Lab3

2024-04-16

Section 1: Importing and sorting data

```
# 2,3,4,5
data.df <- read.csv("cell_infectivity_long.csv")
data.df[, "species" ] == "Finch"
```

```
##  [1]  TRUE  TRUE FALSE FALSE  TRUE  TRUE FALSE FALSE  TRUE  TRUE FALSE FALSE
## [13]  TRUE  TRUE FALSE FALSE  TRUE  TRUE FALSE FALSE  TRUE  TRUE FALSE FALSE
## [25]  TRUE  TRUE FALSE FALSE  TRUE  TRUE FALSE FALSE  TRUE  TRUE FALSE FALSE
```

```
# 6
finch.df <- data.df[ data.df$species == "Finch", ]
# 7
species.col <- data.df$species
which.finch <- species.col == "Finch"
finch.df <- data.df[which.finch, ]
# 8
print(finch.df)
```

```
##           cell species infectivity          group
## 1  Wild-type    Finch   0.2392450 Wild-type Finch
## 2      hLDLR    Finch   1.7215640      hLDLR Finch
## 5  Wild-type    Finch   0.1974520 Wild-type Finch
## 6      hLDLR    Finch   3.3925764      hLDLR Finch
## 9  Wild-type    Finch   0.2137752 Wild-type Finch
## 10     hLDLR    Finch   2.0939034      hLDLR Finch
## 13 Wild-type    Finch   0.1659772 Wild-type Finch
## 14     hLDLR    Finch   3.2264398      hLDLR Finch
## 17 Wild-type    Finch   0.2916330 Wild-type Finch
## 18     hLDLR    Finch   0.4487605      hLDLR Finch
## 21 Wild-type    Finch   0.3327255 Wild-type Finch
## 22     hLDLR    Finch   4.1256479      hLDLR Finch
## 25 Wild-type    Finch   0.3737137 Wild-type Finch
## 26     hLDLR    Finch   2.0673629      hLDLR Finch
## 29 Wild-type    Finch   0.3229060 Wild-type Finch
## 30     hLDLR    Finch   0.7178828      hLDLR Finch
## 33 Wild-type    Finch   0.1458407 Wild-type Finch
## 34     hLDLR    Finch   1.4996970      hLDLR Finch
```

```
# 9
which.chicken <- species.col == "Chicken"
chicken.df <- data.df[which.chicken, ]
print(chicken.df)
```

```
##          cell species infectivity              group
## 3  Wild-type Chicken    4.076517 Wild-type Chicken
## 4       hLDLR Chicken    3.965639       hLDLR Chicken
## 7  Wild-type Chicken    2.046030 Wild-type Chicken
## 8       hLDLR Chicken    3.622098       hLDLR Chicken
## 11 Wild-type Chicken    3.952518 Wild-type Chicken
## 12      hLDLR Chicken    3.136610       hLDLR Chicken
## 15 Wild-type Chicken    3.067056 Wild-type Chicken
## 16      hLDLR Chicken    2.487331       hLDLR Chicken
## 19 Wild-type Chicken    1.343797 Wild-type Chicken
## 20      hLDLR Chicken    4.871601       hLDLR Chicken
## 23 Wild-type Chicken    4.398596 Wild-type Chicken
## 24      hLDLR Chicken    4.596712       hLDLR Chicken
## 27 Wild-type Chicken    4.416107 Wild-type Chicken
## 28      hLDLR Chicken    4.611982       hLDLR Chicken
## 31 Wild-type Chicken    3.243844 Wild-type Chicken
## 32      hLDLR Chicken    3.512496       hLDLR Chicken
## 35 Wild-type Chicken    5.772721 Wild-type Chicken
## 36      hLDLR Chicken    2.553451       hLDLR Chicken
```

```
# 10, 11, 12
WT.finch <- data.df[data.df$species == "Finch" & data.df$cell == "Wild-type", ]
# 13
WT.chicken <- data.df[data.df$species == "Chicken" & data.df$cell =="Wild-type", ]
hLDLR.finch <- data.df[data.df$species == "Finch" & data.df$cell == "hLDLR", ]
hLDLR.chicken <- data.df[data.df$species == "Chicken" & data.df$cell == "hLDLR", ]
print(WT.finch)
```

```
##          cell species infectivity              group
## 1  Wild-type   Finch   0.2392450 Wild-type Finch
## 5  Wild-type   Finch   0.1974520 Wild-type Finch
## 9  Wild-type   Finch   0.2137752 Wild-type Finch
## 13 Wild-type   Finch   0.1659772 Wild-type Finch
## 17 Wild-type   Finch   0.2916330 Wild-type Finch
## 21 Wild-type   Finch   0.3327255 Wild-type Finch
## 25 Wild-type   Finch   0.3737137 Wild-type Finch
## 29 Wild-type   Finch   0.3229060 Wild-type Finch
## 33 Wild-type   Finch   0.1458407 Wild-type Finch
```

```
print(WT.chicken)
```

```
##           cell species infectivity            group
## 3  Wild-type Chicken    4.076517 Wild-type Chicken
## 7  Wild-type Chicken    2.046030 Wild-type Chicken
## 11 Wild-type Chicken    3.952518 Wild-type Chicken
## 15 Wild-type Chicken    3.067056 Wild-type Chicken
## 19 Wild-type Chicken    1.343797 Wild-type Chicken
## 23 Wild-type Chicken    4.398596 Wild-type Chicken
## 27 Wild-type Chicken    4.416107 Wild-type Chicken
## 31 Wild-type Chicken    3.243844 Wild-type Chicken
## 35 Wild-type Chicken    5.772721 Wild-type Chicken
```

```
print(hLDLR.finch)
```

```
##       cell species infectivity       group
## 2  hLDLR    Finch   1.7215640 hLDLR Finch
## 6  hLDLR    Finch   3.3925764 hLDLR Finch
## 10 hLDLR    Finch   2.0939034 hLDLR Finch
## 14 hLDLR    Finch   3.2264398 hLDLR Finch
## 18 hLDLR    Finch   0.4487605 hLDLR Finch
## 22 hLDLR    Finch   4.1256479 hLDLR Finch
## 26 hLDLR    Finch   2.0673629 hLDLR Finch
## 30 hLDLR    Finch   0.7178828 hLDLR Finch
## 34 hLDLR    Finch   1.4996970 hLDLR Finch
```

```
print(hLDLR.chicken)
```

```
##       cell species infectivity        group
## 4  hLDLR Chicken    3.965639 hLDLR Chicken
## 8  hLDLR Chicken    3.622098 hLDLR Chicken
## 12 hLDLR Chicken    3.136610 hLDLR Chicken
## 16 hLDLR Chicken    2.487331 hLDLR Chicken
## 20 hLDLR Chicken    4.871601 hLDLR Chicken
## 24 hLDLR Chicken    4.596712 hLDLR Chicken
## 28 hLDLR Chicken    4.611982 hLDLR Chicken
## 32 hLDLR Chicken    3.512496 hLDLR Chicken
## 36 hLDLR Chicken    2.553451 hLDLR Chicken
```
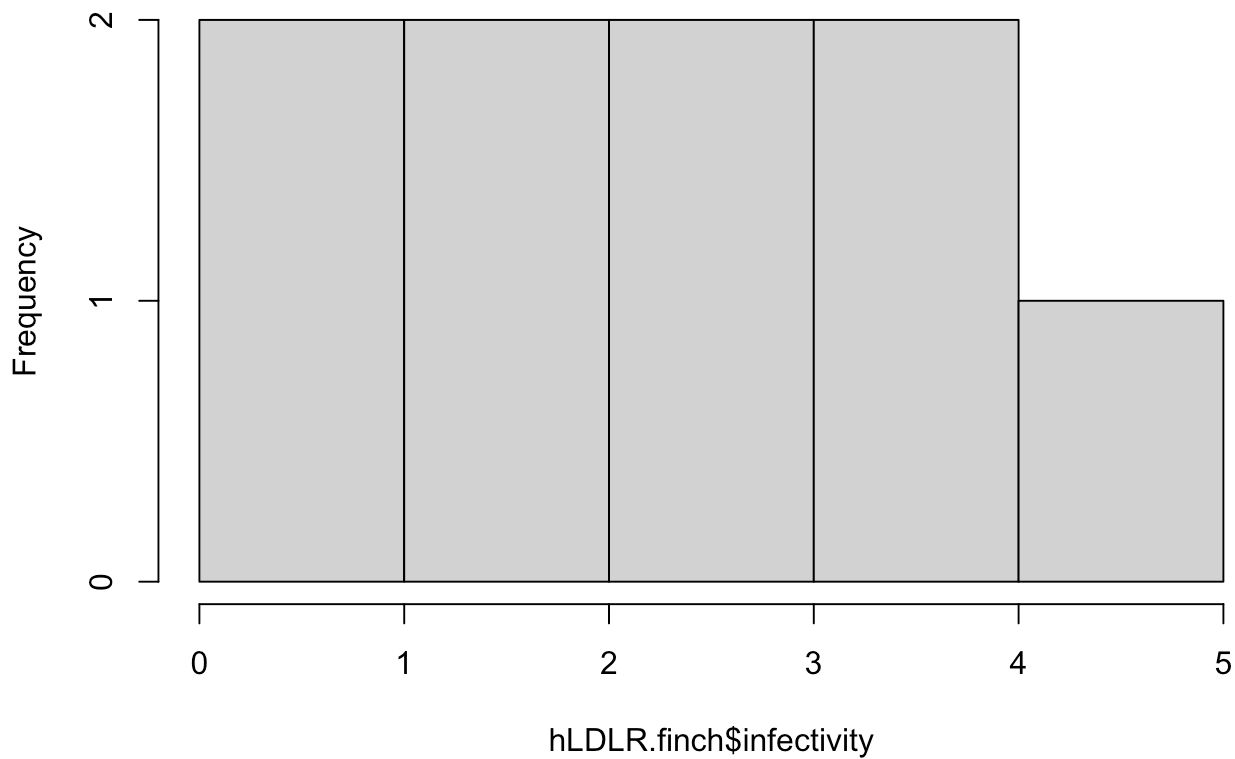
Section 2: t-tests

```
# 14, 15
hist(WT.finch$infectivity)
```

Histogram of WT.finch$infectivity
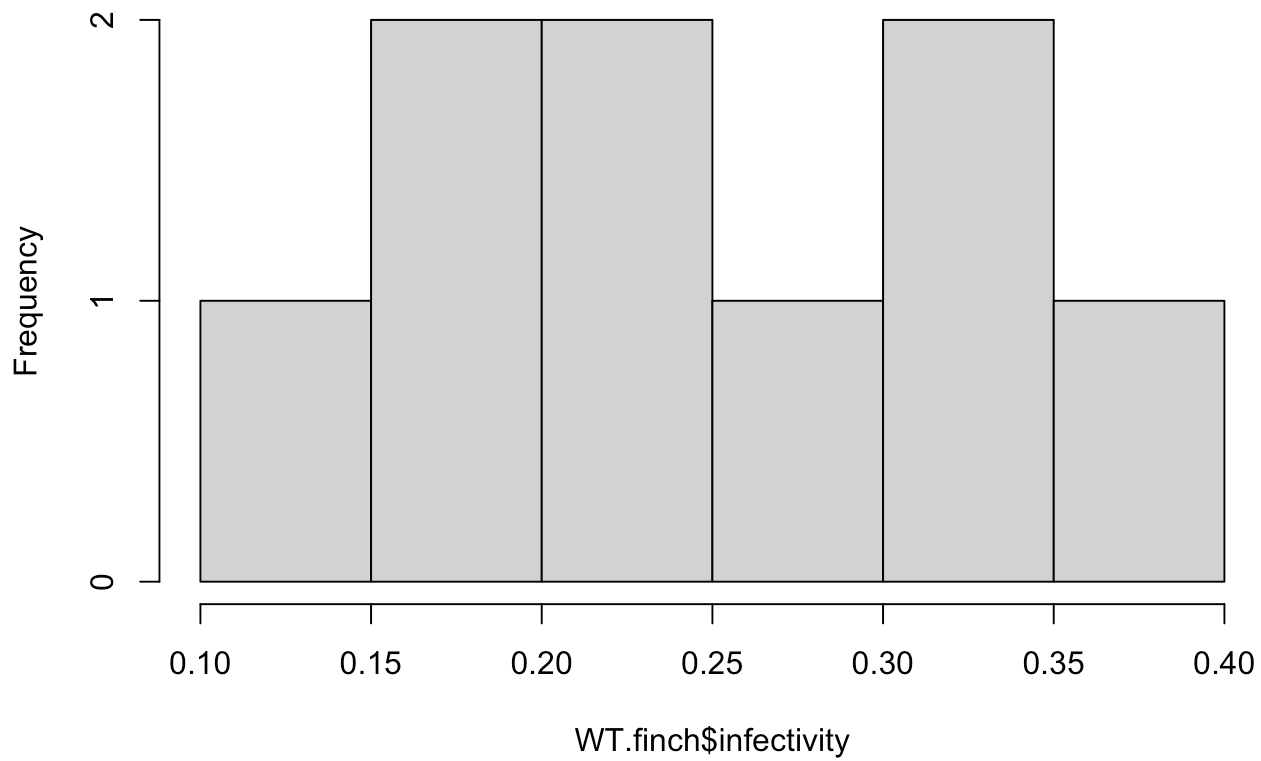

```
hist(hLDLR.finch$infectivity)
```

Histogram of hLDLR.finch$infectivity


```
# 16
shapiro.test(WT.finch$infectivity)
```

```
##
##   Shapiro–Wilk normality test
##
## data:  WT.finch$infectivity
## W = 0.94995, p-value = 0.6895
```

```
shapiro.test(hLDLR.finch$infectivity)
```

```
##
##   Shapiro–Wilk normality test
##
## data:  hLDLR.finch$infectivity
## W = 0.95536, p-value = 0.7487
```

```
# 17
t.test(WT.finch$infectivity, hLDLR.finch$infectivity)
```

```
##
##  Welch Two Sample t-test
##
## data:  WT.finch$infectivity and hLDLR.finch$infectivity
## t = -4.5881, df = 8.0673, p-value = 0.001745
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -2.8386332 -0.9414927
## sample estimates:
## mean of x mean of y
## 0.2536965 2.1437594
```
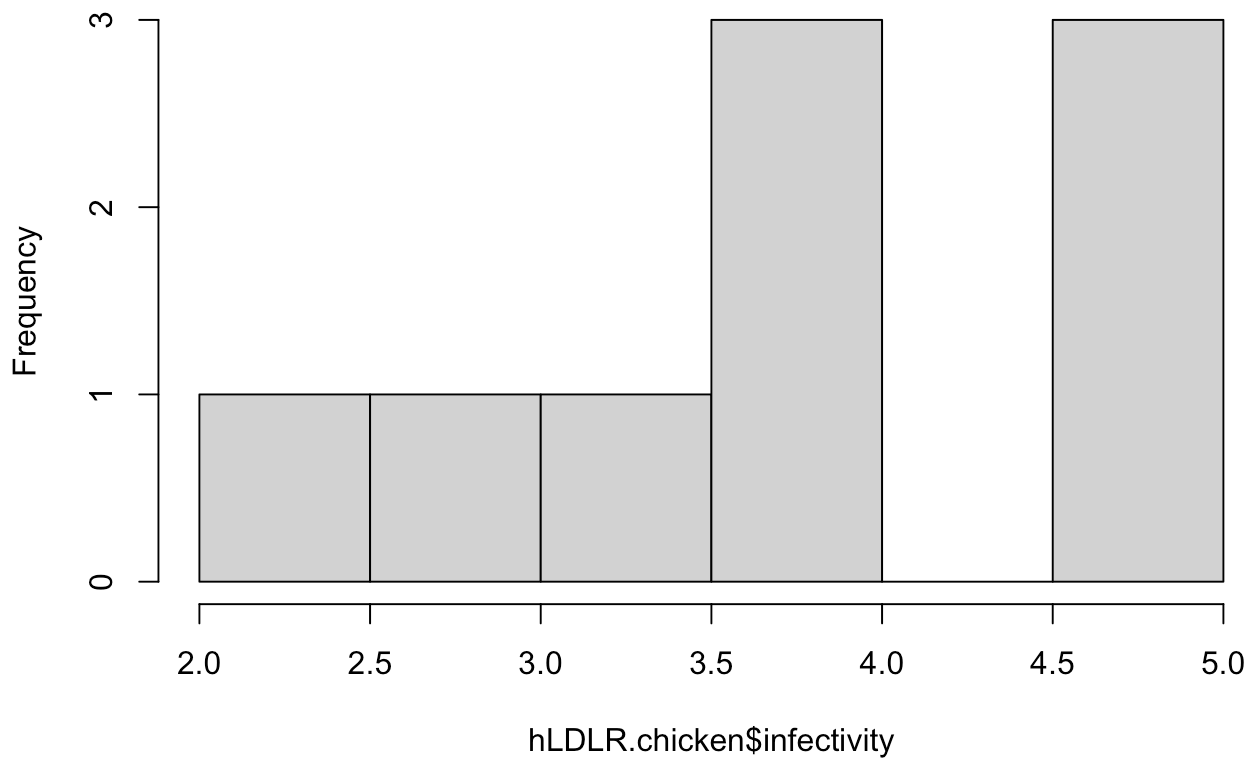
```
# 18, 19
# create histograms for both chicken group
hist(WT.chicken$infectivity)
```

Histogram of WT.chicken$infectivity
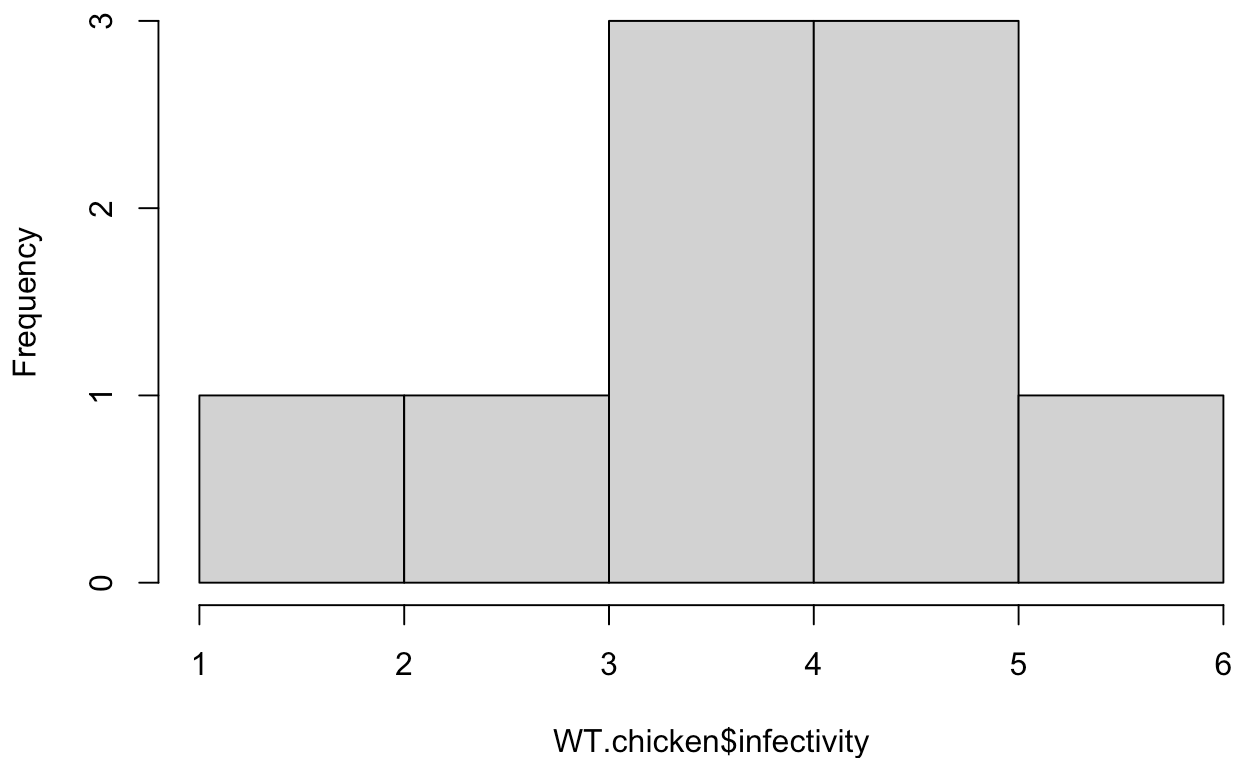

```
hist(hLDLR.chicken$infectivity)
```

Histogram of hLDLR.chicken$infectivity


```
# shapiro-wilk test
shapiro.test(WT.chicken$infectivity)
```

```
##
##   Shapiro-Wilk normality test
##
## data:  WT.chicken$infectivity
## W = 0.96768, p-value = 0.8742
```

```
shapiro.test(hLDLR.chicken$infectivity)
```

```
##
##   Shapiro-Wilk normality test
##
## data:  hLDLR.chicken$infectivity
## W = 0.9284, p-value = 0.4663
```

```
# run t-test
t.test(WT.chicken$infectivity, hLDLR.chicken$infectivity)
```

```
##
##   Welch Two Sample t-test
##
## data:  WT.chicken$infectivity and hLDLR.chicken$infectivity
## t = -0.21664, df = 13.856, p-value = 0.8316
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -1.261578  1.030304
## sample estimates:
## mean of x mean of y
##  3.590798  3.706436
```

Section 3: ANOVA and Tukey's HSD

```
# 20
infectivity.ANOVA <- aov(formula = infectivity ~ group, data=data.df)
# 21
summary(infectivity.ANOVA)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## group         3  70.15  23.384   22.86 4.26e-08 ***
## Residuals    32  32.73   1.023
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# 22
TukeyHSD(infectivity.ANOVA)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = infectivity ~ group, data = data.df)
##
## $group
##                                      diff        lwr        upr     p adj
## hLDLR Finch-hLDLR Chicken       -1.5626761 -2.8544065 -0.2709457 0.0128077
## Wild-type Chicken-hLDLR Chicken -0.1156371 -1.4073675  1.1760933 0.9948807
## Wild-type Finch-hLDLR Chicken   -3.4527391 -4.7444695 -2.1610087 0.0000002
## Wild-type Chicken-hLDLR Finch    1.4470390  0.1553086  2.7387694 0.0233404
## Wild-type Finch-hLDLR Finch     -1.8900630 -3.1817934 -0.5983326 0.0020891
## Wild-type Finch-Wild-type Chicken -3.3371019 -4.6288323 -2.0453715 0.0000004
```

Section 4: Assessment

Q1

Based on the data from step 16 and 18, since all the value of Shapiro-Wilk Test from wildtype finch, wild type chiekcn, hLDLR finch and hLDLR chicken all has a p-value greater than threshold = 0.05, the data is normal.

Q2

From step 17, we have a p value of 0.001745, based on this value and threshold of 0.05, we will reject the null hypothesis as the p value is less than the threshold. This result tell me that there is effect of hLDLR expression on VSV G infectivity in zebra finch cells.

Q3

For step 18, as we get the p value of 0.8316, which is greater than the threshold equal to 0.05. Thus, we fail to reject the null hypothesis. Hence, there is no difference in infectivity between wildtype and hLDLR chicken cell.

Q4

Null hypothesis [H0]: There is no difference in mean of infecivity among all 4 experimental cell groups: Wild type finch, wildtype chicken, hLDLR finch and hLDLR chicken.

Alternative hypothesis [H1]: There is at least one group with a difference in mean of infecivity among all 4 experimental cell groups: Wild type finch, wildtype chicken, hLDLR finch and hLDLR chicken.

Q5

For step 21, we got p value = 4.26e-08, since p value is less than the significance threshold of 0.05, we will reject the null hypothesis. Hence, we can concluded that there is difference in mean of VSV G infectivity in terms of 4 experimental cell groups.

Q6

1. hLDLR finch and hLDLR chicken group has significant comparsion with p value equal to 0.0128077, this suggest that there is a significant difference in mean infectivity between these 2 group.
2. wild-type finch and hLDLR chicken has the most signifiant comparsion as it has the smallest p value among all the group. This suggest that there is a significant difference in mean infectivity between these 2 group.
3. wild-type chicken and hLDLR finch also have a significant comparsion with p value less than 0.05, this suggest that there is a significant difference in mean infectivity between these 2 group.
4. wild type finch and hLDLR finch has a significant compasrsion, but it is not as significant as other group as it has p value 0.0233404, which is the biggest p value for all the p value less than 0.05. This suggest that there is a significant difference in mean infectivity between these 2 group.
5. Wild type finch and wild type Chicken has significant comparsion with p value equal to 0.0000004, this suggest that there is a significant difference in mean infectivity between these 2 group.

Overall, we get to see there is a significant comparsion among finch and chicken group. The mean infectivity between the wild type chicken and hLDLR chicken is very similar to each other.