General Remarks

- I am using the VIF function from the package "usmd" in R to resolve collinearity. Within the VIF functions, I am using the *vifstep* value with a threshold of 10 vif_function
- The variables chosen were: Soil temperature, SOM, pH, CN, NH4, PO4, SO4, Silt, Litter, LTN, BB, SR, E2.E3, E4.E6, BIX, PeakC, PeakB, HIX, LTC_LTN and altitude.
- Based on the additional function *vifstep*, I added the following variables that might consider important: water content, TC, FB and clay.
- Additionally, I am adding aridity index that must be correlated with other variables, but we want to test their effects on the soil functions.

1. **Respiration model**

- We followed first outlier elimination using the cook distance function in R cook_distance

Influential Obs by Cooks distance
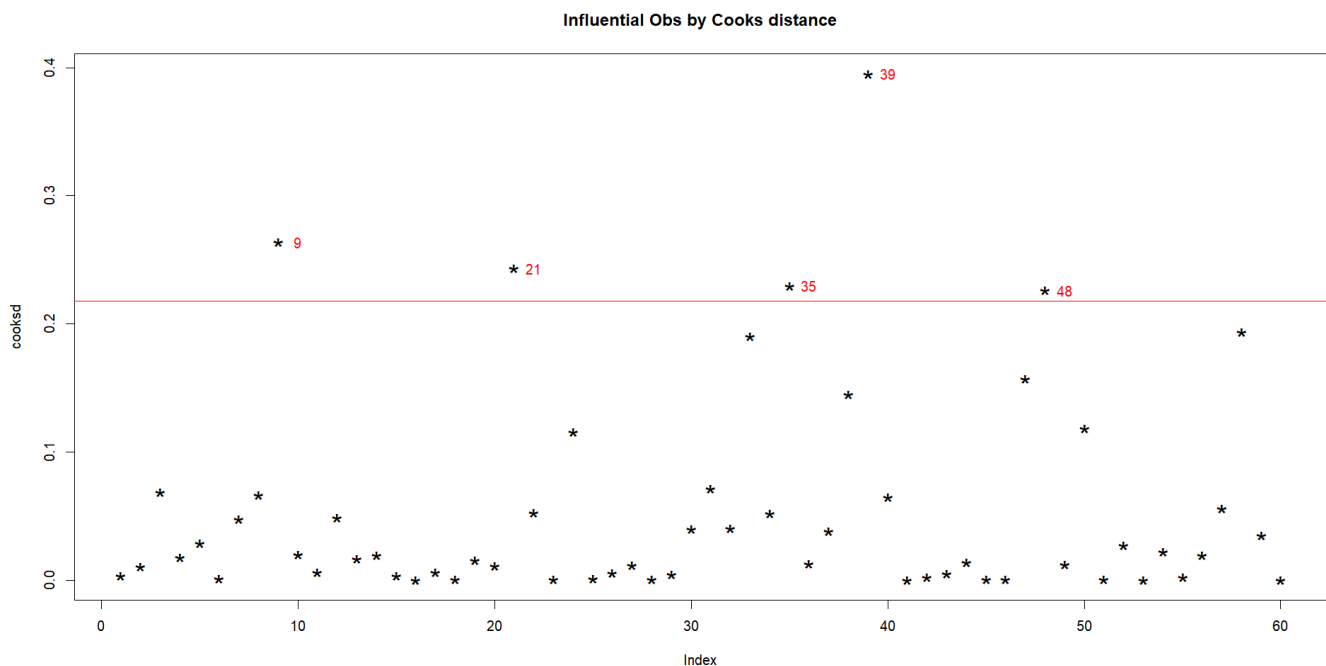
- Final model:

```
Respiration ~ 1 + Water_content + Clay + BIX + AI + BIX:AI + Clay:AI + (1|Site)
AIC_full = -481.72  AIC_new = -472.65
Marginal R2 = 0.5980825  Total R2 = 0.9821801
```

```
![[Pasted image 20240205174220.png]]
![[Pasted image 20240205174233.png]]
```

## 2. Bacterial biomass BB model

- For this model, I needed to take the log of the total bacterial biomass.
- For this model, I did not eliminate the statistical outliers because the model assumptions are still acceptable (feedback needed)
- Final model:

  `log(BB) ~ 1 + Water_content + Peak_B + L_TN + PO43 + E2.E3 + Peak_C + AI +`
  `E2.E3:AI + Peak_B:AI + Soil_Temp + Peak_C:AI + (1|Site)`
  `AIC_full = 81.79` AIC_new = 55.85
  `Marginal R2 = 0.6075355`
  `Total R2 = 0.9240806`

Normal Q-Q Plot
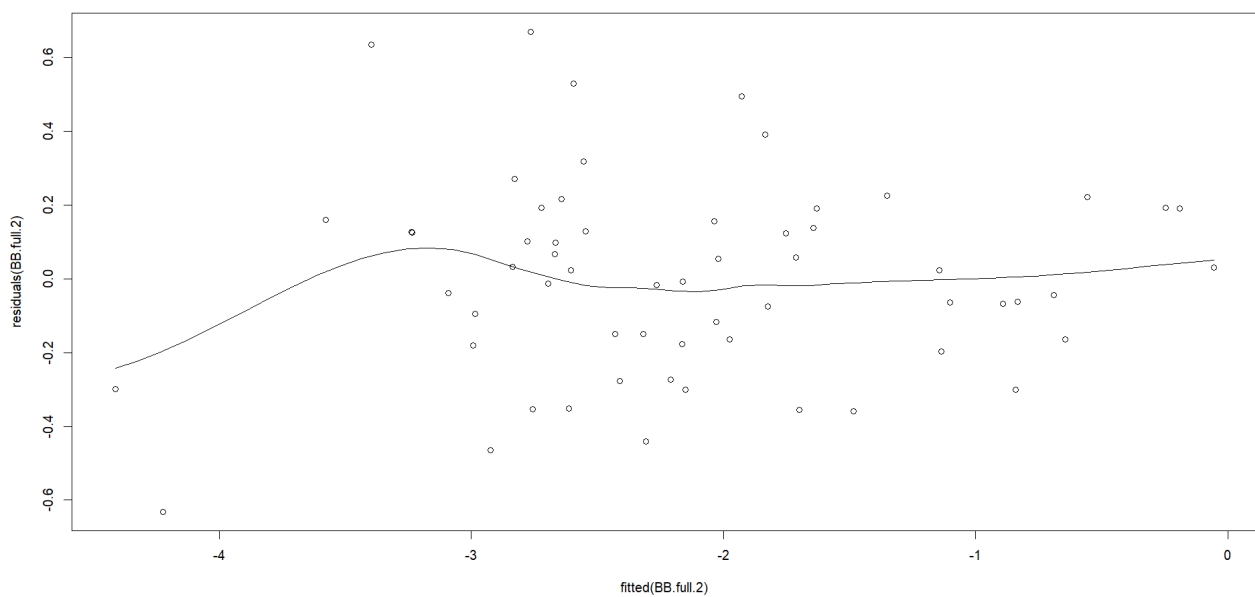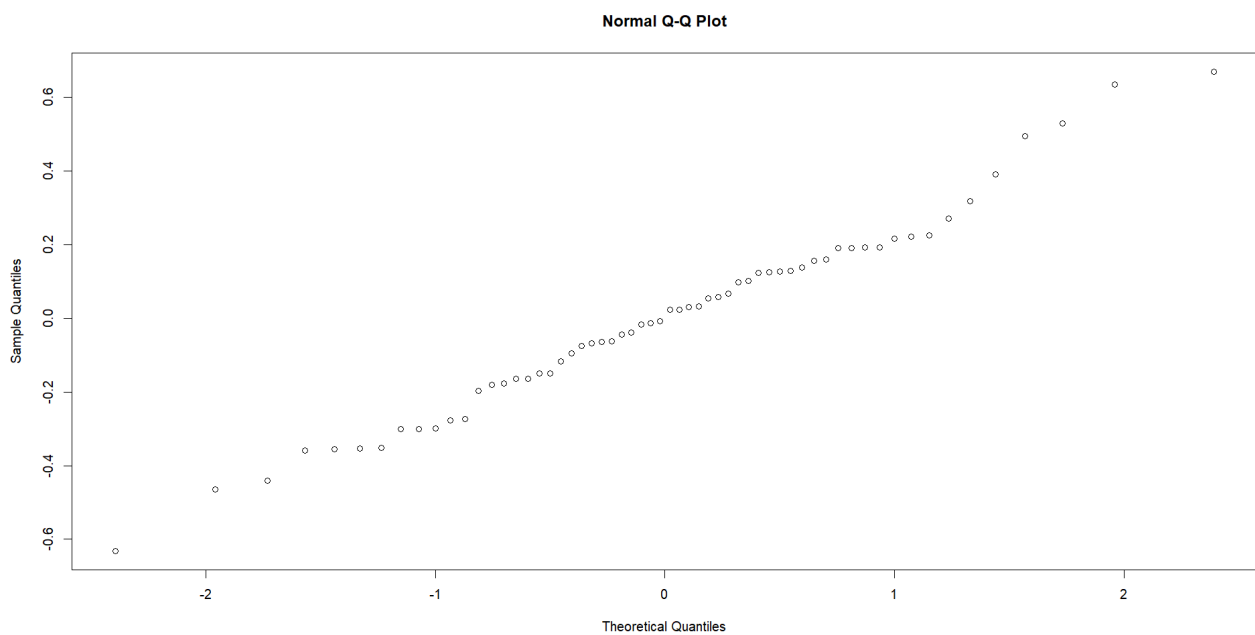
3. **Fungal biomass FB model**

- For this model, I needed to take the log of the total fungal biomass.
- Final model:

```
log(FB) ~ 1 + TC + C_N + Peak_C + Litter + (1 | Site)
AIC_full = 59.71  AIC_new = 45.57
Marginal R2 = 0.5749925  Total R2 = 0.9111168
```

```
![[Pasted image 20240205165415.png]]
![[Pasted image 20240205165432.png]]
```

4. **Total biomass MB model**

- For this model, I needed to take the log of the total biomass.
- Final model:

```
log(MB) ~ 1 + TC + Peak_B + Water_content + C_N + Silt + Clay + PO43 + Peak_C +
(1|Site)
AIC_full = 44.06  AIC_new = 35.39
Marginal R2 = 0.8166648  Total R2 = 0.9068883
```
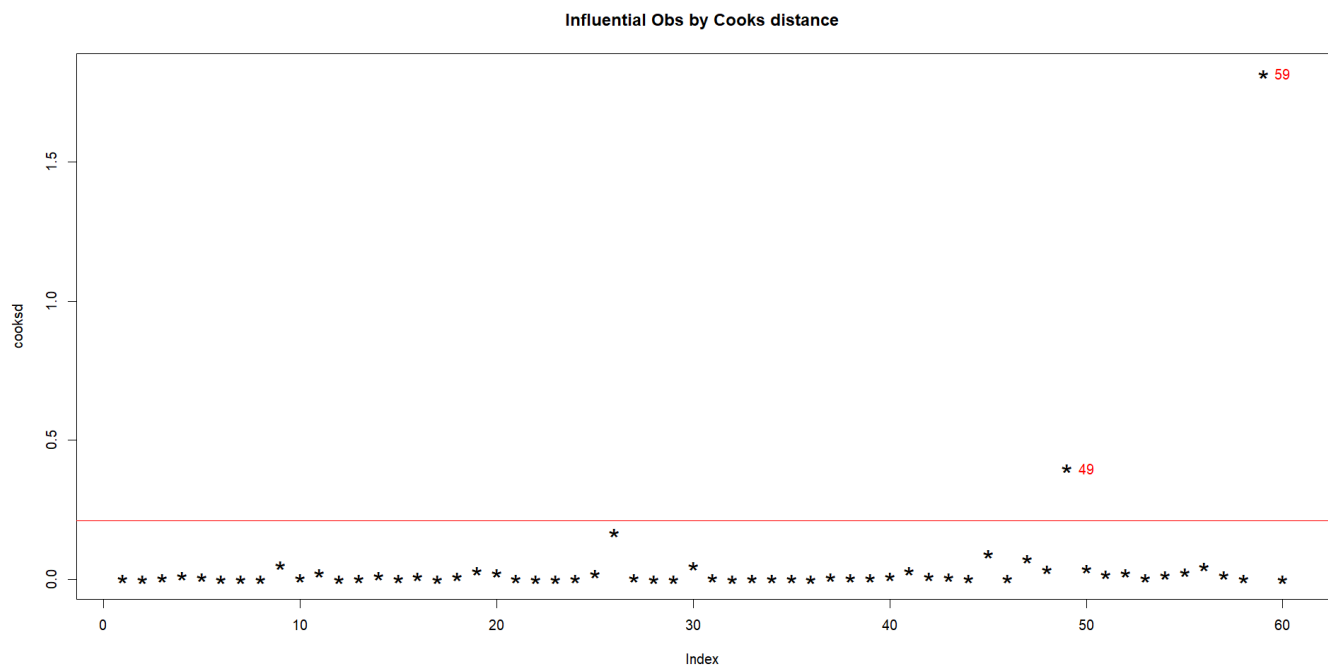
```
![[Pasted image 20240205170747.png]]
![[Pasted image 20240205170803.png]]
```

5. **Enzyme - alpha**

- We followed first outlier elimination using the cook distance function in R:

Influential Obs by Cooks distance

- Final model:

```
alpha ~ 1 + Soil_Temp + (1|Site)
AIC_full = -336.48  AIC_new = -479.97
Marginal R2 = 0.3858346  Total R2 = 0.5419623
```
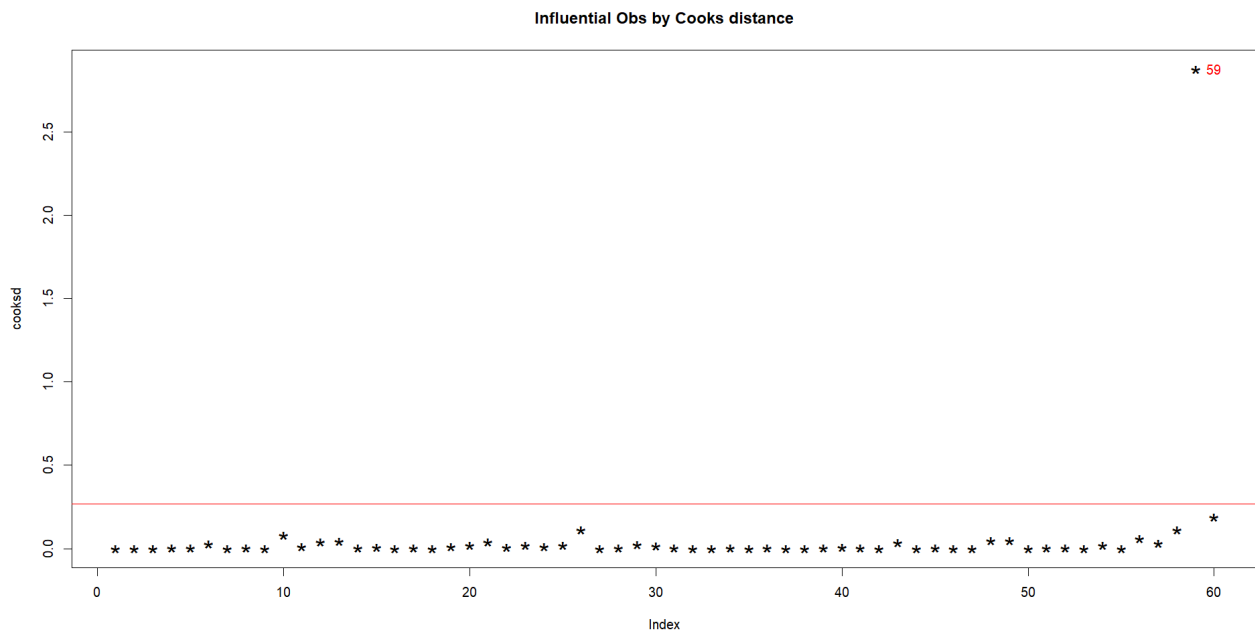
```
![[Pasted image 20240205173143.png]]
![[Pasted image 20240205173201.png]]
```

6. Enzyme - beta

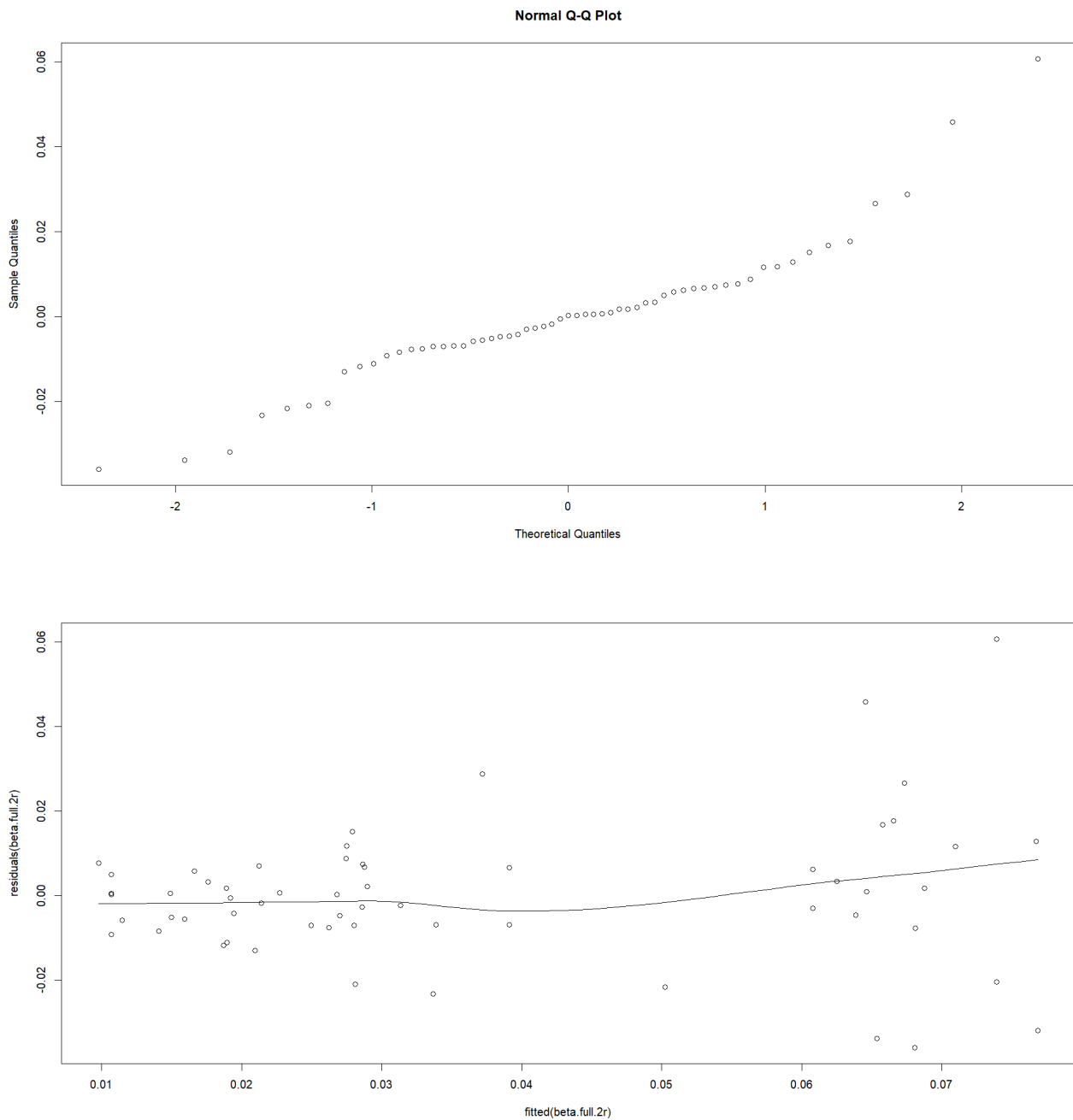- We followed first outlier elimination using the cook distance function in R:

- Final model:

```
beta ~ 1 + Silt + HIX + Peak_C + (1|Site)
AIC_full = -131.19   AIC_new = -290.82
Marginal R2 = 0.2455794   Total R2 = 0.6658517
```
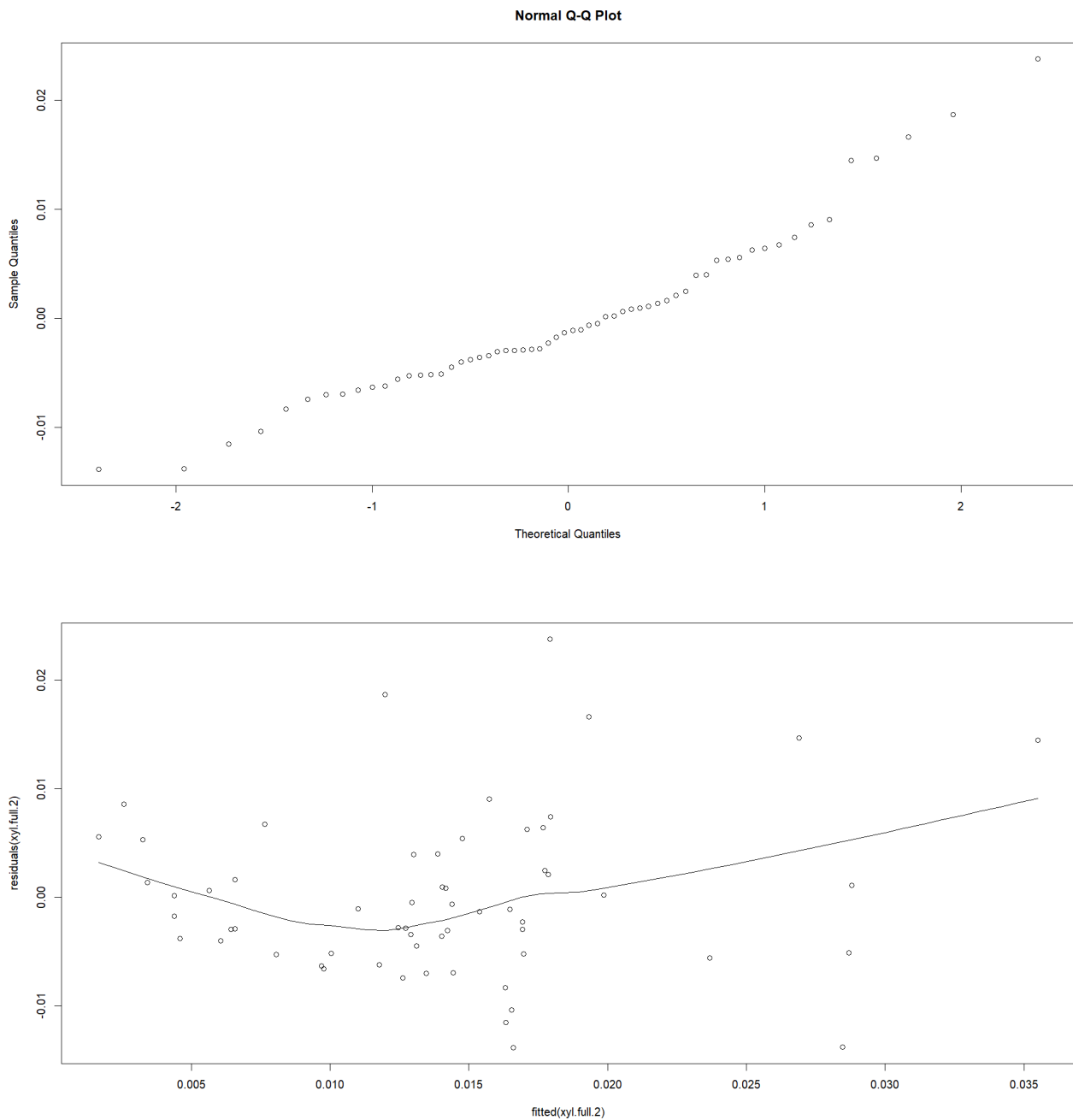
Normal Q-Q Plot

7. Enzyme - xyl

- Final model:

```
xyl ~ 1 + L_TN + HIX + AI + Litter + Soil_Temp + Soil_Temp:AI + (1|Site)
AIC_full = -369.63   AIC_new = -390.01
Marginal R2 = 0.3242244   Total R2 = 0.4598999
```
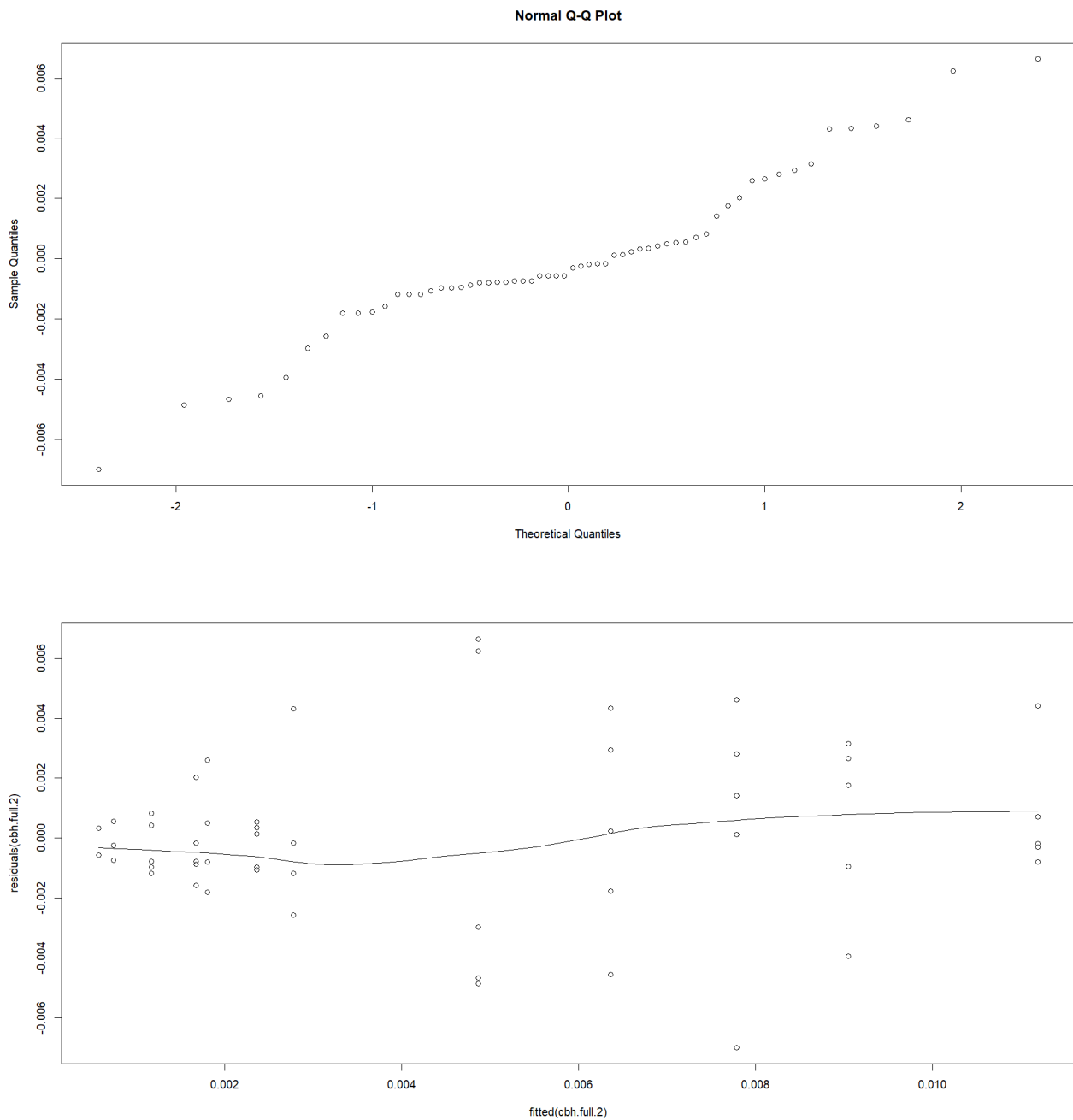
Normal Q-Q Plot

8. **Enzyme - cbh**

- For this model, the final model does not contain any of the variables measured, which I do not know what it means.
- Final model:

```
cbh ~ 1 + (1|Site)
AIC_full = -468.73  AIC_new = -521.62
Marginal R2 = 0.0  Total R2 = 0.6460922
```

Normal Q-Q Plot

9. **Enyzme - gla**

- For this model, I needed to take the log of the enyzme gla.
- Final model:

```
log(gla) ~ 1 + Water_content + SR + Soil_Temp + C_N + altitude + pH + TC +
(1|Site)
AIC_full = --- I cannot calculate it   AIC_new = 120.92
Marginal R2 = 0.638128   Total R2 = 0.7537349
```
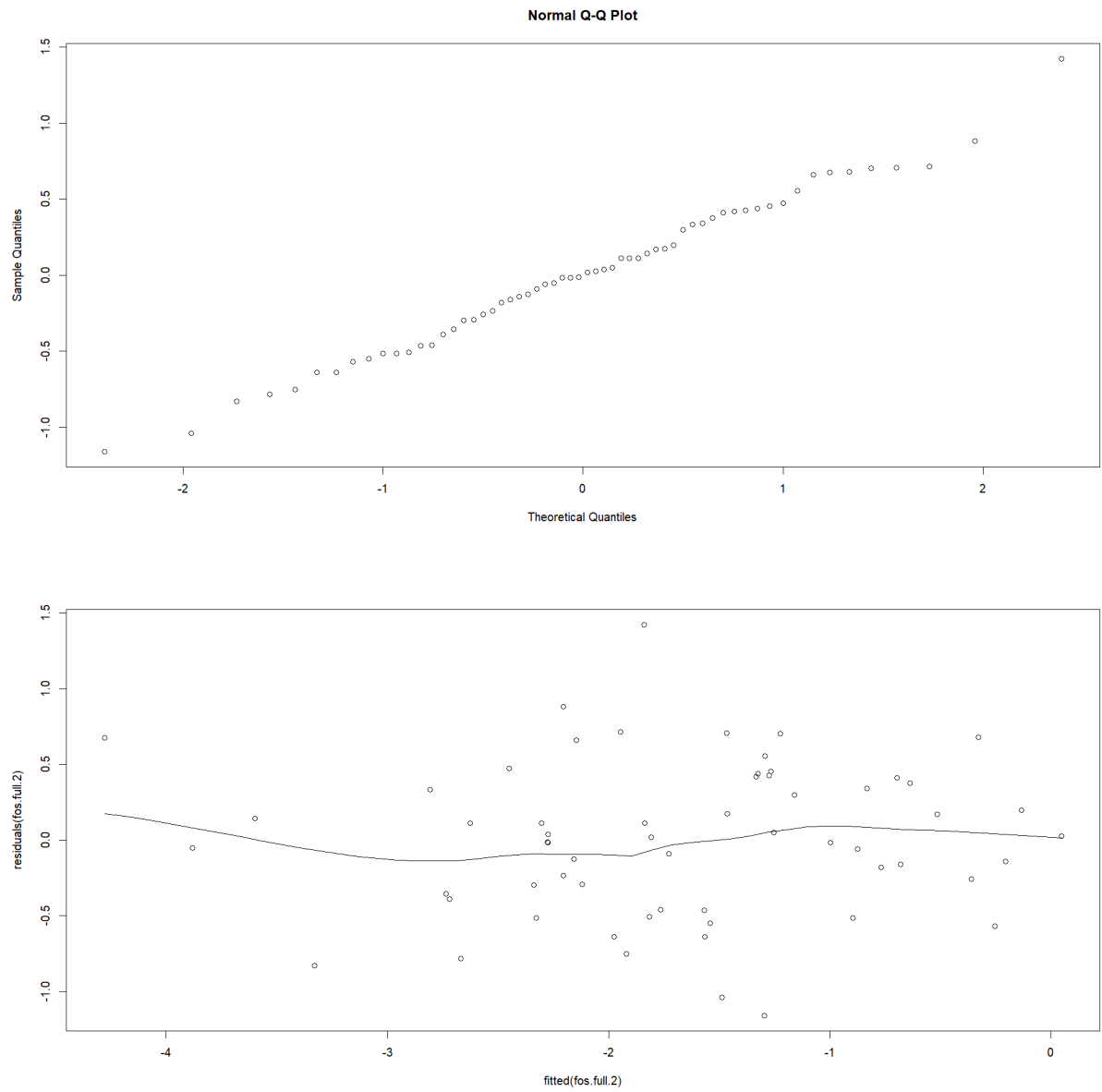
Normal Q-Q Plot
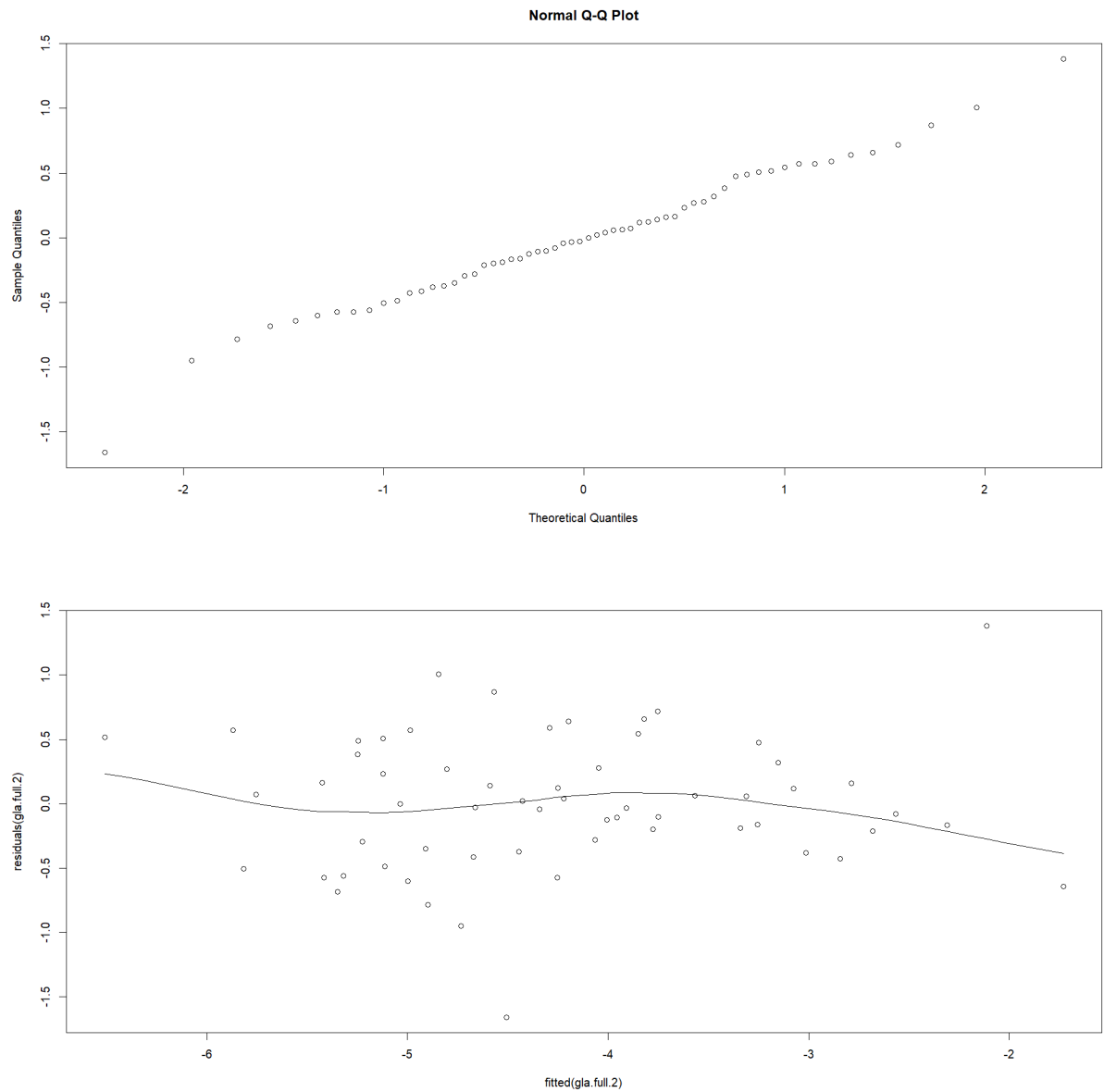
10. **Enyzme - fos**

- For this model, I needed to take the log of the enyzme fos.
- Final model:

```
log(fos) ~ 1 + SOM + Litter + PO43 + BB + Clay + Silt + (1|Site)
AIC_full = 160.05   AIC_new = 116.56
Marginal R2 = 0.6298265   Total R2 = 0.7123375
```
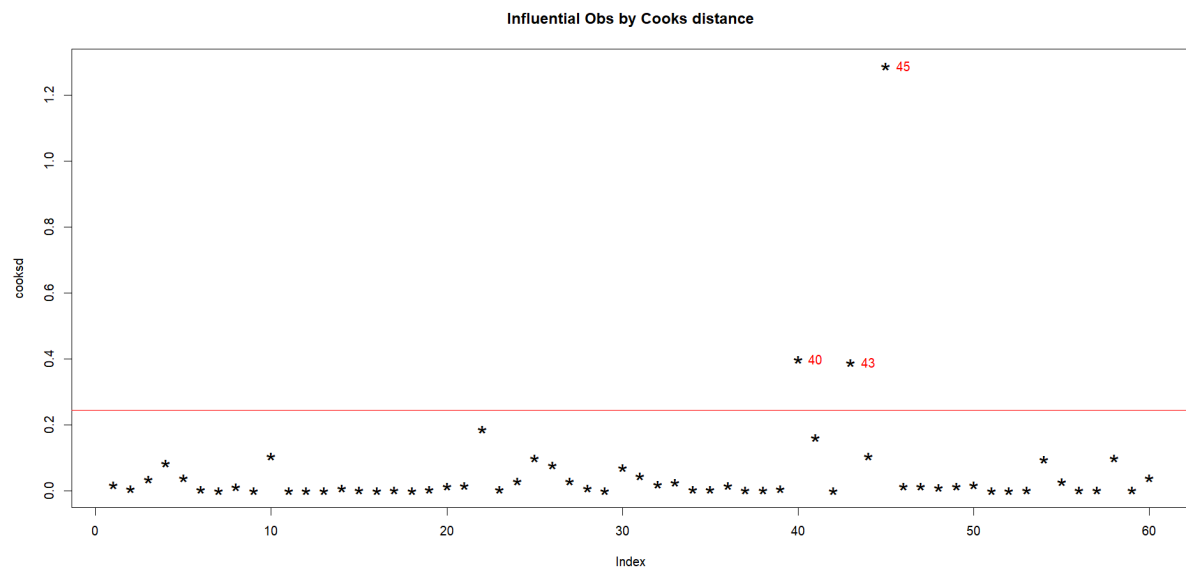
Normal Q-Q Plot

11. **Enyzme - leu**

- For this model, I needed to take the log of the enyzme leu.
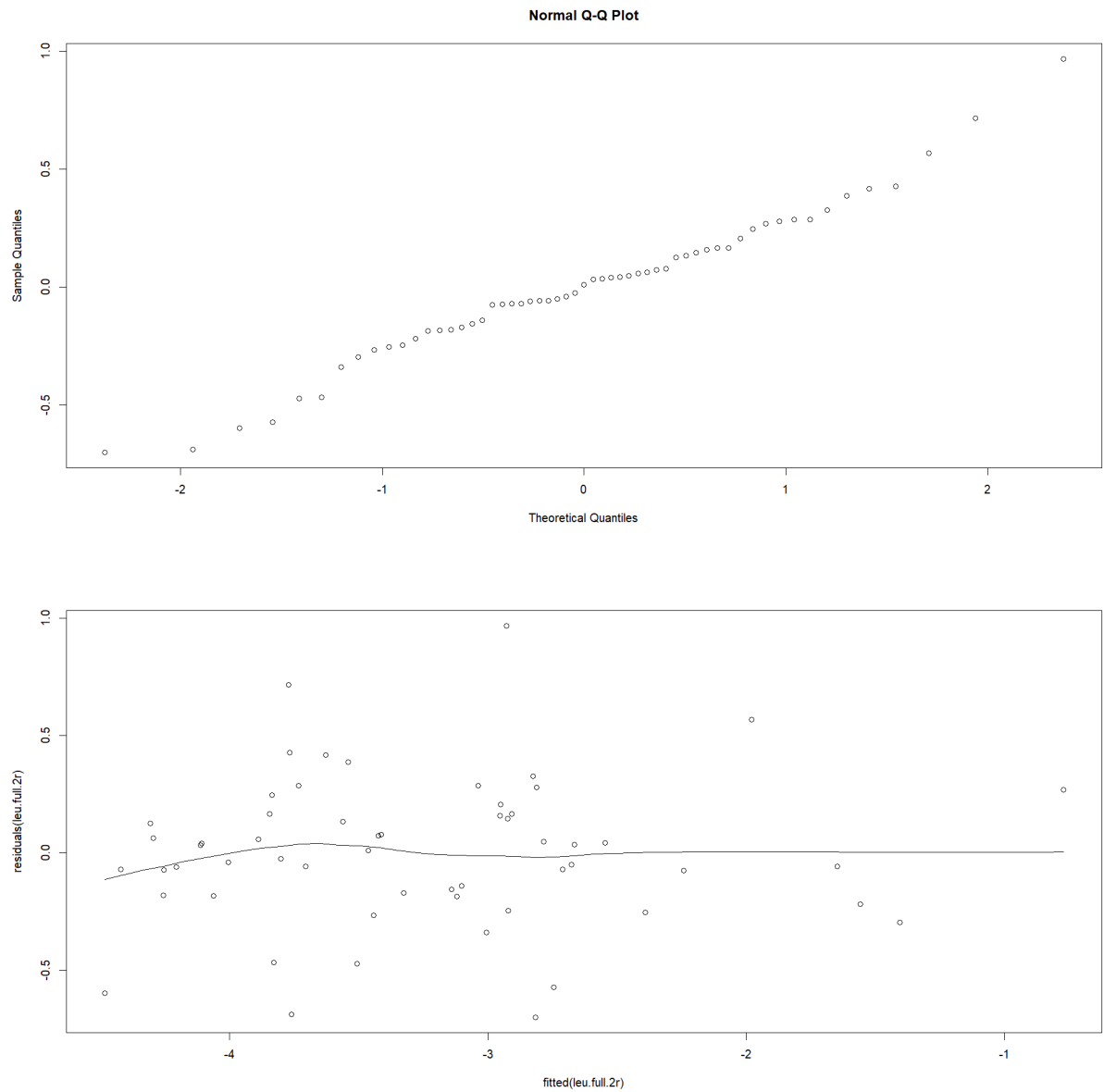- We followed first outlier elimination using the cook distance function in R:

Influential Obs by Cooks distance

- Final model:

```
log(leu) ~ 1 + TC + pH + C_N + (1|Site)
```

`AIC_full = 134.65` AIC_new = 54.14

`Marginal R2 = 0.7877693` Total R2 = 0.8444413
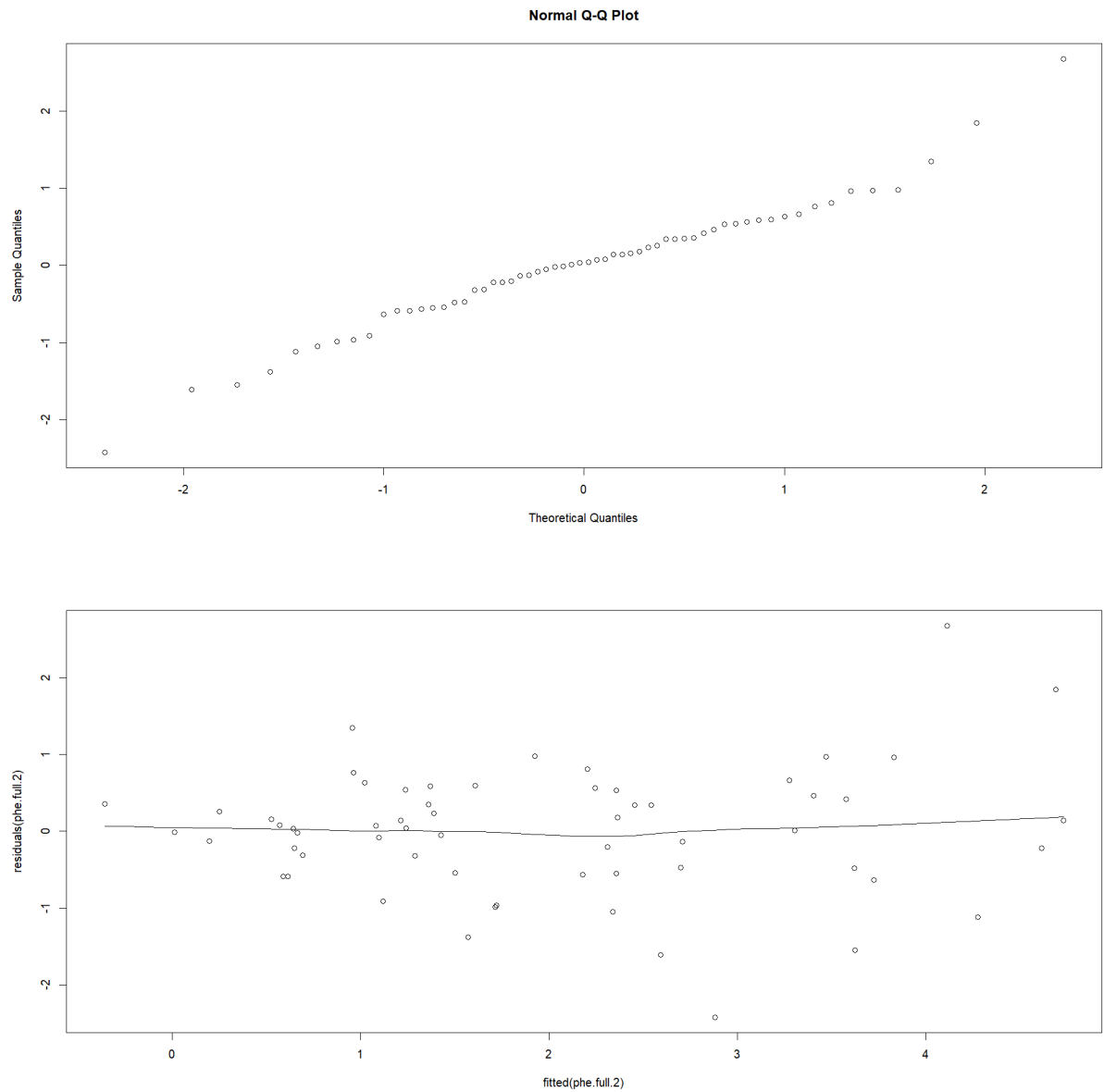
Normal Q-Q Plot

12. **Enyzme - phe**

- Final model:

  ```
  phe ~ phe ~ 1 + LTC_LTN + TC + SOM + Water_content + Peak_B + E4.E6 + HIX +
  Soil_Temp + (1|Site)
  ```

  `AIC_full = 223.77` AIC_new = 181.05

  `Marginal R2 = 0.4886686` Total R2 = 0.657342
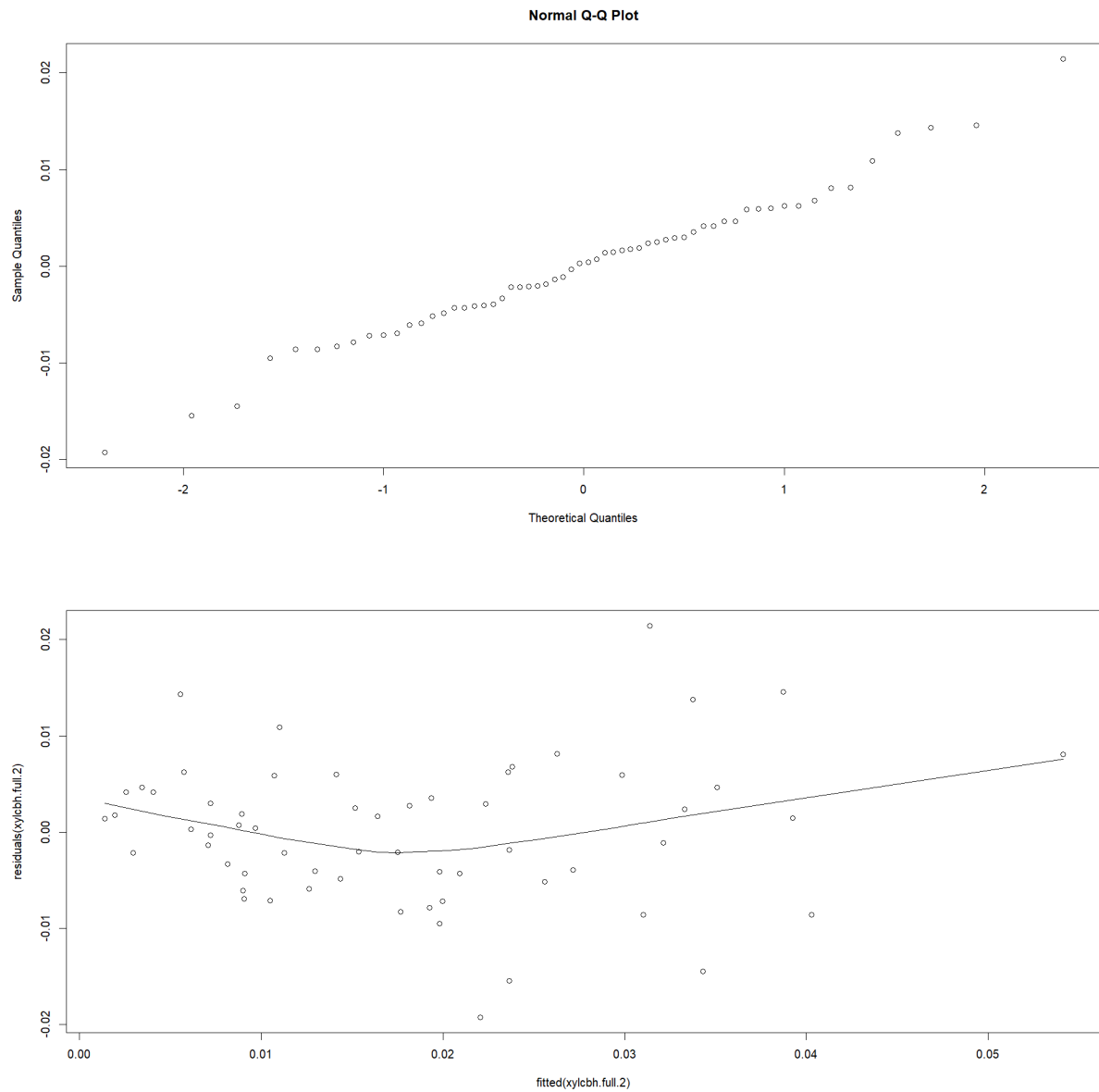
Normal Q-Q Plot

13. **Enzyme xylcbh**

- Final model:

```
xylcbh ~ 1 + L_TN + HIX + AI + L_TN:AI + C_N + Soil_Temp + E4.E6 + Silt + FB +
TC + Silt:AI + (1|Site)
```

`AIC_full = -329.92` AIC_new = -381.30

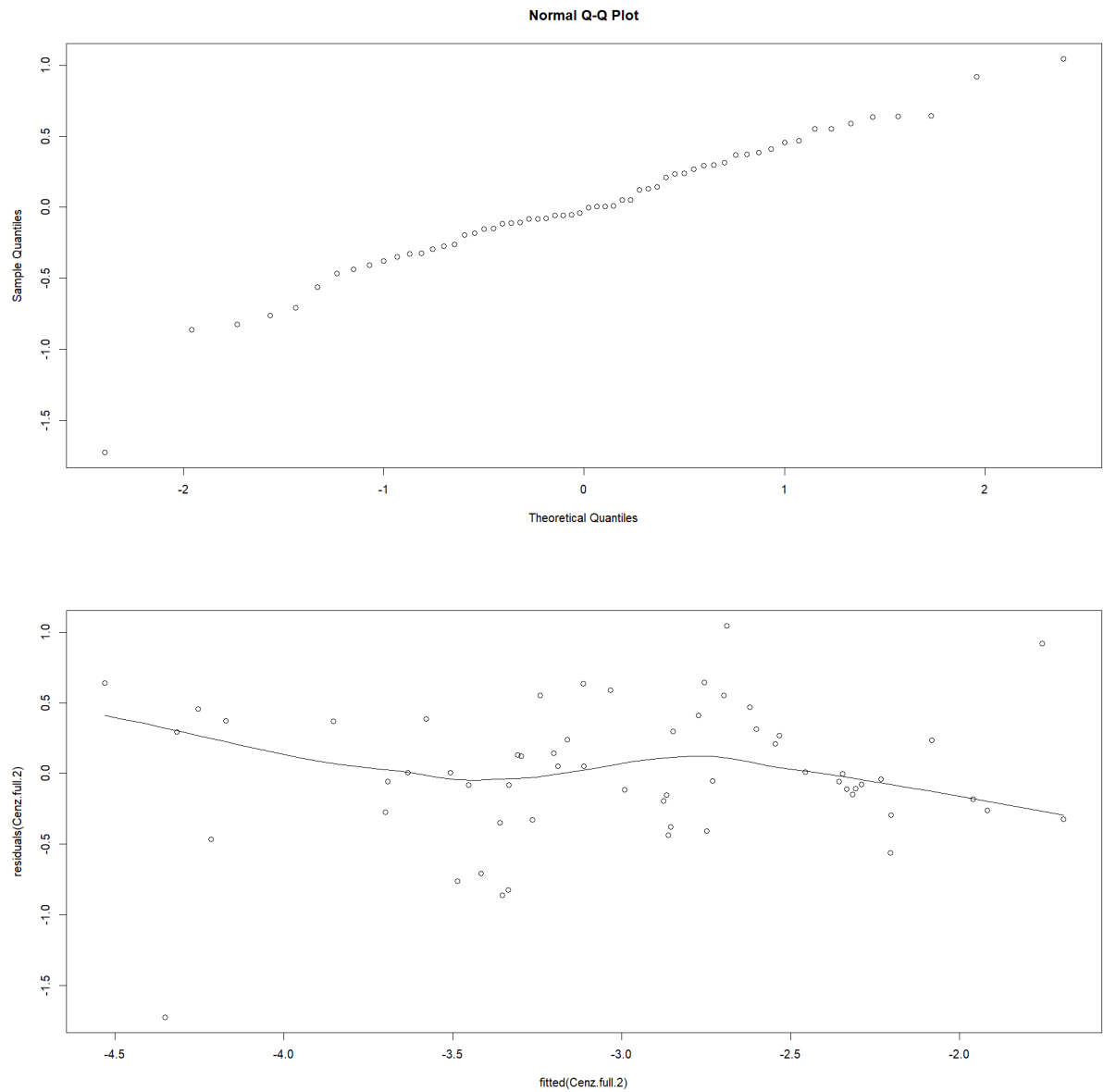`Marginal R2 = 0.5508247` Total R2 = 0.6855857

Normal Q-Q Plot

14. **Enzyme Cenz**

- For this model, I needed to take the log of the enyzme Cenz.
- Final model:
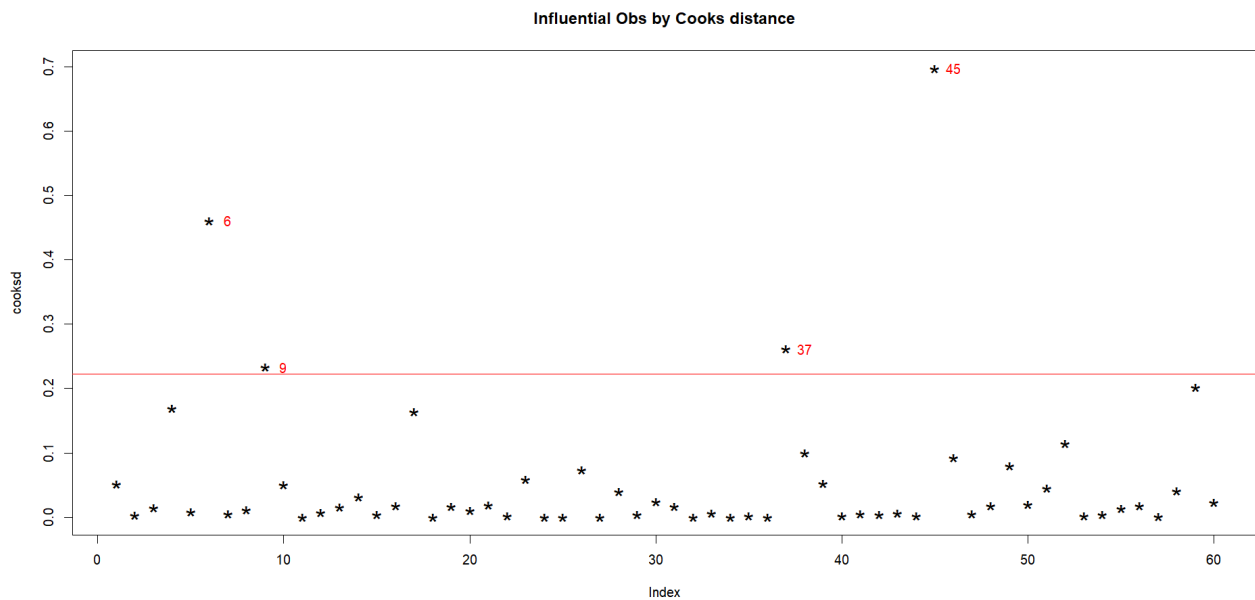
```
log(Cenz) ~ 1 + Soil_Temp + C_N + TC + HIX + (1|Site)
AIC_full = 127.97   AIC_new = 105.96
Marginal R2 = 0.4458457   Total R2 = 0.6598602
```

Normal Q-Q Plot

15. Enzyme alphabeta

- For this model, I needed to take the log of the enyzme alphabeta.
- We followed first outlier elimination using the cook distance function in R:

Influential Obs by Cooks distance

- Final model:

```
log(alphabeta) ~ 1 + Silt + L_TN + HIX + Soil_Temp + C_N + SR + FB + PO43 +
Water_content + SO42 + AI + C_N:AI + PO43:AI + E4.E6 + L_TN:AI + BIX + LTC_LTN +
HIX:AI + SO42:AI + Litter + AI:Litter + BB + AI:BIX + SR:AI + SOM + NH4 + (1|Site)
AIC_full = 130.73  AIC_new = 71.45
Marginal R2 = 0.6822995  Total R2 = 0.9215226
```

Normal Q-Q Plot