

Updated Results Diagnostics

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3/22/2021

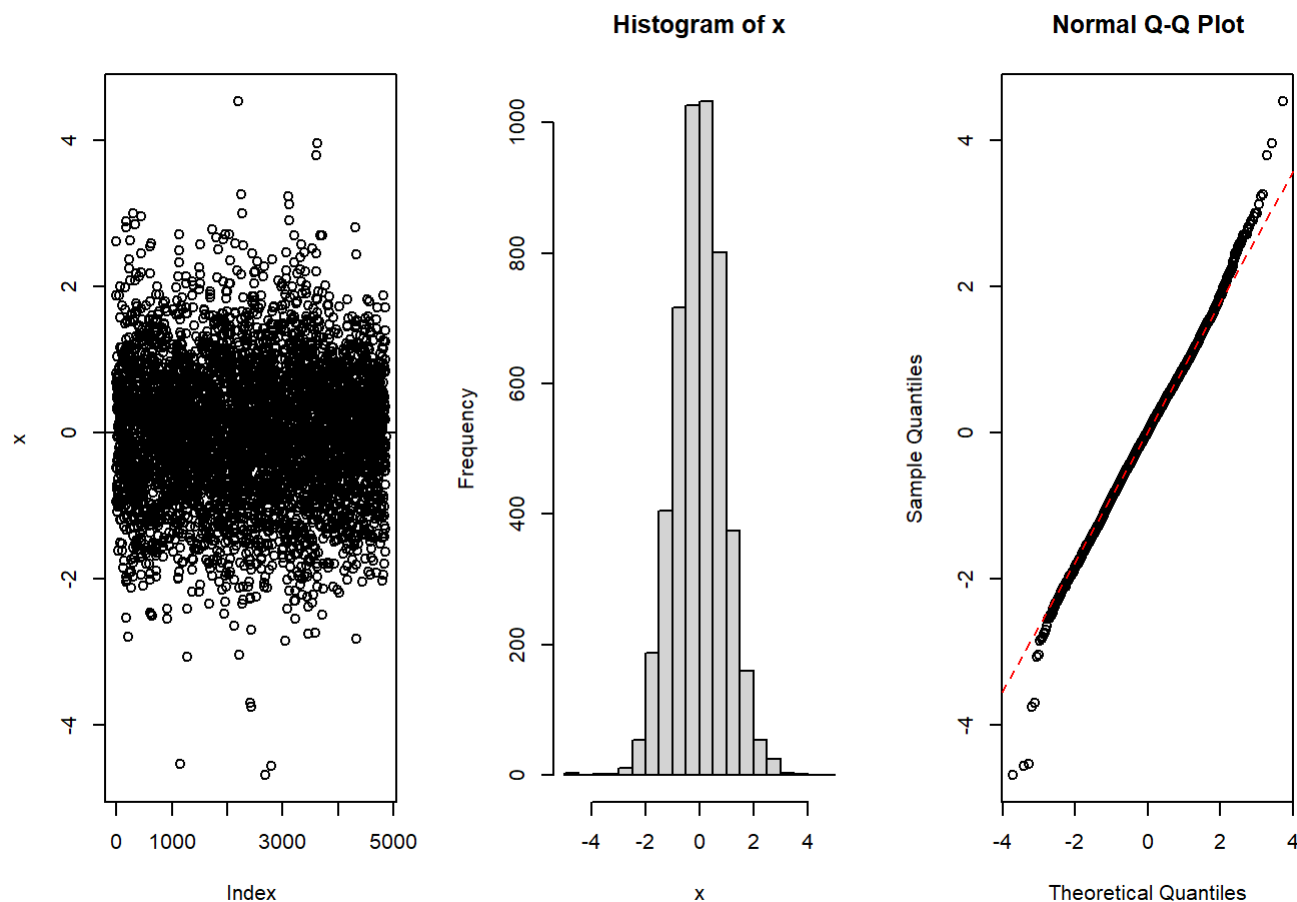
Model 1: $\text{trait} \sim \text{mainland/island} + \text{year} + (1|\text{ID})$

This model looks at the differences between *Tribulus* mericarps, flowers and leaves from mainland and island populations.

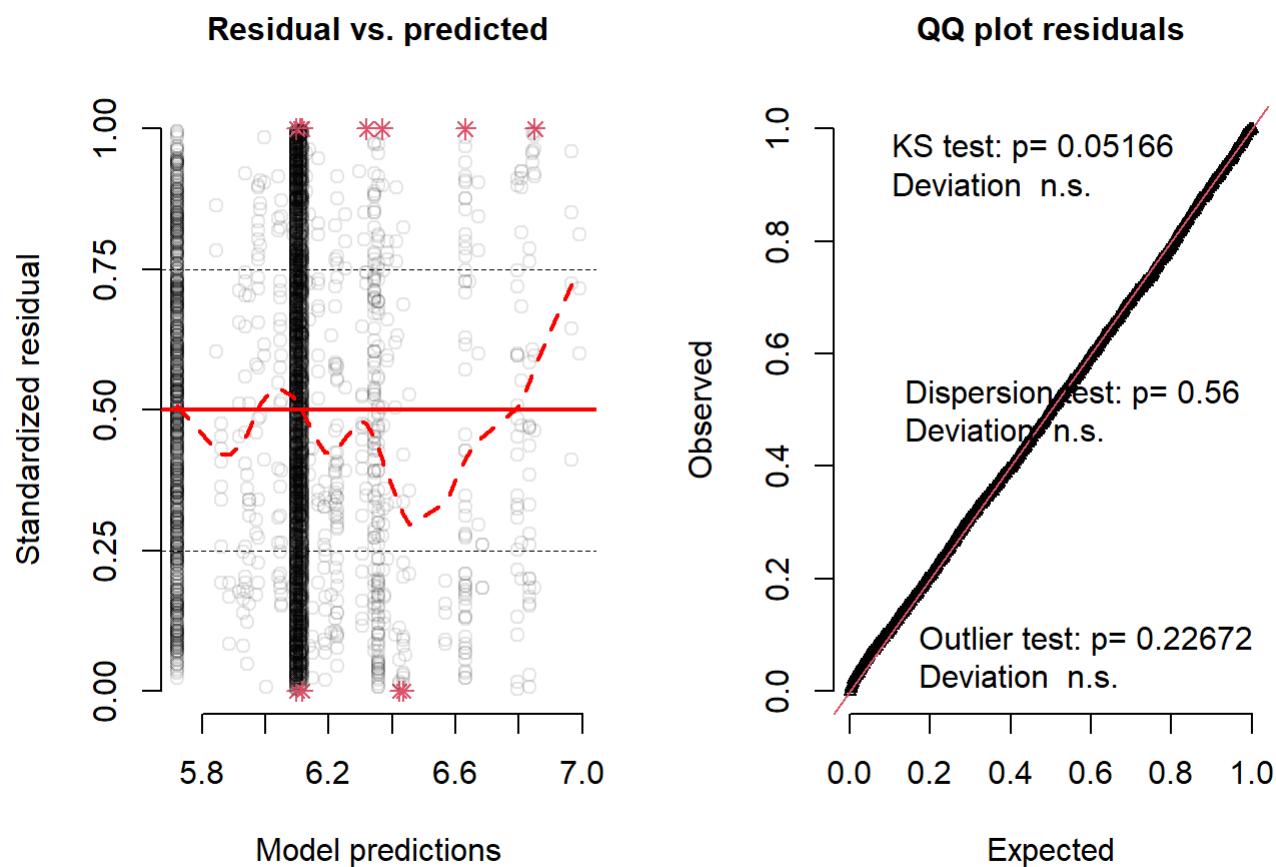
Mericaarp traits:

Length

Best fitted data: Untransformed data

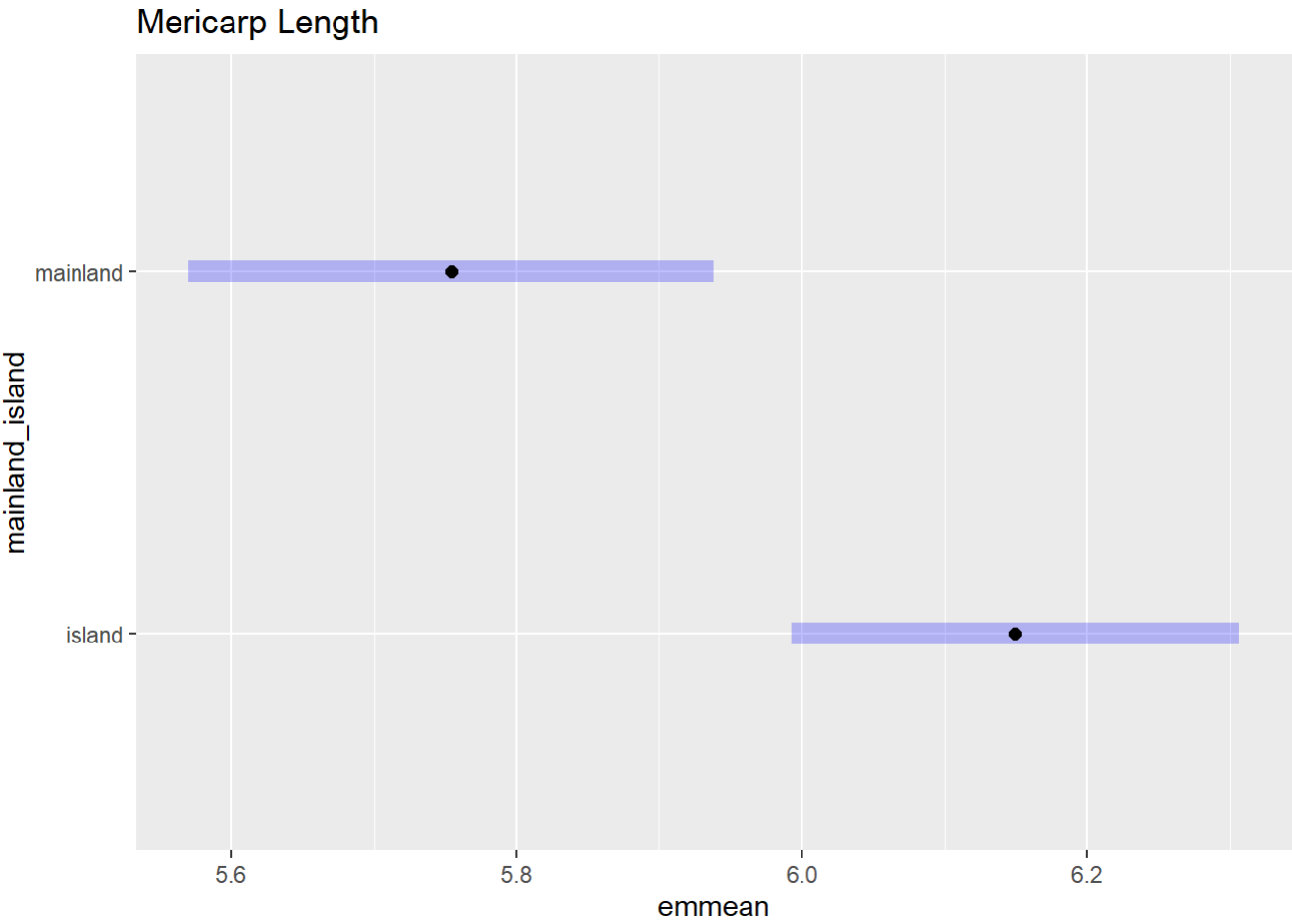


```
## [1] "Kurtosis=0.64698123476754"
## [1] "Skew=-0.0153024526537272"
```



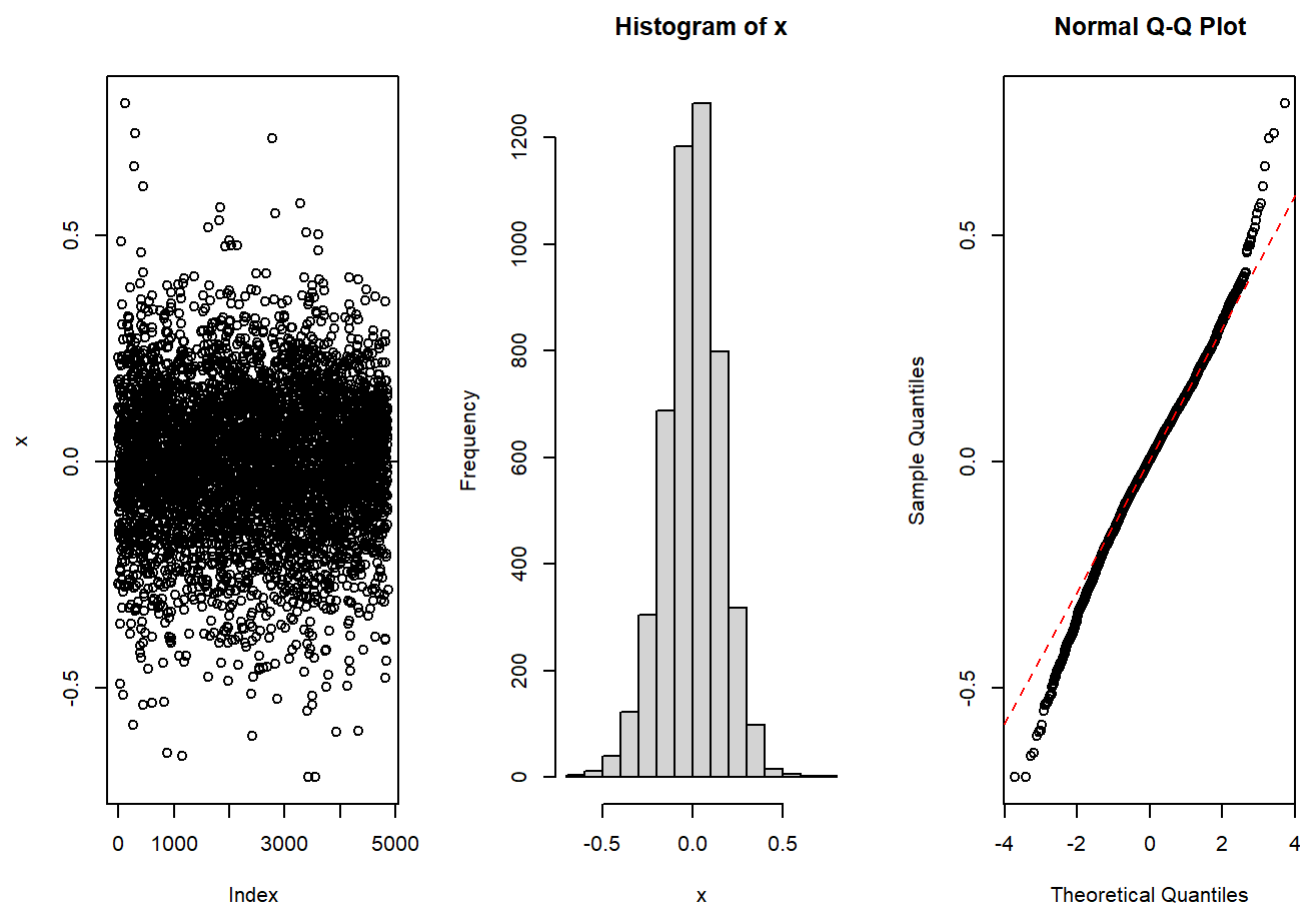
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: length
##           Chisq Df Pr(>Chisq)
## mainland_island 10.731  1  0.001054 **
## year_collected 10.827  1  0.001000 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Emmeans: Length

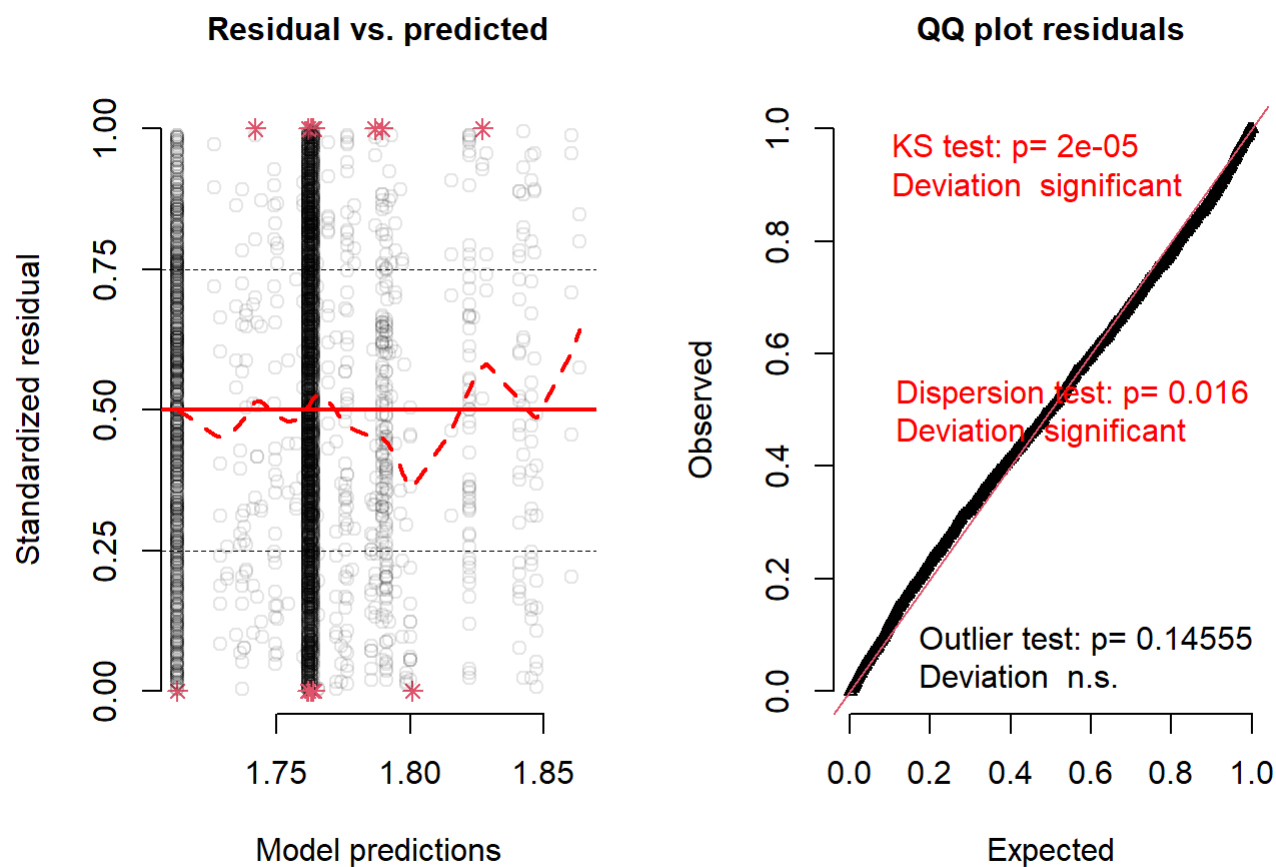


Width

Best fitted data: Square root transformed data

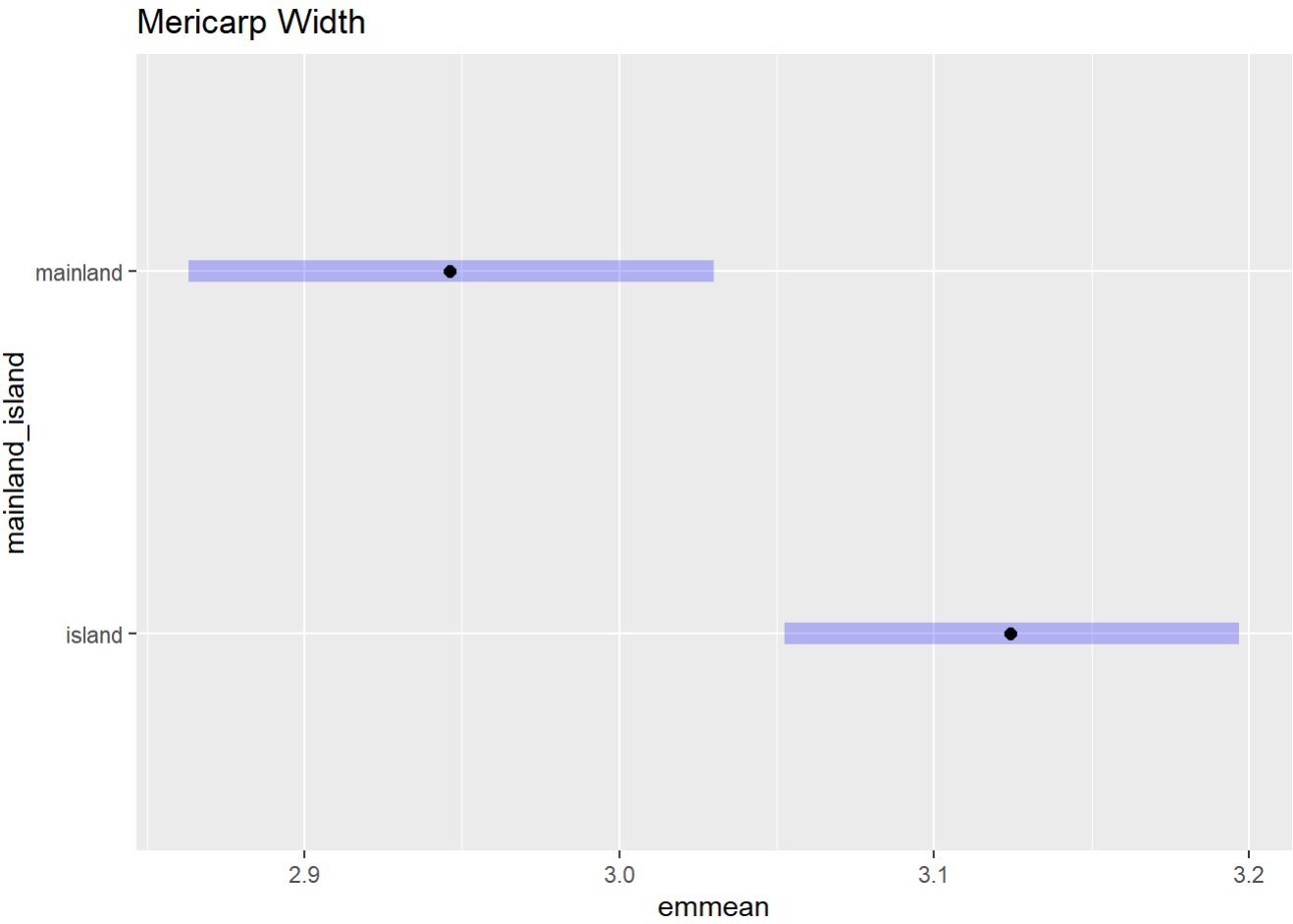


```
## [1] "Kurtosis=0.915288926843053"
## [1] "Skew=-0.184236416326029"
```



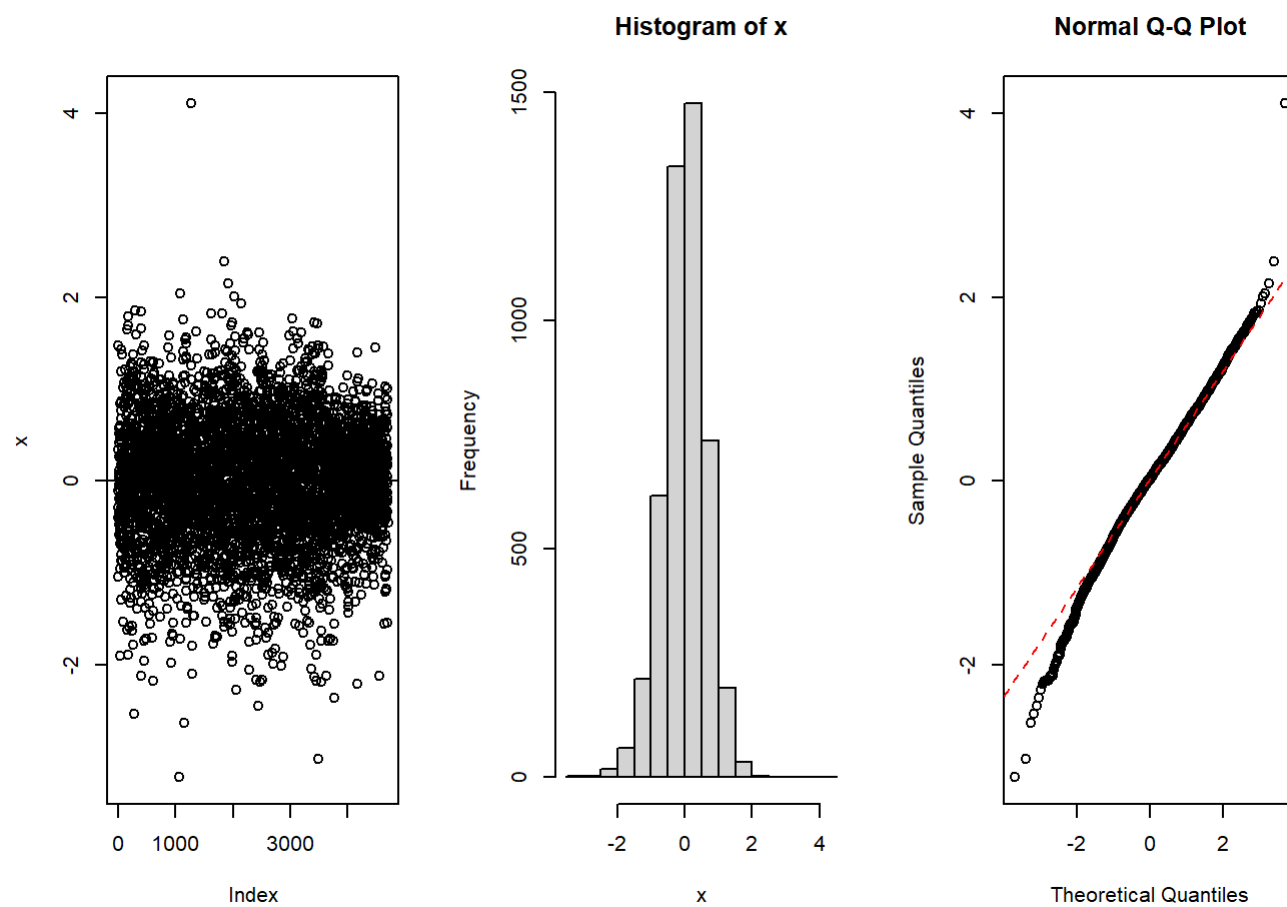
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(width)
##           Chisq Df Pr(>Chisq)
## mainland_island 10.36 1 0.001288 **
## year_collected  7.84 1 0.005110 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Emmeans: Width

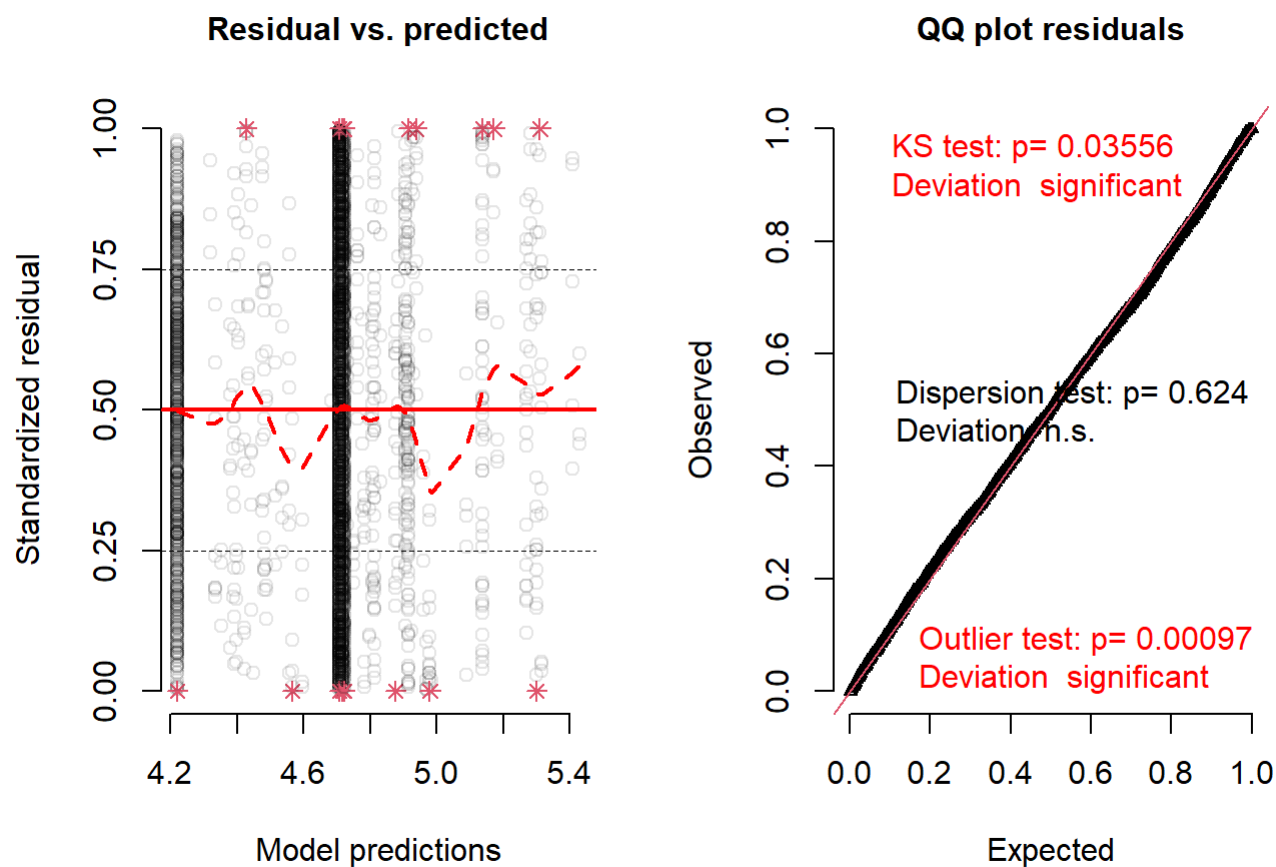


Depth

Best fitted data: Untransformed data

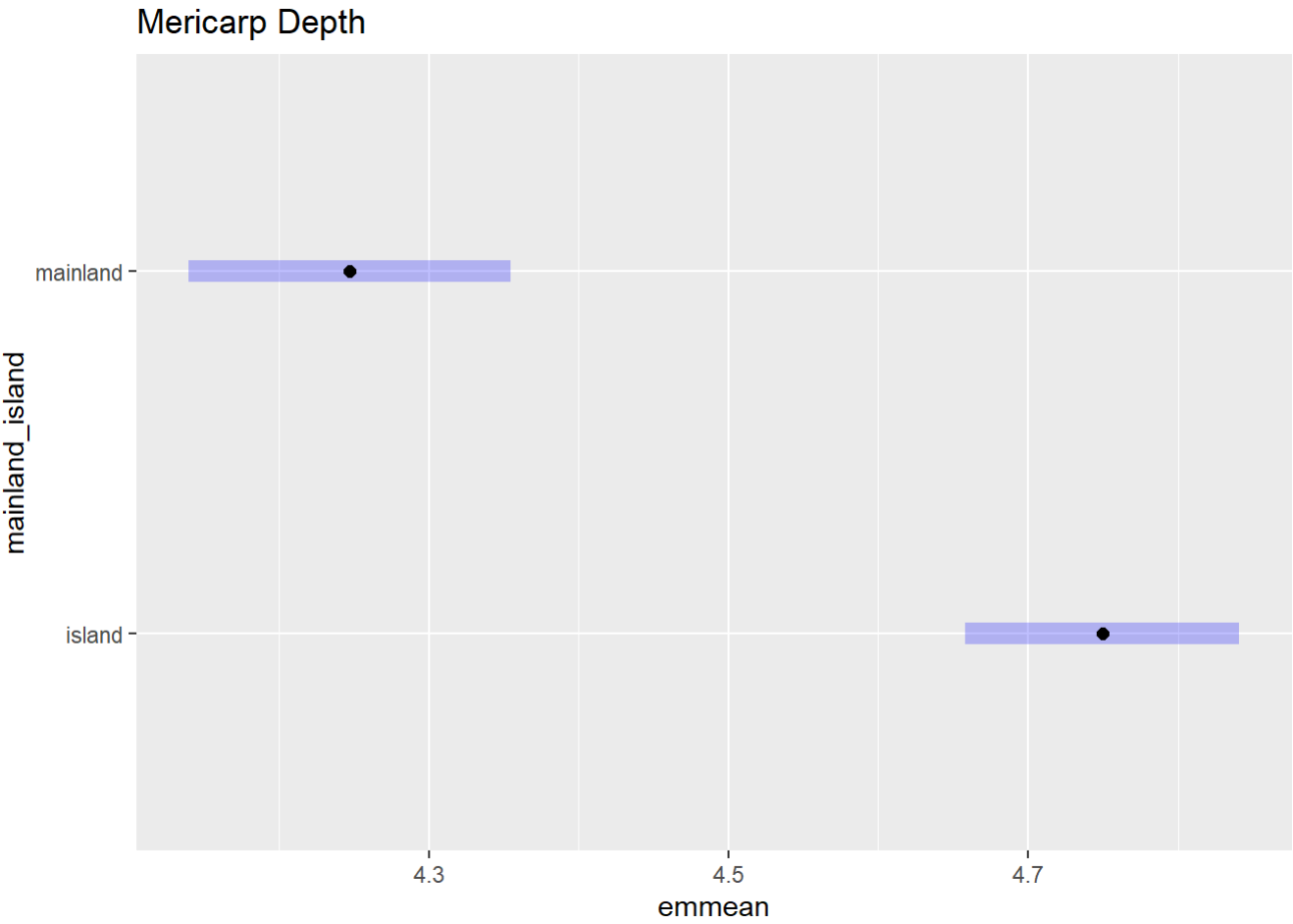


```
## [1] "Kurtosis=0.989267427953835"
## [1] "Skew=-0.241253118215469"
```



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: depth
##           Chisq Df Pr(>Chisq)
## mainland_island 50.871  1 9.865e-13 ***
## year_collected  20.387  1 6.325e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Emmeans: Depth



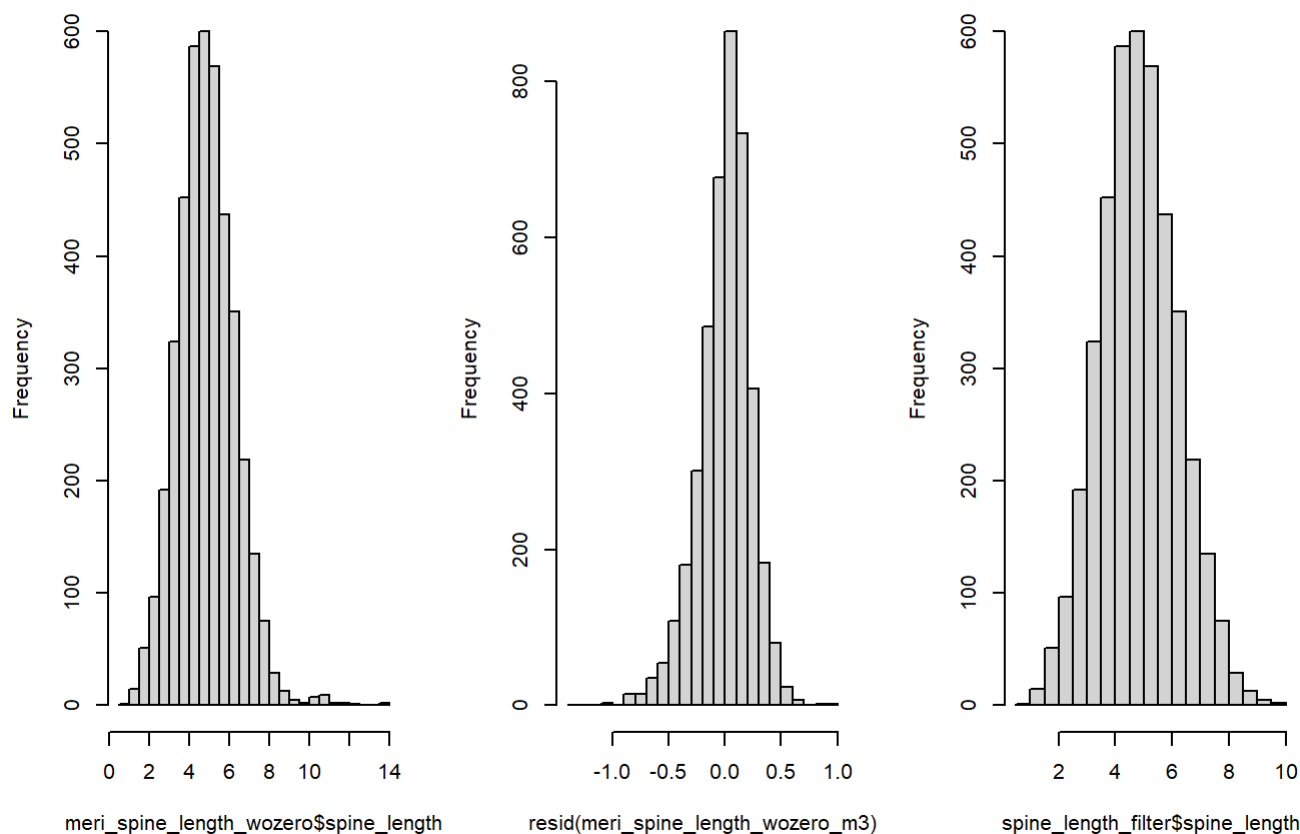
Spine length

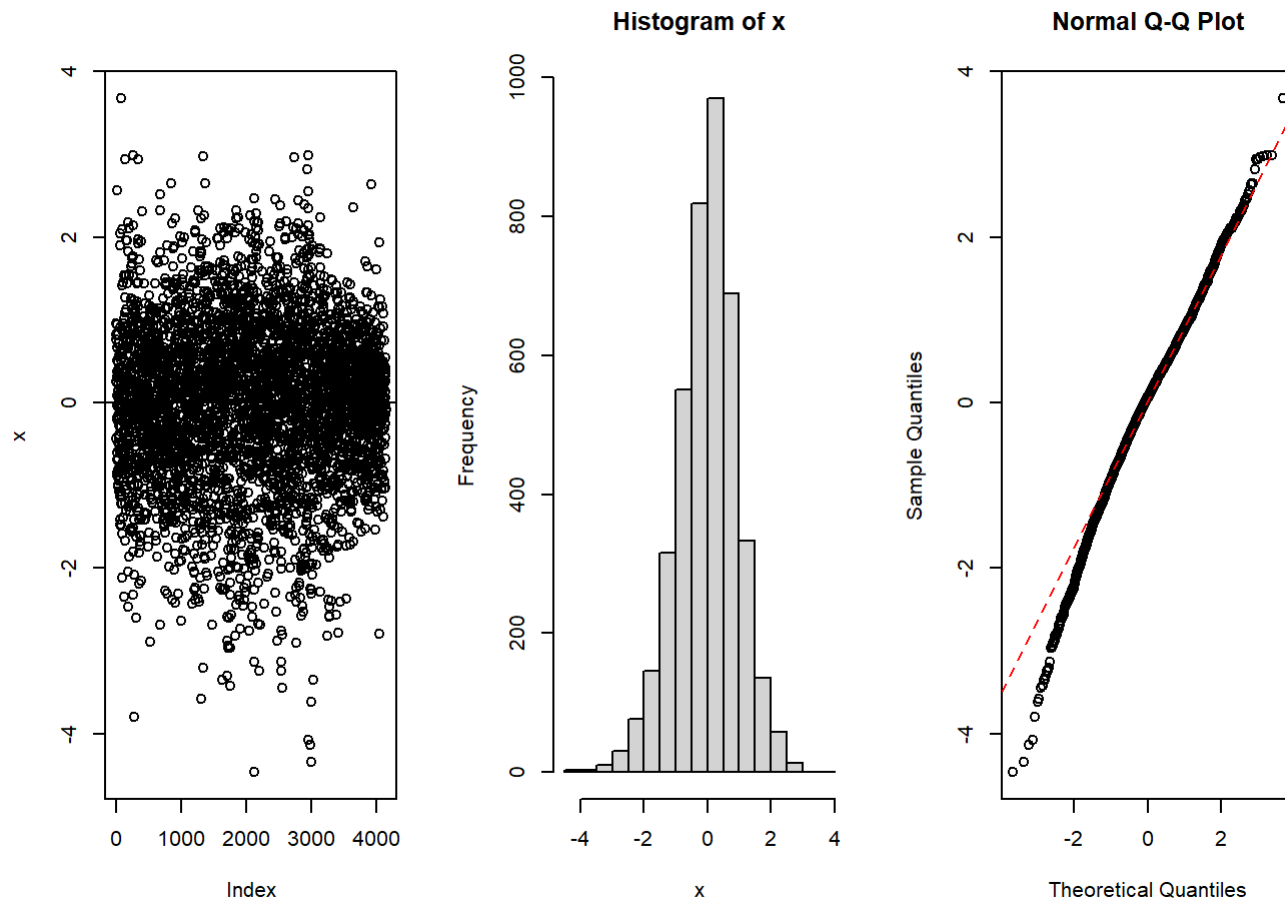
Spine length had a lot zeroes that were removed, also I filter the data again because the residual distribution was skewed. I removed spines larger than 10 mm. This filter removed some individuals from Baltra Island. Here I show the best model fit after filtering.

The histograms show the distribution of spine length measurements. The residual distribution of the unfiltered model, and the spine length distribution of the filtered data.

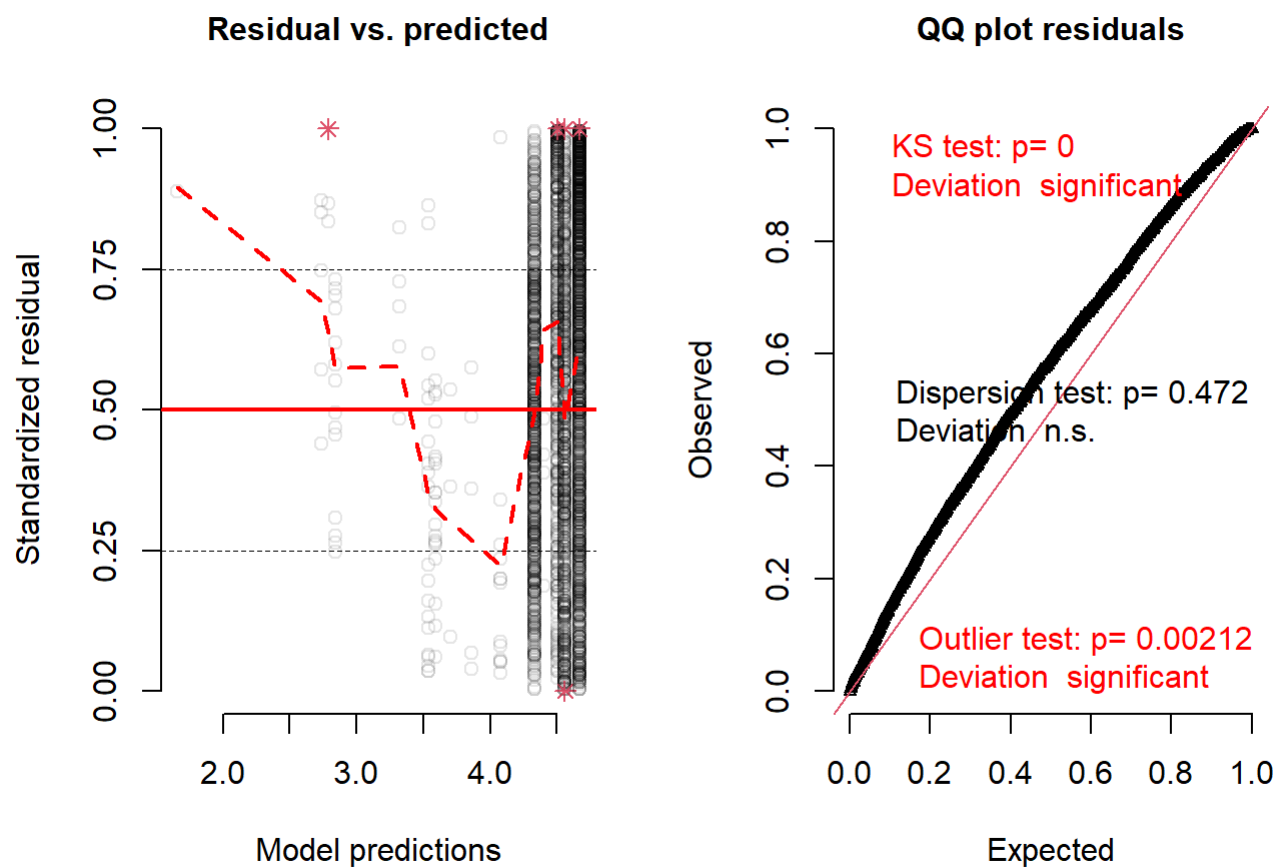
Best fitted data: Untransformed data.

Diagram of meri_spine_length_wozero\$spine_length Histogram of resid(meri_spine_length_wozero_m3) Histogram of spine_length_filter\$spine_length





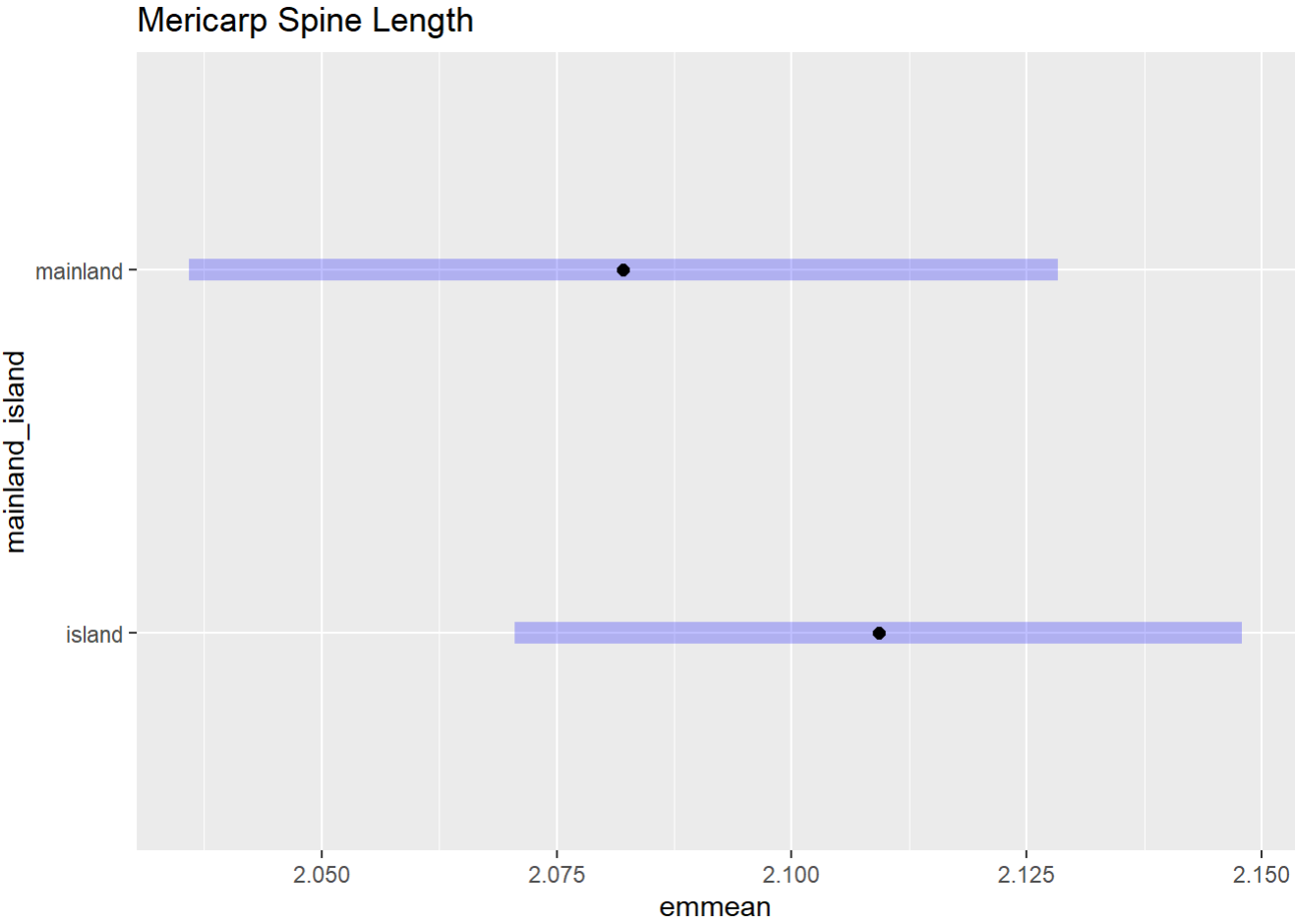
```
## [1] "Kurtosis=0.748351232224566"
## [1] "Skew=-0.359277318386279"
```



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: spine_length
##               Chisq Df Pr(>Chisq)
## mainland_island  2.1413  1    0.1434
## year_collected 25.6152  1 4.168e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Mainland/island groups non significant

Emmeans: Spine length



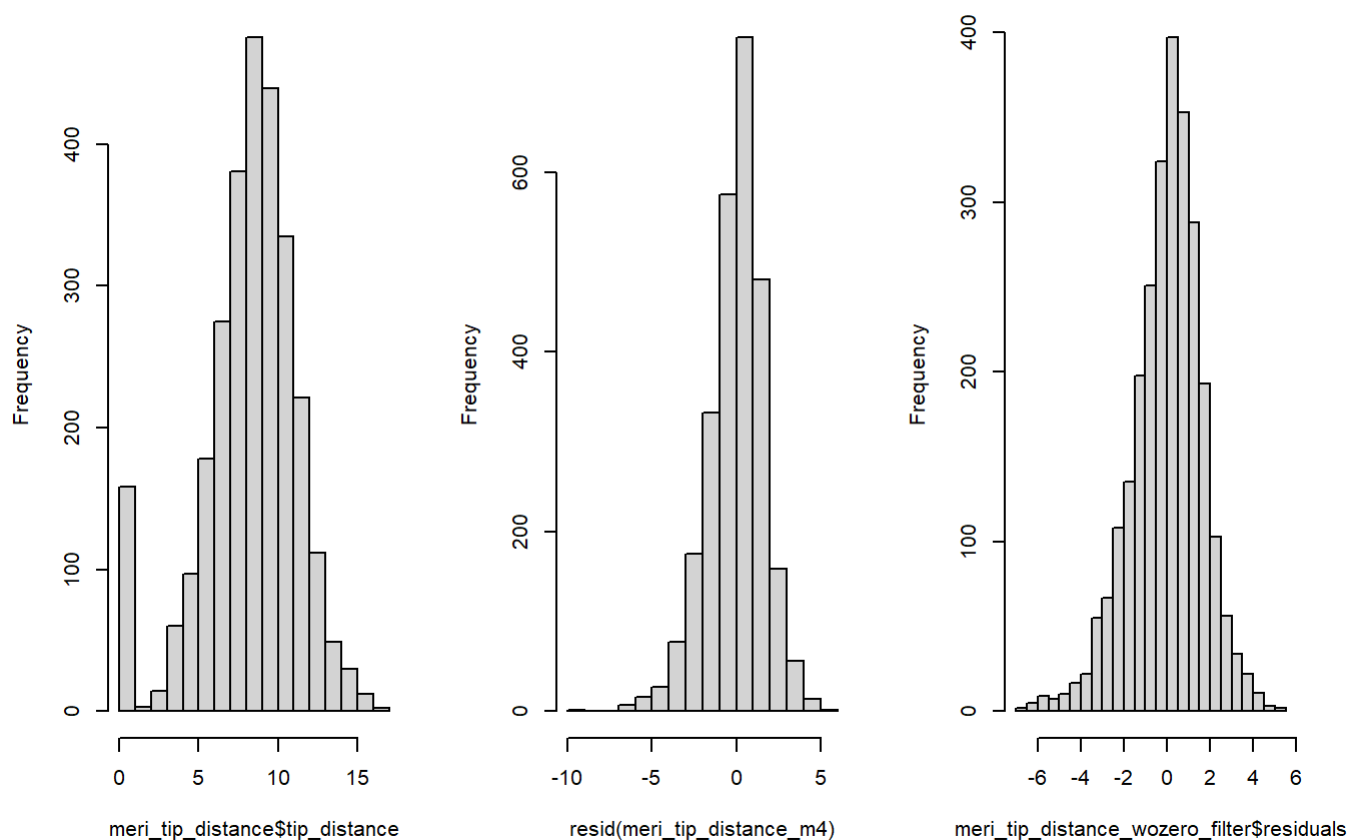
Tip distance

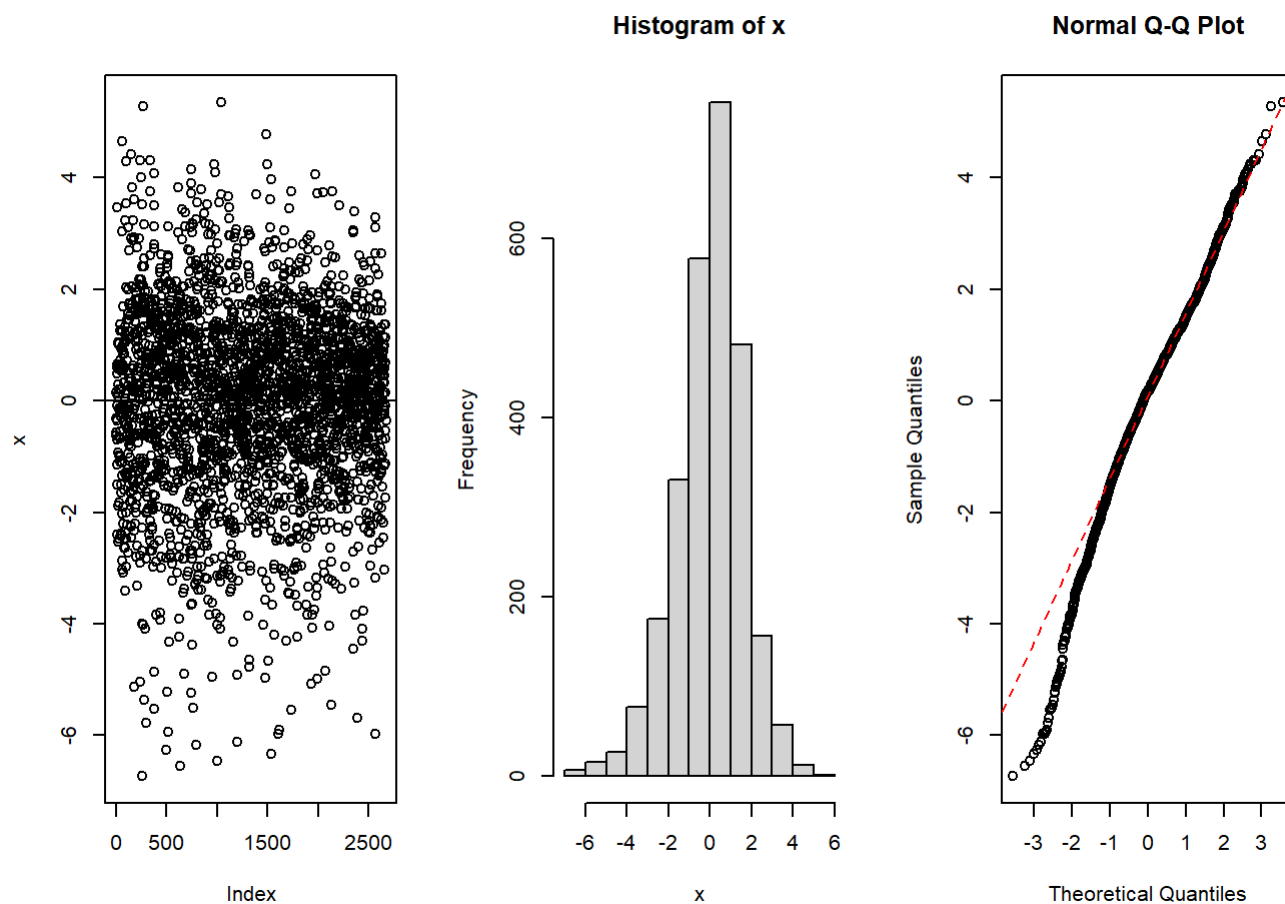
In a similar way, tip distance had a lot zeroes that were removed. I show three histograms with the distributions of tip distance measurements with zeros included. The residuals of the original model and the residuals distribution after filtering.

The diagnostic function shows the residuals distribution after removing zeros and filtering residuals that were lower than -5. This removed specimen 383.

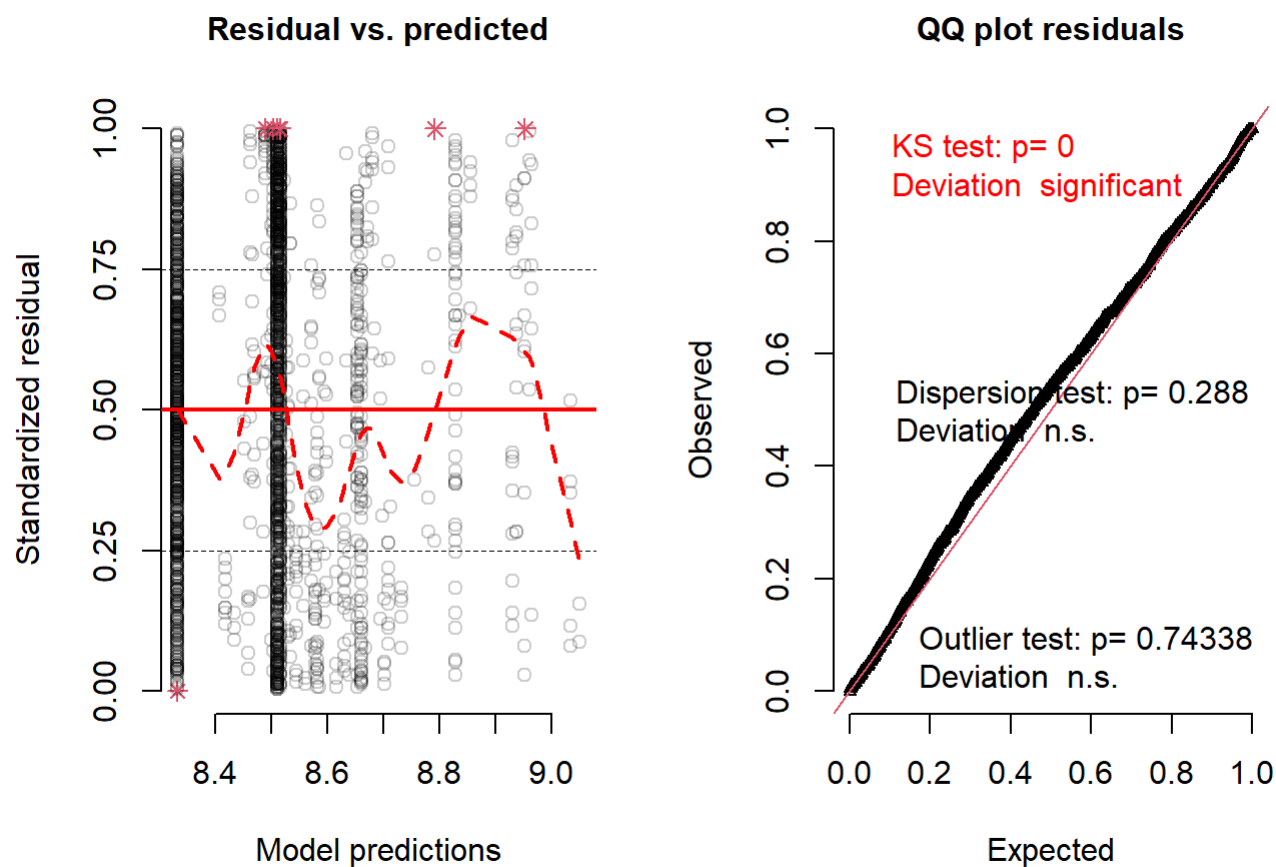
Best fitted data: Untransformed data.

Histogram of meri_tip_distance\$tip_dis Histogram of resid(meri_tip_distance_ram of meri_tip_distance_wozero_filte





```
## [1] "Kurtosis=0.981641657570068"
## [1] "Skew=-0.521061407190251"
```

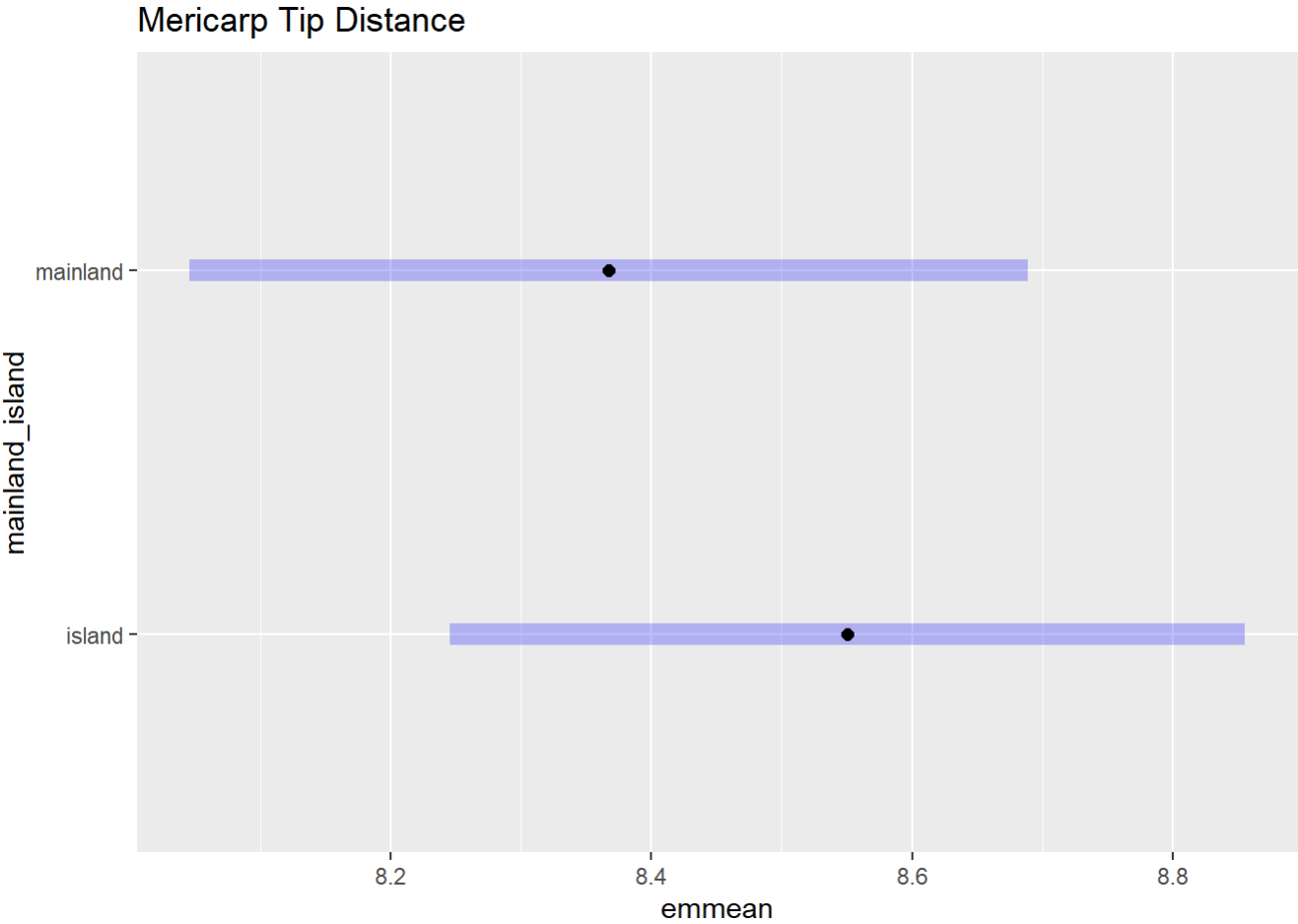


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: tip_distance
##           Chisq Df Pr(>Chisq)
## mainland_island 0.6821 1    0.4089
## year_collected 1.1957 1    0.2742
```

Mainland/island groups non significant

Year groups non significant

Emmeans: Tip distance



Lower spines

Presence/absence of lower spines is a binomial trait for this one I used two models that showed different outcomes. The first one is a glm: **glm(lower_spines ~ mainland_island + year_collected)**.

This model includes year as a factor but does not contain ID as a random effect.

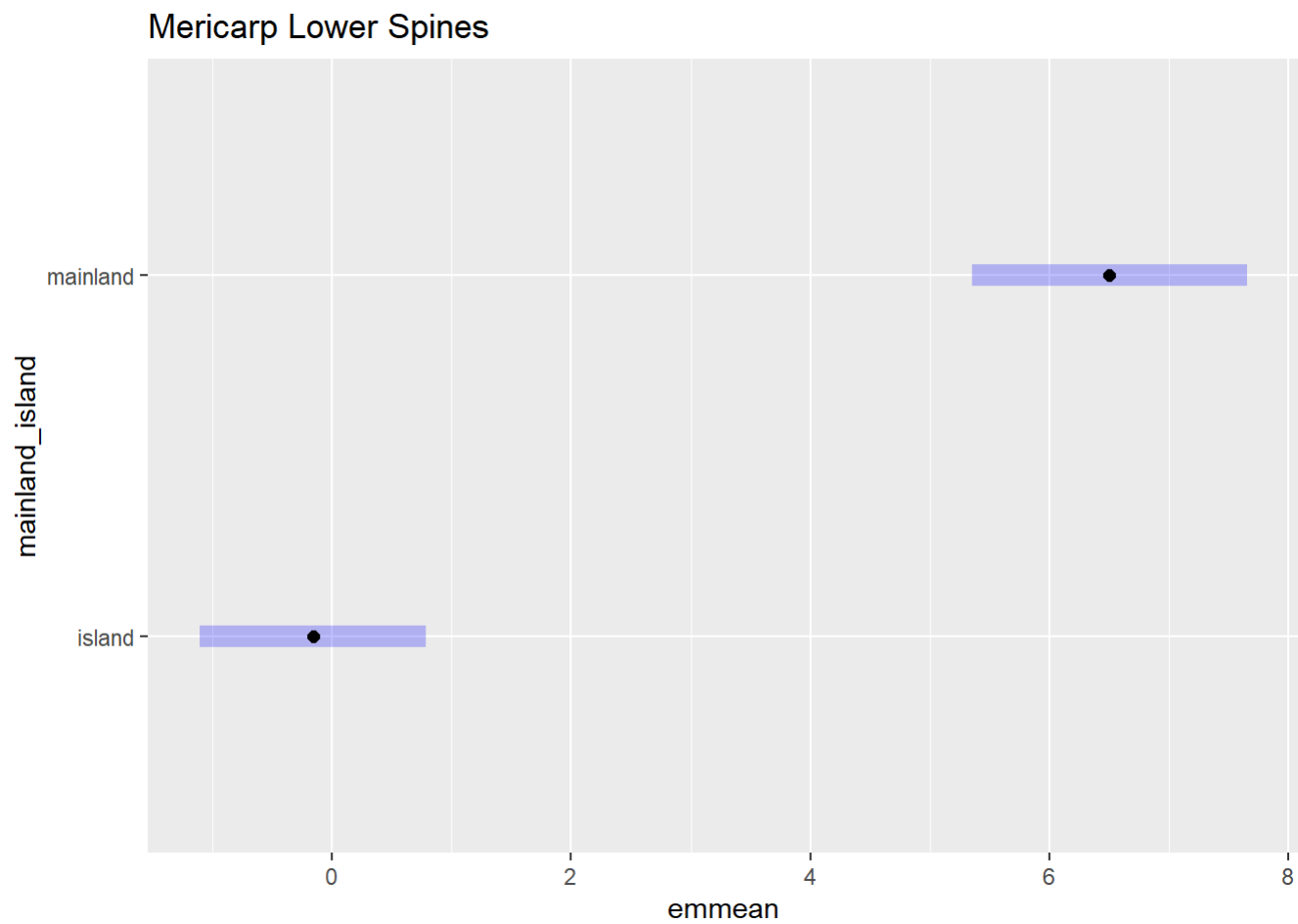
The second one using the *glmmTMB* package: **glmmTMB(lower_spines ~ mainland_island + (1|ID))**

The glmmTMB model does not include the year factor but does include the random ID effect.

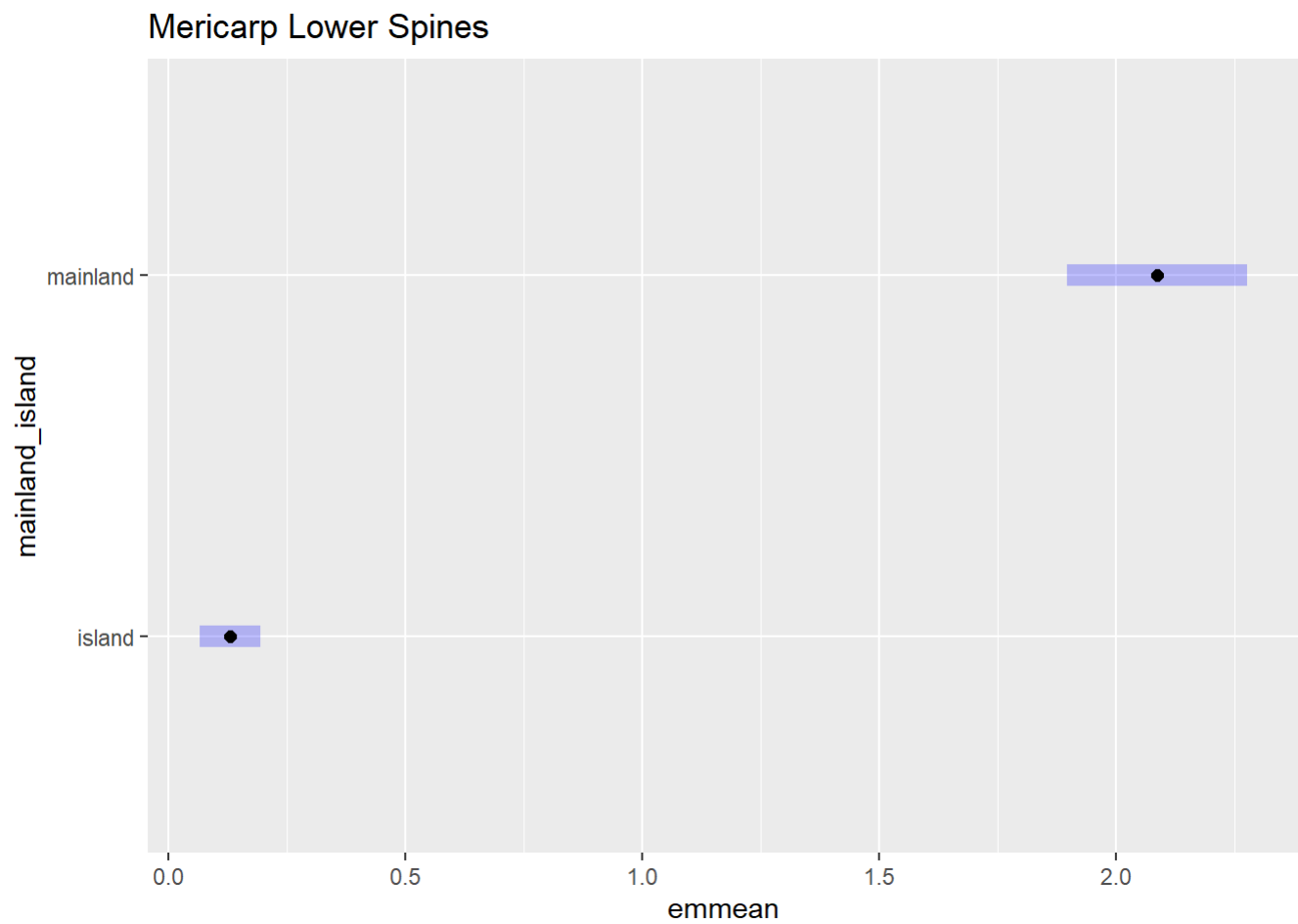
```
## Analysis of Deviance Table (Type II tests)
##
## Response: lower_spines
##              LR Chisq Df Pr(>Chisq)
## mainland_island  515.40  1  < 2.2e-16 ***
## year_collected   11.99  1  0.0005335 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: lower_spines
##              Chisq Df Pr(>Chisq)
## mainland_island 73.898  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Emmeans: Lower spines



First plot, glm model. Second plot, glmmTMB model.



First plot, glm model. Second plot, glmmTMB model.

Upper spines

Presence/absence of upper spines is a binomial trait that replaced spine number. Similar as lower spines, I used two models that showed different outcomes. The first one is a glm: **glm(upper_spines ~ mainland_island + year_collected)**.

This model includes year as a factor but does not contain ID as a random effect.

The second one using the *glmmTMB* package: **glmmTMB(upper_spines ~ mainland_island + (1|ID))**

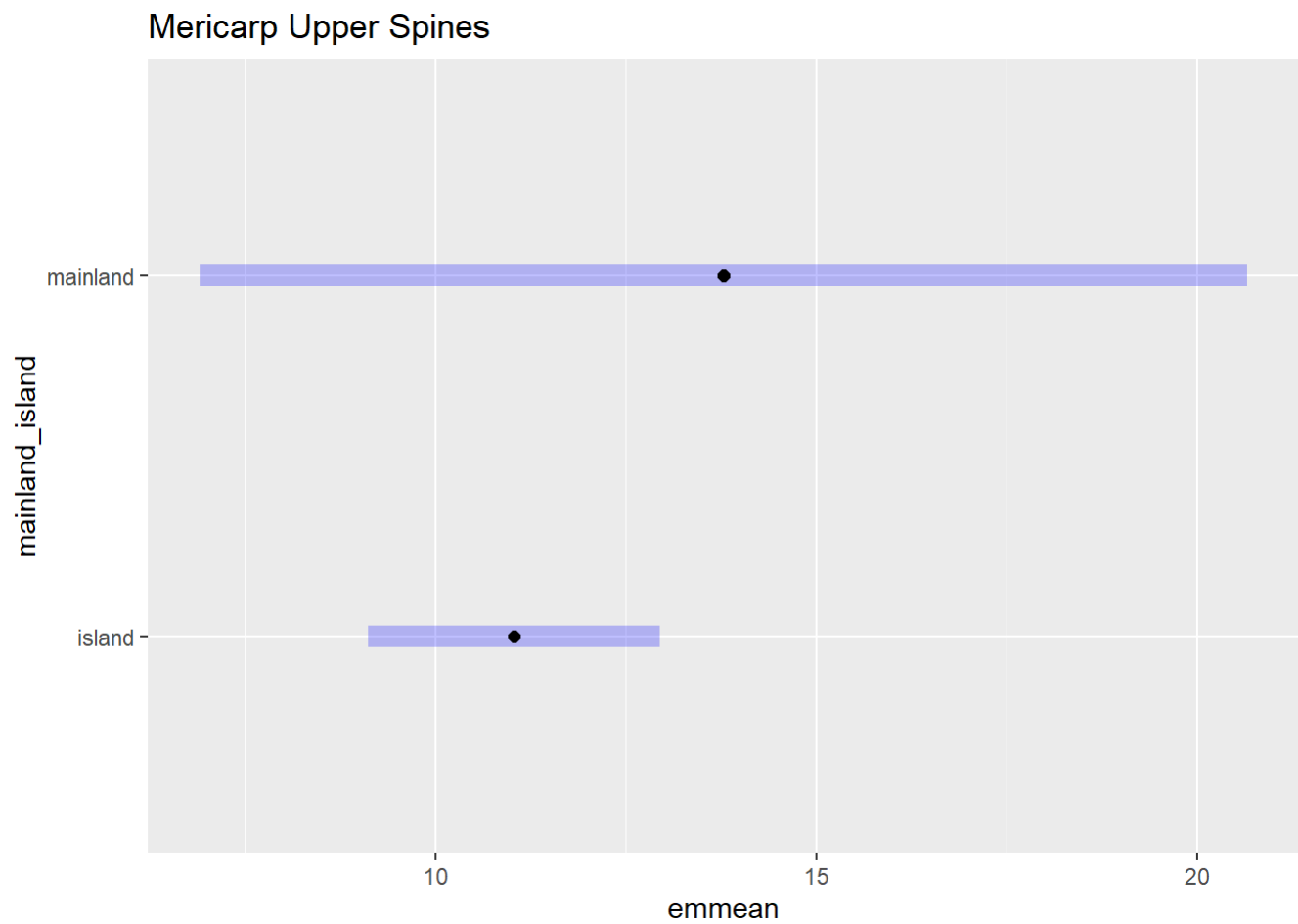
The glmmTMB model does not include the year factor but does include the random ID effect.

```
## Analysis of Deviance Table (Type II tests)
##
## Response: upper_spines
##              LR Chisq Df Pr(>Chisq)
## mainland_island   94.046  1 < 2.2e-16 ***
## year_collected    34.208  1 4.953e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

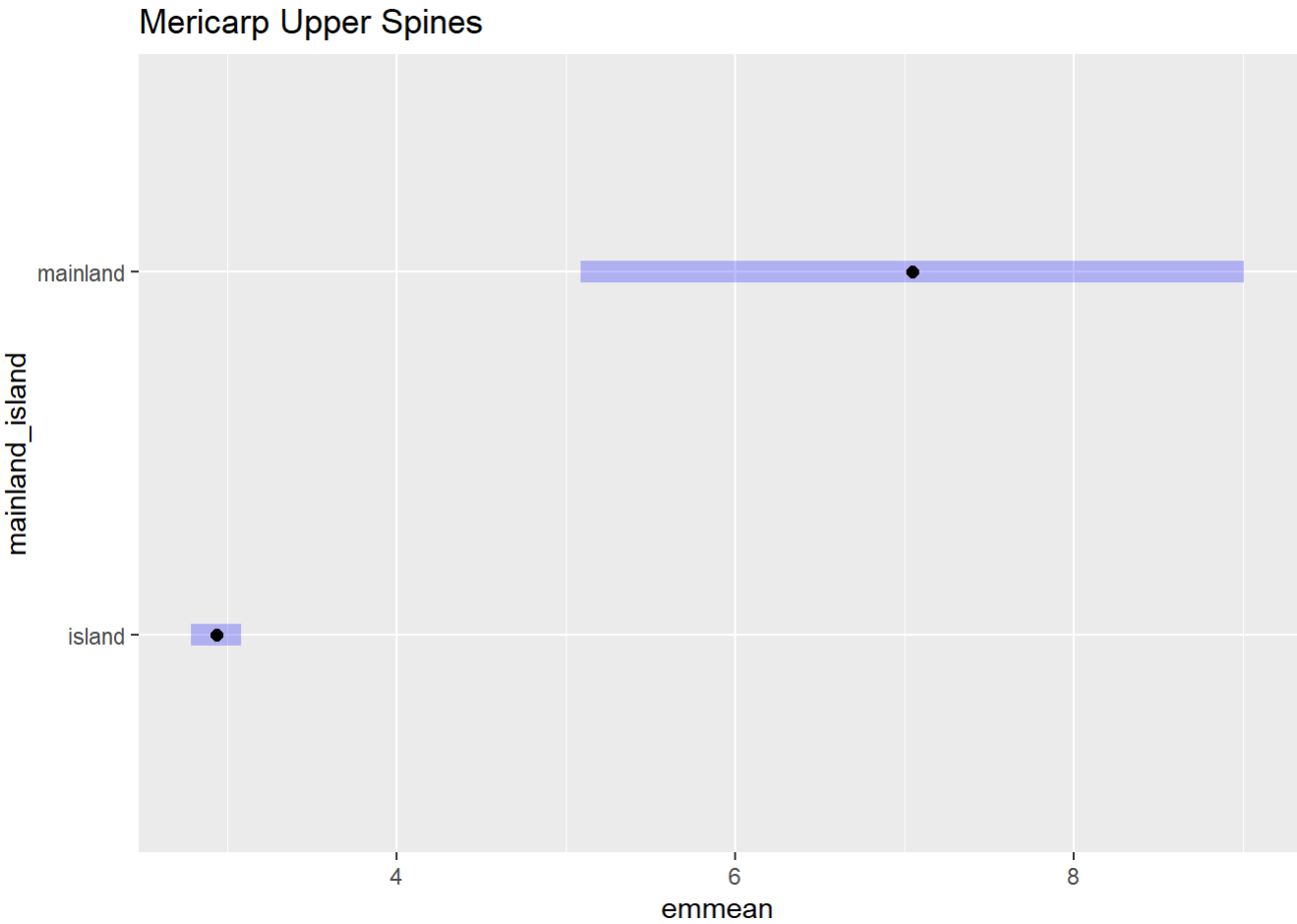
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: upper_spines
##              Chisq Df Pr(>Chisq)
## mainland_island 0.6146  1      0.433
```

Here, for the glm model the results are significant, but for the glmmTMB the differences between mainland and island populations are not significant.

Emmeans: Lower spines



First plot, glm model. Second plot, glmmTMB model.

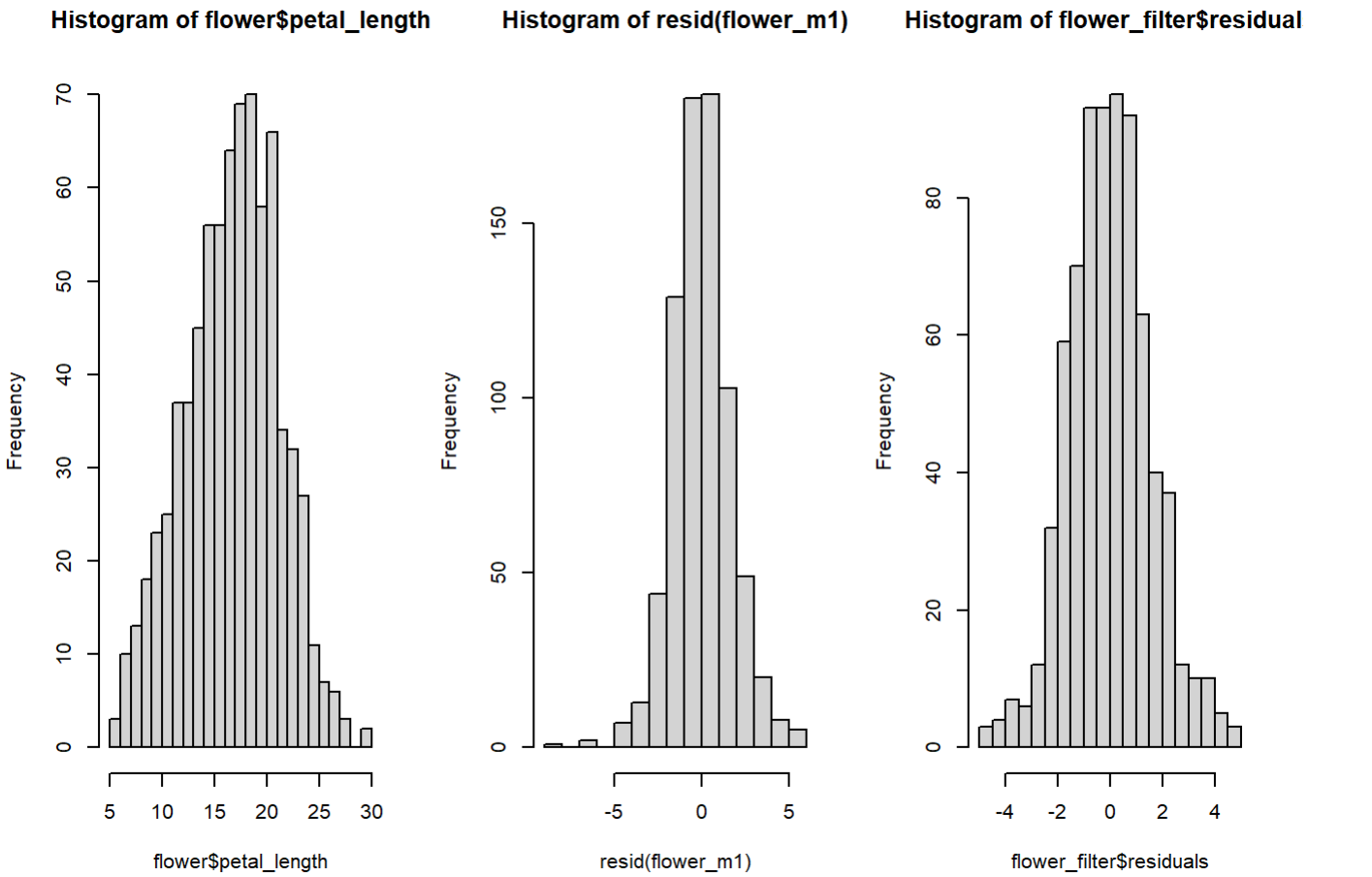


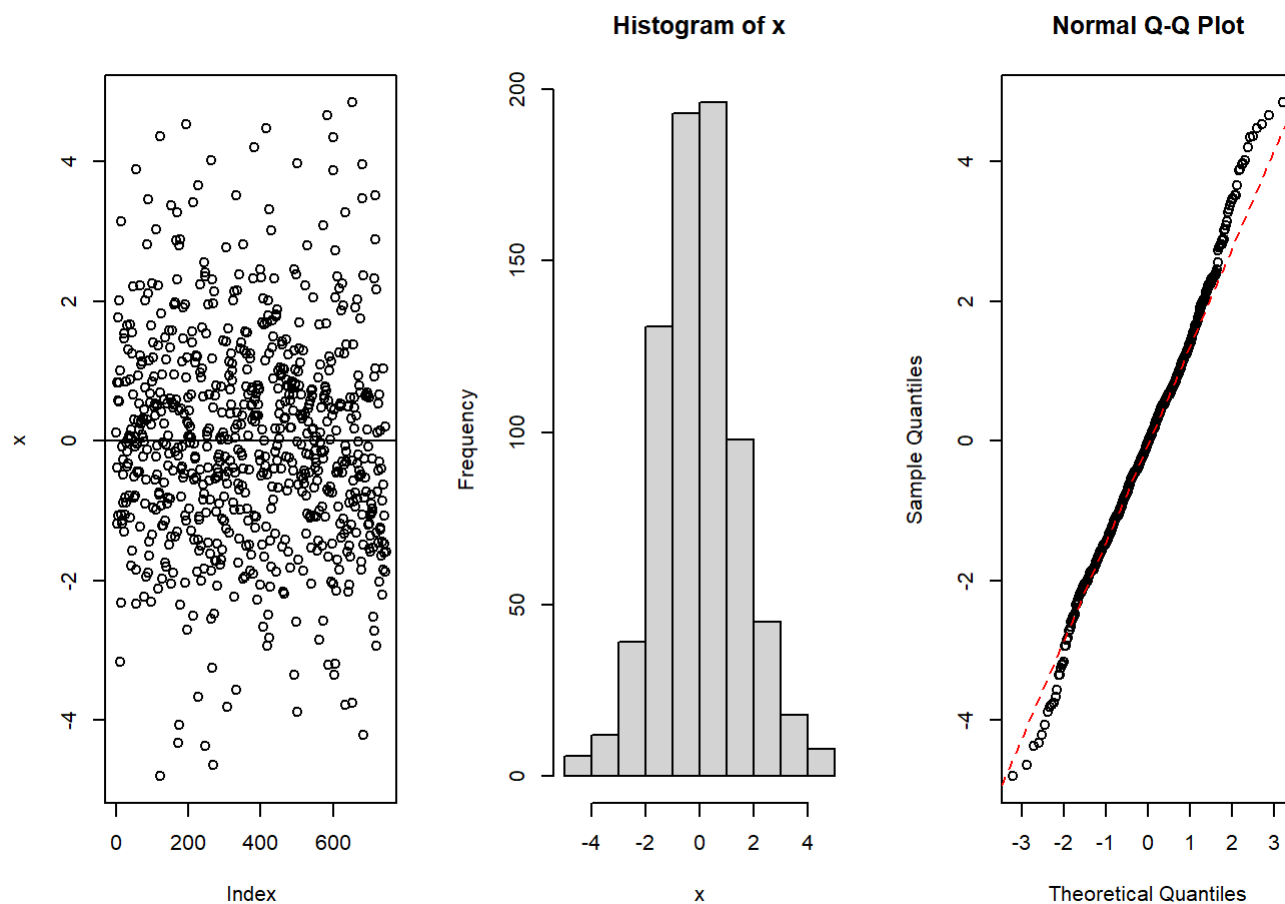
First plot, glm model. Second plot, glmmTMB model.

Flower traits:

Petal length

Best fitted data: Untransformed data Filter residuals. This filter removed specimens 240, 351, 320 (<-5) and 454, 319, 207, 249, 340 (>5)

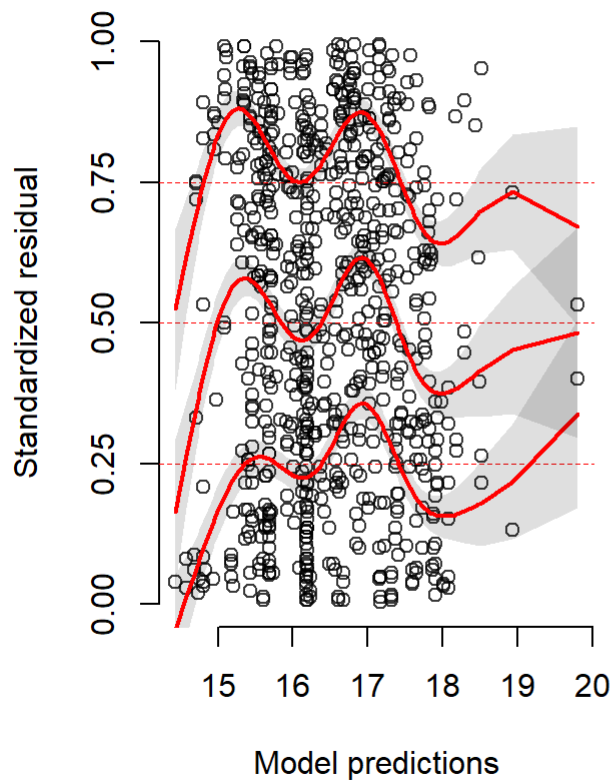




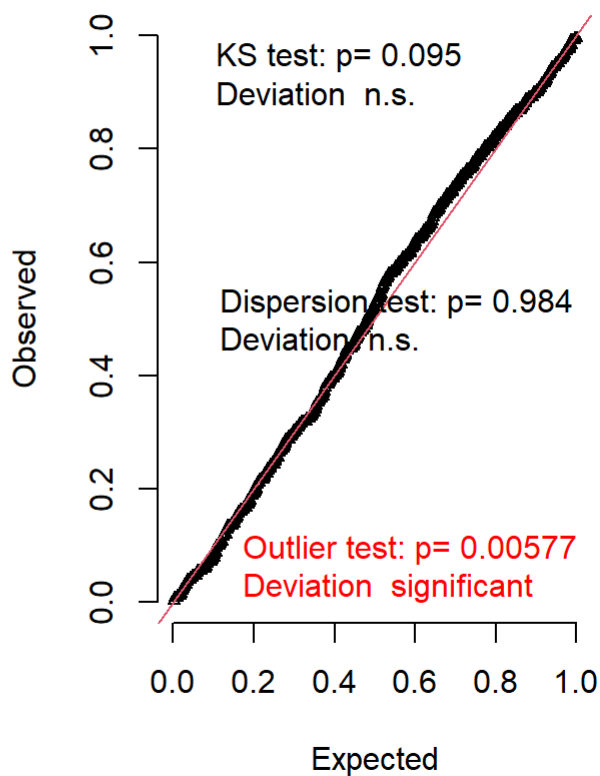
```
## [1] "Kurtosis=0.548589780356622"
## [1] "Skew=0.149144911337373"
```

```
## qu = 0.75, log(sigma) = -2.582137 : outer Newton did not converge fully.
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



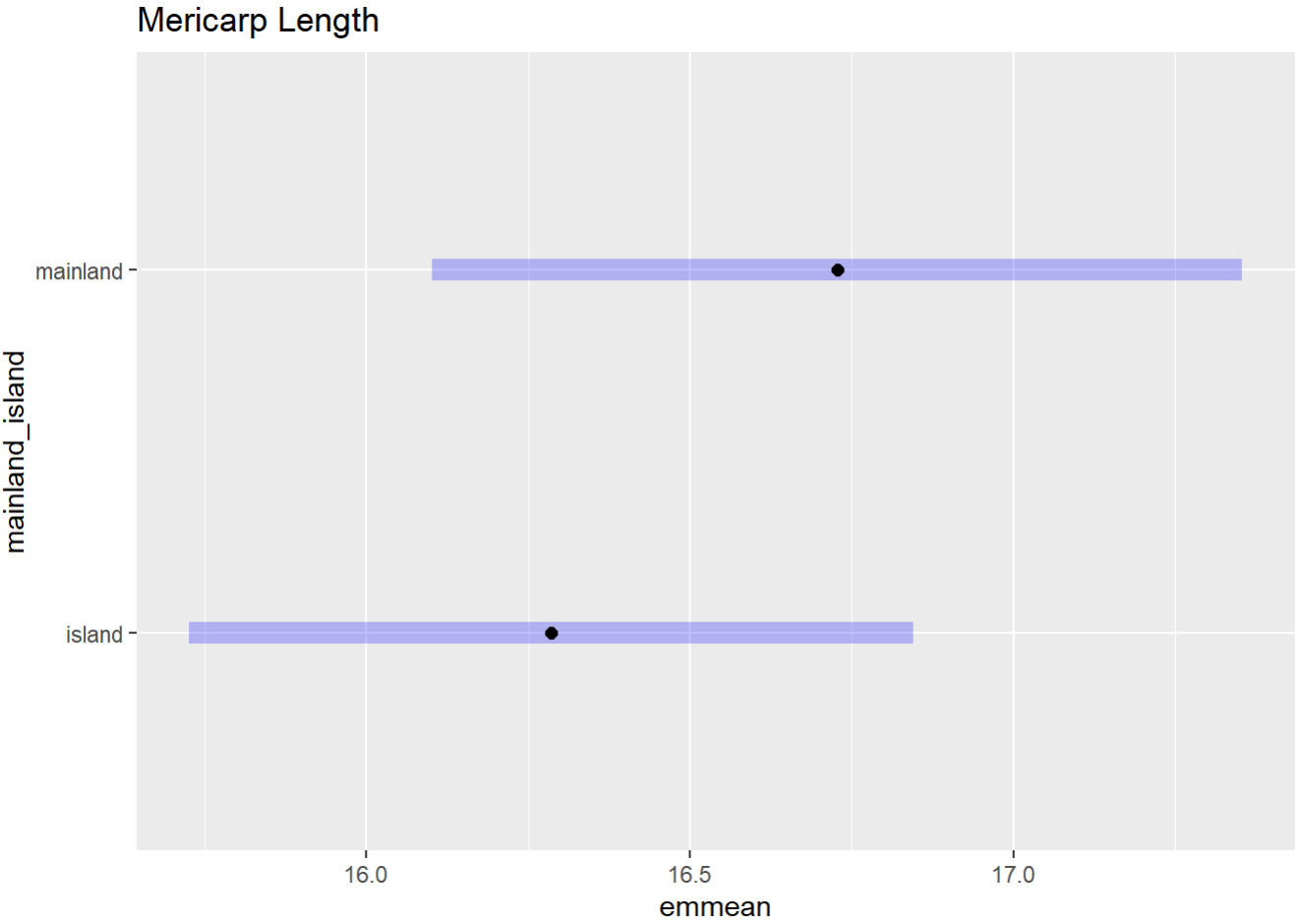
QQ plot residuals



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: petal_length
##               Chisq Df Pr(>Chisq)
## mainland_island  1.0773  1    0.2993
## year_collected 15.8995  1   6.68e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Mainland and island differences are not significant. Year differences are significant.

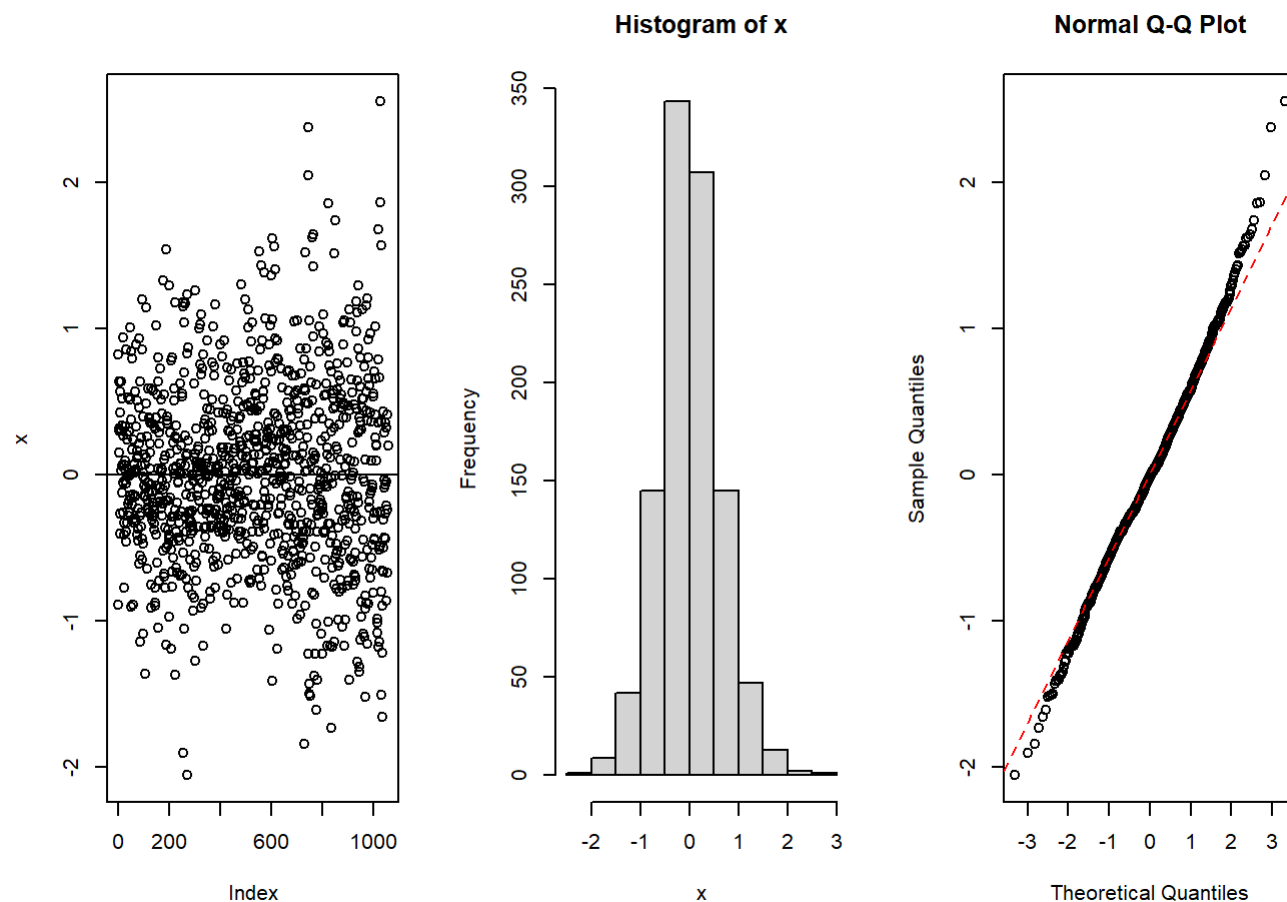
Emmeans: Petal length



Leaf traits:

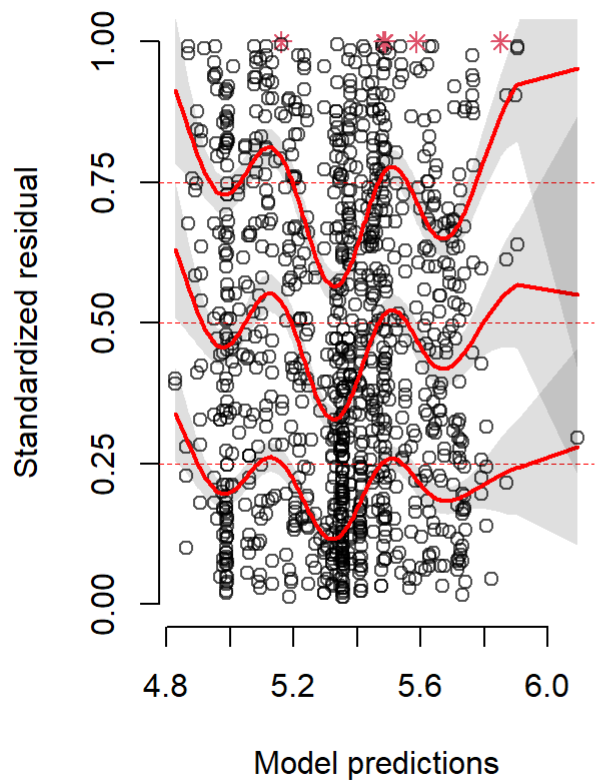
Leaf length

Best fitted data: Square root transformed data

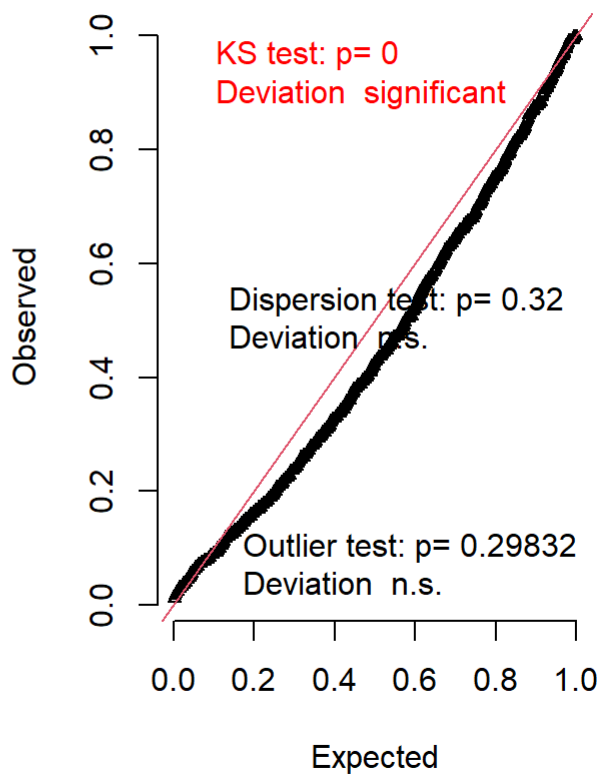


```
## [1] "Kurtosis=0.62252769325954"
## [1] "Skew=0.180396615854015"
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



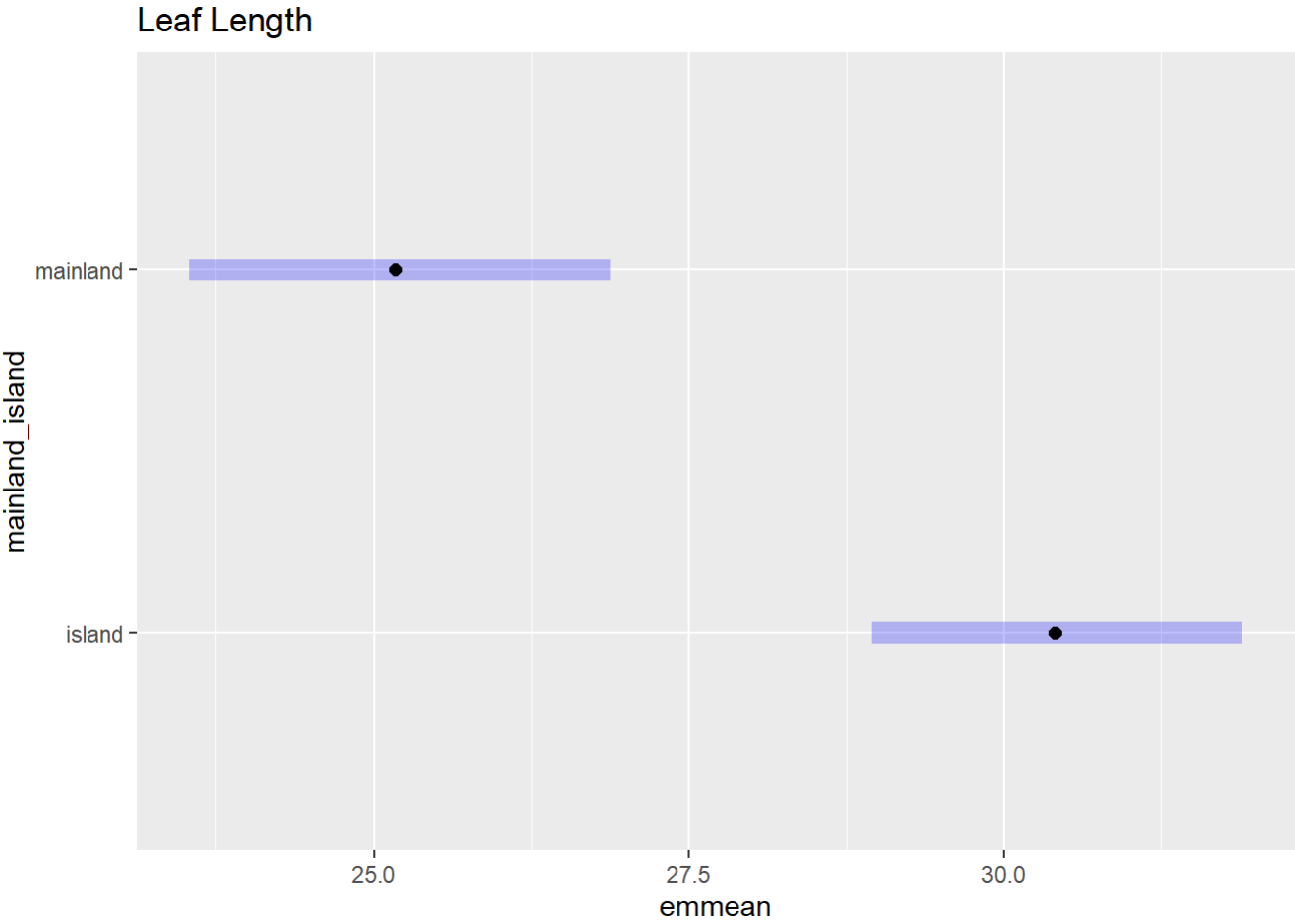
QQ plot residuals



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(leaf_length)
##               Chisq Df Pr(>Chisq)
## mainland_island 21.8619  1  2.93e-06 ***
## year_collected  6.5025  1  0.01077 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Mainland and island differences and year differences are significant.

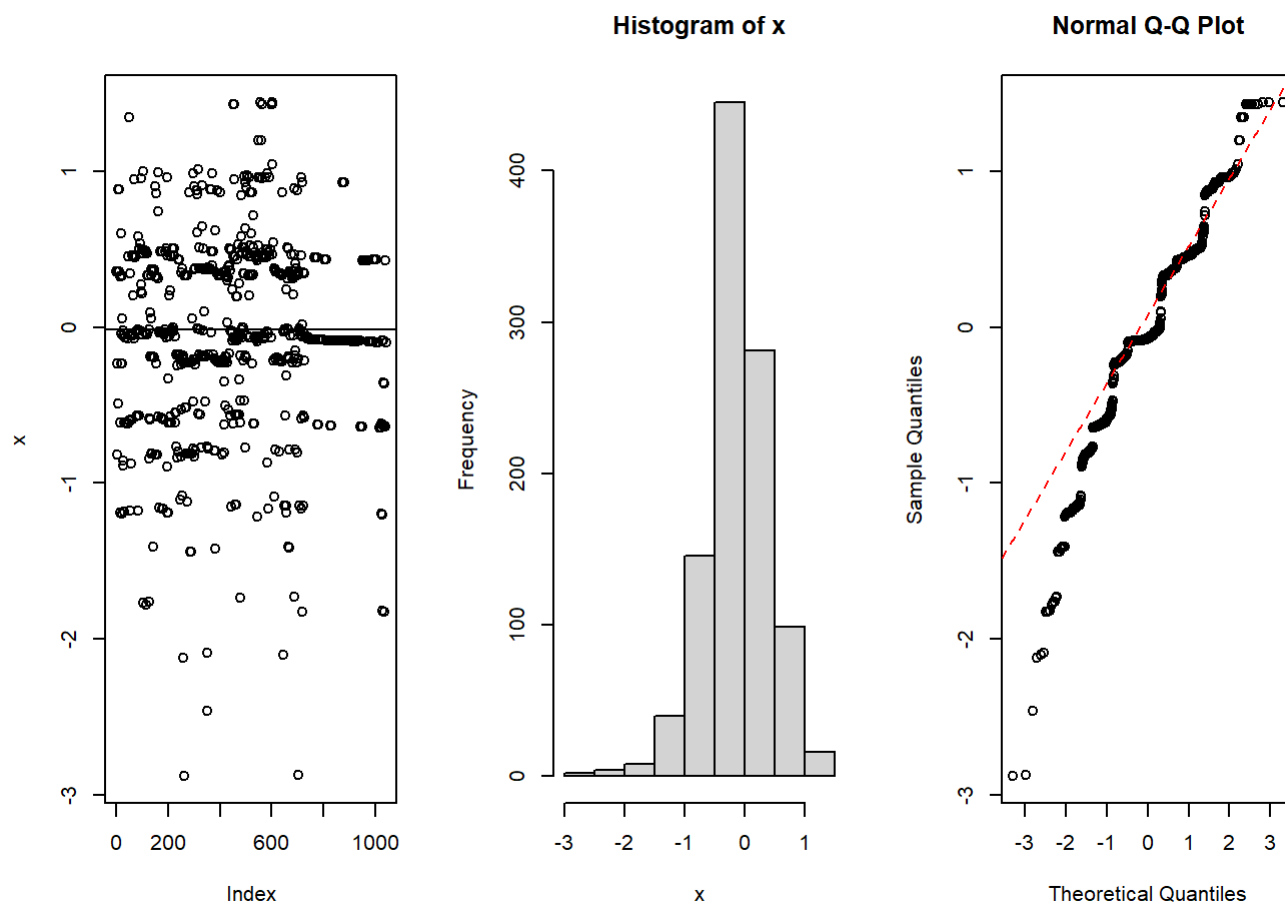
Emmeans: Leaf length



Leaflet number

For this trait I used a glm model with a Poisson distribution:

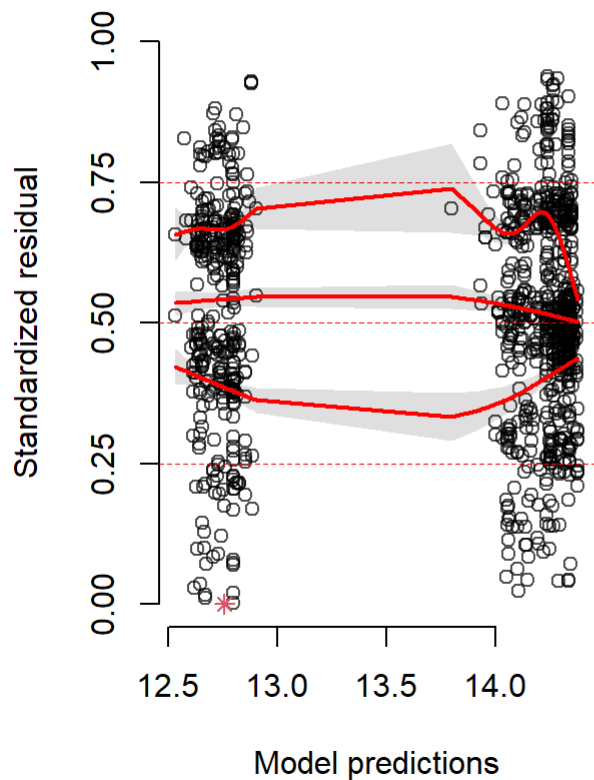
```
glm(number_of_leaflets ~ mainland_island + year_collected)
```



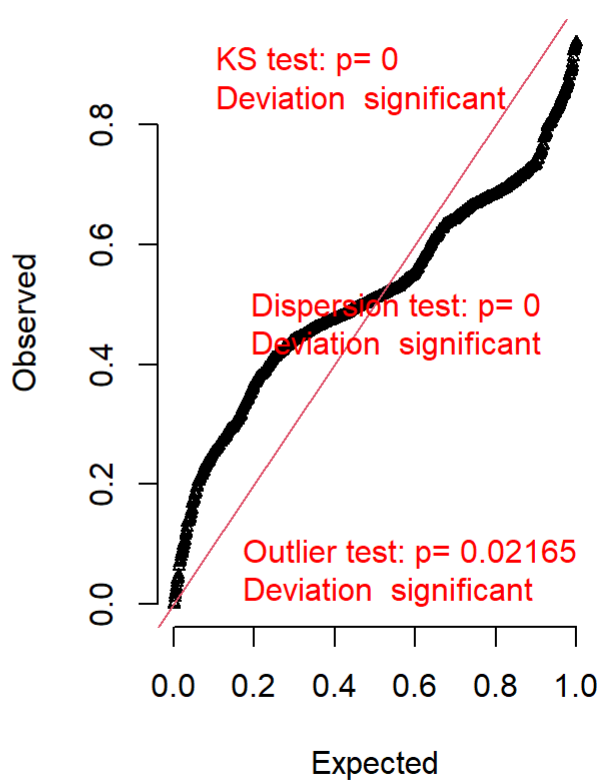
```
## [1] "Kurtosis=2.06742376370439"
## [1] "Skew=-0.665090322563763"
```

```
## DHARMA:plot used testOutliers with type = binomial for computational reasons (nobs > 500). Note that this method may not have inflated Type I error rates for integer-valued distributions. To get a more exact result, it is recommended to re-run testOutliers with type = 'bootstrap'. See ?testOutliers for details
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



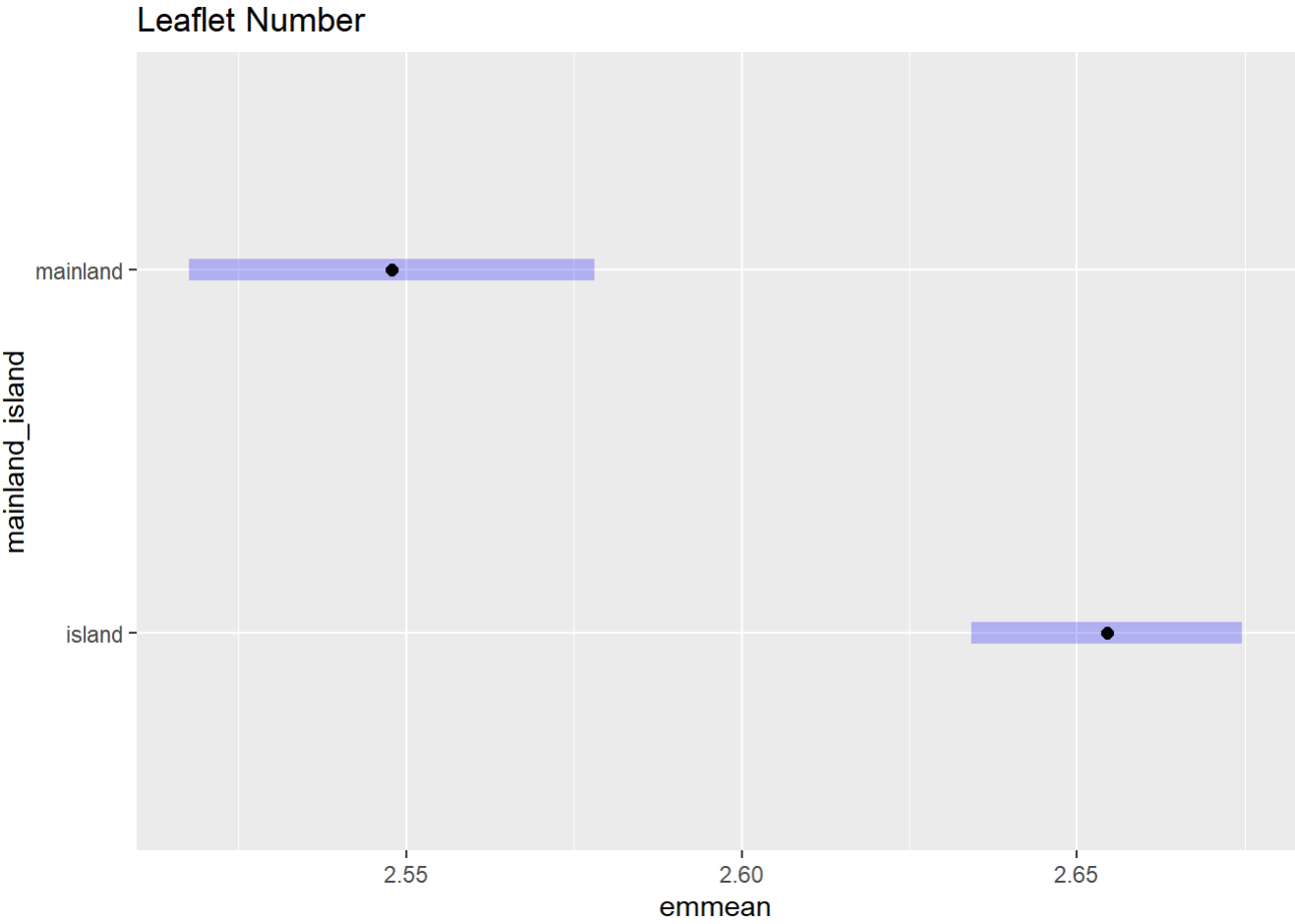
QQ plot residuals



```
## Analysis of Deviance Table (Type II tests)
##
## Response: number_of_leaflets
##           LR Chisq Df Pr(>Chisq)
## mainland_island  31.808  1  1.702e-08 ***
## year_collected    0.687  1    0.407
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

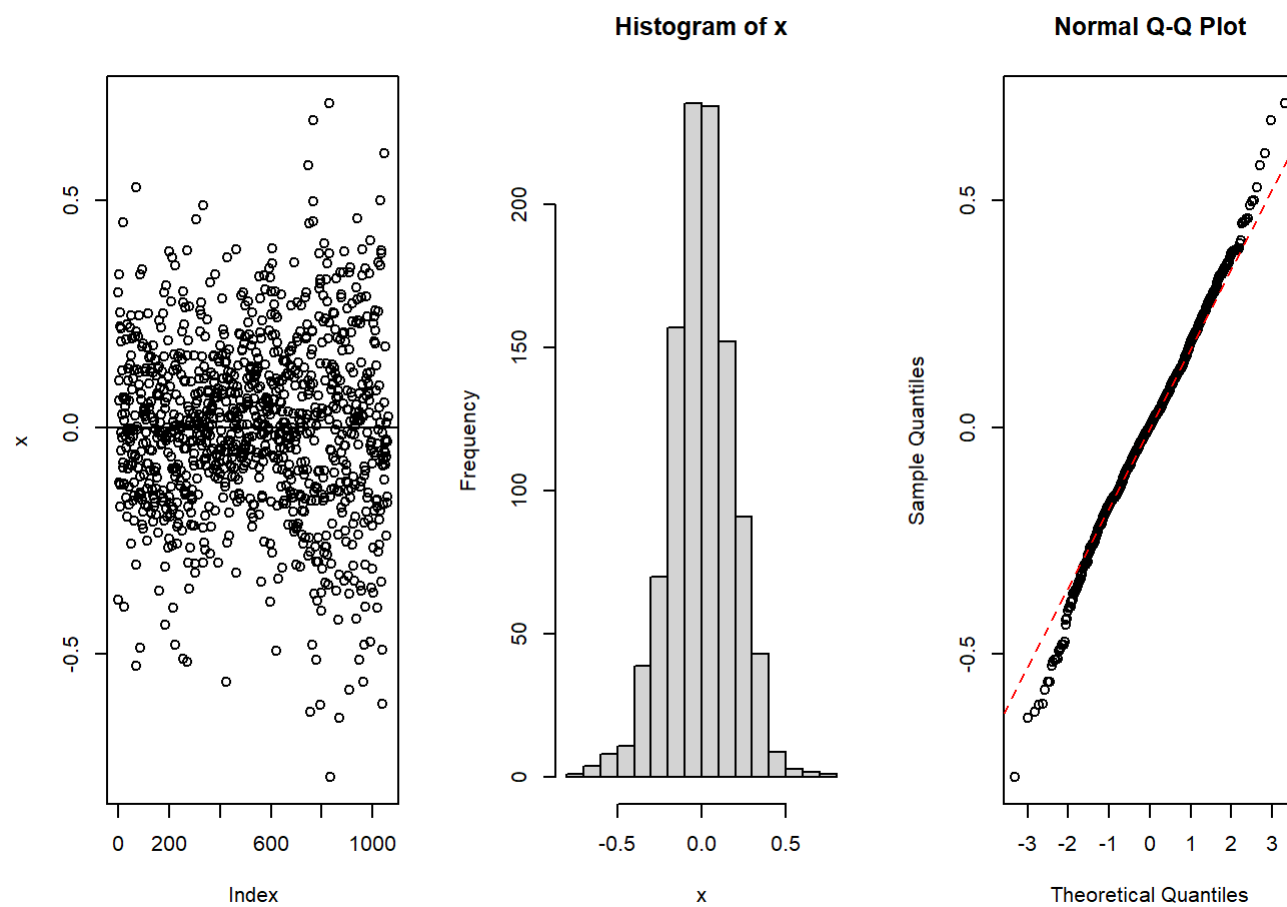
Mainland and island differences are significant.

Emmeans: Leaflet number



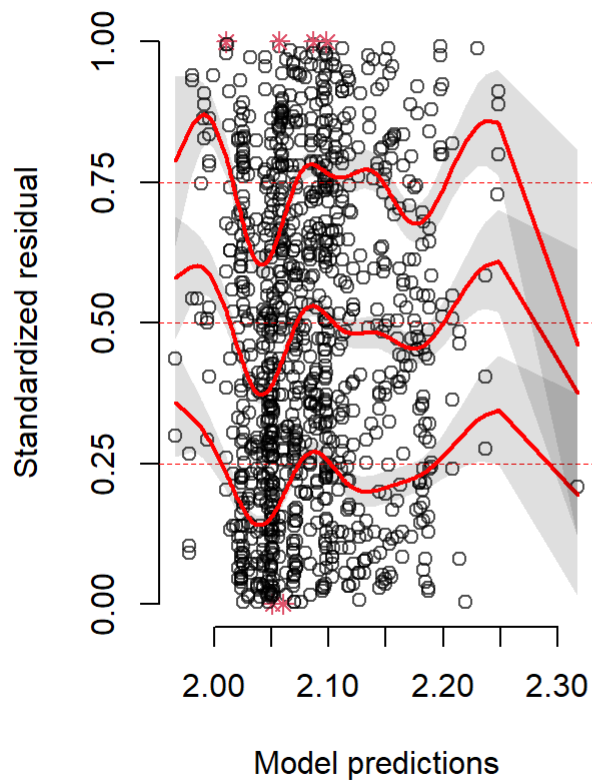
Leaflet length

Best fitted data: Log transformed data

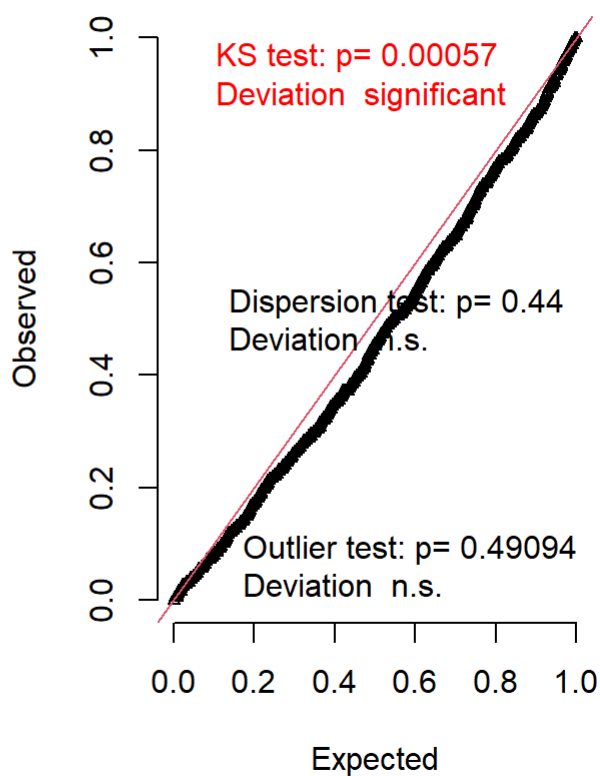


```
## [1] "Kurtosis=0.798536670239446"
## [1] "Skew=-0.132164114832064"
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



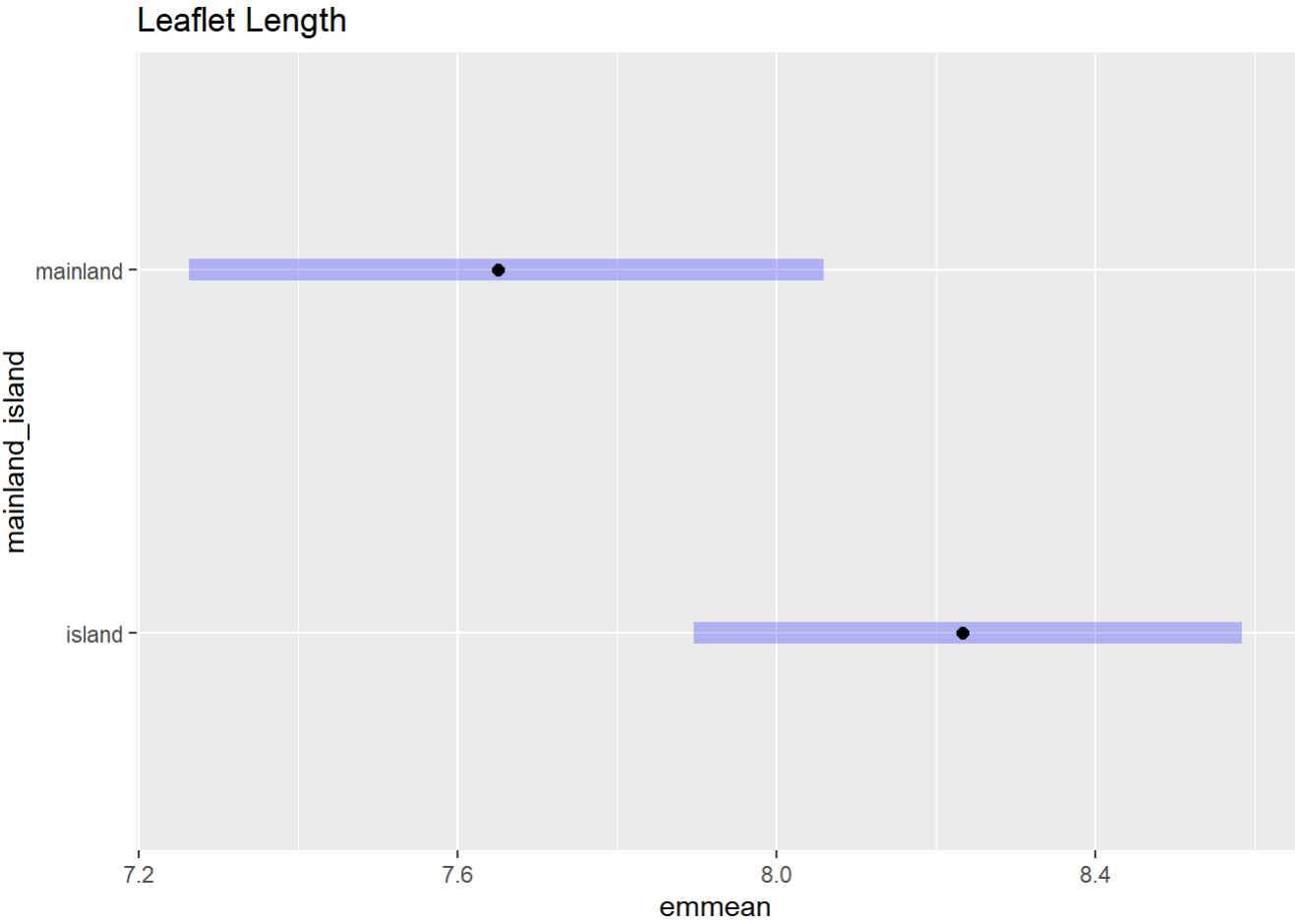
QQ plot residuals



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: log(leaflet_length)
##           Chisq Df Pr(>Chisq)
## mainland_island 4.8651 1 0.027405 *
## year_collected 8.6928 1 0.003195 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Mainland and island differences and year differences are significant.

Emmeans: Leaflet length



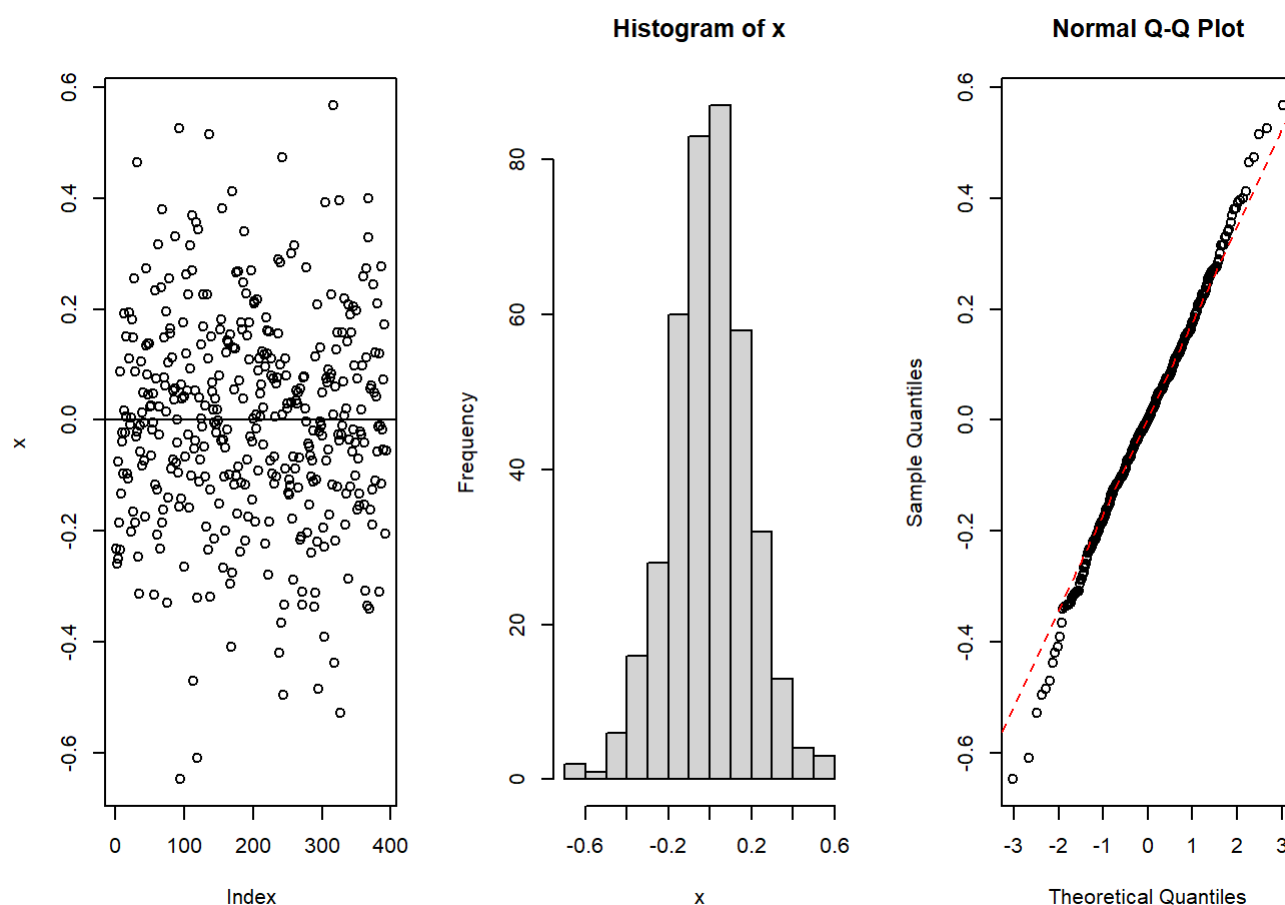
Model 2: trait ~ galapagos/other + year + (1|ID)

This model looks at the differences between *Tribulus* flowers and leaves from Galapagos and other island systems. We do not have mericarp data from other islands so they are not included.

Flower traits:

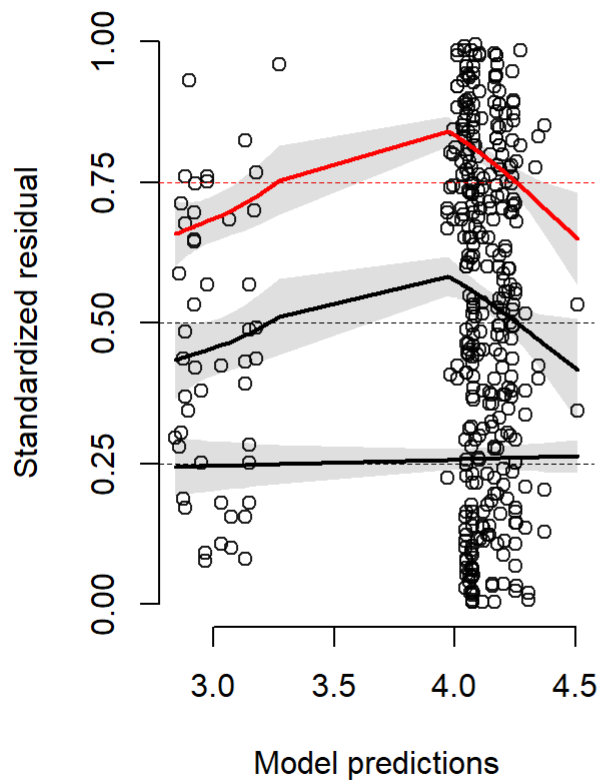
Petal length

Best fitted data: Squared root data

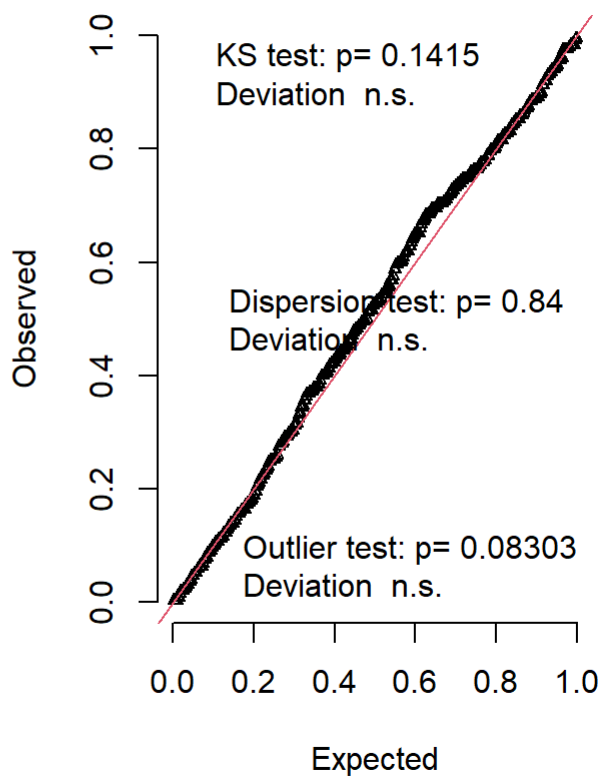


```
## [1] "Kurtosis=0.526417690150699"
## [1] "Skew=-0.114096244913898"
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



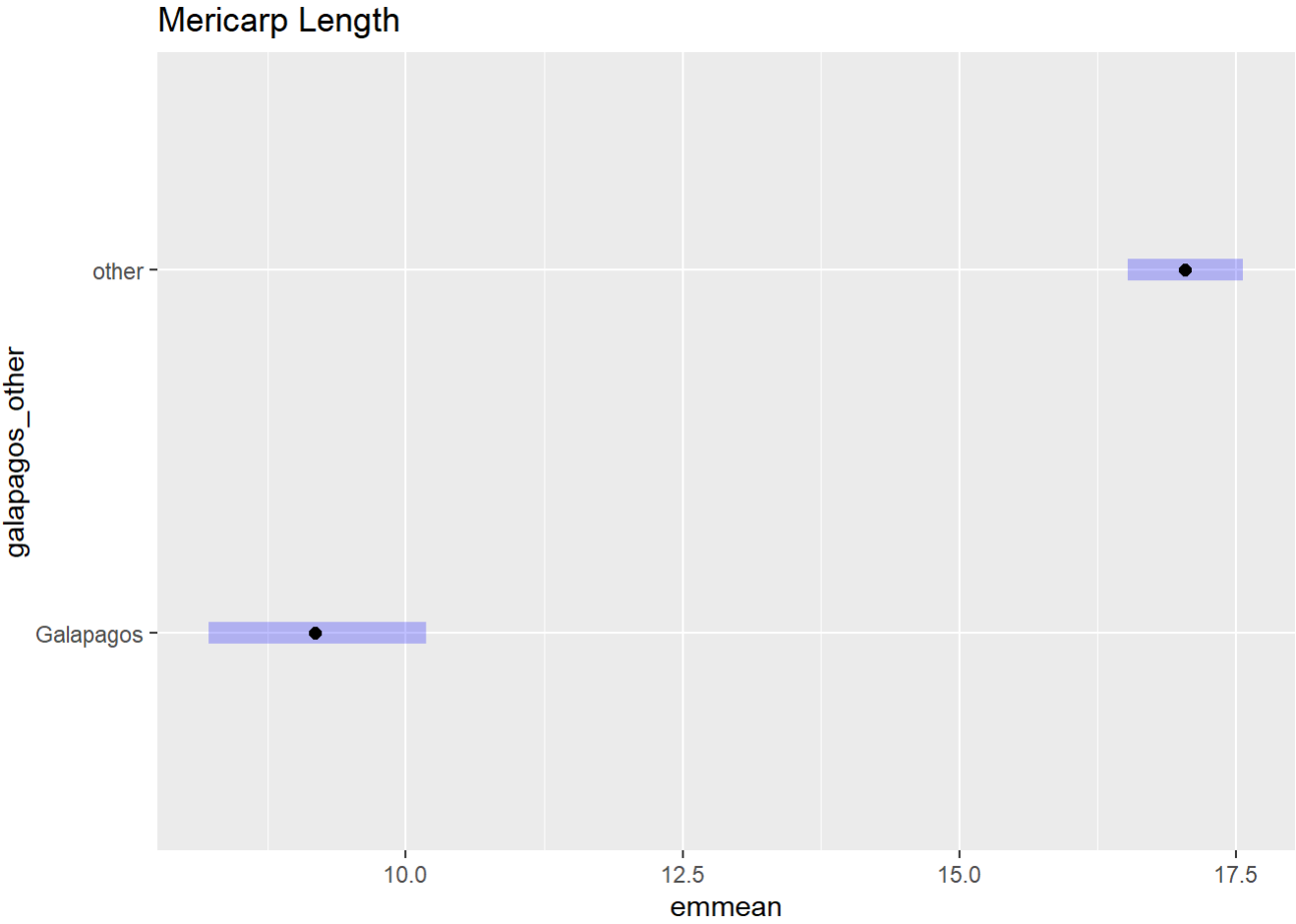
QQ plot residuals



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(petal_length)
##               Chisq Df Pr(>Chisq)
## galapagos_other 156.398 1 < 2.2e-16 ***
## year_collected  10.133 1  0.001456 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Mainland and island differences are significant. Year differences are significant.

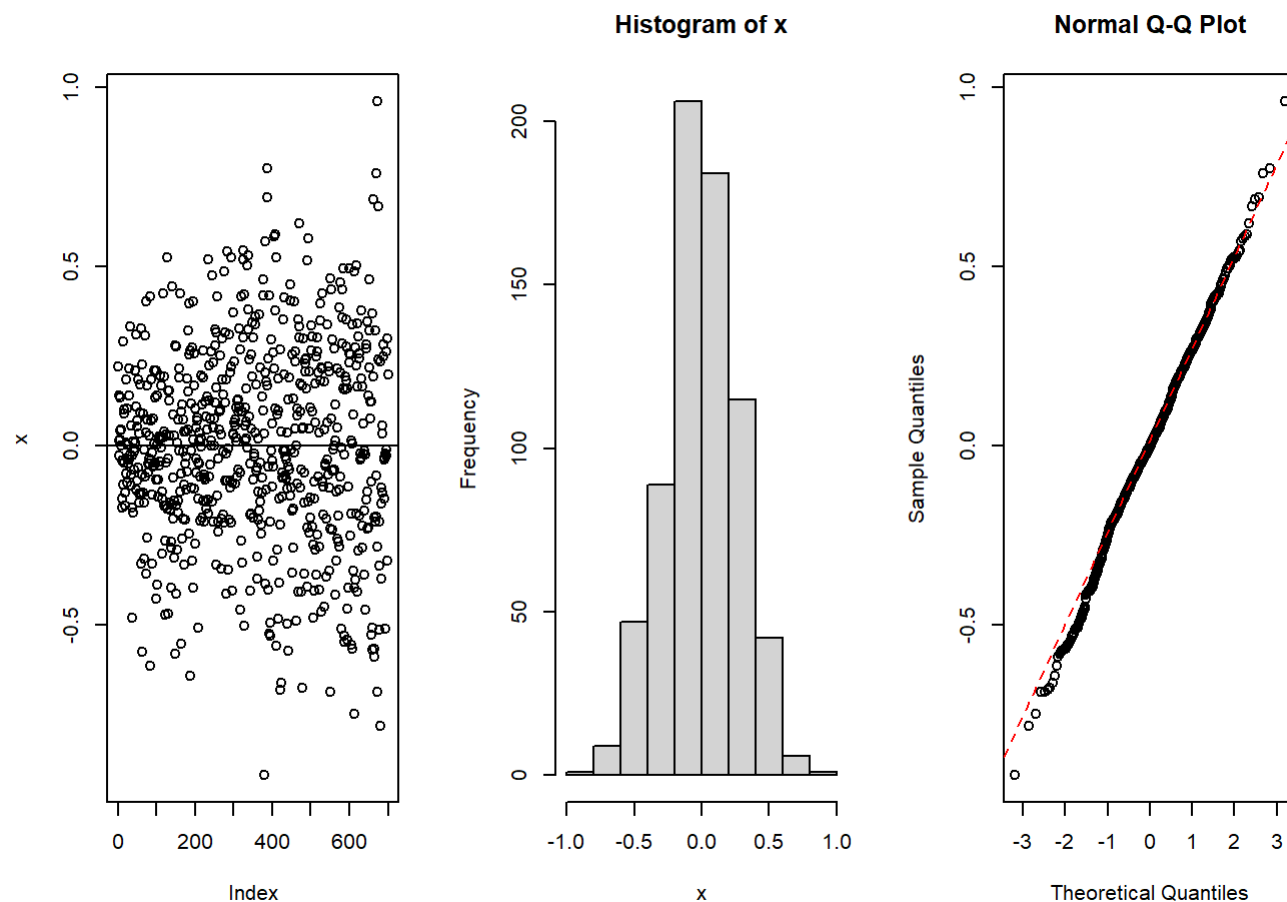
Emmeans: Petal length



Leaf traits:

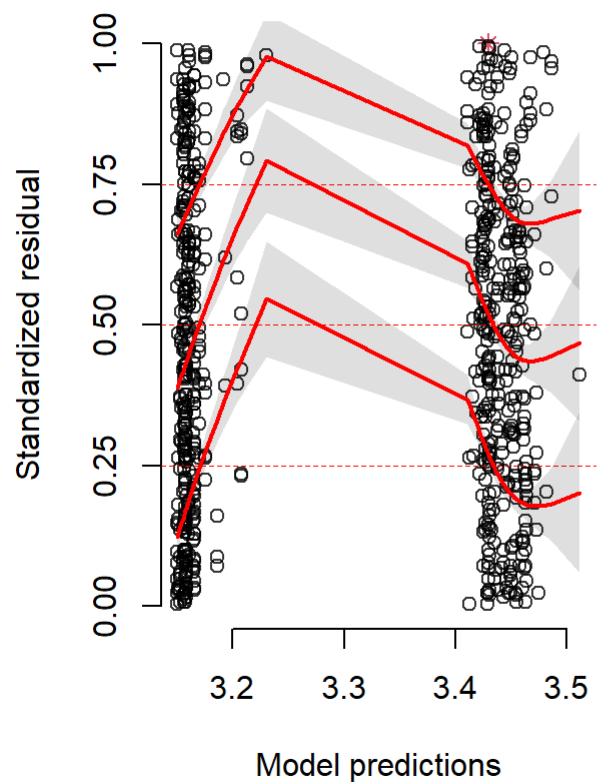
Leaf length

Best fitted data: Log transformed data

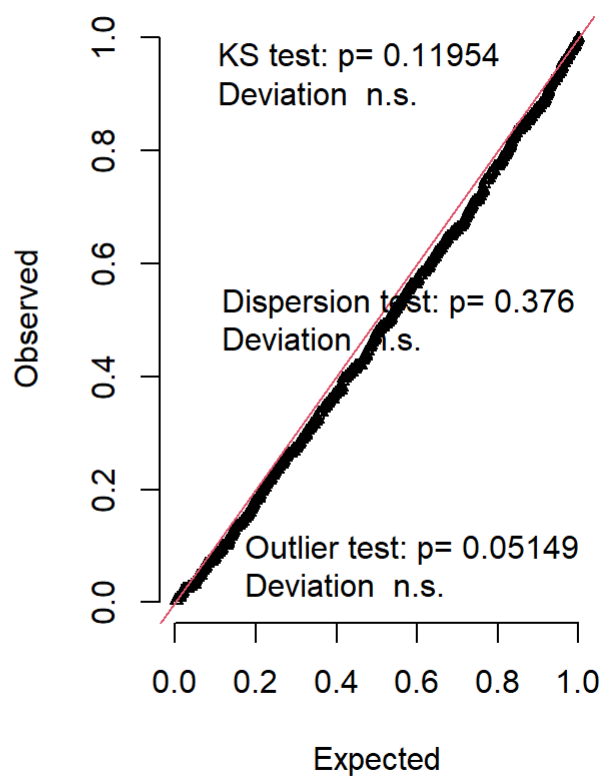


```
## [1] "Kurtosis=0.193135255752809"
## [1] "Skew=-0.0988914986843238"
```


Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



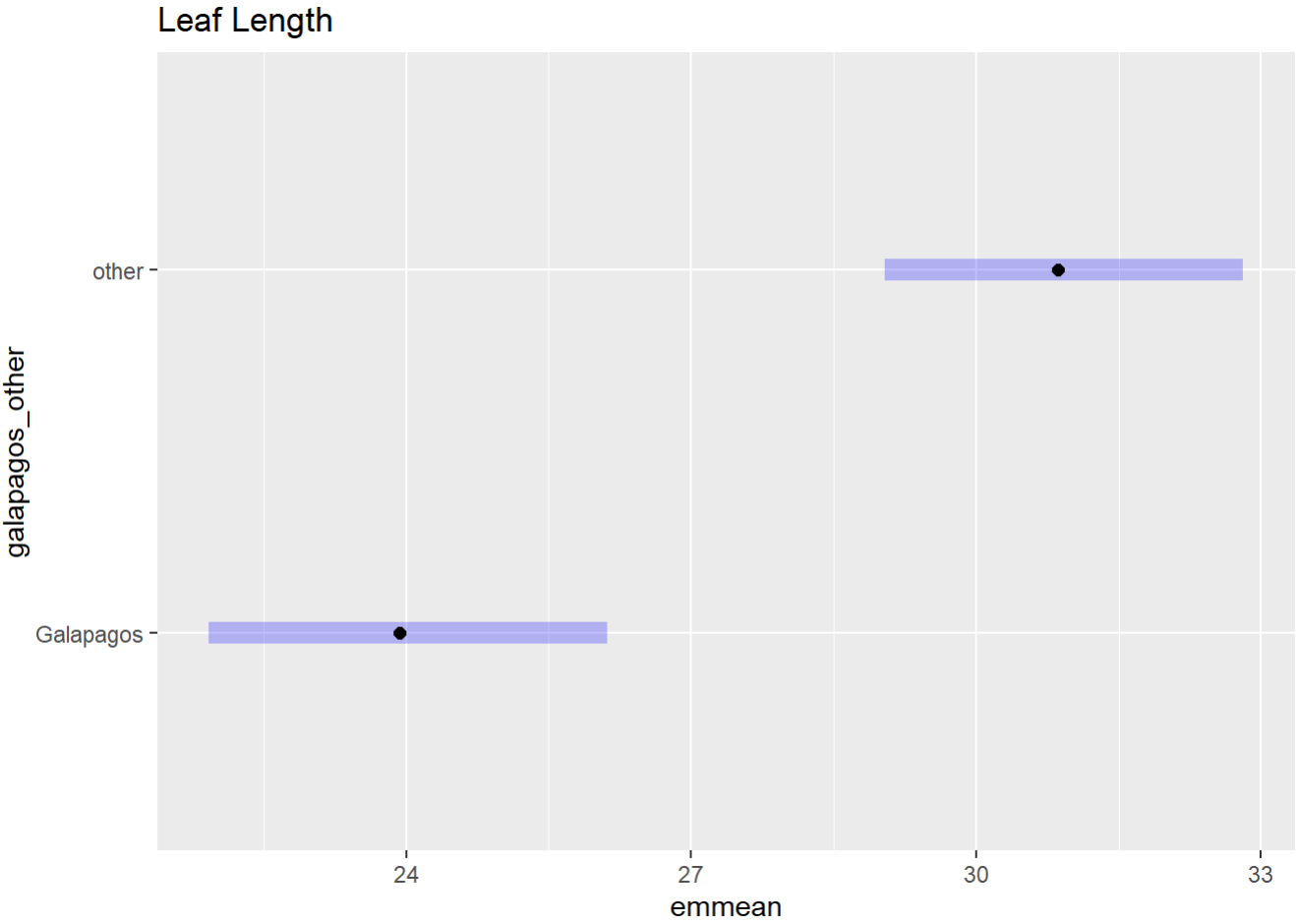
QQ plot residuals



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: log(leaf_length)
##               Chisq Df Pr(>Chisq)
## galapagos_other 20.3974 1 6.291e-06 ***
## year_collected  0.5726 1  0.4492
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Differences between galapagos and other islands are significant

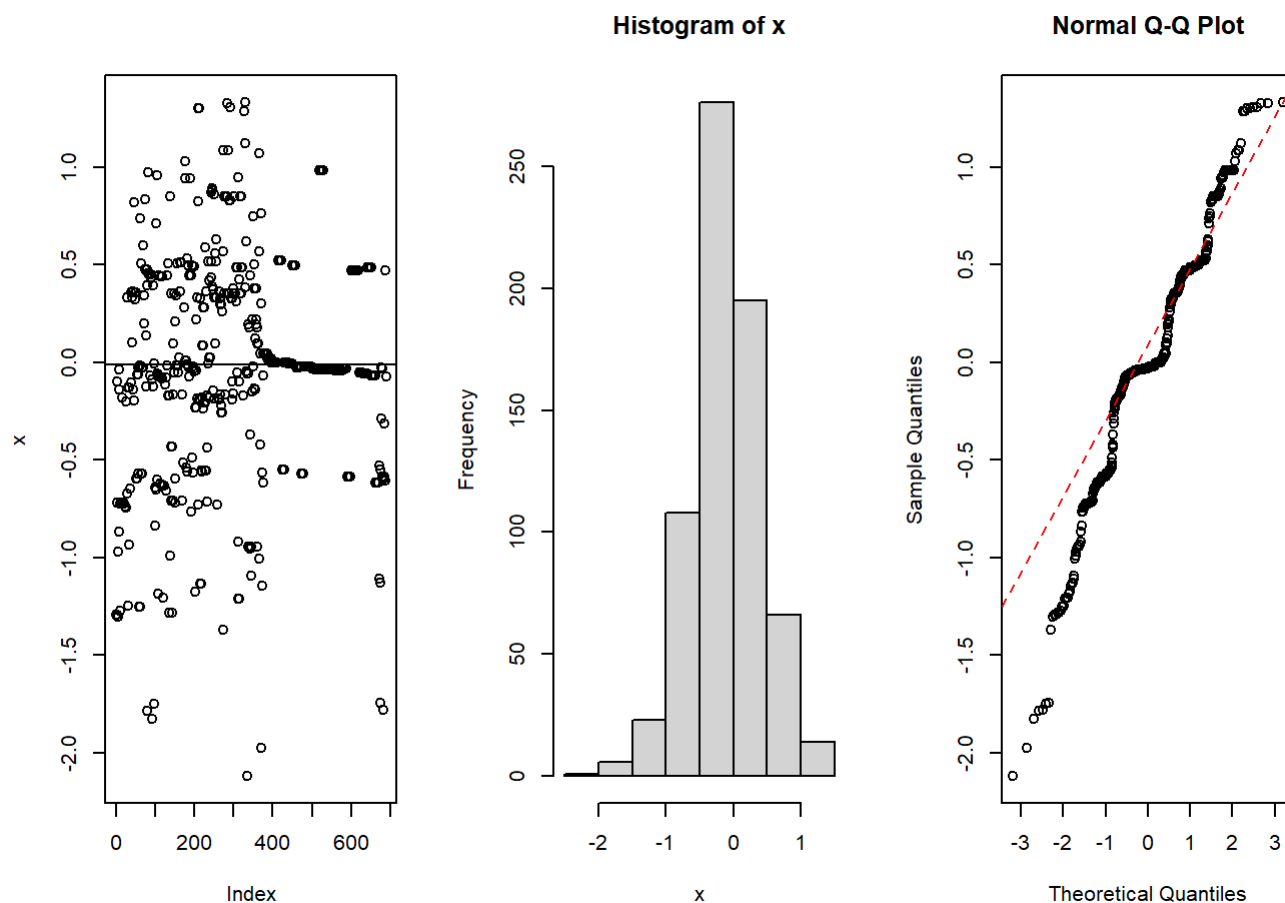
Emmeans: Leaf length



Leaflet number

For this trait I used a glm model with a Poisson distribution:

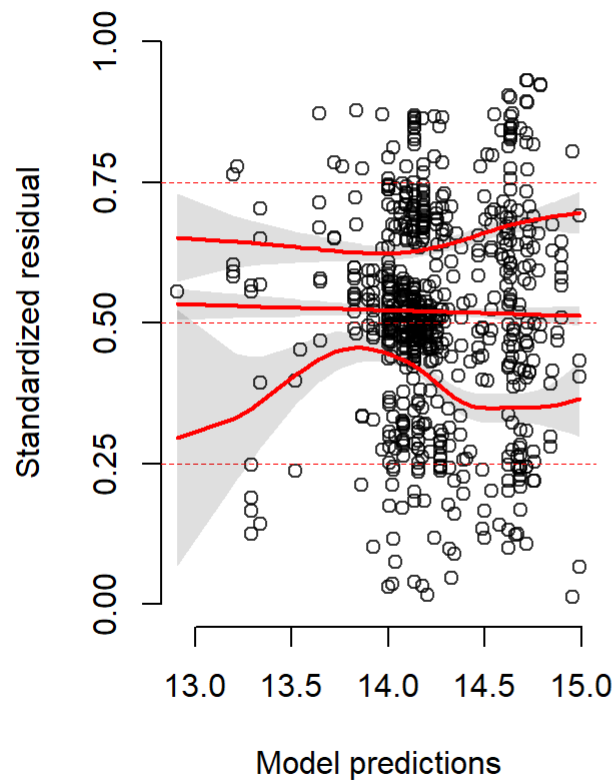
```
glm(number_of_leaflets ~ mainland_island + year_collected)
```



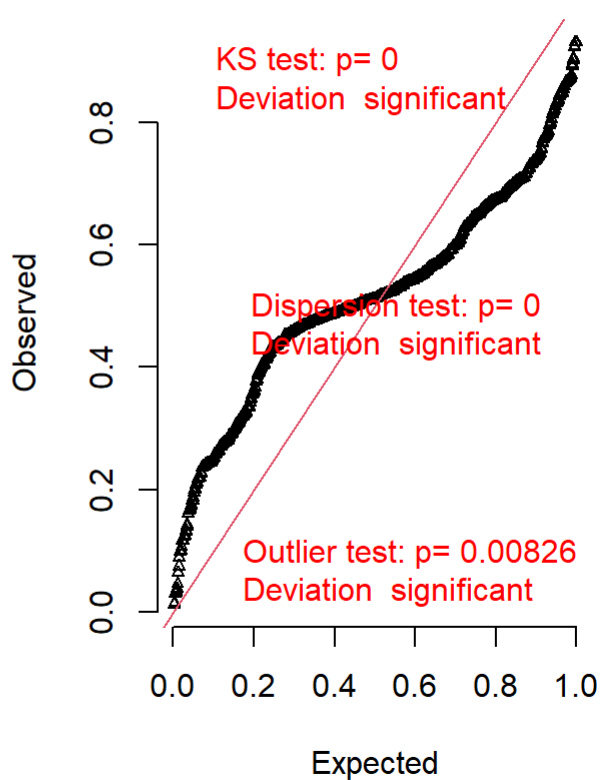
```
## [1] "Kurtosis=1.14450585157219"
## [1] "Skew=-0.450482991123054"
```

```
## DHARMA:plot used testOutliers with type = binomial for computational reasons (nobs > 500). Note that this method may not have inflated Type I error rates for integer-valued distributions. To get a more exact result, it is recommended to re-run testOutliers with type = 'bootstrap'. See ?testOutliers for details
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



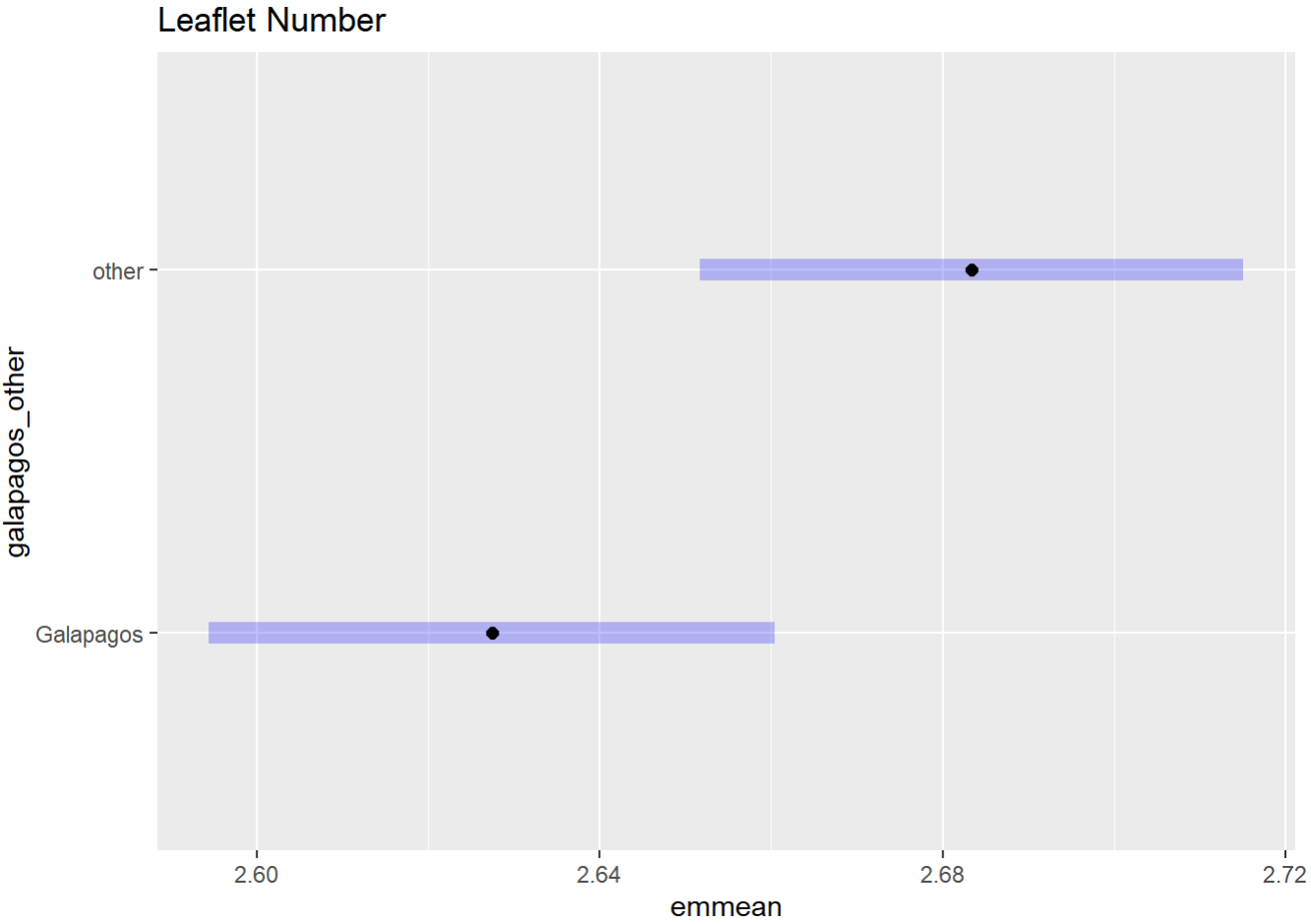
QQ plot residuals



```
## Analysis of Deviance Table (Type II tests)
##
## Response: number_of_leaflets
##           LR Chisq Df Pr(>Chisq)
## galapagos_other  4.5993 1  0.03198 *
## year_collected  3.2926 1  0.06959 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

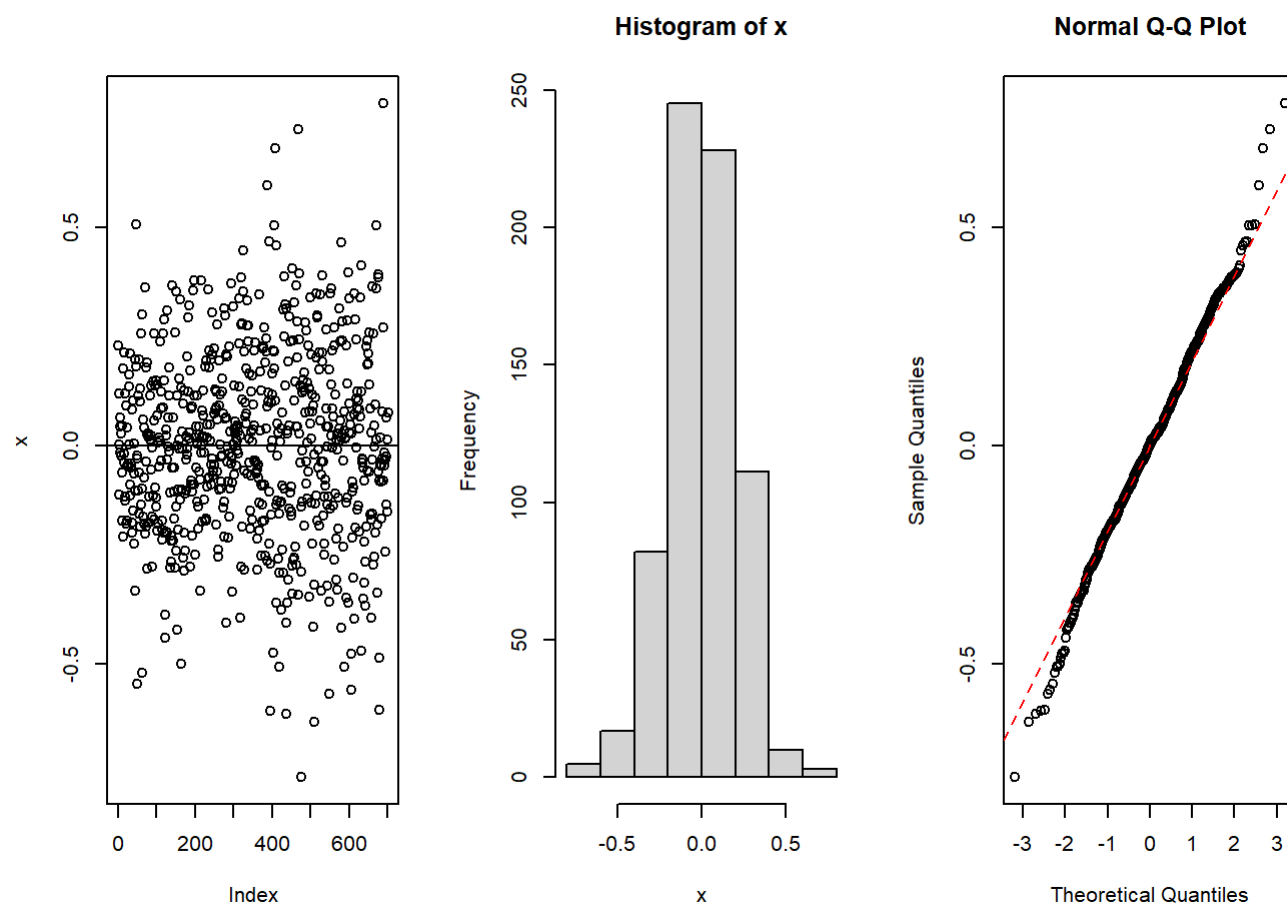
Mainland and island differences are *barely* significant.

Emmeans: Leaflet number



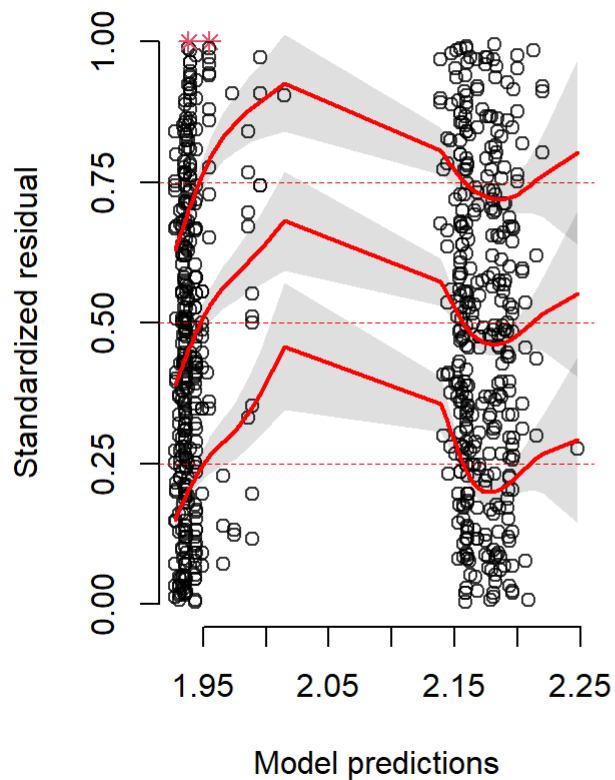
Leaflet length

Best fitted data: Log transformed data

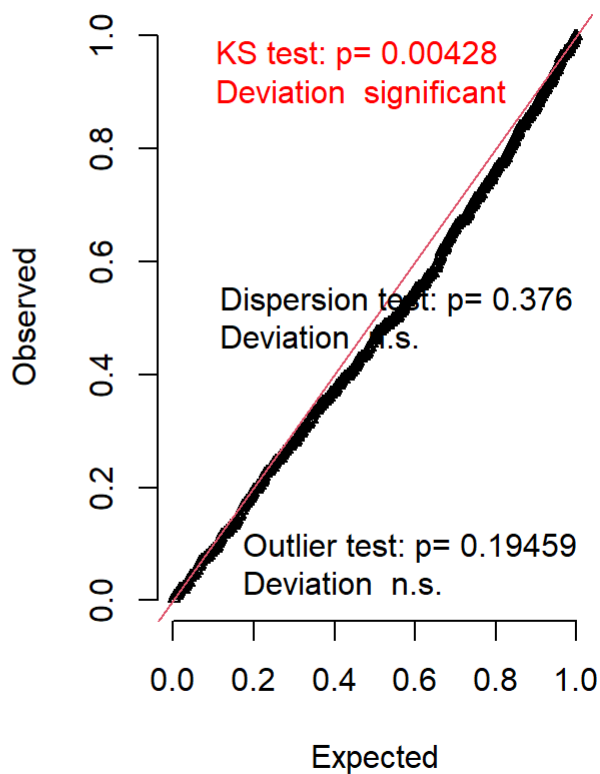


```
## [1] "Kurtosis=0.542906559522408"
## [1] "Skew=-0.0347332872064938"
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



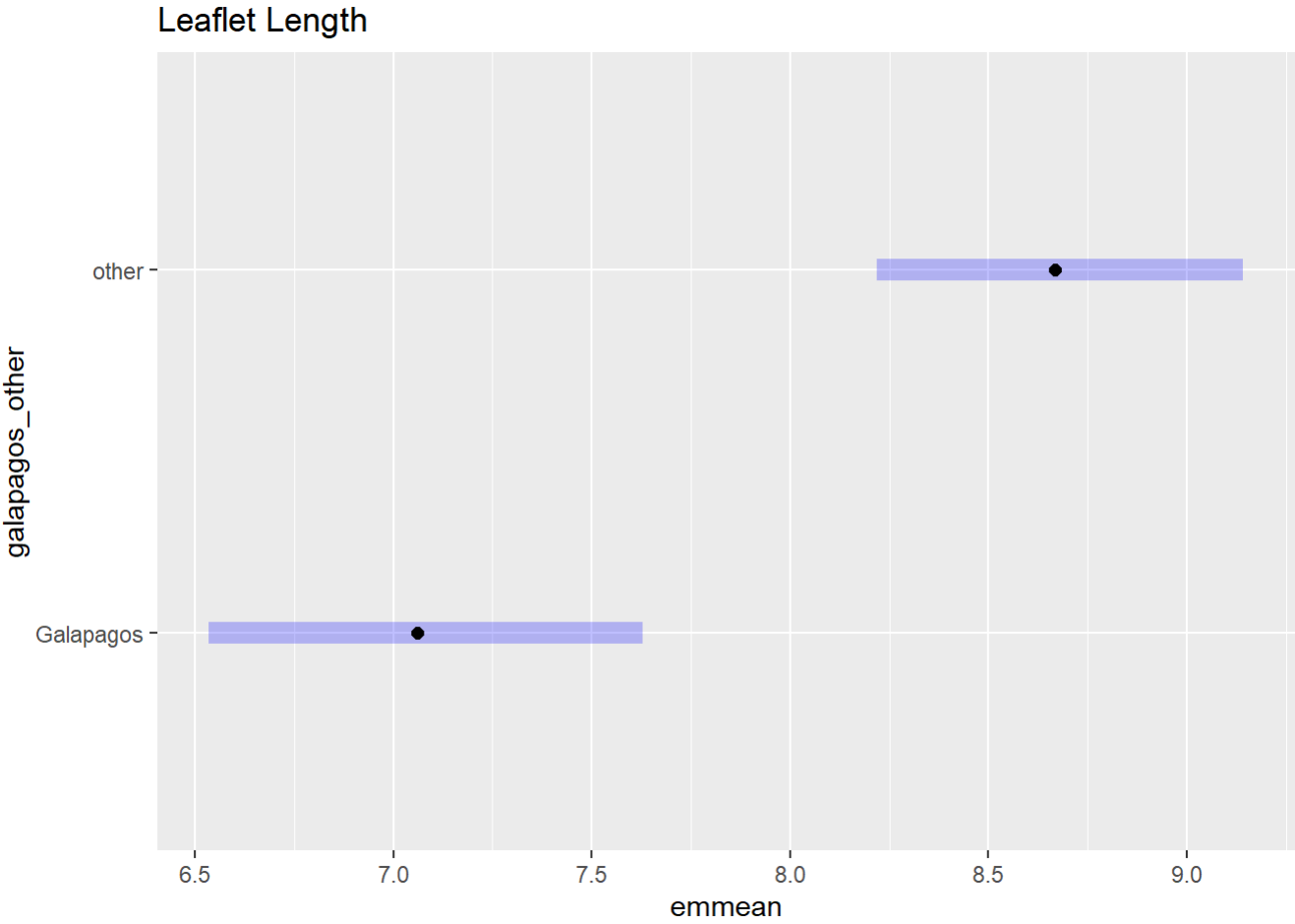
QQ plot residuals



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: log(leaflet_length)
##               Chisq Df Pr(>Chisq)
## galapagos_other 17.2063  1 3.353e-05 ***
## year_collected  0.8816  1  0.3478
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Galapagos and other island differences are significant.

Emmeans: Leaflet length



Model 3: trait ~ finch beak + year + (1|ID)

This model looks at the differences between *Tribulus mericarps*, flowers and leaves within the Galapagos islands that differ in the distribution of seed predators *G. magnirostris* and *G. cornirostris*. Darwin's finches that are known to easily predate mericarps.

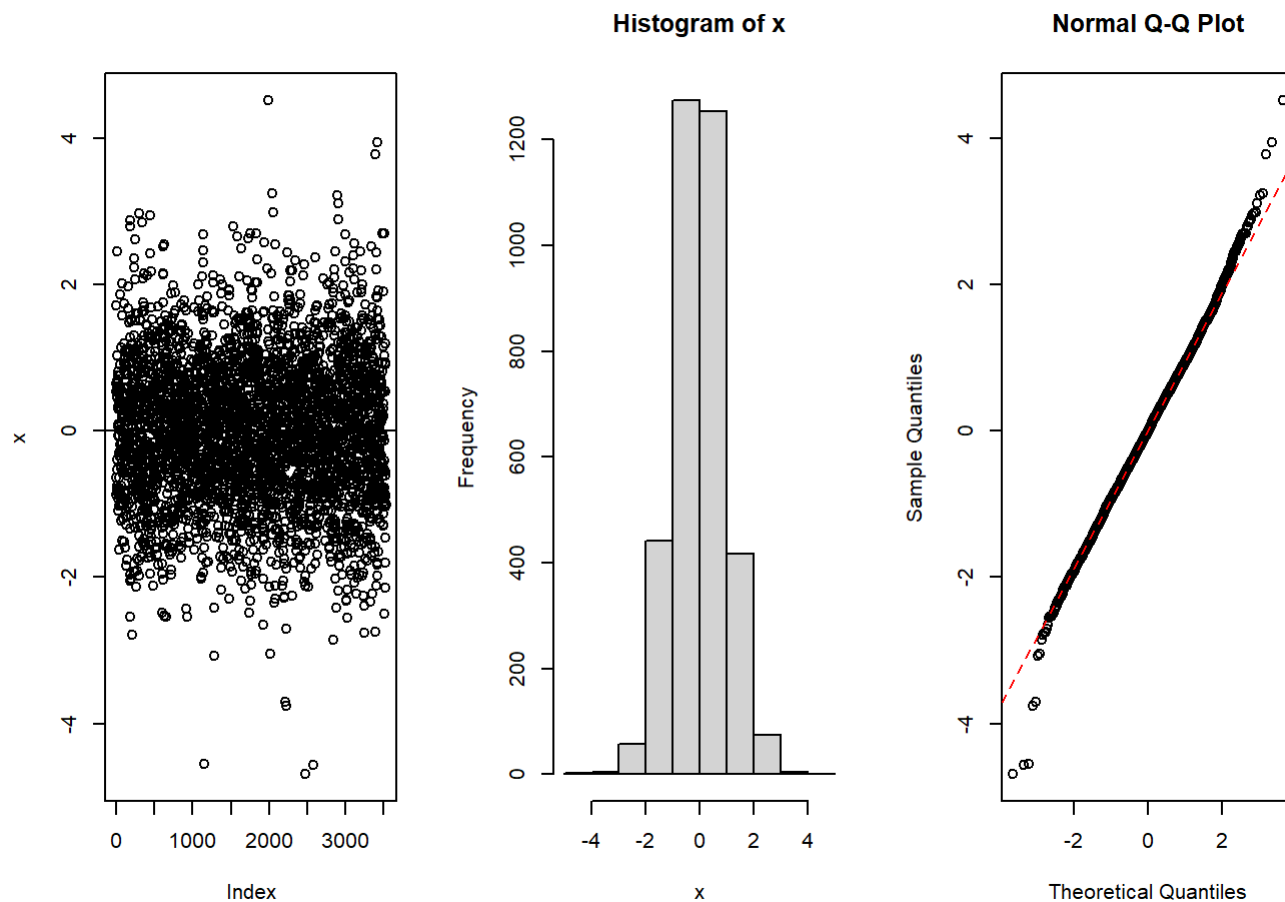
Finch Island distribution. *Magnirostris arrived to Daphne Major after 1984

Presence of <i>G. magnirostris</i> and <i>G. Cornirrostris</i>	Absence of <i>G. magnirostris</i> and <i>G. Cornirrostris</i>
Daphne Major	Floreana
Daphne Minor	San Cristobal
Darwin	Santa Fe
Fernandina	Champion
Genovesa	Baltra
Guy Fawkes Oeste	Enderby
Isabela	Gardner
Pinta	Daphne Major <1983
Plaza Norte	
Rabida	
Santa Cruz	
Santiago	
Seymour Norte	
Espanola	

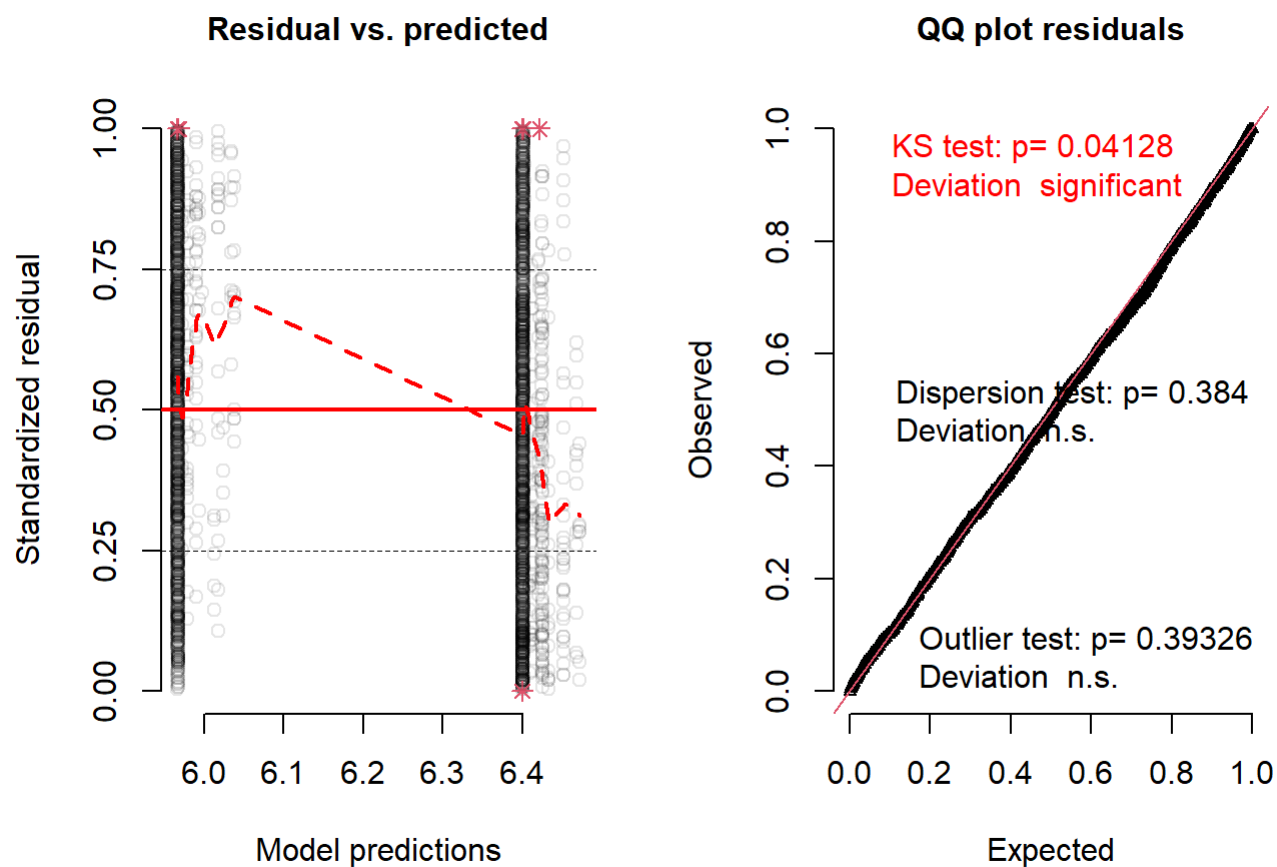
Mericaarp traits:

Length

Best fitted data: Untransformed data

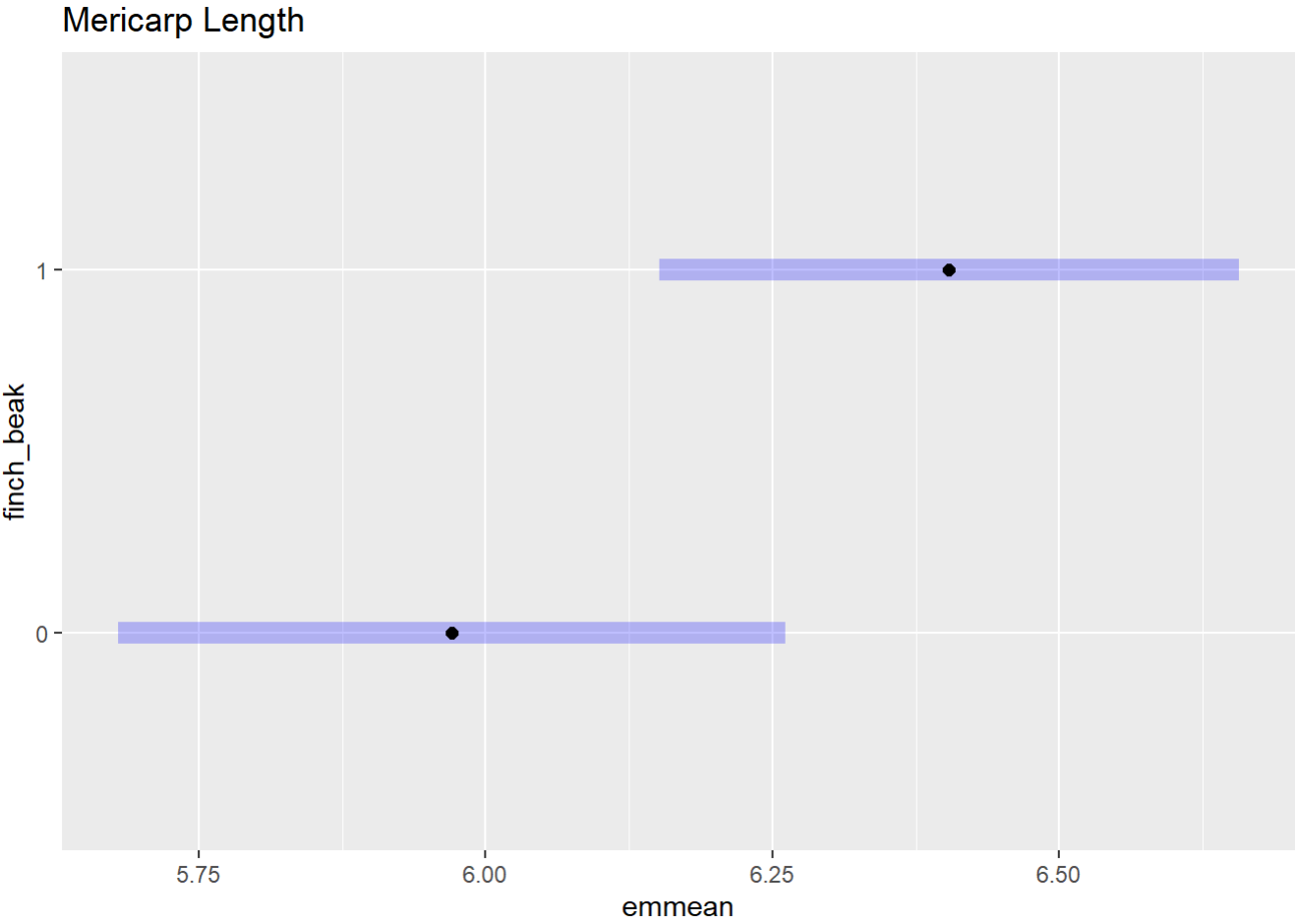


```
## [1] "Kurtosis=0.641070100215158"
## [1] "Skew=0.00706886345866648"
```



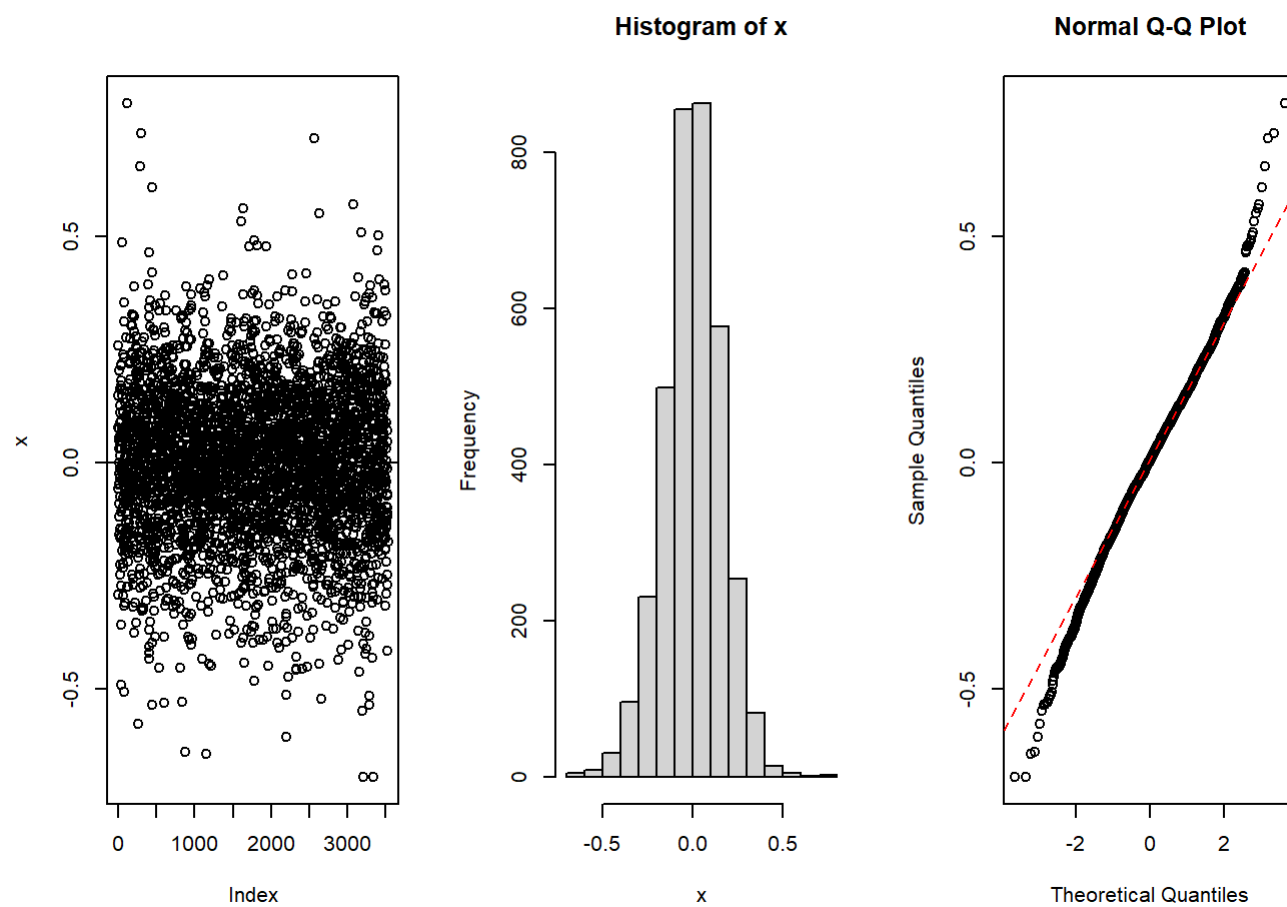
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: length
##               Chisq Df Pr(>Chisq)
## finch_beak      5.1150  1   0.02372 *
## year_collected 0.0384  1   0.84464
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Emmeans: Length

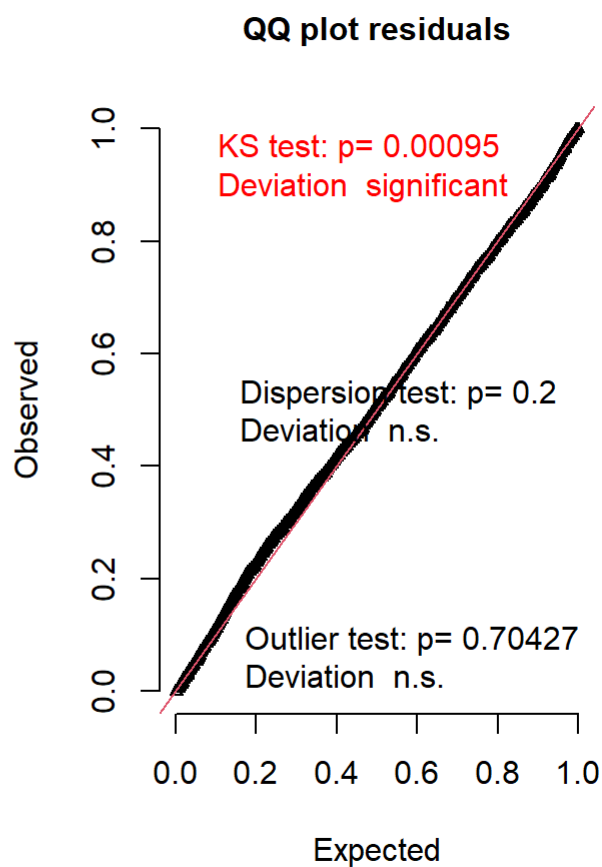
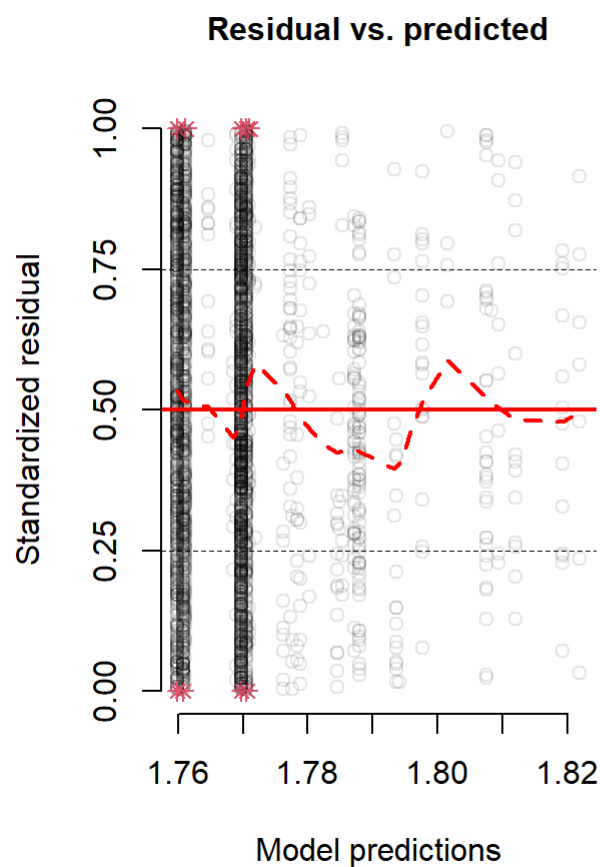


Width

Best fitted data: Square root transformed data

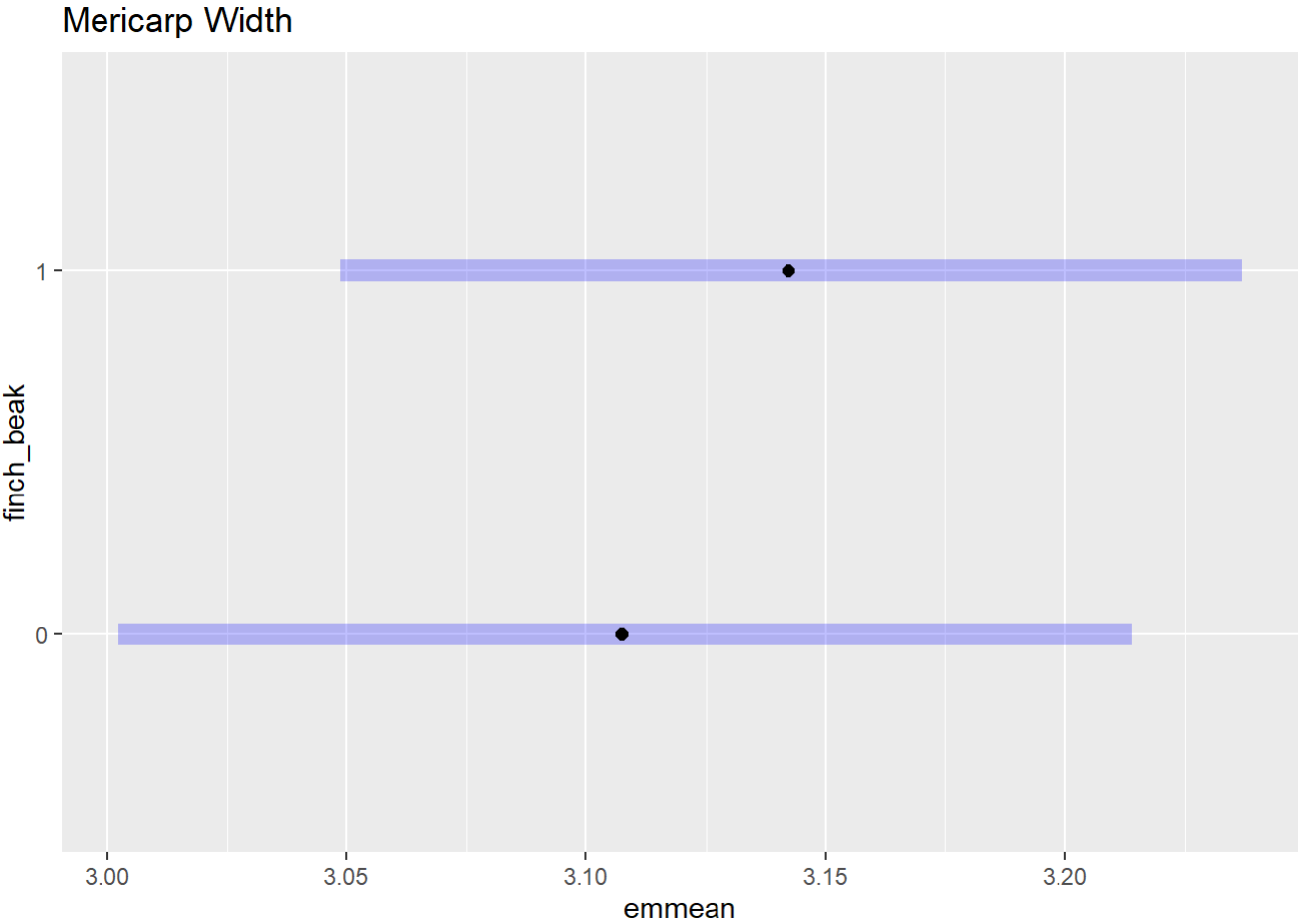


```
## [1] "Kurtosis=0.865895540669791"
## [1] "Skew=-0.131502833504471"
```



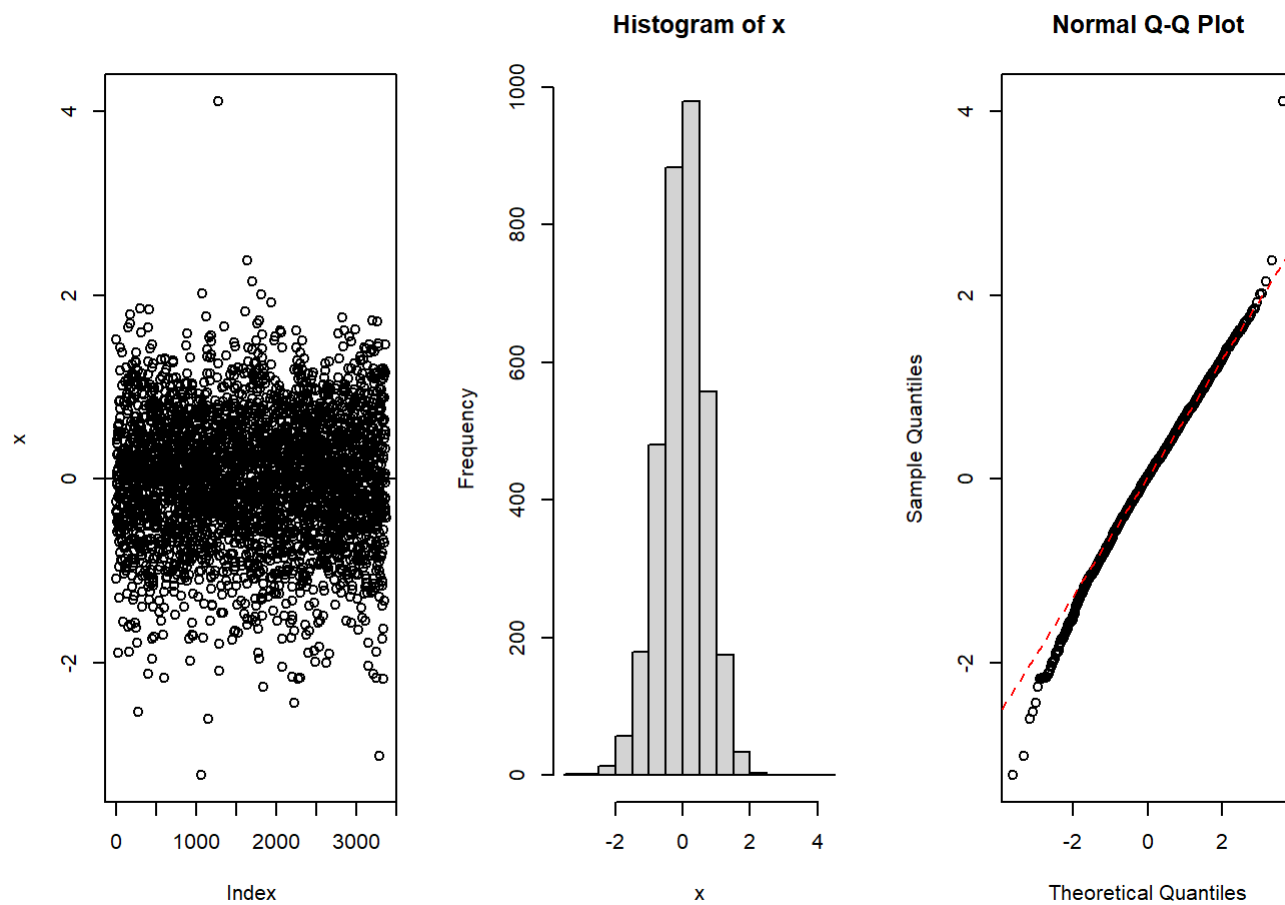
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(width)
##           Chisq Df Pr(>Chisq)
## finch_beak    0.2415  1    0.6231
## year_collected 1.6943  1    0.1930
```

Emmeans: Width

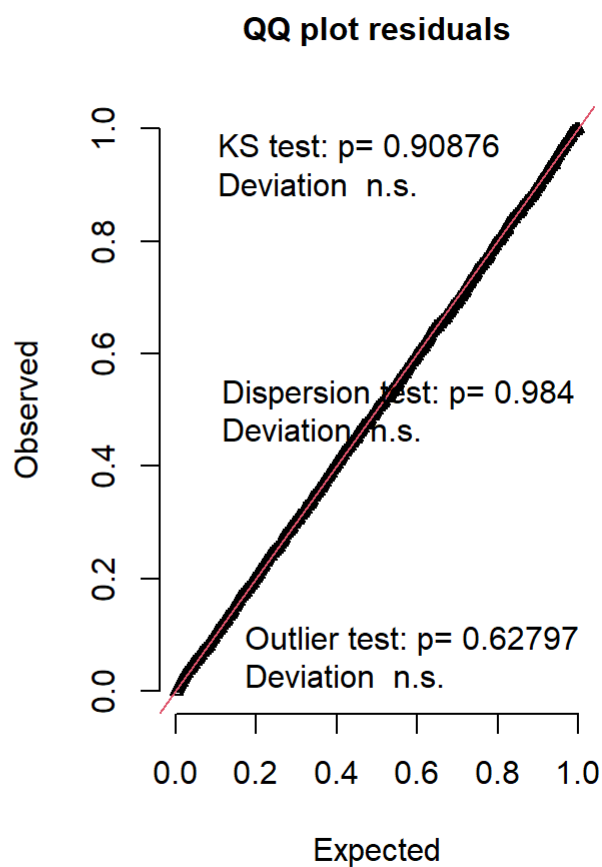
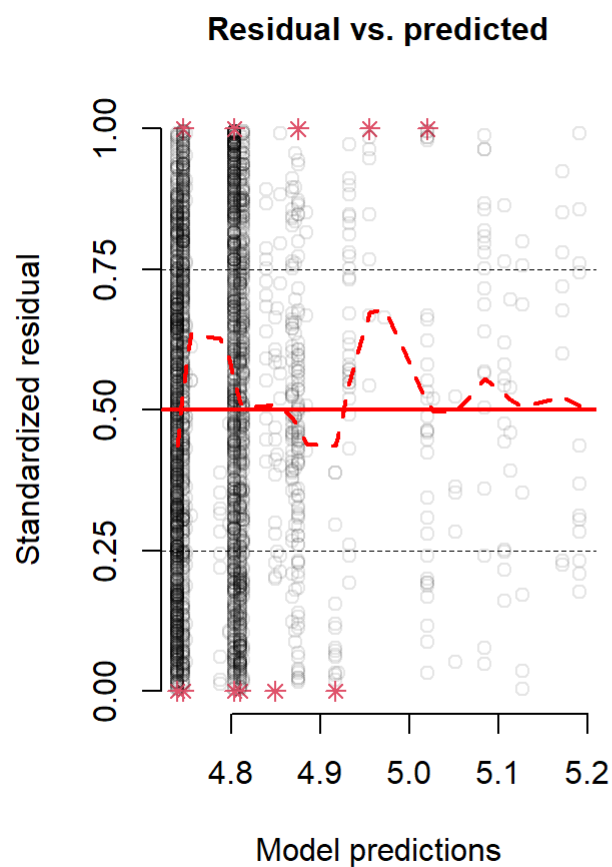


Depth

Best fitted data: Untransformed data

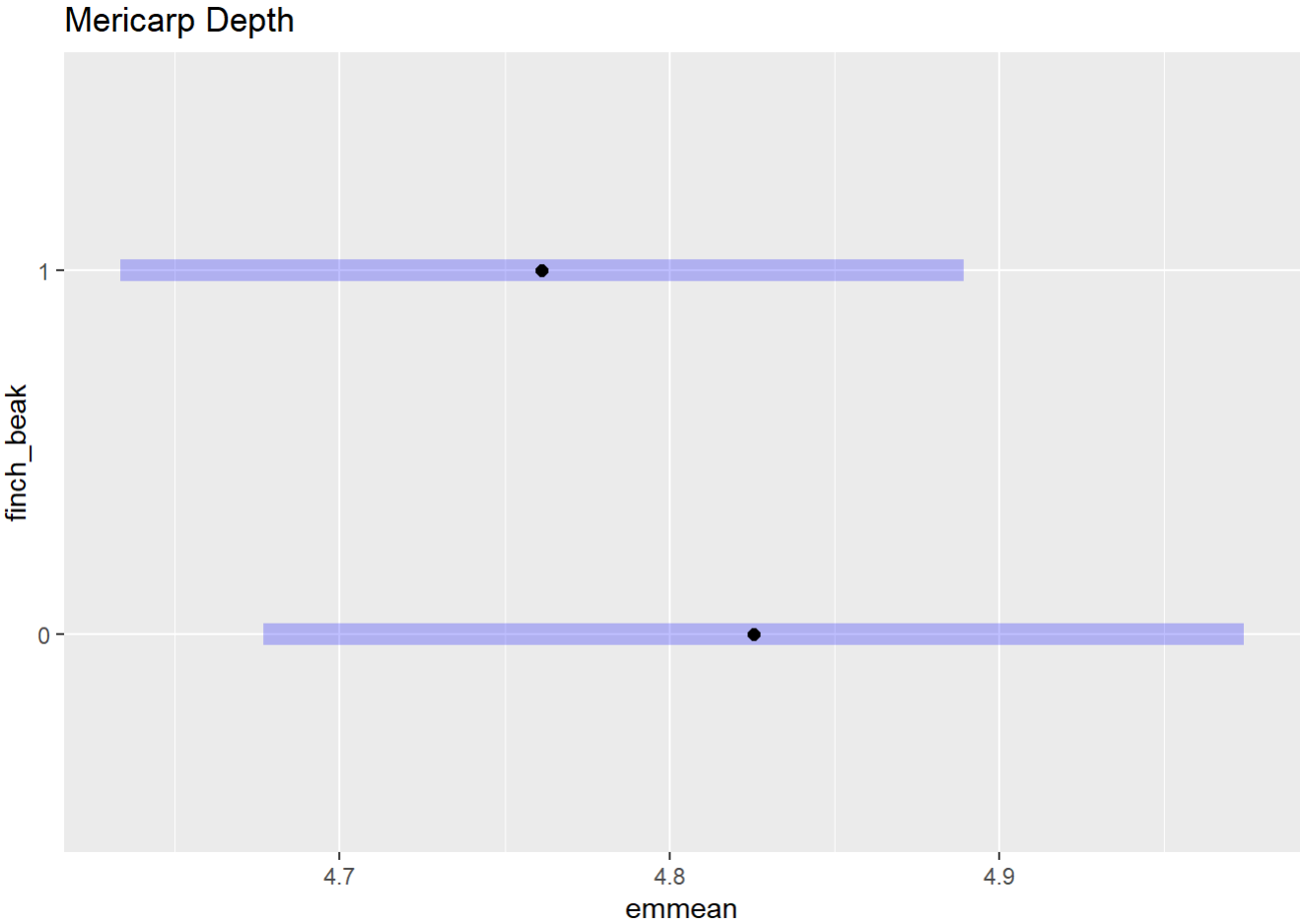


```
## [1] "Kurtosis=0.742071142705659"
## [1] "Skew=-0.204346797146509"
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: depth
##           Chisq Df Pr(>Chisq)
## finch_beak    0.4309  1    0.51155
## year_collected 4.1036  1    0.04279 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

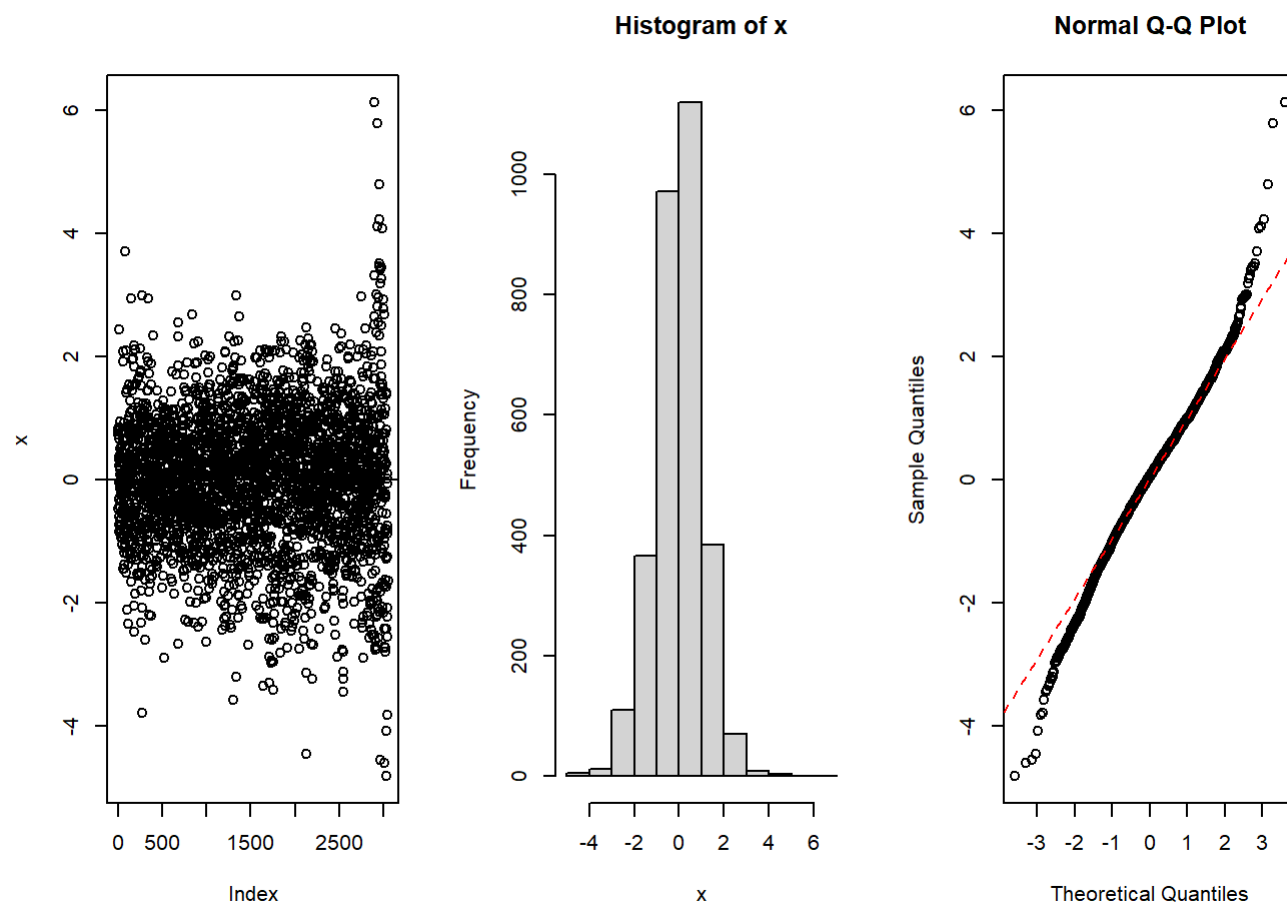
Emmeans: Depth



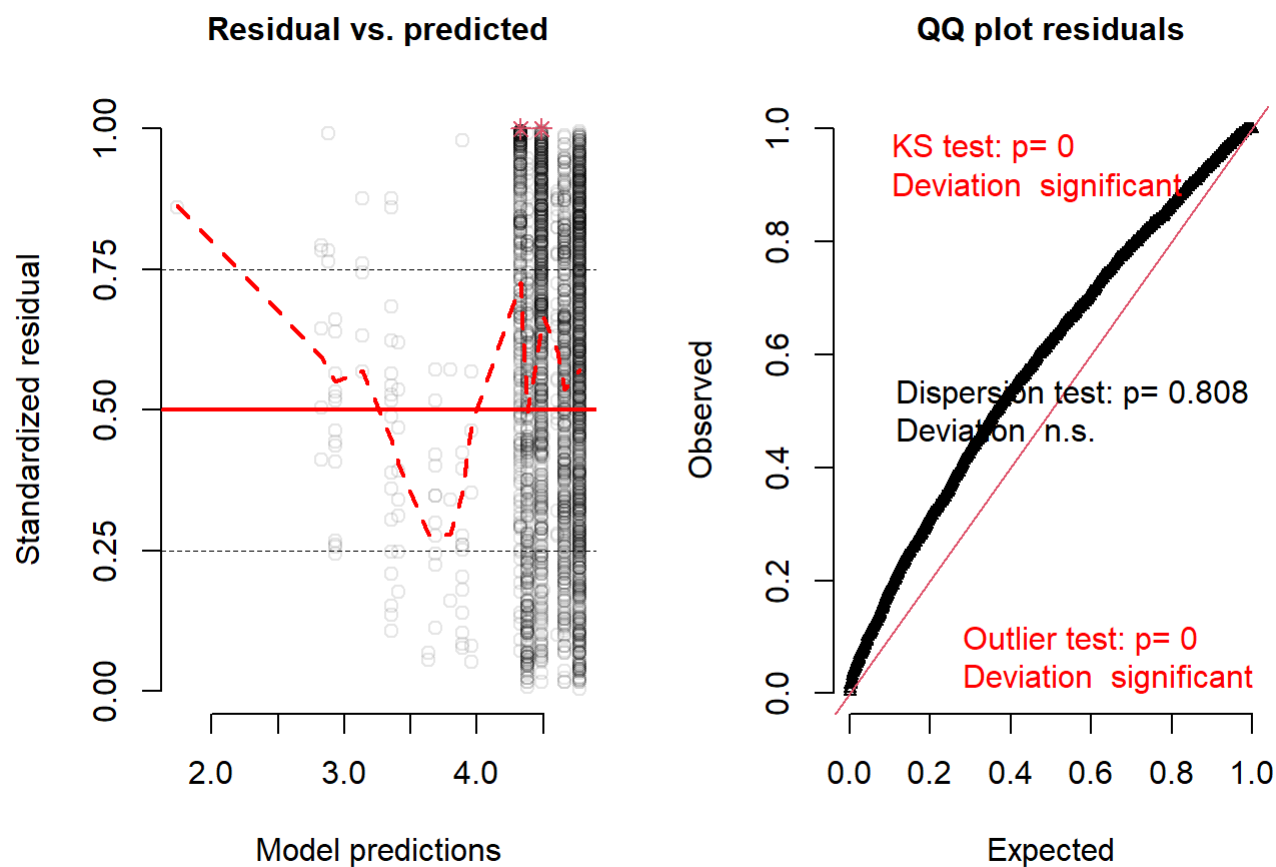
Spine length

Spine length had a lot zeroes that were removed.

Best fitted data: Untransformed data.



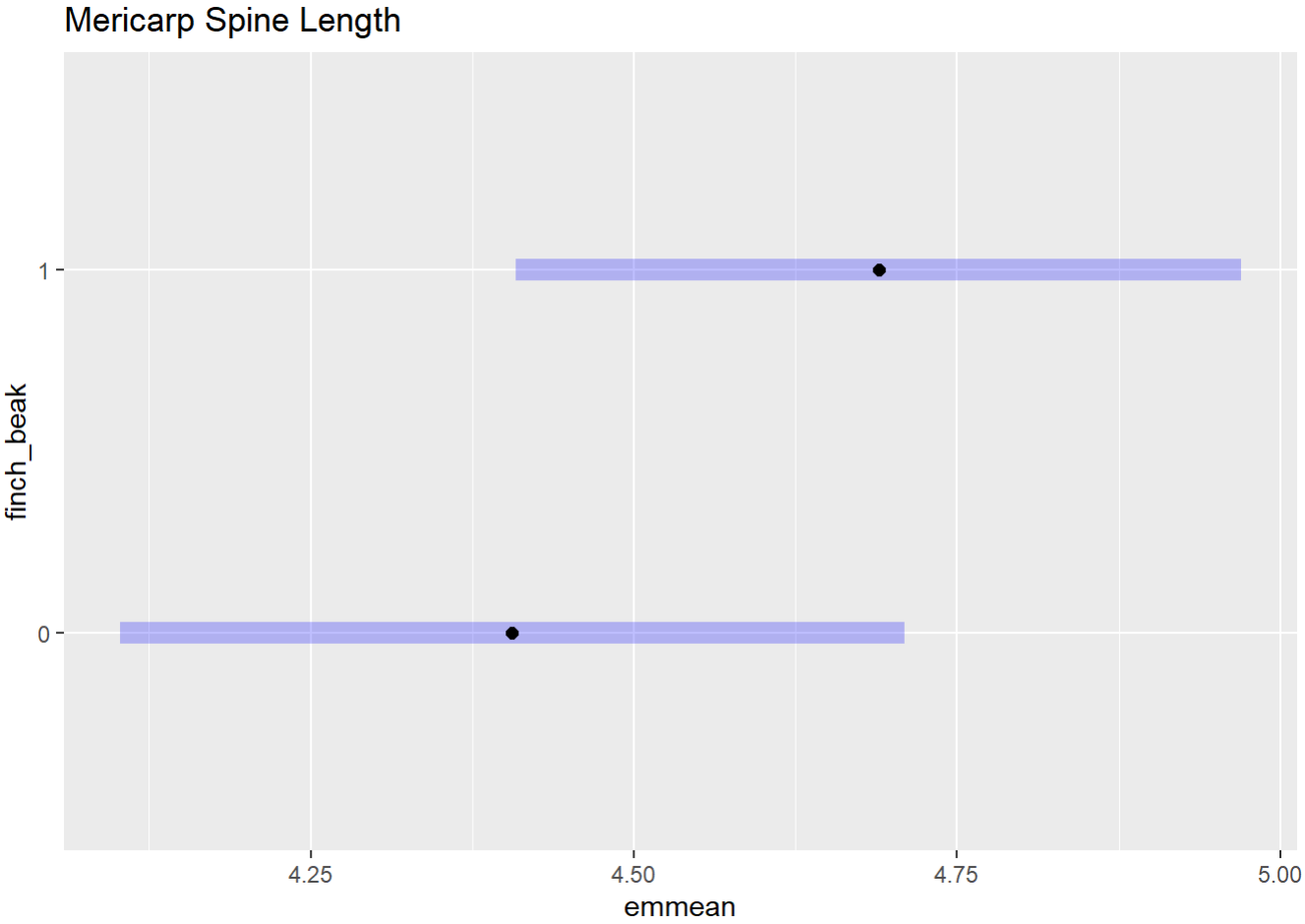
```
## [1] "Kurtosis=1.39547873017004"
## [1] "Skew=-0.109215601223584"
```



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: spine_length
##               Chisq Df Pr(>Chisq)
## finch_beak      1.8926  1    0.1689
## year_collected 17.4551  1  2.942e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Mainland/island groups non significant

Emmeans: Spine length



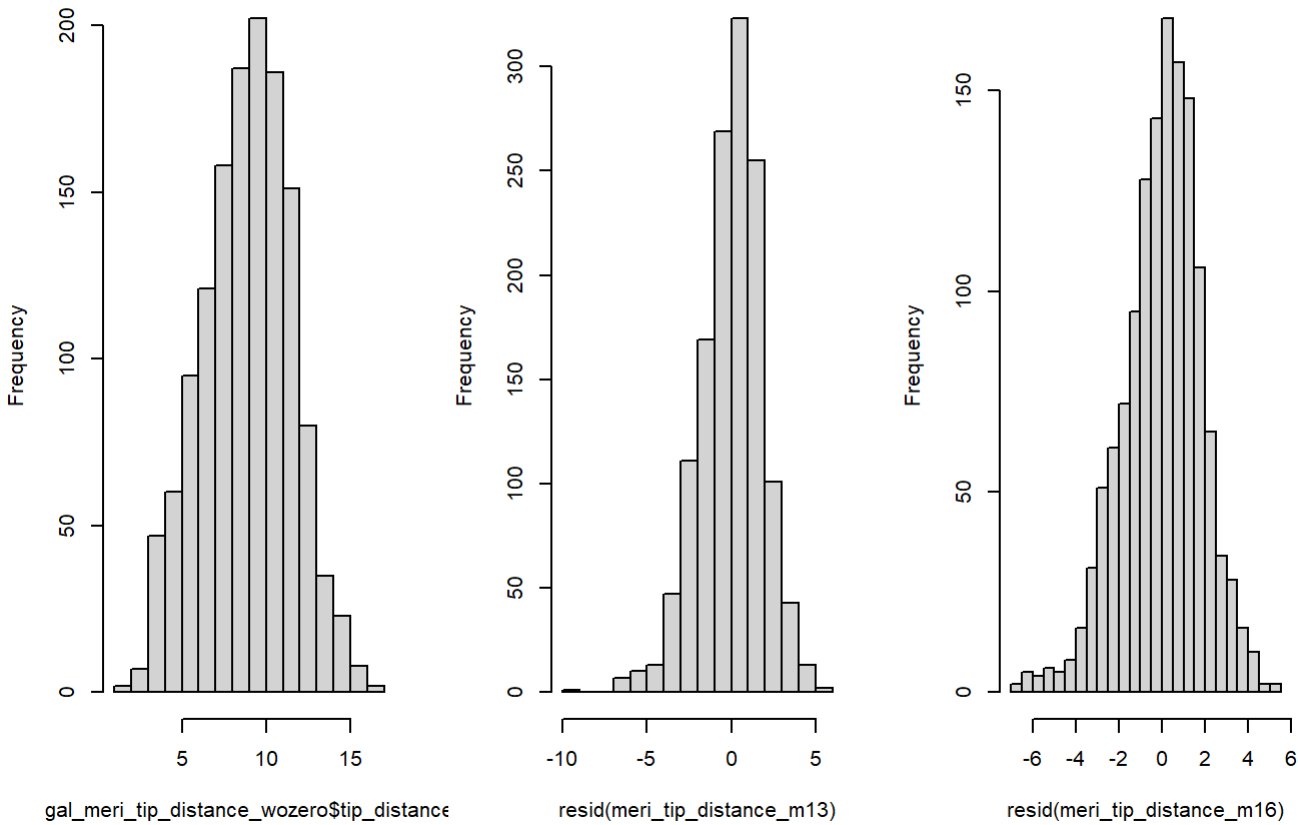
Tip distance

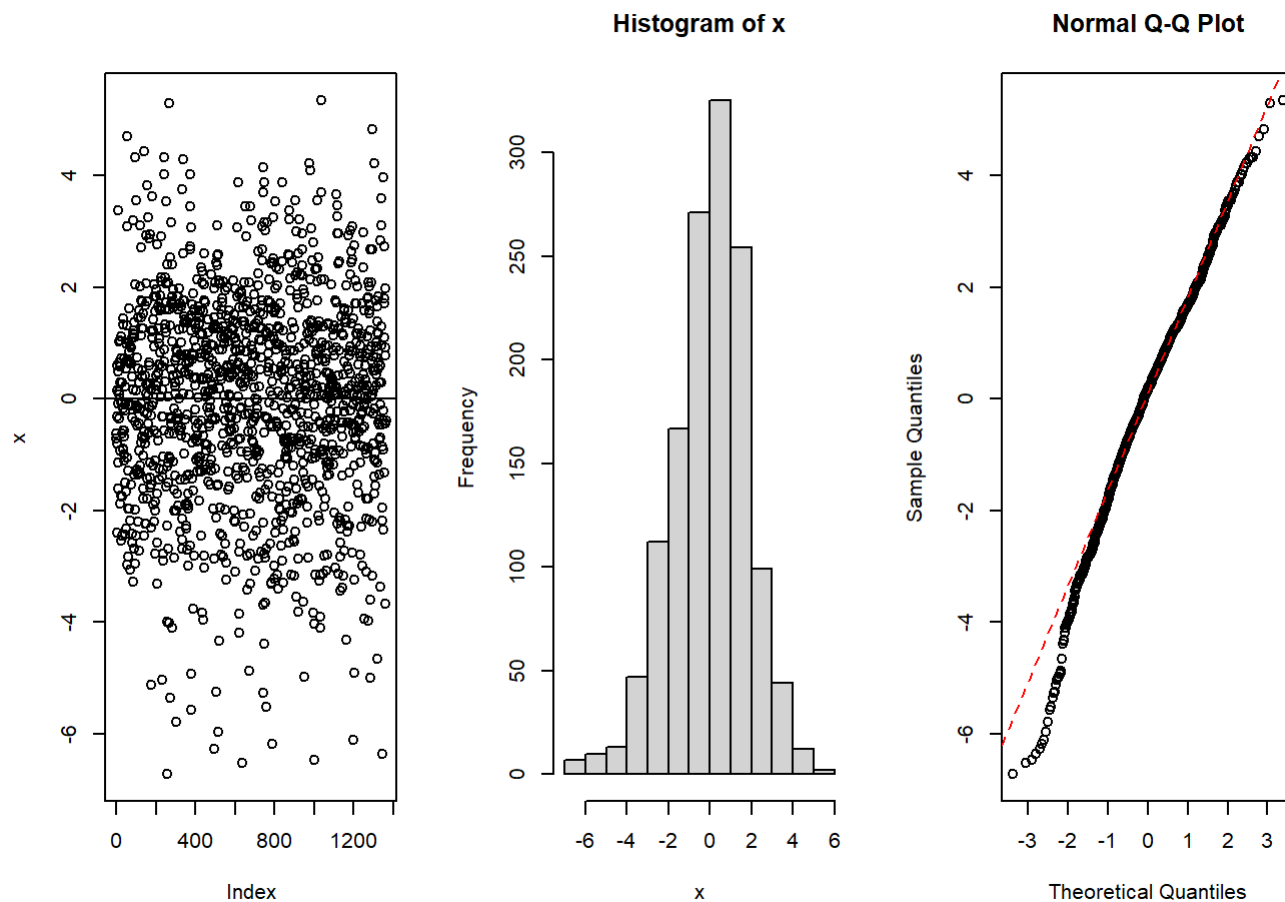
In a similar way, tip distance had a lot zeroes that were removed. I show three histograms with the distributions of tip distance measurements with zeros included. The residuals of the original model and the residuals distribution after filtering.

The diagnostic function shows the residuals distribution after removing zeros and filtering residuals that were lower than -9.

Best fitted data: Untransformed data.

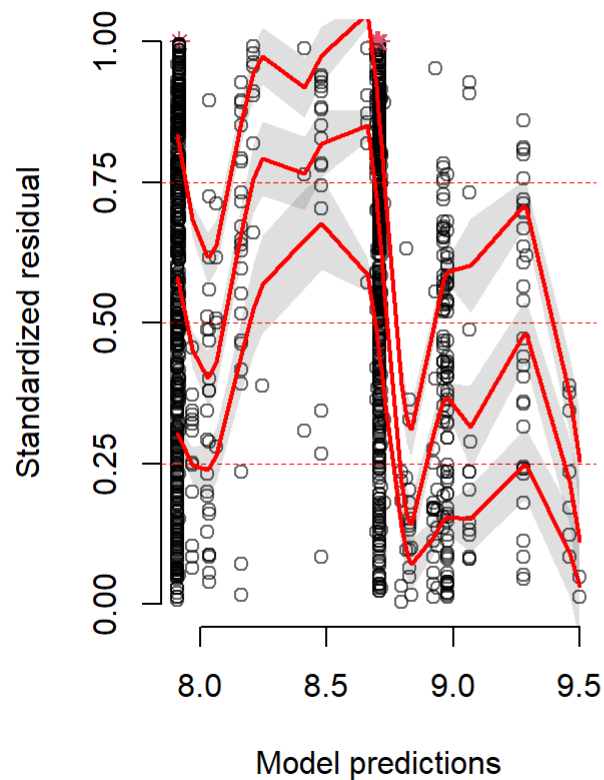
am of gal_meri_tip_distance_wozero\$Histogram of resid(meri_tip_distance_Histogram of resid(meri_tip_distance_



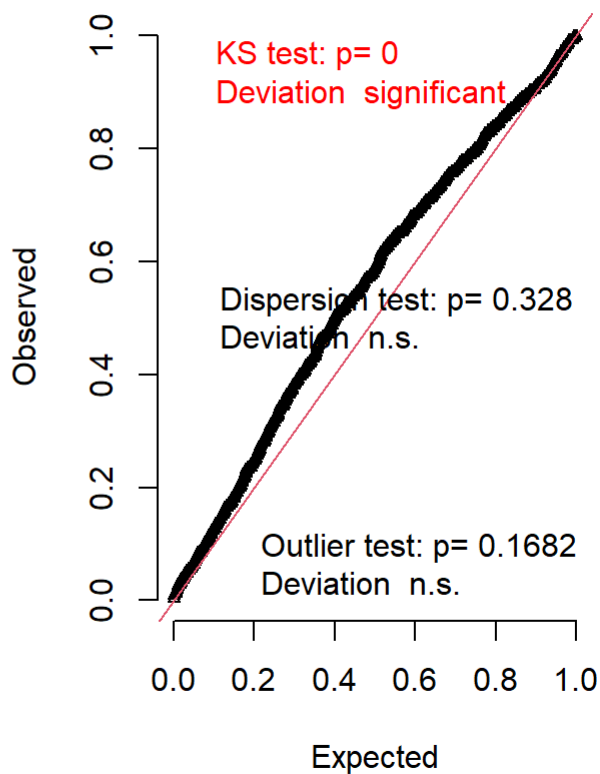


```
## [1] "Kurtosis=0.583306801964268"
## [1] "Skew=-0.428815505578938"
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



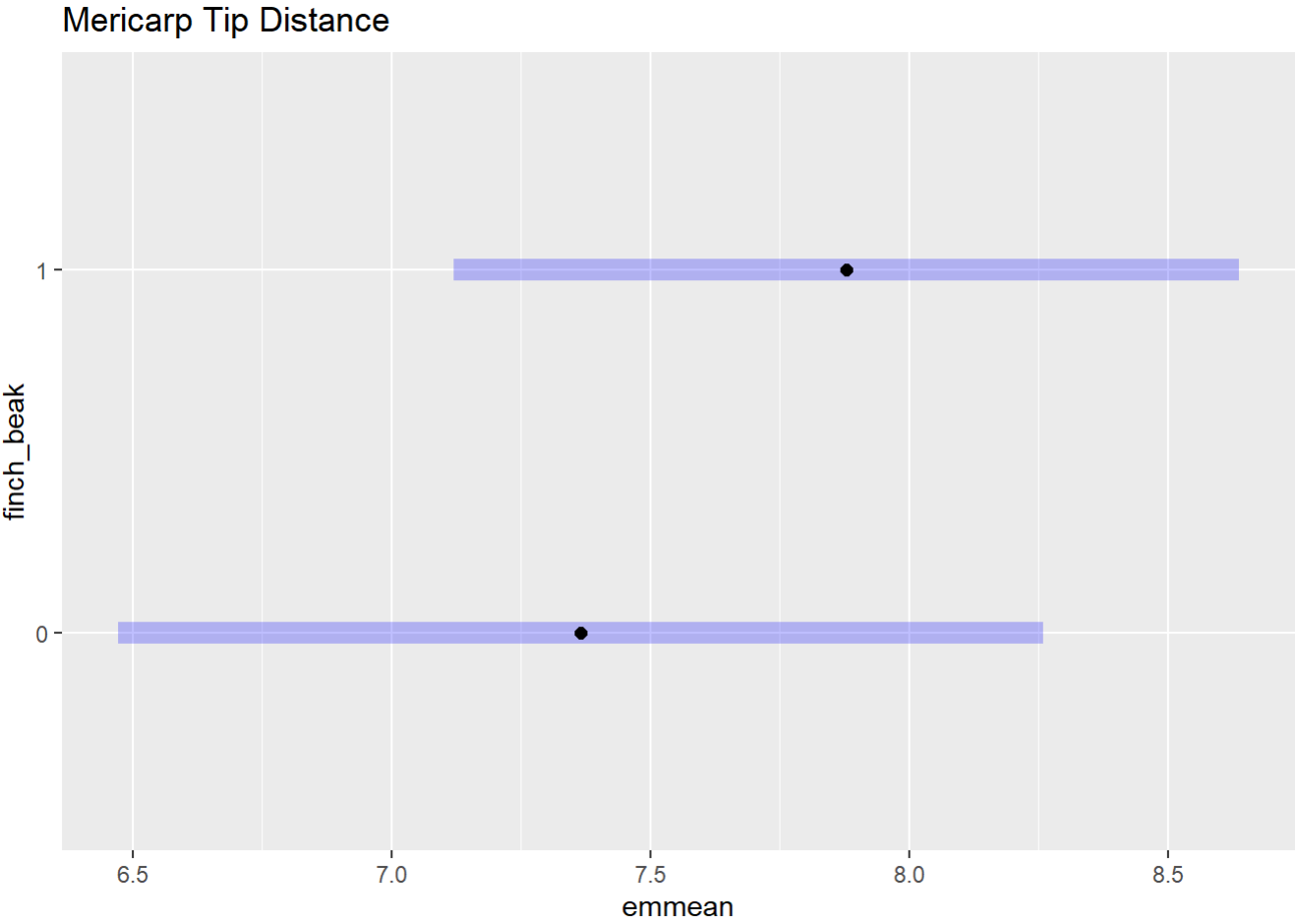
QQ plot residuals



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: tip_distance
##           Chisq Df Pr(>Chisq)
## finch_beak   4.0870  1   0.04321 *
## year_collected 1.2434  1   0.26481
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Finch beak groups significant

Emmeans: Tip distance



Lower spines

Presence/absence of lower spines is a binomial trait for this one I used two models that showed different outcomes. The first one is a glm: **glm(lower_spines ~ mainland_island + year_collected)**.

This model includes year as a factor but does not contain ID as a random effect.

The second one using the *glmmTMB* package: **glmmTMB(lower_spines ~ mainland_island + (1|ID)**

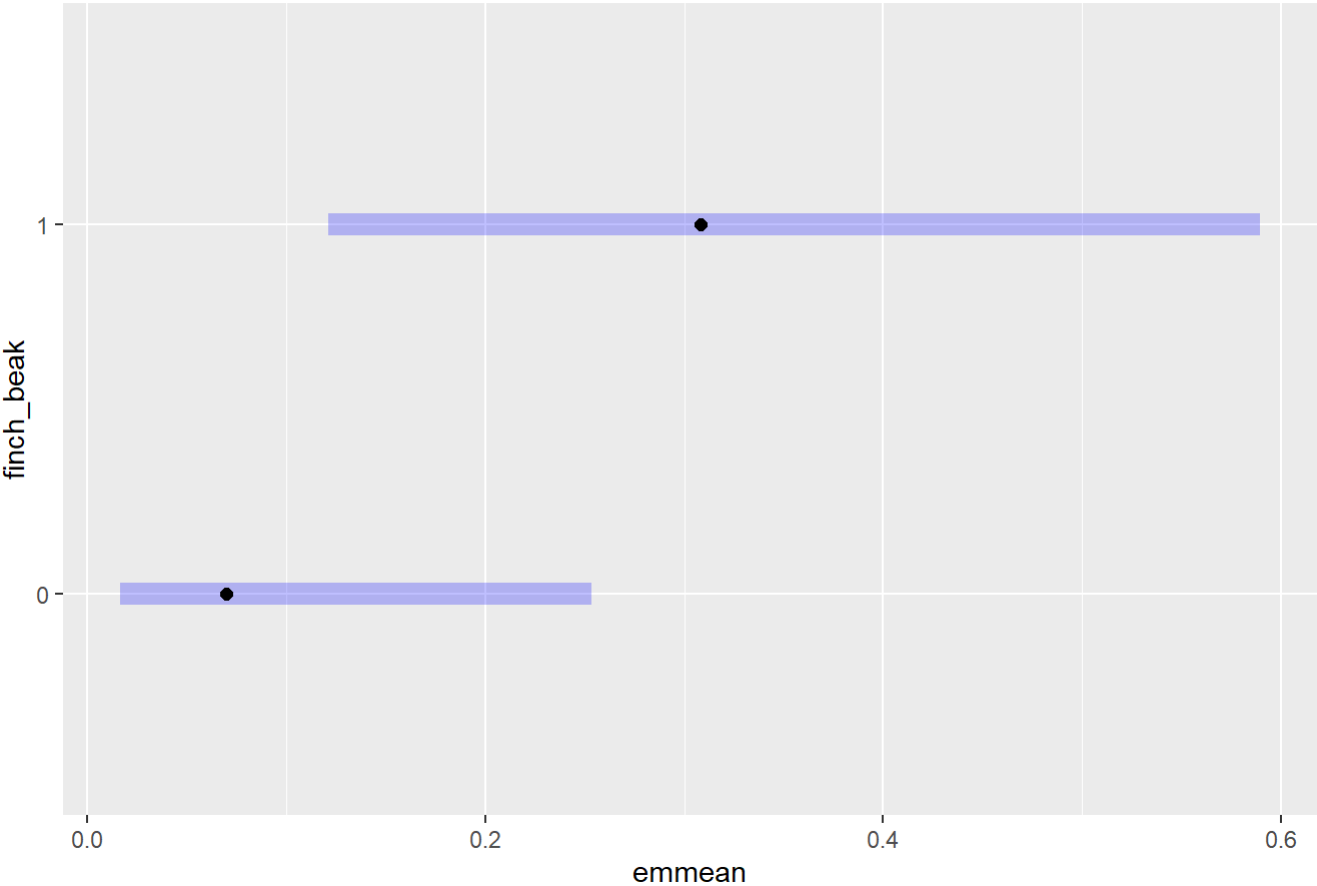
The glmmTMB model does not include the year factor but does include the random ID effect.

```
## Analysis of Deviance Table (Type II tests)
##
## Response: lower_spines
##              LR Chisq Df Pr(>Chisq)
## finch_beak      214.413  1  < 2.2e-16 ***
## year_collected   26.534  1  2.589e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: lower_spines
##              Chisq Df Pr(>Chisq)
## finch_beak 3.6226  1      0.057 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

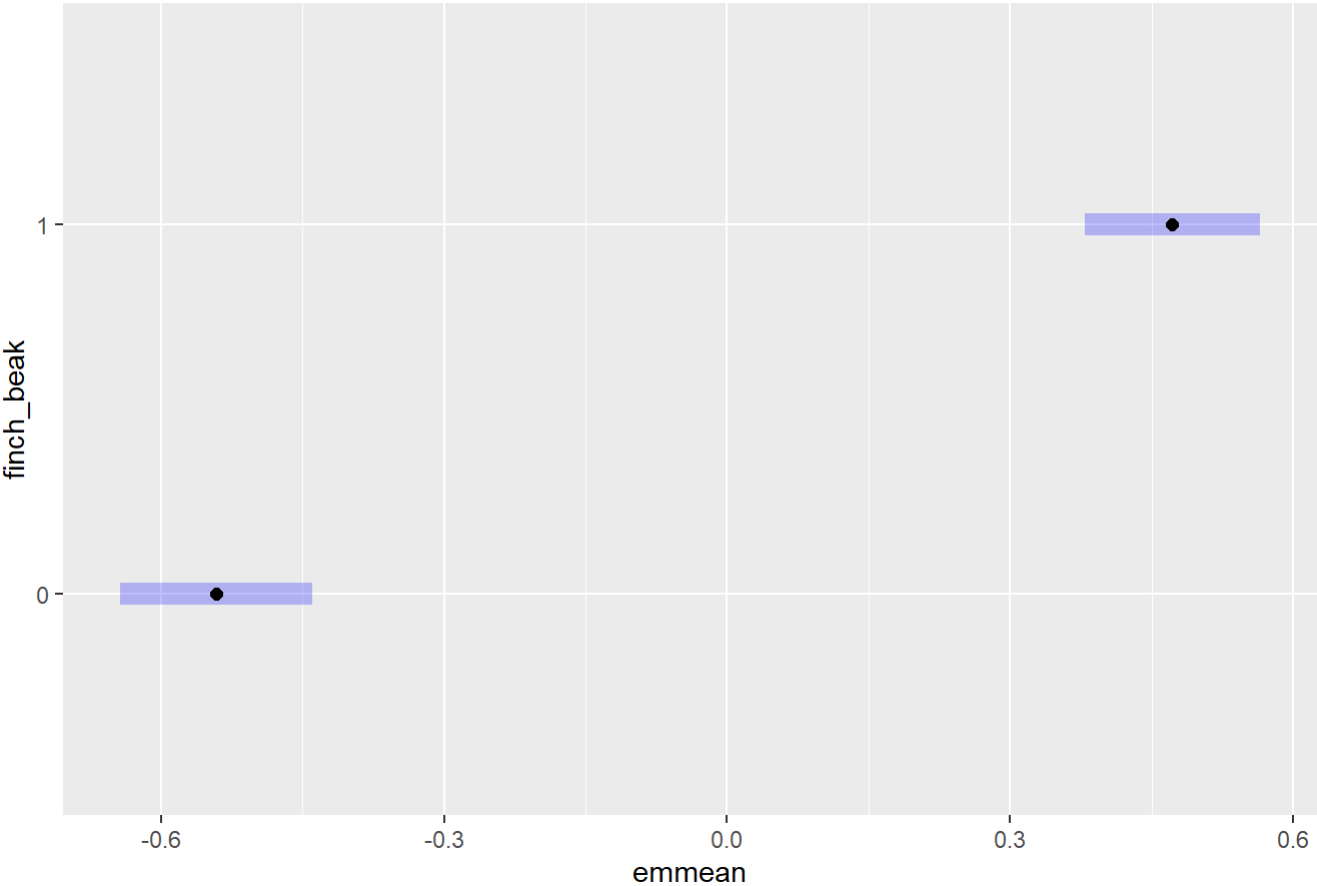
Emmeans: Lower spines

Merica­ Lower Spines



First plot, glm model. Second plot, glmmTMB model.

Merica­rp Lower Spines



First plot, glm model. Second plot, glmmTMB model.

Upper spines

Presence/absence of upper spines is a binomial trait that replaced spine number. Similar as lower spines, I used two models that showed different outcomes. The first one is a glm: **glm(upper_spines ~ mainland_island + year_collected)**.

This model includes year as a factor but does not contain ID as a random effect.

The second one using the *glmmTMB* package: **glmmTMB(upper_spines ~ mainland_island + (1|ID)**

The glmmTMB model does not include the year factor but does include the random ID effect.

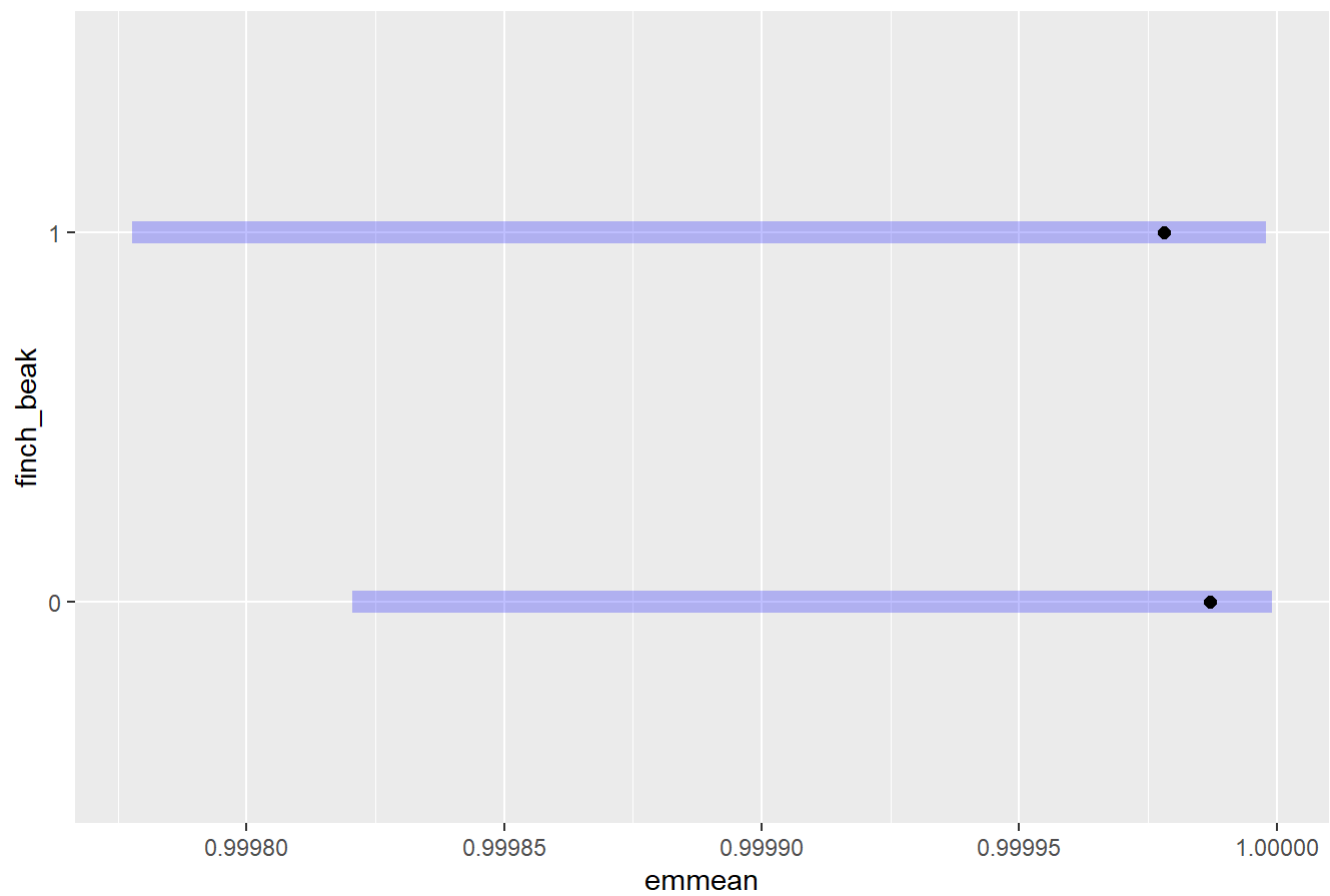
```
## Analysis of Deviance Table (Type II tests)
##
## Response: lower_spines
##              LR Chisq Df Pr(>Chisq)
## finch_beak      214.413  1 < 2.2e-16 ***
## year_collected   26.534  1 2.589e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: upper_spines
##              Chisq Df Pr(>Chisq)
## finch_beak 0.138  1    0.7103
```

Here, for the glm model the results are significant, but for the glmmTMB the differences between mainland and island populations are not significant.

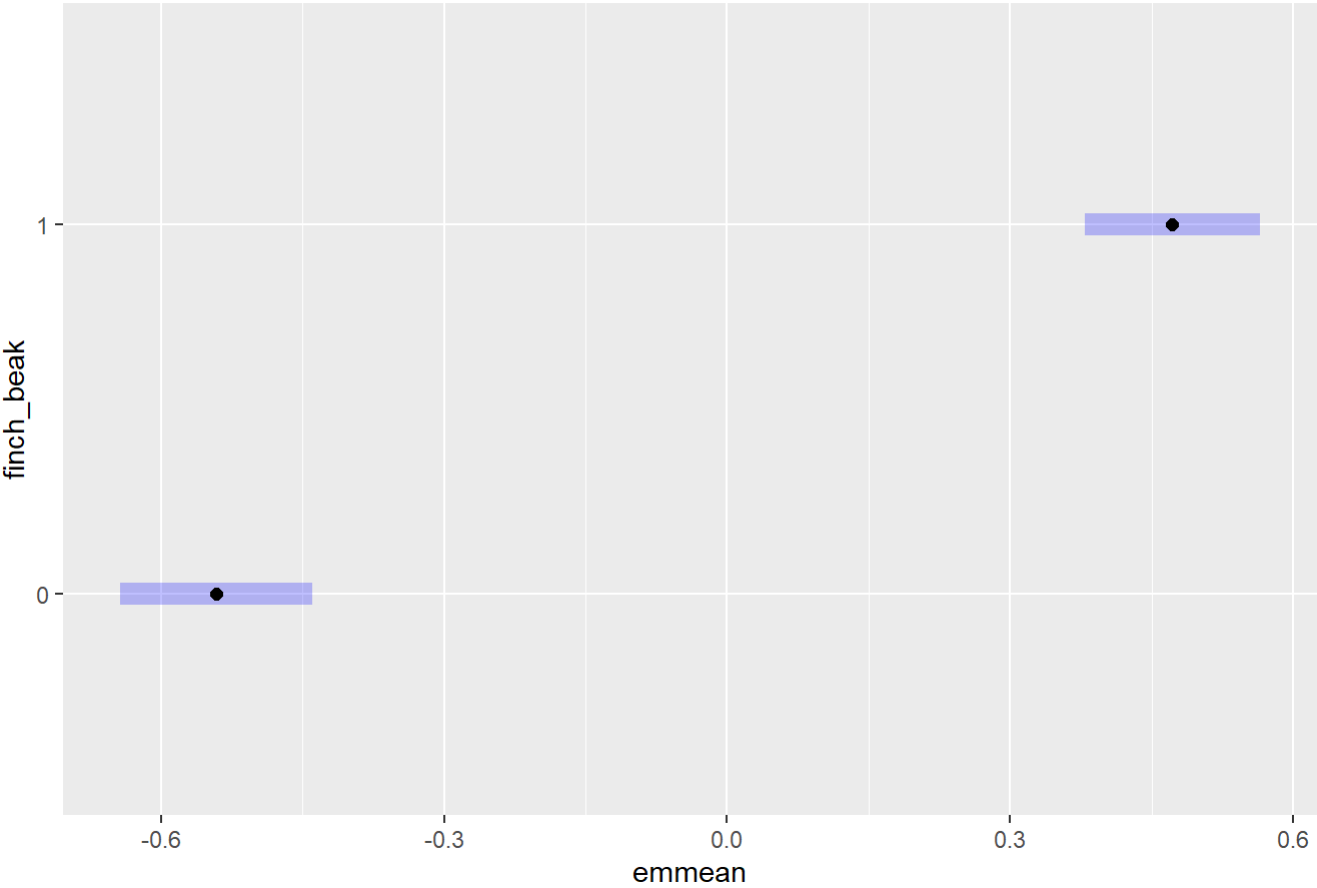
Emmeans: Lower spines

Mericaup Upper Spines



First plot, glm model. Second plot, glmmTMB model.

Merica­rp Upper Spines

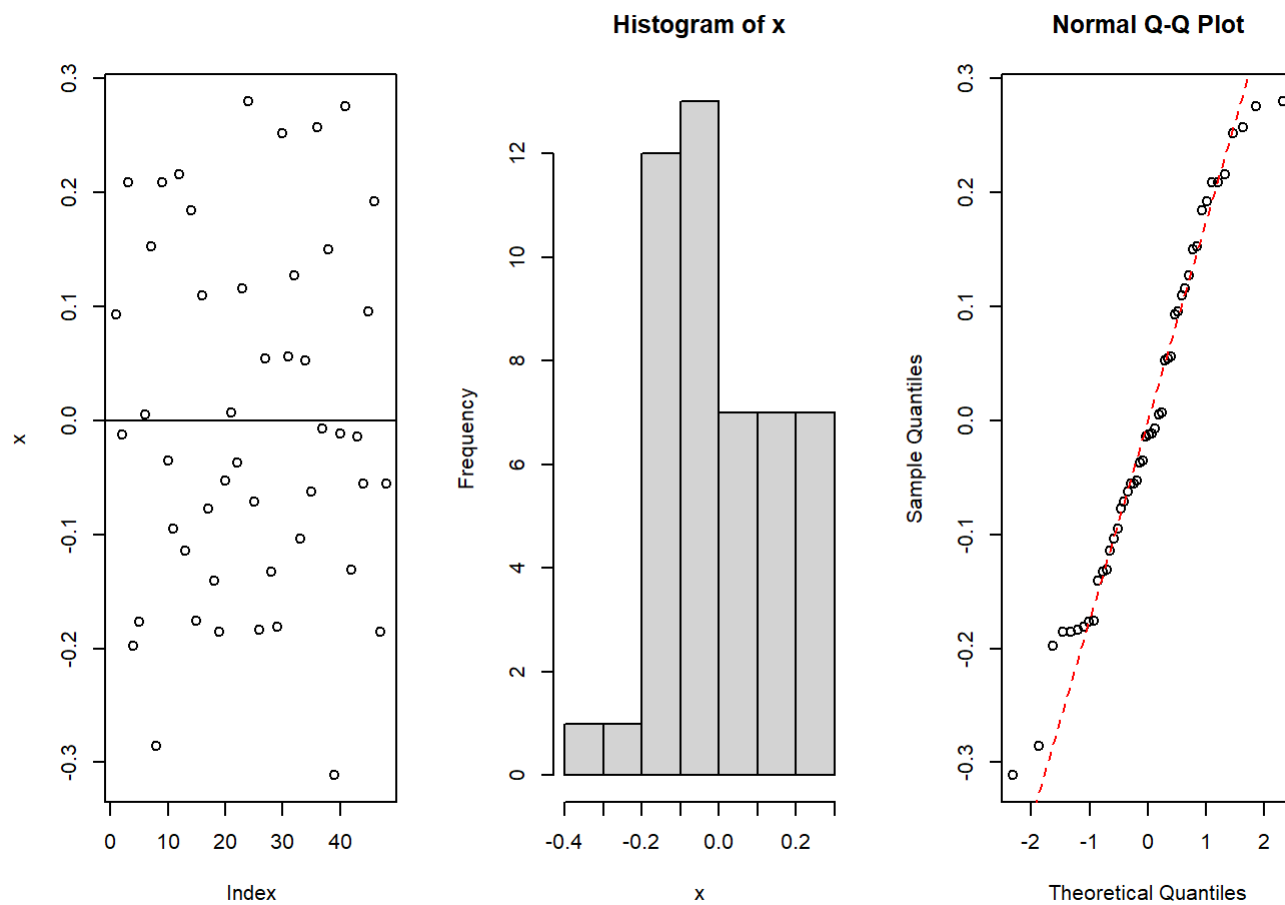


First plot, glm model. Second plot, glmmTMB model.

Flower traits:

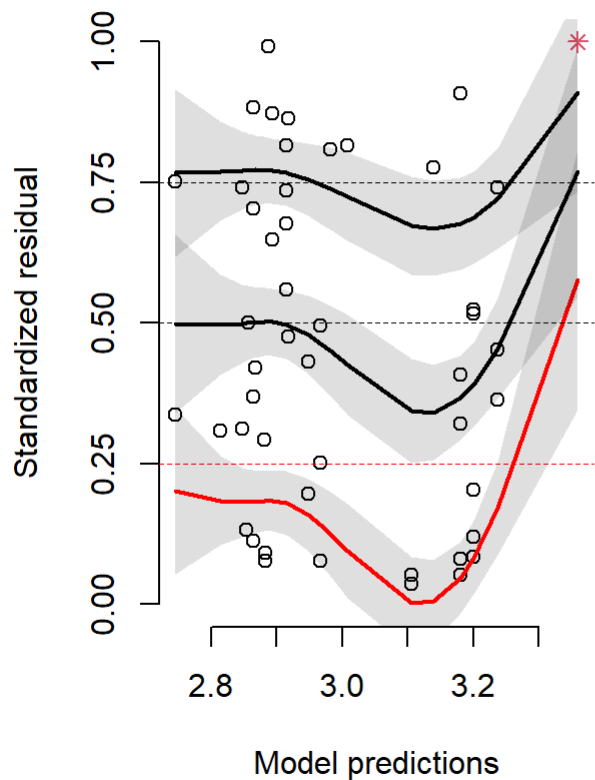
Petal length

Best fitted data: Square root data

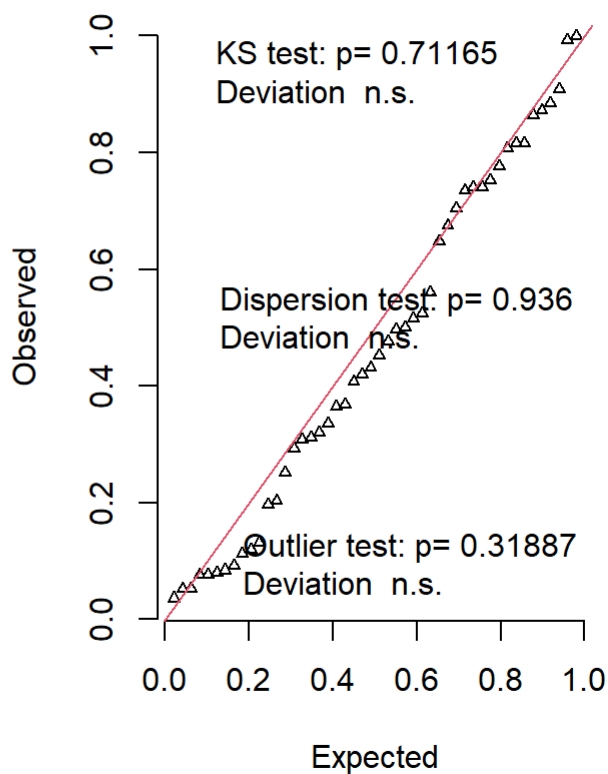


```
## [1] "Kurtosis=-0.984219631146156"
## [1] "Skew=0.122007465363433"
```


Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



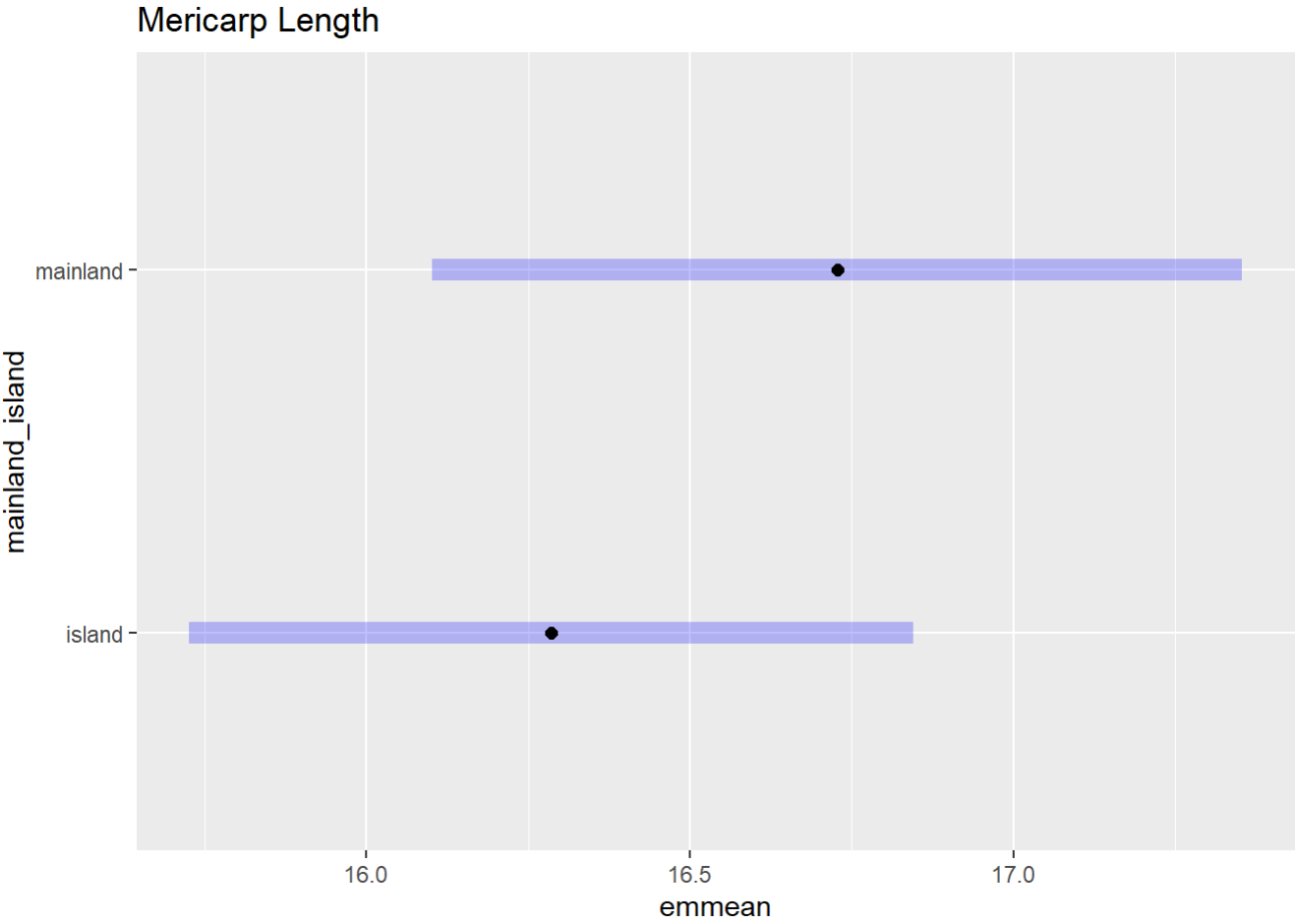
QQ plot residuals



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(petal_length)
##           Chisq Df Pr(>Chisq)
## finch_beak    0.3459  1  0.556418
## year_collected 6.7203  1  0.009532 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Year differences are significant.

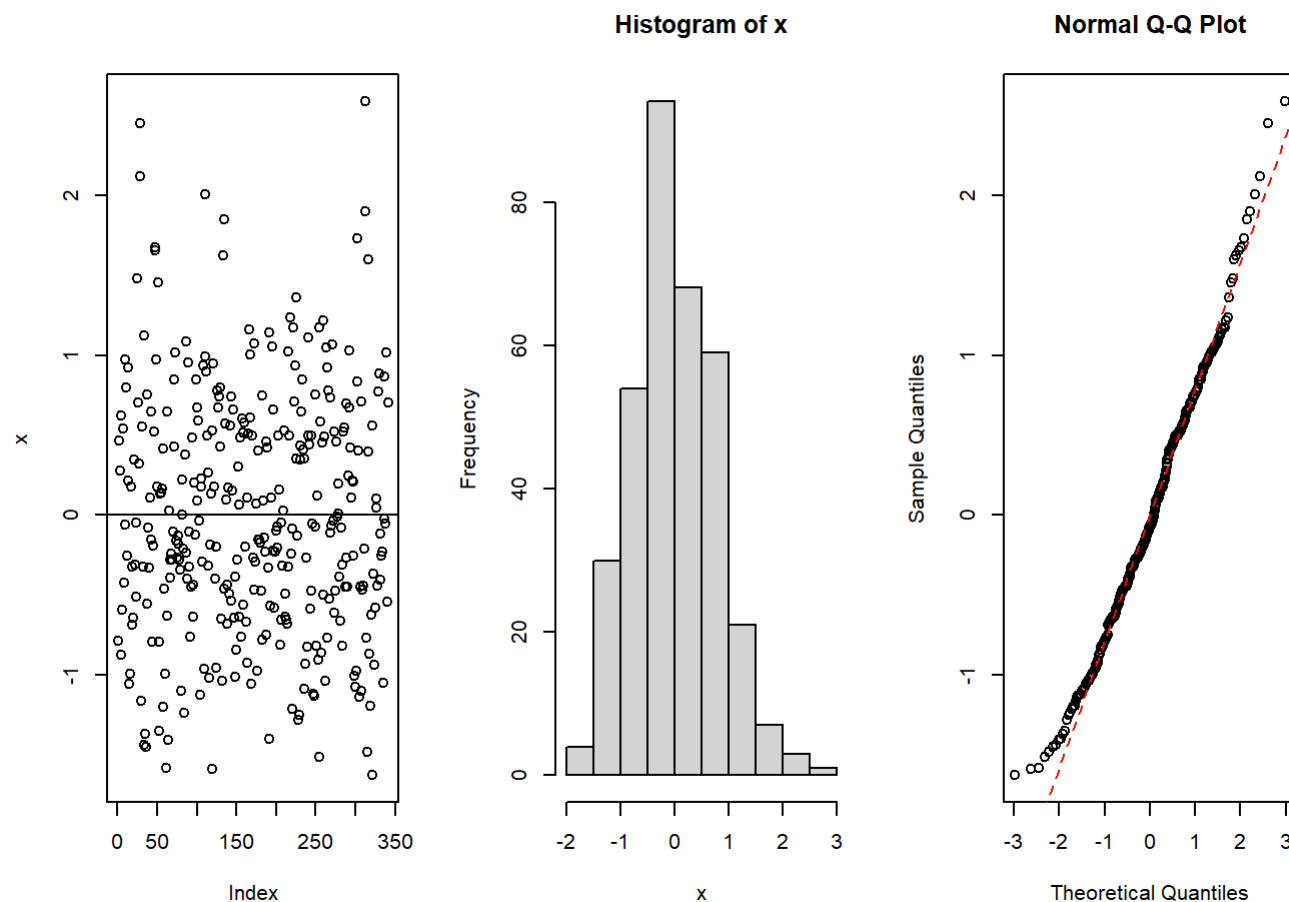
Emmeans: Petal length



Leaf traits:

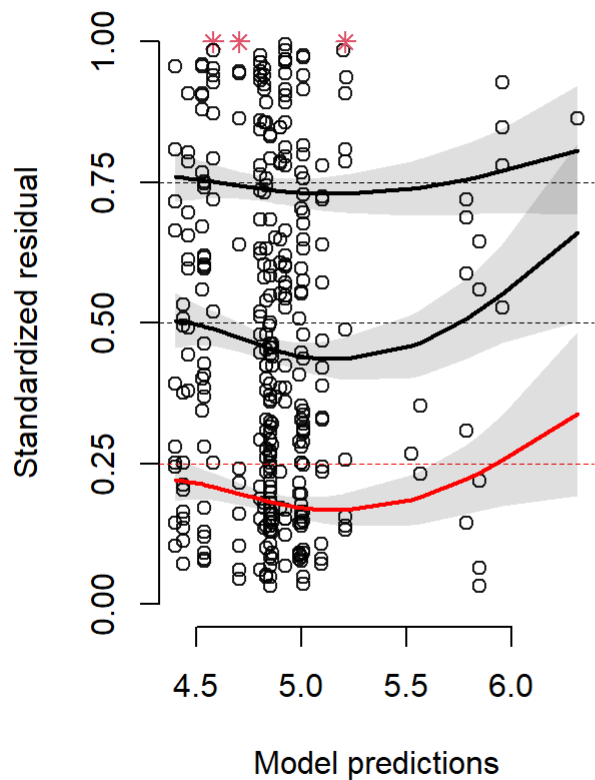
Leaf length

Best fitted data: Square root transformed data

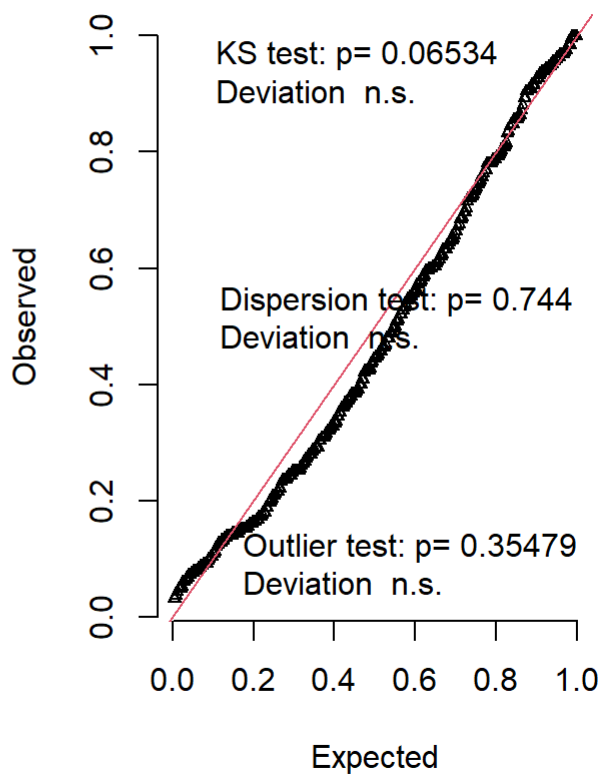


```
## [1] "Kurtosis=-0.016632520030861"
## [1] "Skew=0.32922404767702"
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



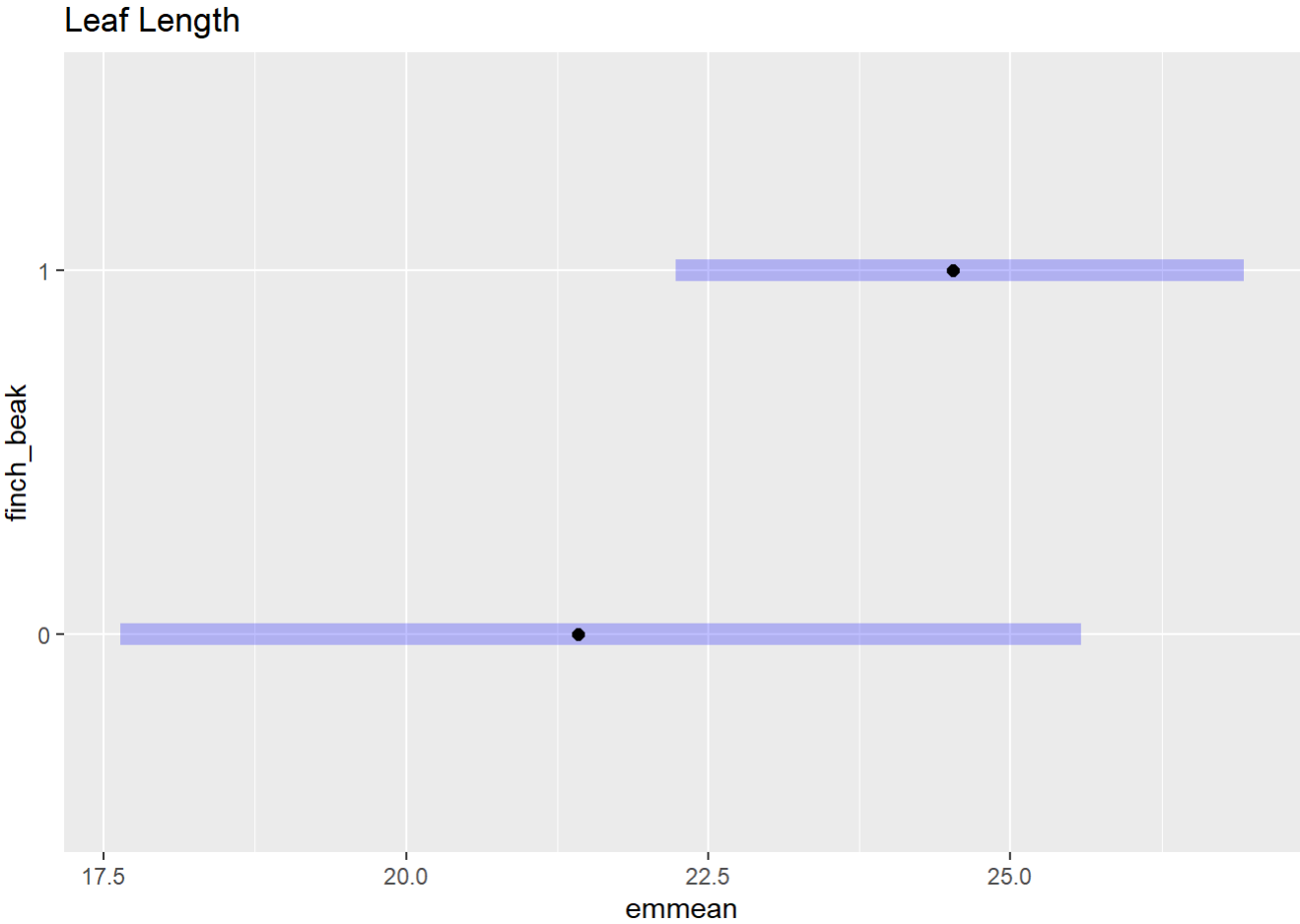
QQ plot residuals



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(leaf_length)
##           Chisq Df Pr(>Chisq)
## finch_beak    1.8787  1  0.1704780
## year_collected 12.8565  1  0.0003363 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Year differences are significant.

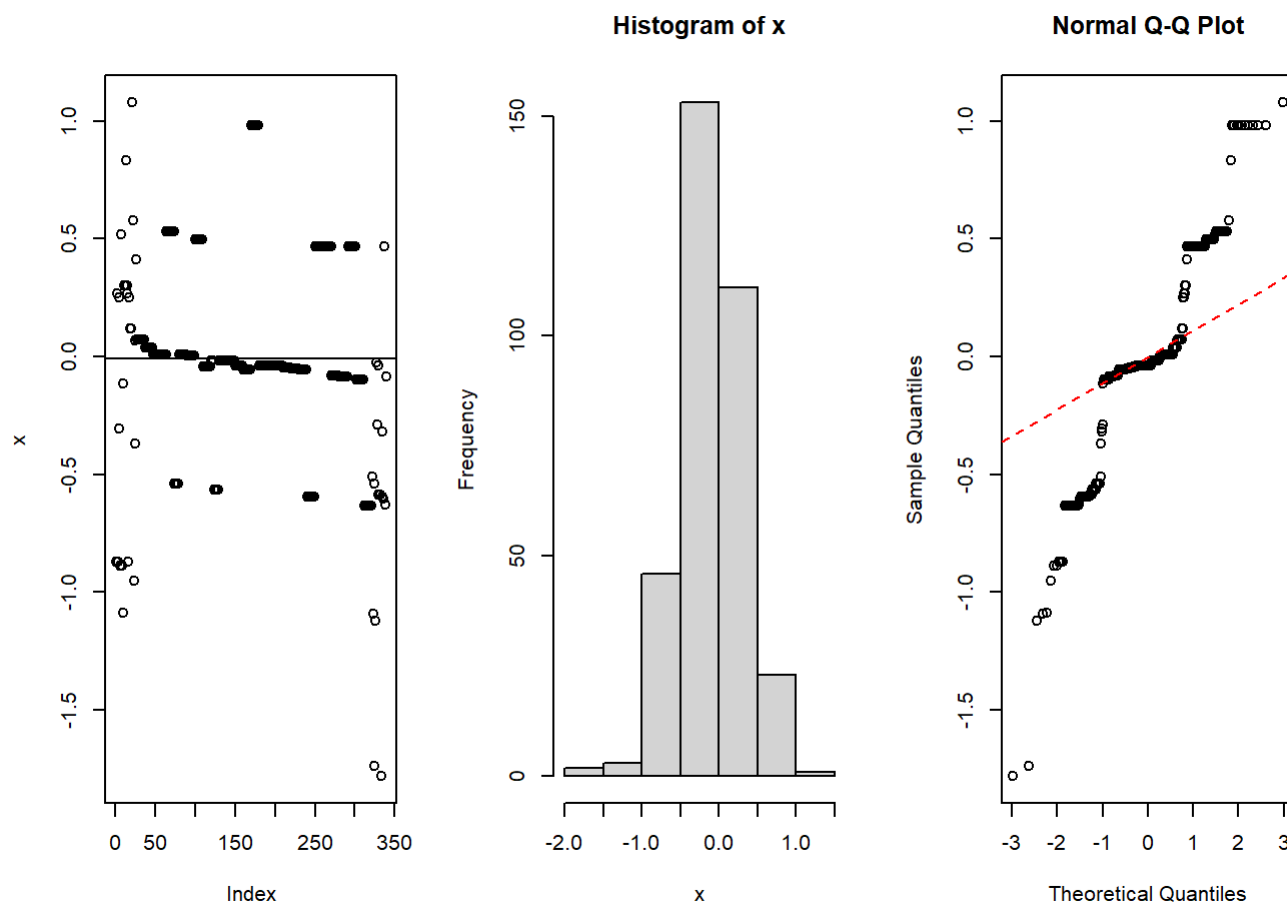
Emmeans: Leaf length



Leaflet number

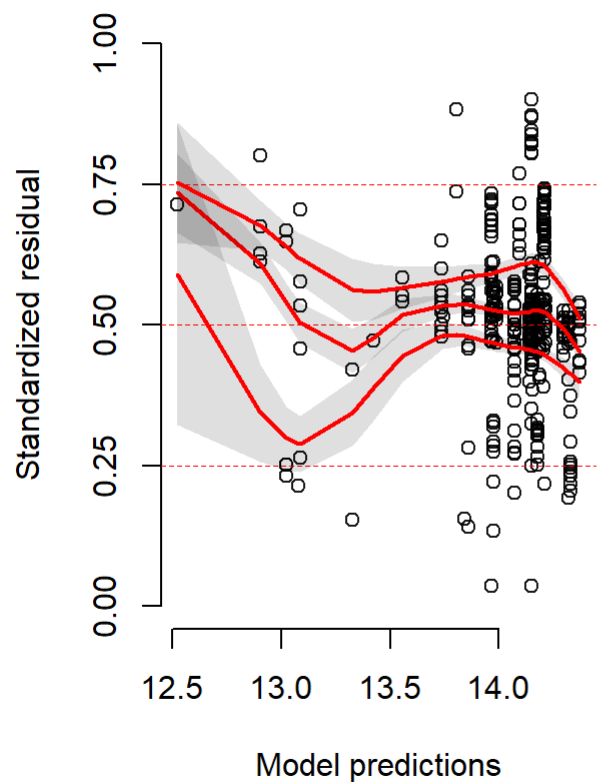
For this trait I used a glm model with a Poisson distribution:

```
glm(number_of_leaflets ~ mainland_island + year_collected)
```

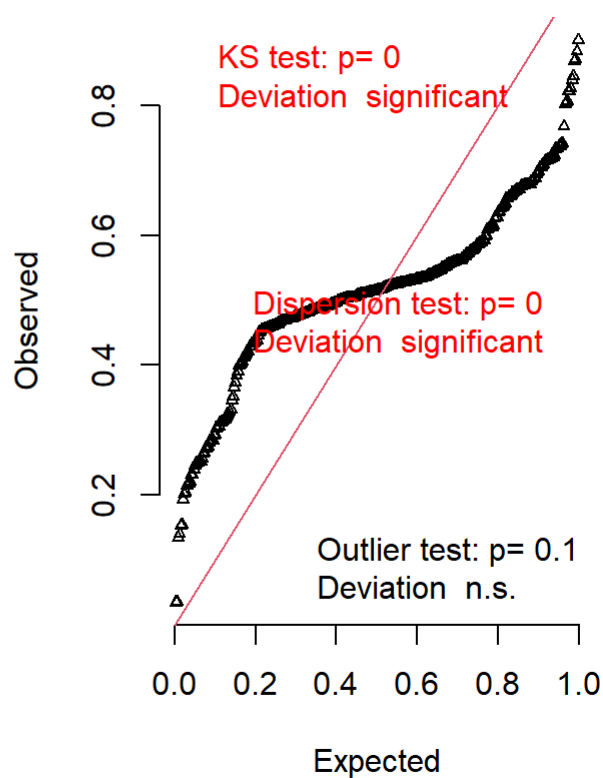


```
## [1] "Kurtosis=2.25505743315769"
## [1] "Skew=-0.393494785165159"
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant

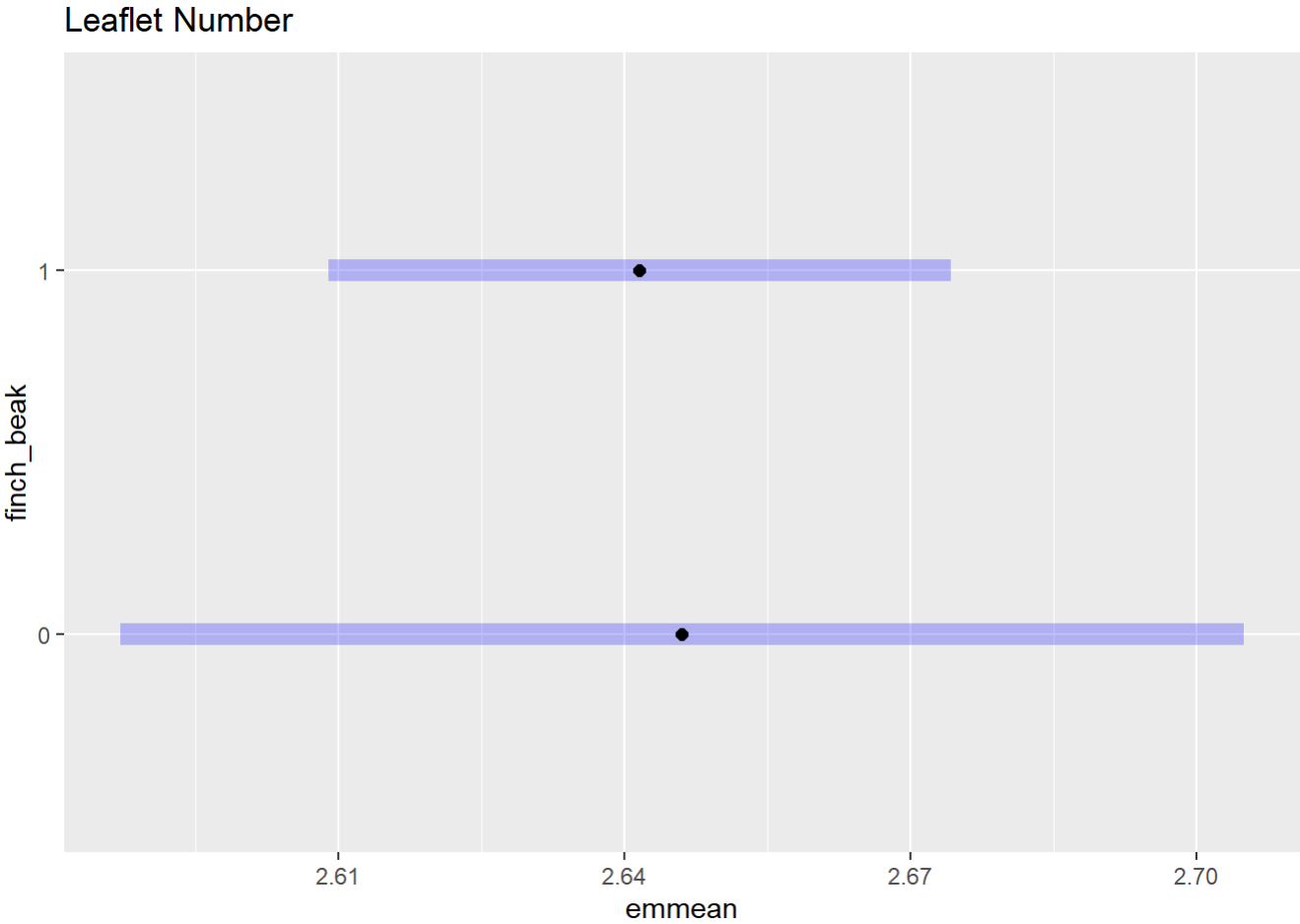


QQ plot residuals



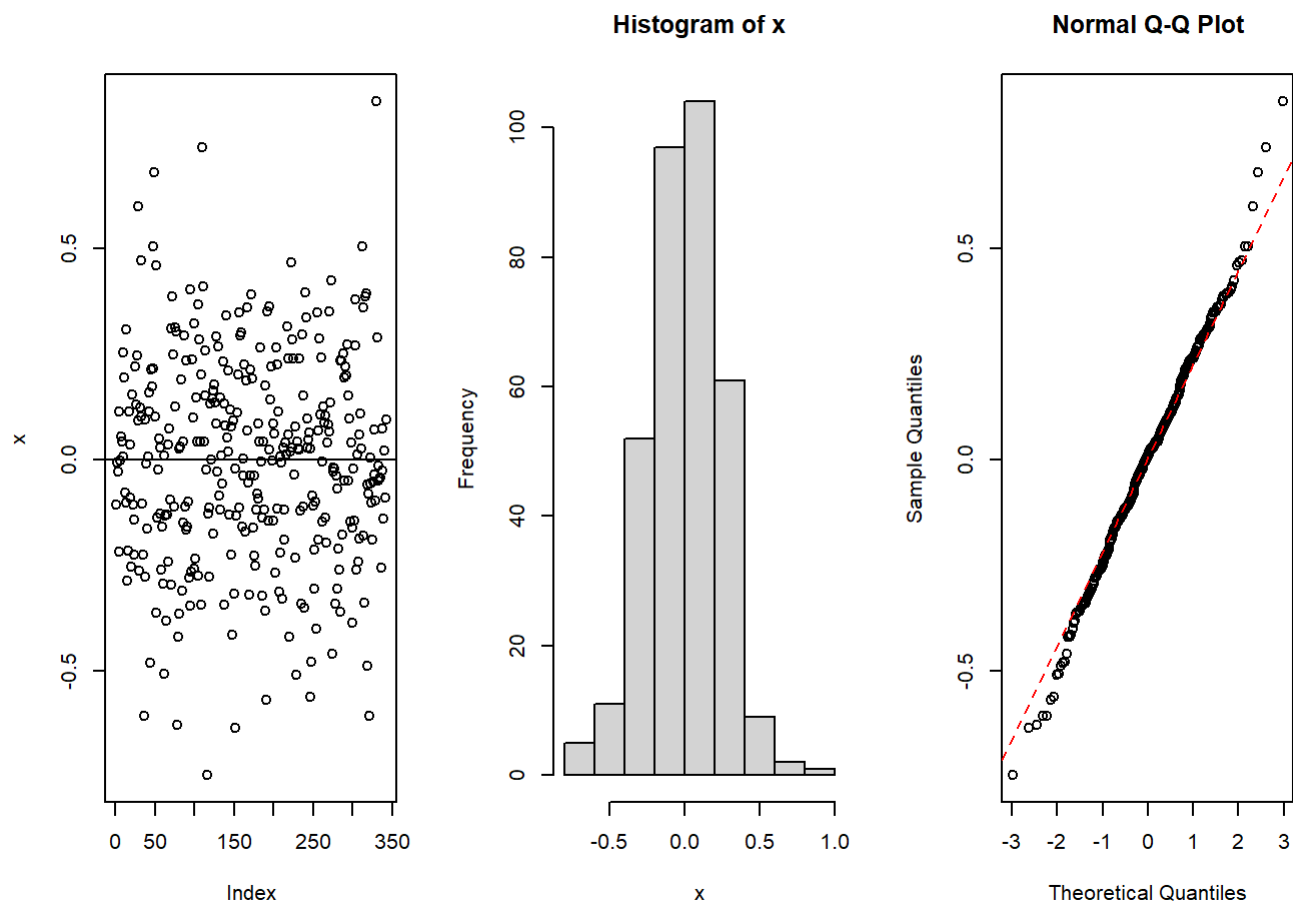
```
## Analysis of Deviance Table (Type II tests)
##
## Response: number_of_leaflets
##           LR Chisq Df Pr(>Chisq)
## finch_beak    0.01664 1    0.8974
## year_collected 1.94310 1    0.1633
```

Emmeans: Leaflet number



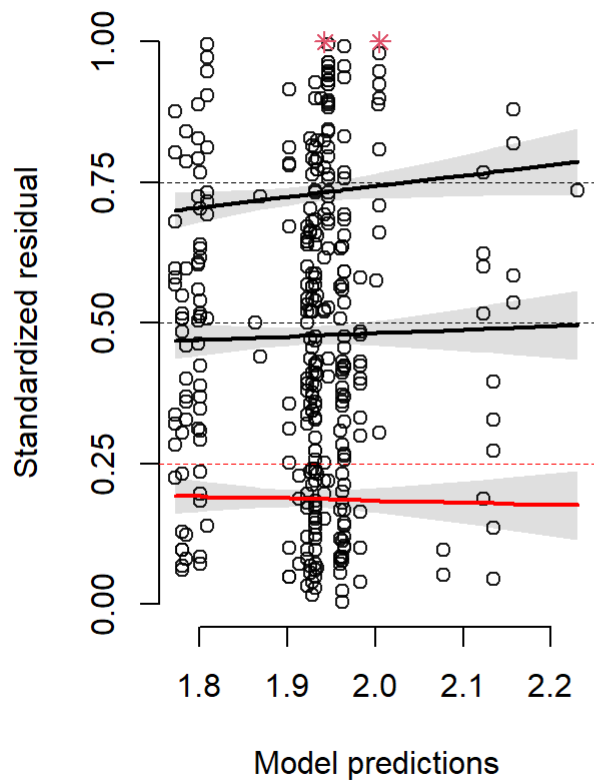
Leaflet length

Best fitted data: Log transformed data

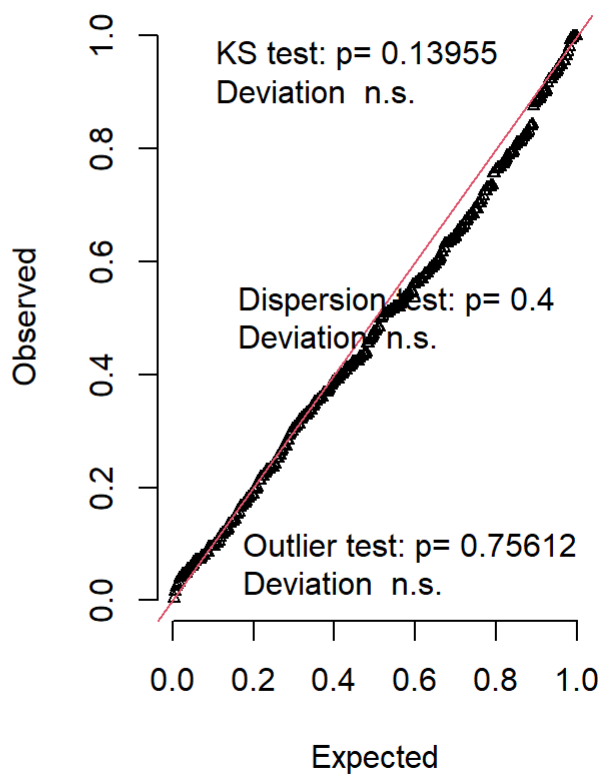


```
## [1] "Kurtosis=0.339413441190826"
## [1] "Skew=-0.0191508261482862"
```

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



QQ plot residuals



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: log(leaflet_length)
##           Chisq Df Pr(>Chisq)
## finch_beak    2.0280  1    0.15442
## year_collected 3.7091  1    0.05412 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Mainland and island differences and year differences are significant.

Emmeans: Leaflet length

