433 2.1e-06 ***
## male$plt2TRUE   0.4436     0.2110   2.102  0.05288 .
## male$poundTRUE -0.8108     0.2669  -3.038  0.00831 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 636.7405)
##
##     Null deviance: 34940.8  on 17  degrees of freedom
## Residual deviance:  9559.1  on 15  degrees of freedom
##   (2 observations deleted due to missingness)
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

```
table(male$Animal_type)
```

```
##
```

```
##  PLT2_male Pound_male    WT_male
##         9        7         4
```

```
plot(male$Animal_type,male$CD19pos_B220pos_3_prop,main="CD19pos_B220pos_3_prop")
```

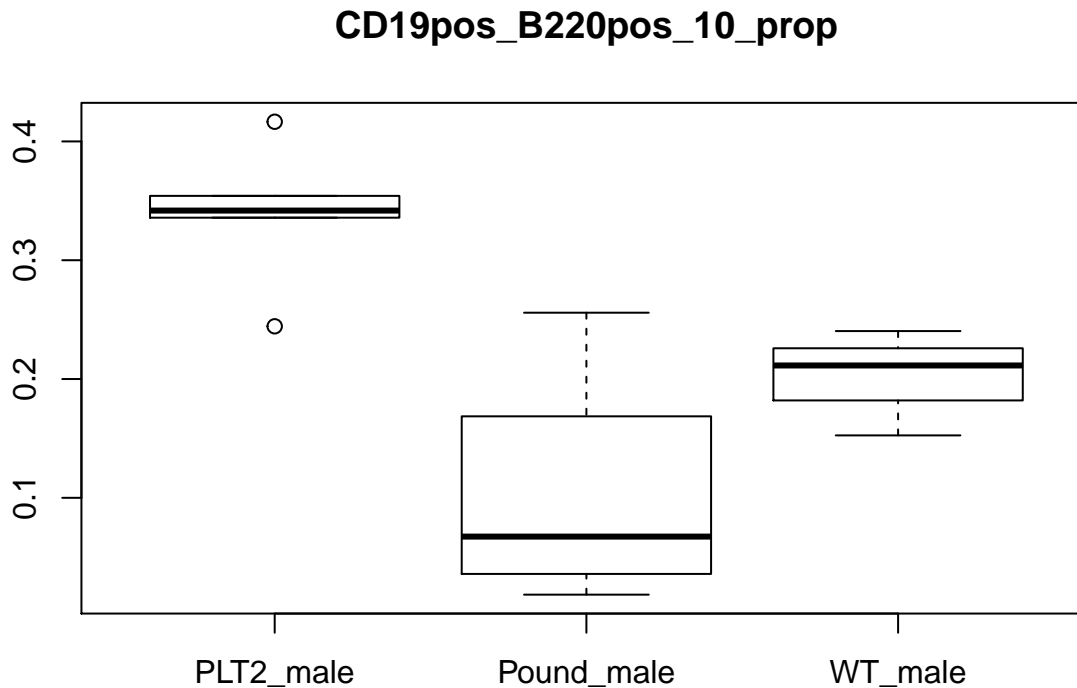**CD19pos_B220pos_3_prop**


```
m <- glm(male$CD19pos_B220pos_3_prop ~ 1 + male$plt2 + male$pound, weights = male$Live_cells_3,
         family='quasibinomial')
summary(m)
```

```
##
## Call:
## glm(formula = male$CD19pos_B220pos_3_prop ~ 1 + male$plt2 + male$pound,
##     family = "quasibinomial", weights = male$Live_cells_3)
##
## Deviance Residuals:
##     Min      1Q   Median      3Q      Max
## -48.500  -25.150   -6.412    9.216   69.882
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.2907     0.2725  -4.737 0.000265 ***
## male$plt2TRUE   0.5307     0.2898   1.831 0.087020 .
## male$poundTRUE -0.3178     0.3159  -1.006 0.330418
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 1042.498)
##
##     Null deviance: 39561  on 17  degrees of freedom
## Residual deviance: 15742  on 15  degrees of freedom
##   (2 observations deleted due to missingness)
## AIC: NA
##
```

```
## Number of Fisher Scoring iterations: 4
```

```
plot(male$Animal_type,male$CD19pos_B220pos_10_prop,main="CD19pos_B220pos_10_prop")
```

CD19pos_B220pos_10_prop


```
m <- glm(male$CD19pos_B220pos_10_prop ~ 1 + male$plt2 + male$pound, weights = male$Live_cells_10,
         family='quasibinomial')
summary(m)
```

```
##
## Call:
## glm(formula = male$CD19pos_B220pos_10_prop ~ 1 + male$plt2 +
##     male$pound, family = "quasibinomial", weights = male$Live_cells_10)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -49.56  -27.81  -11.42   13.51   79.16
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.4551     0.2823  -5.154   0.0006 ***
## male$plt2TRUE   0.8772     0.3216   2.728   0.0233 *
## male$poundTRUE -0.7224     0.4445  -1.625   0.1385
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 1730.052)
##
##     Null deviance: 58598  on 11  degrees of freedom
## Residual deviance: 14359  on  9  degrees of freedom
##   (8 observations deleted due to missingness)
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
```

9

```
plot(male$Animal_type,male$CD19pos_B220pos_17_prop,main="CD19pos_B220pos_17_prop")
```

CD19pos_B220pos_17_prop
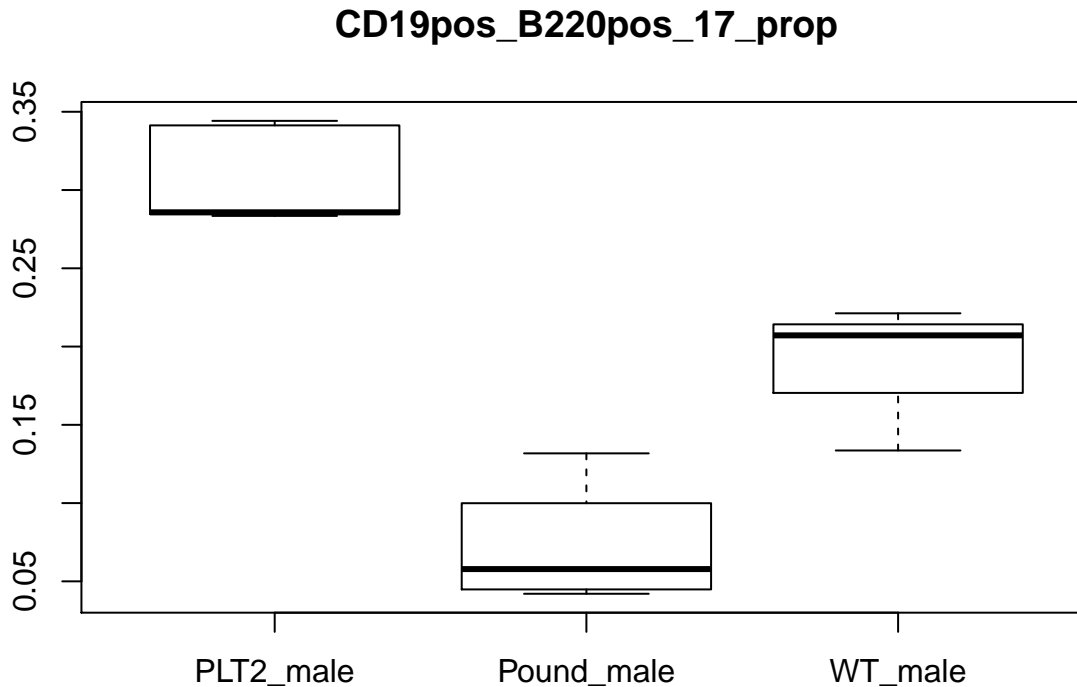

```
m <- glm(male$CD19pos_B220pos_17_prop ~ 1 + male$plt2 + male$pound, weights = male$Live_cells_17,
          family='quasibinomial')
summary(m)
```

```
##
## Call:
## glm(formula = male$CD19pos_B220pos_17_prop ~ 1 + male$plt2 +
##     male$pound, family = "quasibinomial", weights = male$Live_cells_17)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -37.273  -19.437   -9.665   14.587   57.462
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -1.4022     0.1838  -7.630 3.23e-05 ***
## male$plt2TRUE    0.6044     0.2121   2.850  0.01908 *
## male$poundTRUE  -1.1285     0.2829  -3.988  0.00316 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 951.9488)
##
##     Null deviance: 72558.6  on 11  degrees of freedom
## Residual deviance:  8231.7  on  9  degrees of freedom
##   (8 observations deleted due to missingness)
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

```
plot(male$Animal_type,male$CD19pos_B220pos_24_prop,main="CD19pos_B220pos_24_prop")
```

CD19pos_B220pos_24_prop
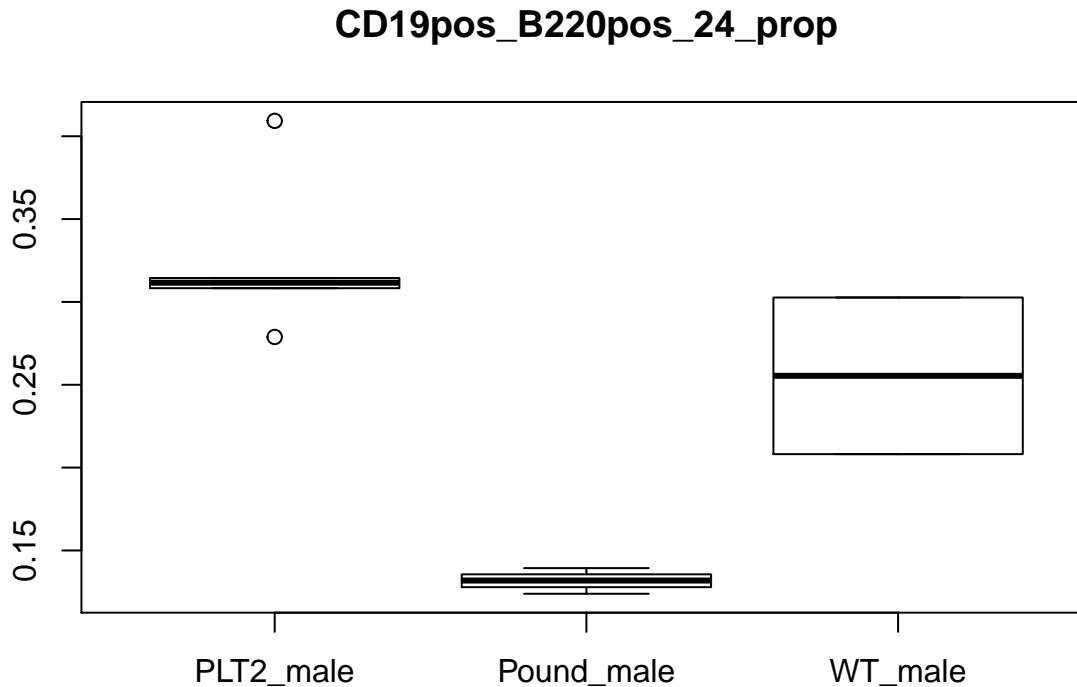

```
m <- glm(male$CD19pos_B220pos_24_prop ~ 1 + male$plt2 + male$pound, weights = male$Live_cells_24,
         family='quasibinomial')
summary(m)
```

```
##
## Call:
## glm(formula = male$CD19pos_B220pos_24_prop ~ 1 + male$plt2 +
##     male$pound, family = "quasibinomial", weights = male$Live_cells_24)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -23.500   -8.635   -5.073    3.134   41.625
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -1.2005     0.2461  -4.878   0.0018 **
## male$plt2TRUE    0.4755     0.2604   1.826   0.1105
## male$poundTRUE  -0.6756     0.2913  -2.320   0.0534 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 413.8843)
##
##     Null deviance: 22898.4  on 9  degrees of freedom
## Residual deviance:  2833.7  on 7  degrees of freedom
##   (10 observations deleted due to missingness)
## AIC: NA
##
## Number of Fisher Scoring iterations: 3
```

```
#plot(male$Animal_type,male$CD19pos_B220pos_31_prop,main="CD19pos_B220pos_31_prop")
#m <- glm(male$CD19pos_B220pos_31_prop ~ 1 + male$plt2 + male$pound, weights = male$Live_cells_31,
#        family='quasibinomial')
#summary(m)
```

```
plot(male$Animal_type,male$CD19pos_B220pos_0_prop)
```