final-test-analysis.R

Shawn

2021-03-28

```
pollutants <- read.csv("C:/Users/Shawn/Downloads/pollutants.csv")
library("car")
```

```
## Loading required package: carData
```

```
library(ggplot2)
library(ggcorrplot)
library(caret)
```

```
## Loading required package: lattice
```

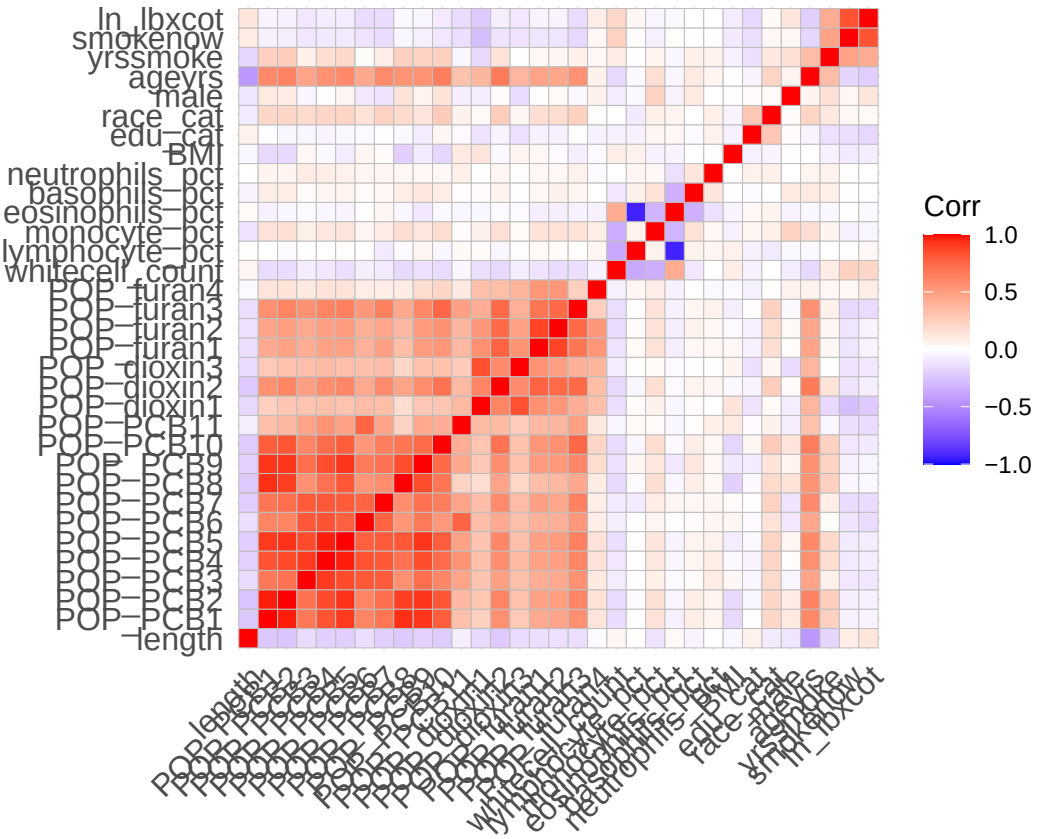
```
library(glmnet)
```

```
## Loading required package: Matrix
```

```
## Loaded glmnet 4.1-1
```

```
library(MASS)
#remove the x
pollutants["X"] = NULL

#calculate correlation matrix before removing the multicolinearity covariates
corr_mat = cor(pollutants)
#graph colored corr matrix
ggcorrplot(corr_mat)
```




```
#set the factor
pollutants$edu_cat = as.factor(pollutants$edu_cat)
pollutants$race_cat = as.factor(pollutants$race_cat)
pollutants$male = as.factor(pollutants$male)
pollutants$smokenow = as.factor(pollutants$smokenow)
#fit model
model = lm(length ~ .,data = pollutants)
#summary
summary(model)
```

```
##
## Call:
## lm(formula = length ~ ., data = pollutants)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5023 -0.1540 -0.0290  0.1224  1.1904
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -5.516e-02  9.700e+00  -0.006   0.9955
## POP_PCB1        -1.604e-06  1.075e-06  -1.492   0.1361
## POP_PCB2         7.240e-07  3.023e-06   0.240   0.8108
## POP_PCB3         1.189e-06  2.157e-06   0.551   0.5816
## POP_PCB4        -1.800e-07  1.026e-06  -0.175   0.8608
## POP_PCB5         1.496e-07  1.070e-06   0.140   0.8889
```

```
## POP_PCB6         2.754e-07  1.059e-06   0.260   0.7949
## POP_PCB7        -5.768e-07  1.207e-06  -0.478   0.6328
## POP_PCB8         1.644e-06  2.447e-06   0.672   0.5021
## POP_PCB9         6.043e-07  2.115e-06   0.286   0.7751
## POP_PCB10        1.181e-03  8.919e-04   1.324   0.1858
## POP_PCB11        3.405e-05  3.079e-04   0.111   0.9120
## POP_dioxin1      2.773e-05  3.056e-04   0.091   0.9277
## POP_dioxin2     -1.732e-04  4.398e-04  -0.394   0.6939
## POP_dioxin3     -1.876e-05  3.027e-05  -0.620   0.5356
## POP_furan1       2.522e-03  3.846e-03   0.656   0.5122
## POP_furan2      -2.915e-04  4.504e-03  -0.065   0.9484
## POP_furan3       4.498e-03  2.762e-03   1.629   0.1038
## POP_furan4      -6.489e-04  9.201e-04  -0.705   0.4808
## whitecell_count -5.233e-03  4.410e-03  -1.186   0.2358
## lymphocyte_pct   1.420e-02  9.698e-02   0.146   0.8836
## monocyte_pct     9.448e-03  9.697e-02   0.097   0.9224
## eosinophils_pct  1.545e-02  9.697e-02   0.159   0.8734
## basophils_pct    1.651e-02  9.706e-02   0.170   0.8650
## neutrophils_pct  2.754e-02  9.816e-02   0.281   0.7791
## BMI             -1.367e-03  1.411e-03  -0.969   0.3329
## edu_cat2         2.439e-02  2.218e-02   1.100   0.2718
## edu_cat3         4.781e-02  2.166e-02   2.207   0.0276 *
## edu_cat4         3.259e-02  2.557e-02   1.275   0.2028
## race_cat2       -2.198e-02  3.267e-02  -0.673   0.5013
## race_cat3        2.464e-02  3.372e-02   0.730   0.4653
## race_cat4       -3.479e-02  2.993e-02  -1.162   0.2455
## male1           -3.947e-02  1.772e-02  -2.227   0.0262 *
## ageyrs          -6.234e-03  7.447e-04  -8.372 2.41e-16 ***
## yrssmoke        -5.325e-04  7.276e-04  -0.732   0.4645
## smokenow1        1.914e-03  3.587e-02   0.053   0.9575
## ln_lbxcot        5.371e-03  3.928e-03   1.367   0.1719
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2221 on 827 degrees of freedom
## Multiple R-squared:  0.2448, Adjusted R-squared:  0.2119
## F-statistic: 7.447 on 36 and 827 DF,  p-value: < 2.2e-16
```

```
#show the VIF
vif(model)
```

```
##                       GVIF Df GVIF^(1/(2*Df))
## POP_PCB1         33.044120  1        5.748401
## POP_PCB2         34.281125  1        5.855009
## POP_PCB3          9.351143  1        3.057964
## POP_PCB4         31.742239  1        5.634025
## POP_PCB5         59.896895  1        7.739308
## POP_PCB6         11.386658  1        3.374412
## POP_PCB7          4.870075  1        2.206825
## POP_PCB8         12.982575  1        3.603134
## POP_PCB9         12.441595  1        3.527264
## POP_PCB10         6.020678  1        2.453707
## POP_PCB11         4.725769  1        2.173883
## POP_dioxin1       5.276251  1        2.297009
## POP_dioxin2       5.413132  1        2.326614
```

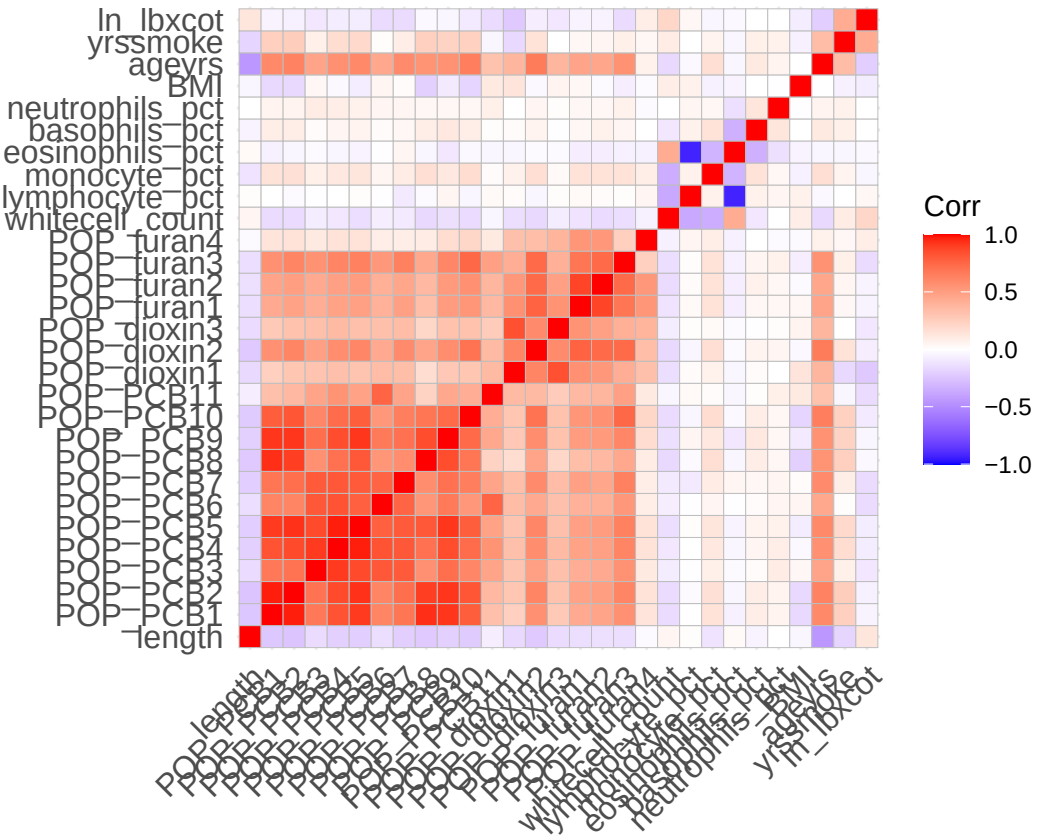
```
## POP_dioxin3         4.398509  1        2.097262
## POP_furan1          6.154213  1        2.480769
## POP_furan2          6.195336  1        2.489043
## POP_furan3          4.464346  1        2.112900
## POP_furan4          1.821809  1        1.349744
## whitecell_count     1.548380  1        1.244339
## lymphocyte_pct  12250.336528  1      110.681238
## monocyte_pct      726.843372  1       26.960033
## eosinophils_pct 15071.561945  1      122.766290
## basophils_pct     867.412798  1       29.451873
## neutrophils_pct    37.984114  1        6.163125
## BMI                 1.263662  1        1.124127
## edu_cat             1.543109  3        1.074978
## race_cat            2.052848  3        1.127352
## male                1.350324  1        1.162034
## ageyrs              3.238631  1        1.799620
## yrssmoke            2.204139  1        1.484634
## smokenow            4.006708  1        2.001676
## ln_lbxcot           3.963407  1        1.990831
```

```
#get set a dataset with no categorical covariates
no_cat = pollutants
no_cat$edu_cat = NULL
no_cat$race_cat = NULL
no_cat$male = NULL
no_cat$smokenow = NULL
#summary of the dataset
summary(no_cat)
```

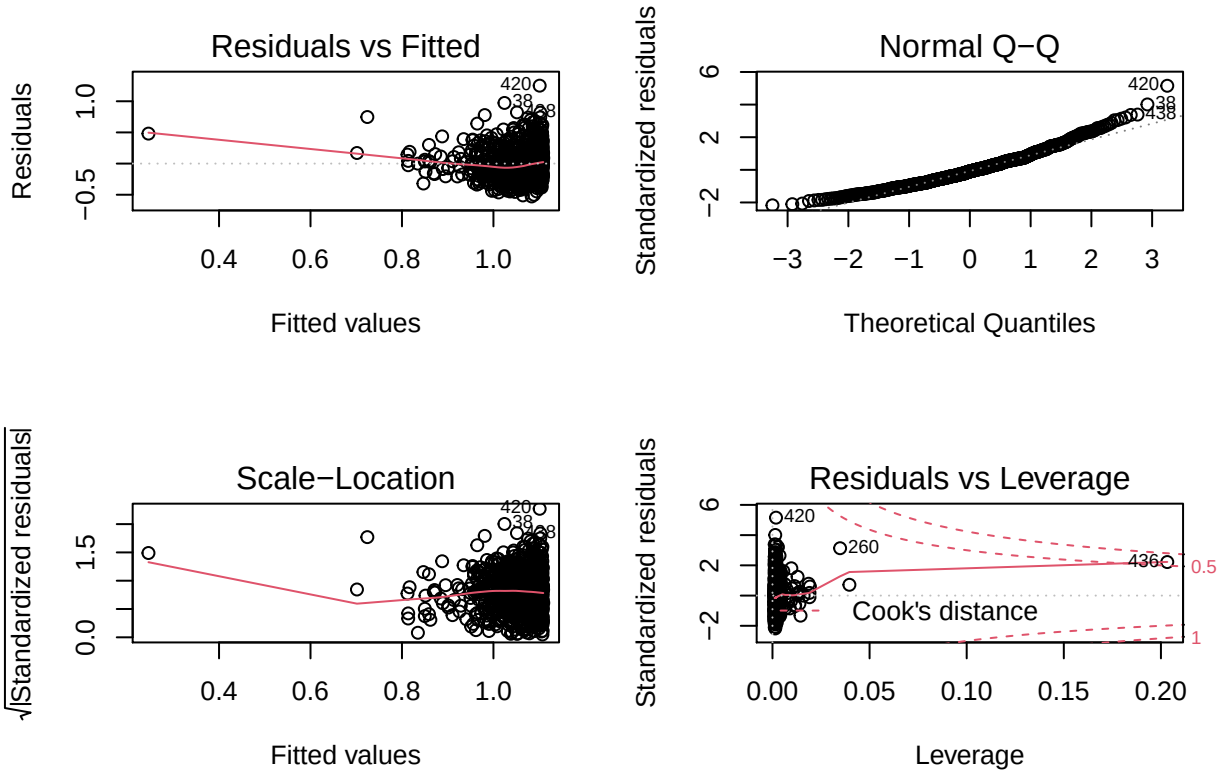
```
##      length          POP_PCB1         POP_PCB2         POP_PCB3
##  Min.   :0.5266   Min.   :  2000   Min.   :  2000   Min.   :  2000
##  1st Qu.:0.8754   1st Qu.:  9975   1st Qu.:  4800   1st Qu.:  3700
##  Median :1.0286   Median : 27600   Median : 11500   Median :  6200
##  Mean   :1.0543   Mean   : 38082   Mean   : 15637   Mean   : 10158
##  3rd Qu.:1.2095   3rd Qu.: 53325   3rd Qu.: 21825   3rd Qu.: 12000
##  Max.   :2.3512   Max.   :572000   Max.   :165000   Max.   :123000
##     POP_PCB4         POP_PCB5         POP_PCB6         POP_PCB7
##  Min.   :  2100   Min.   :  2100   Min.   :  2000   Min.   :  1100
##  1st Qu.: 11475   1st Qu.: 15600   1st Qu.:  4400   1st Qu.:  4000
##  Median : 25550   Median : 36300   Median :  9400   Median :  7450
##  Mean   : 38456   Mean   : 52650   Mean   : 16820   Mean   : 12682
##  3rd Qu.: 50650   3rd Qu.: 68625   3rd Qu.: 19500   3rd Qu.: 15625
##  Max.   :487000   Max.   :708000   Max.   :319000   Max.   :144000
##     POP_PCB8         POP_PCB9        POP_PCB10        POP_PCB11
##  Min.   :  1100   Min.   :  1100   Min.   :  1.70   Min.   :  1.30
##  1st Qu.:  3800   1st Qu.:  3900   1st Qu.:  9.10   1st Qu.: 14.80
##  Median :  6950   Median :  8050   Median : 18.35   Median : 24.50
##  Mean   : 10530   Mean   : 12220   Mean   : 24.49   Mean   : 38.15
##  3rd Qu.: 14425   3rd Qu.: 16025   3rd Qu.: 34.90   3rd Qu.: 42.95
##  Max.   :187000   Max.   :144000   Max.   :172.00   Max.   :845.00
##   POP_dioxin1      POP_dioxin2      POP_dioxin3       POP_furan1
##  Min.   :  1.90   Min.   :  1.40   Min.   :  36.8   Min.   : 1.000
##  1st Qu.: 23.90   1st Qu.: 21.27   1st Qu.: 197.0   1st Qu.: 3.200
##  Median : 41.35   Median : 37.80   Median : 342.5   Median : 5.200
##  Mean   : 57.65   Mean   : 47.81   Mean   : 494.4   Mean   : 6.371
```

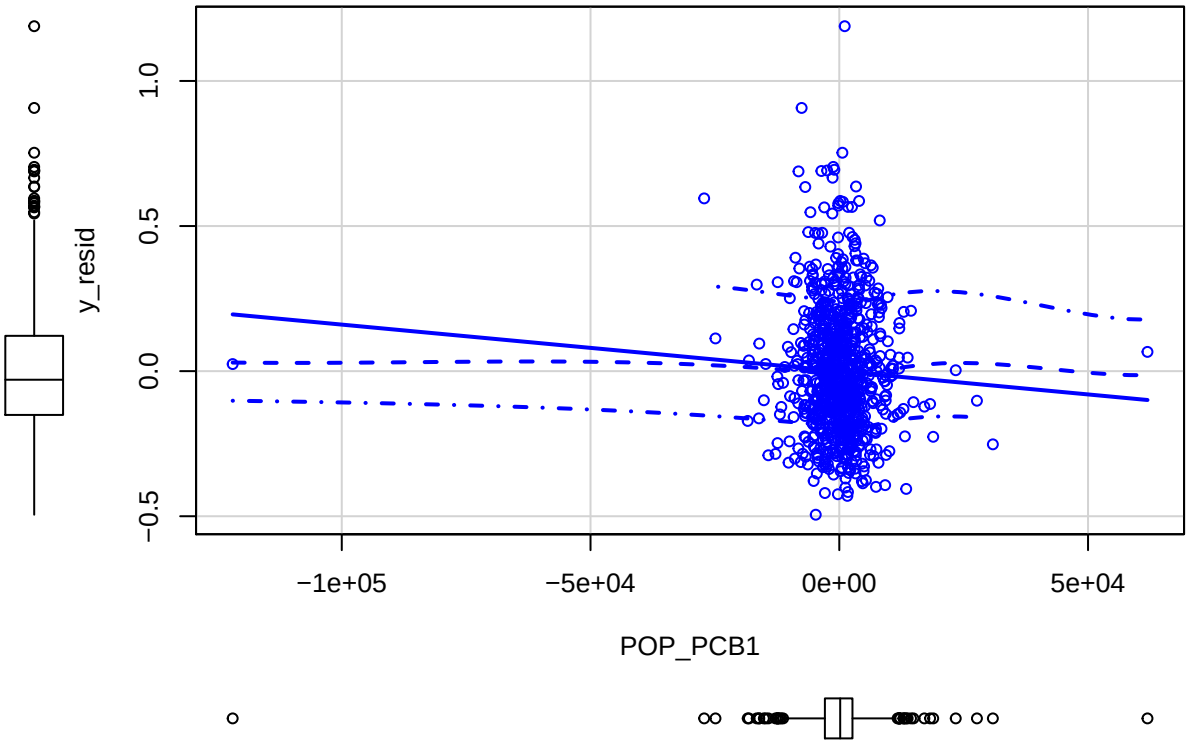
```
##  3rd Qu.: 71.62   3rd Qu.: 62.42   3rd Qu.: 603.0   3rd Qu.: 7.700
##  Max.   :760.00   Max.   :281.00   Max.   :8190.0   Max.   :44.400
##    POP_furan2       POP_furan3       POP_furan4     whitecell_count
##  Min.   : 0.800   Min.   : 0.700   Min.   :  0.90   Min.   : 2.300
##  1st Qu.: 2.600   1st Qu.: 2.200   1st Qu.:  6.40   1st Qu.: 5.600
##  Median : 4.200   Median : 5.050   Median :  9.65   Median : 6.900
##  Mean   : 5.390   Mean   : 6.669   Mean   : 11.54   Mean   : 7.191
##  3rd Qu.: 6.825   3rd Qu.: 9.300   3rd Qu.: 14.00   3rd Qu.: 8.300
##  Max.   :33.500   Max.   :38.300   Max.   :234.00   Max.   :20.100
##  lymphocyte_pct   monocyte_pct    eosinophils_pct basophils_pct
##  Min.   : 5.80   Min.   : 1.600   Min.   :21.60   Min.   : 0.000
##  1st Qu.:24.00   1st Qu.: 6.600   1st Qu.:52.35   1st Qu.: 1.500
##  Median :28.95   Median : 7.700   Median :59.30   Median : 2.300
##  Mean   :29.92   Mean   : 7.936   Mean   :58.62   Mean   : 2.903
##  3rd Qu.:35.42   3rd Qu.: 9.100   3rd Qu.:65.22   3rd Qu.: 3.700
##  Max.   :73.40   Max.   :23.800   Max.   :88.10   Max.   :28.200
##  neutrophils_pct       BMI            ageyrs         yrssmoke
##  Min.   :0.0000   Min.   :16.16   Min.   :20.00   Min.   : 0.0
##  1st Qu.:0.4000   1st Qu.:23.88   1st Qu.:34.00   1st Qu.: 0.0
##  Median :0.6000   Median :27.38   Median :46.00   Median : 0.0
##  Mean   :0.6669   Mean   :28.09   Mean   :48.36   Mean   :10.6
##  3rd Qu.:0.8000   3rd Qu.:31.17   3rd Qu.:63.00   3rd Qu.:20.0
##  Max.   :5.5000   Max.   :62.99   Max.   :85.00   Max.   :69.0
##    ln_lbxcot
##  Min.   :-4.5099
##  1st Qu.:-4.0745
##  Median :-2.7334
##  Mean   :-0.9804
##  3rd Qu.: 2.8000
##  Max.   : 6.5848
```

```r
#calculate correlation matrix
corr_matrix = cor(no_cat)
#graph colored corr matrix
ggcorrplot(corr_matrix)
```




```
#find the linearity (residual y against residual x)
covariates = names(no_cat)
#remove response name
covariates = covariates[-1]
for (name in covariates){
  y_model = lm(paste("length", "~", ".", "-", name), data = pollutants)
  x_model = lm(paste(name, "~", ".", "- length"), data = pollutants)
  y_resid = resid(y_model)
  x_resid = resid(x_model)
  #residual QQ studentized - show the qqPlot of all covariates that is not categorical
  studentized_model = lm(paste("length", "~", name), data = pollutants)
  #find the AIC model fit for homoscedasticity after removing multicolinearity
  par(mfrow=c(2,2))
  plot(studentized_model)
  par(mfrow=c(1,1))
  #linearity
  scatterplot(x_resid, y_resid, xlab = name)
}
```


Residuals vs Fitted
Residuals
Fitted values
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Cook's distance
Leverage
420
260
436
38


y_resid
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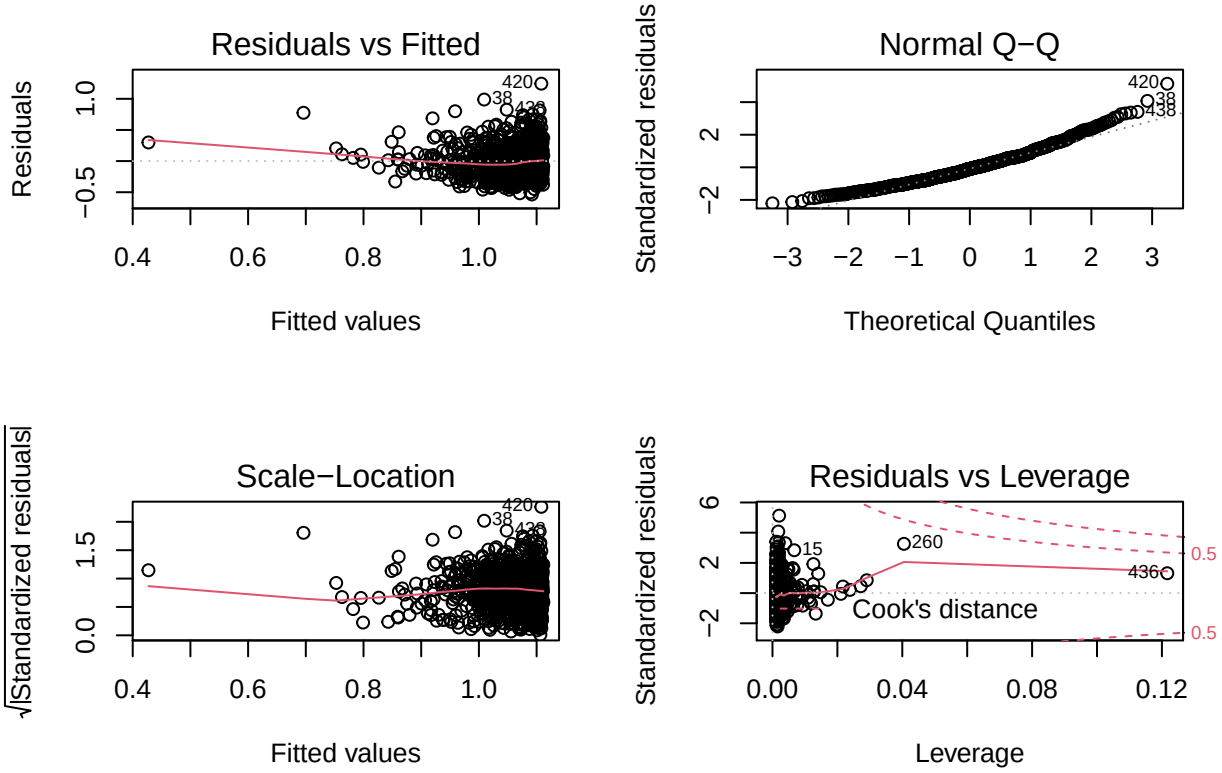
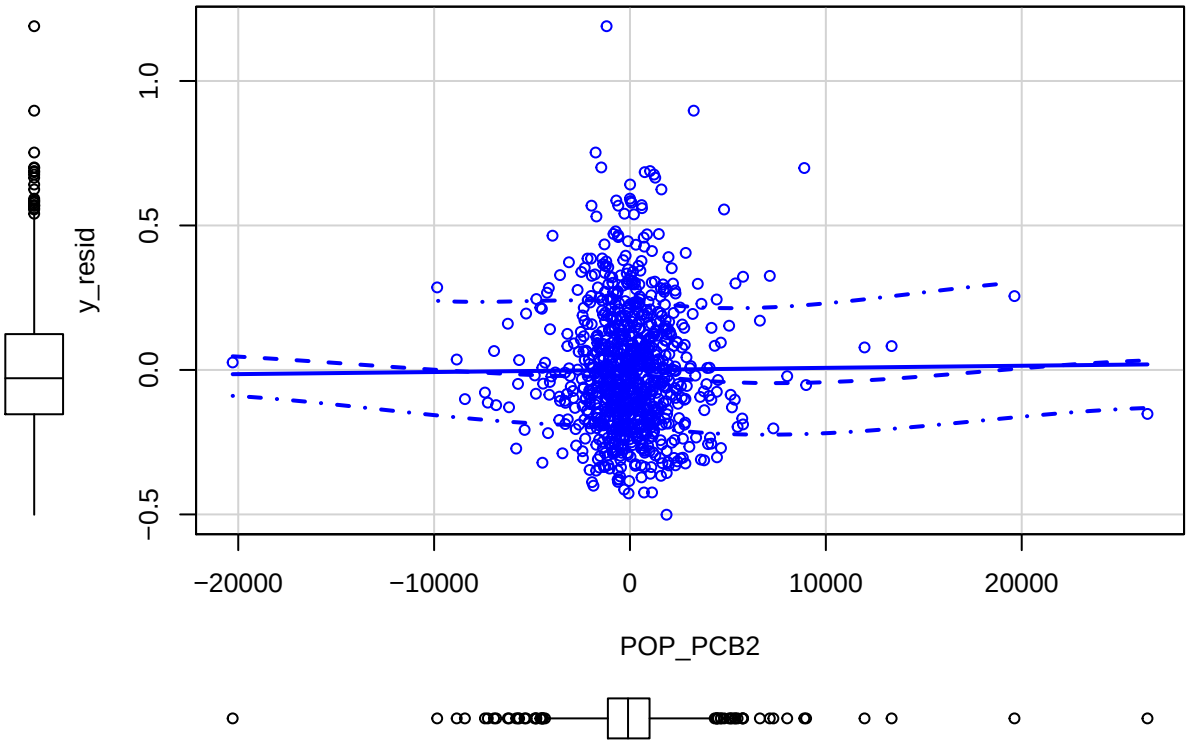
0.5
0.0
−0.5
−1e+05
−5e+04
0e+00
5e+04
POP_PCB1


Residuals vs Fitted
Residuals
Fitted values
420
38
438
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
Leverage
15
260
436
0.5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0.0
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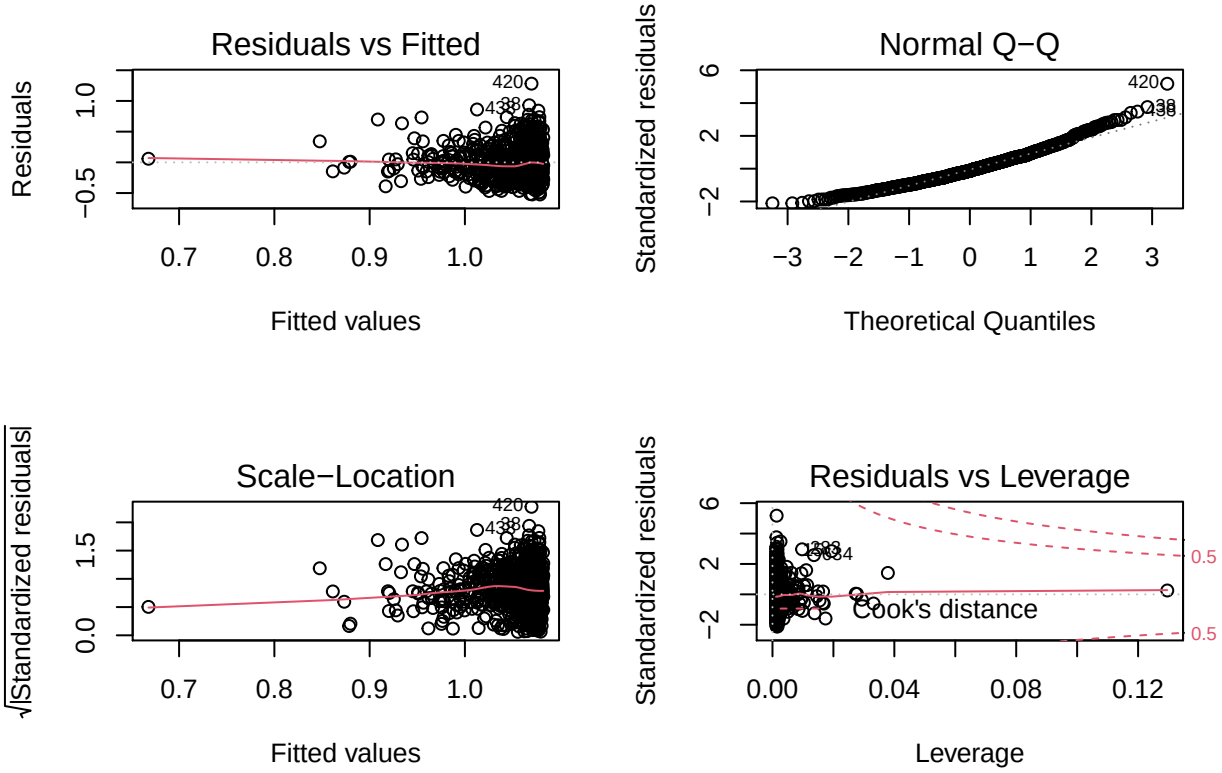
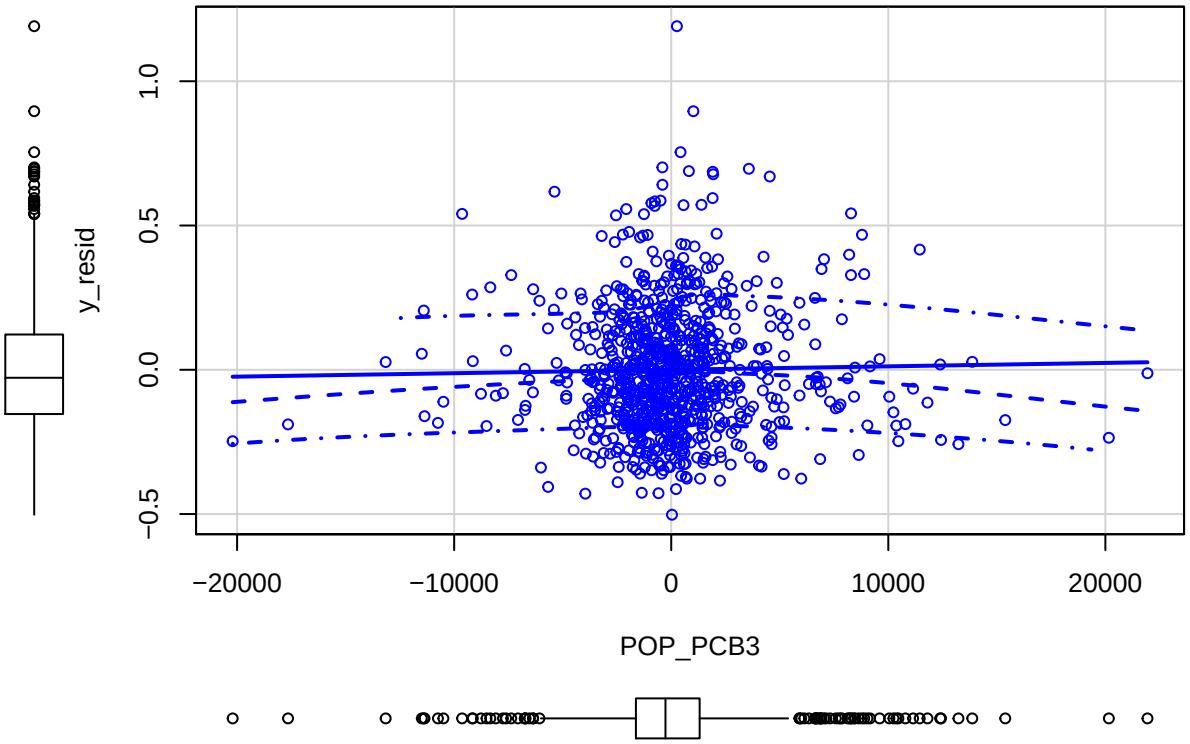
−20000
−10000
0
10000
20000
POP_PCB2


Residuals vs Fitted
Residuals
Fitted values
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Cook's distance
Leverage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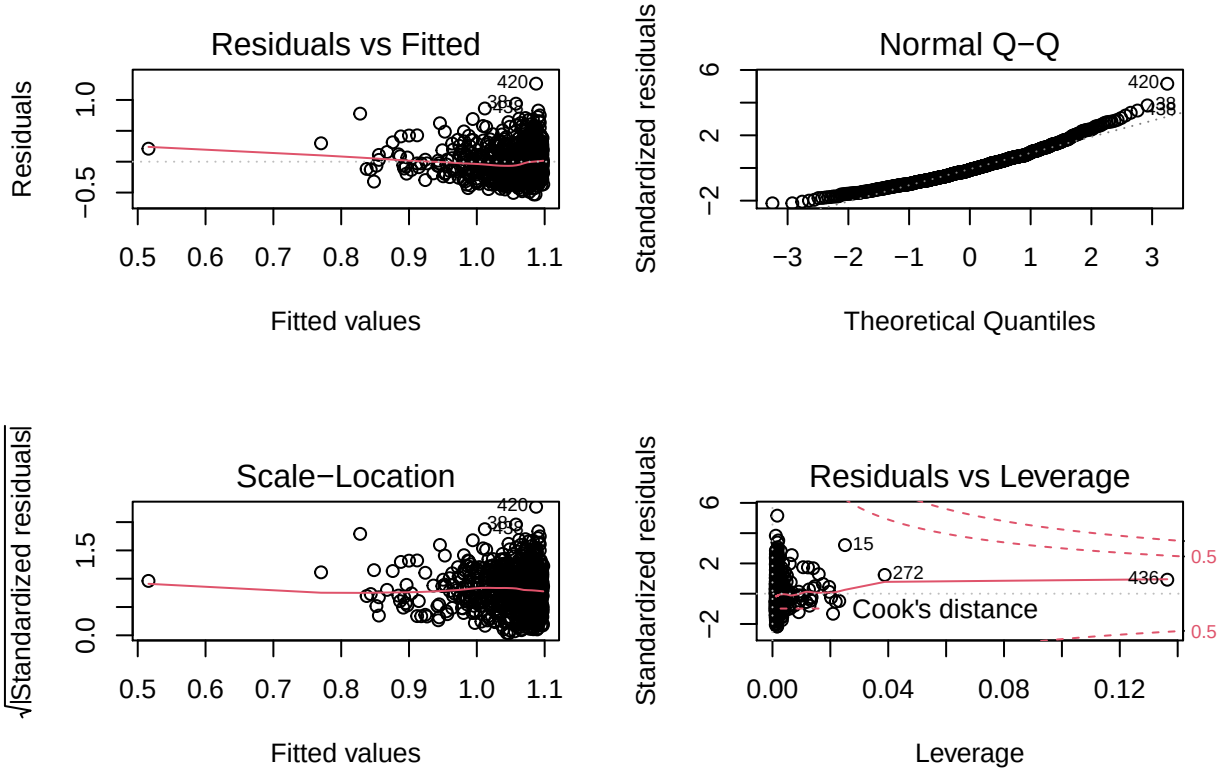
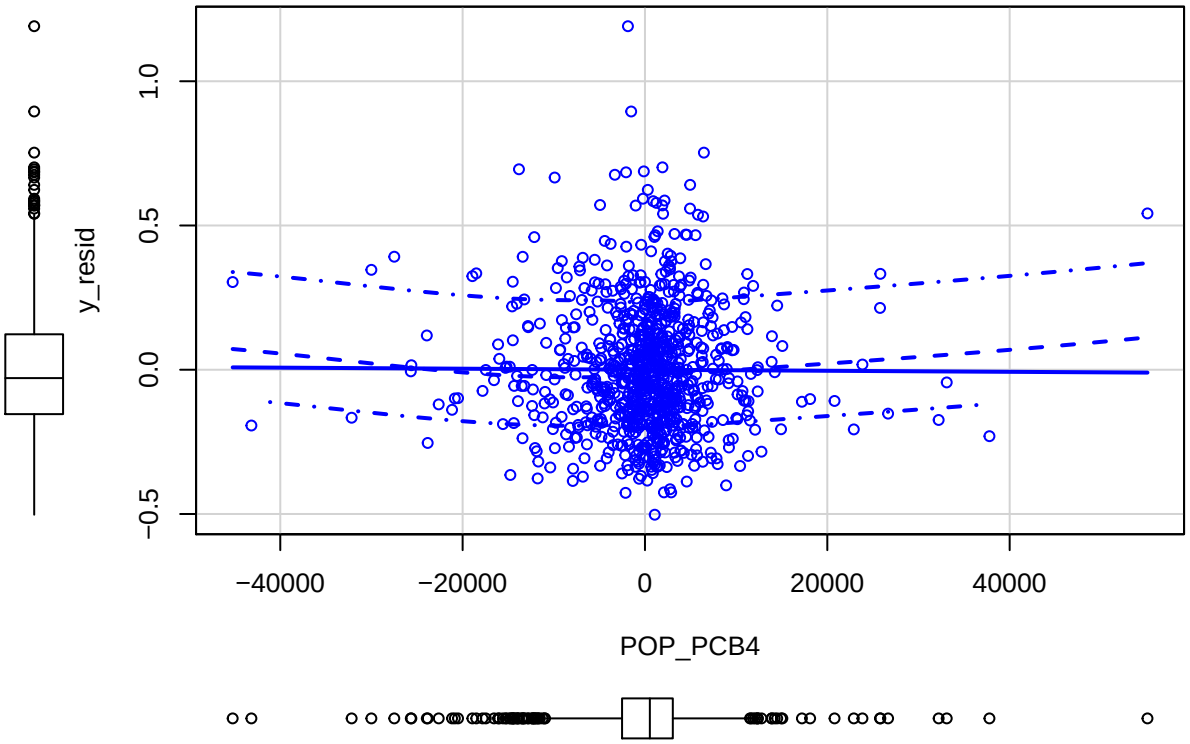
0.0
−0.5
−20000
−10000
0
10000
20000
POP_PCB3


Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
15
272
436
0.5
Leverage


y_resid
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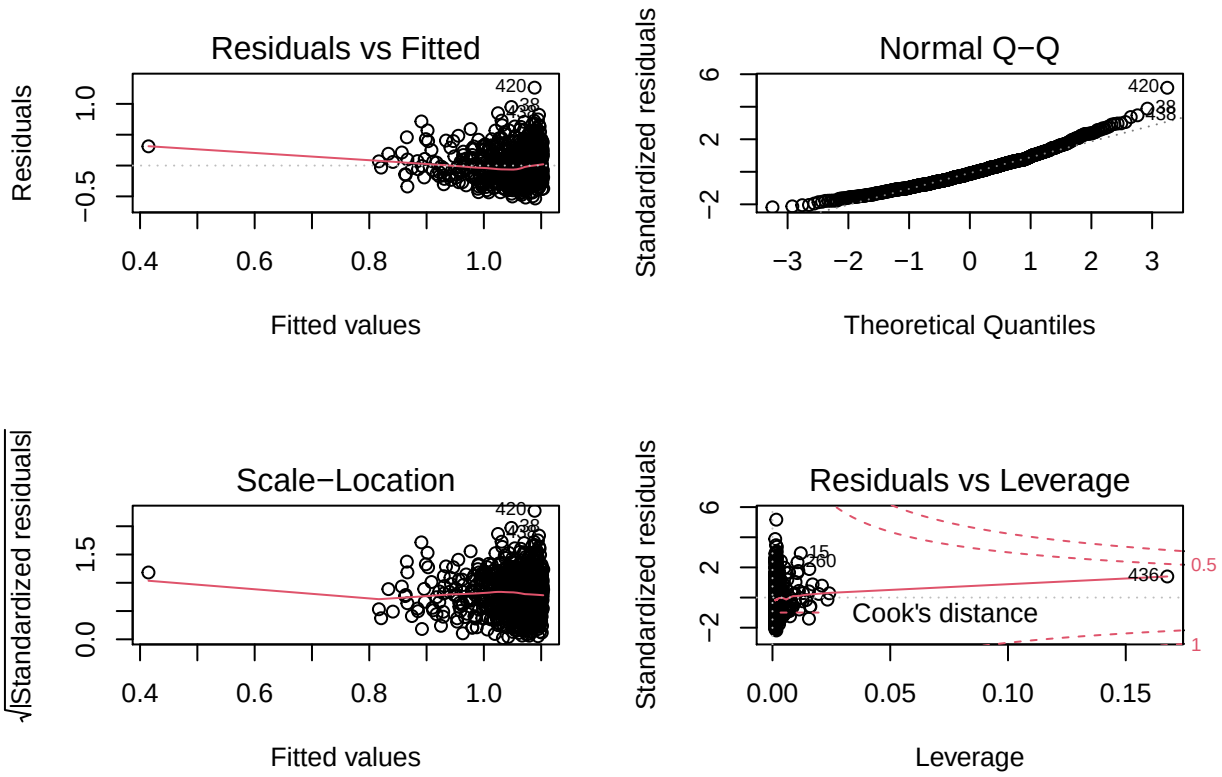
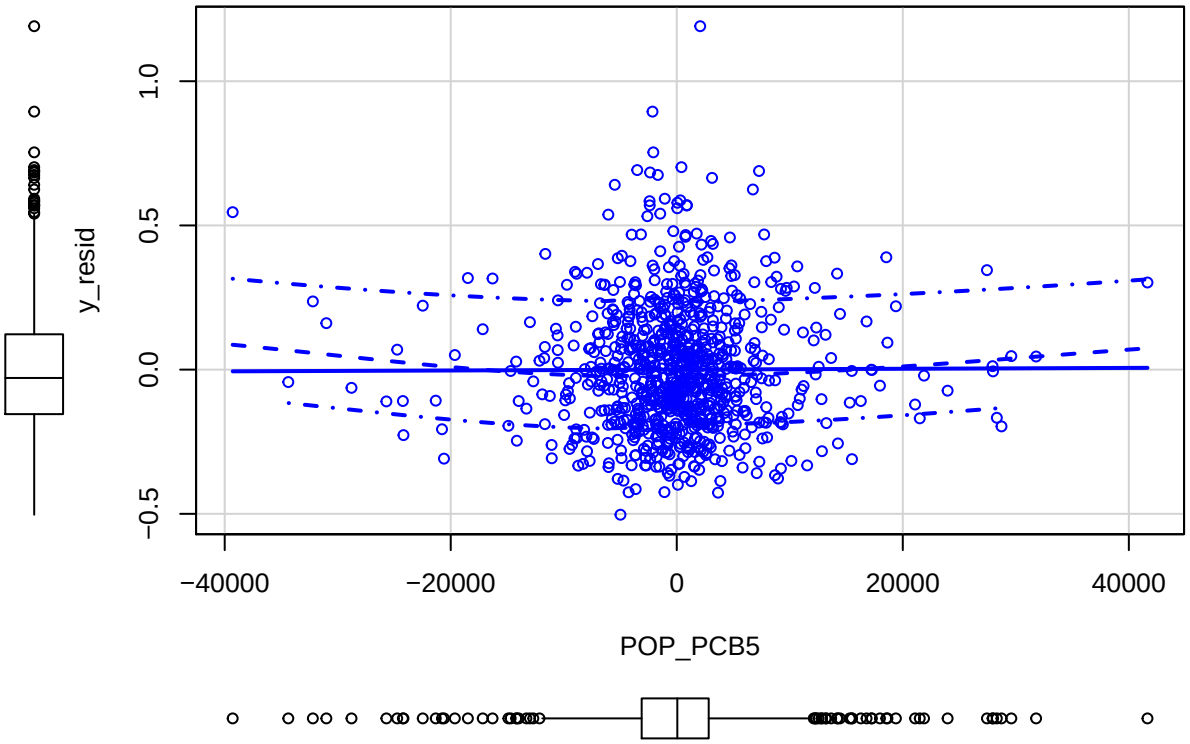
0.5
0.0
−0.5
−40000
−20000
0
20000
40000
POP_PCB4


Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
420
438
Scale−Location
√|Standardized residuals|
Fitted values
420
Residuals vs Leverage
Standardized residuals
Leverage
Cook's distance
436
0.5
1


y_resid
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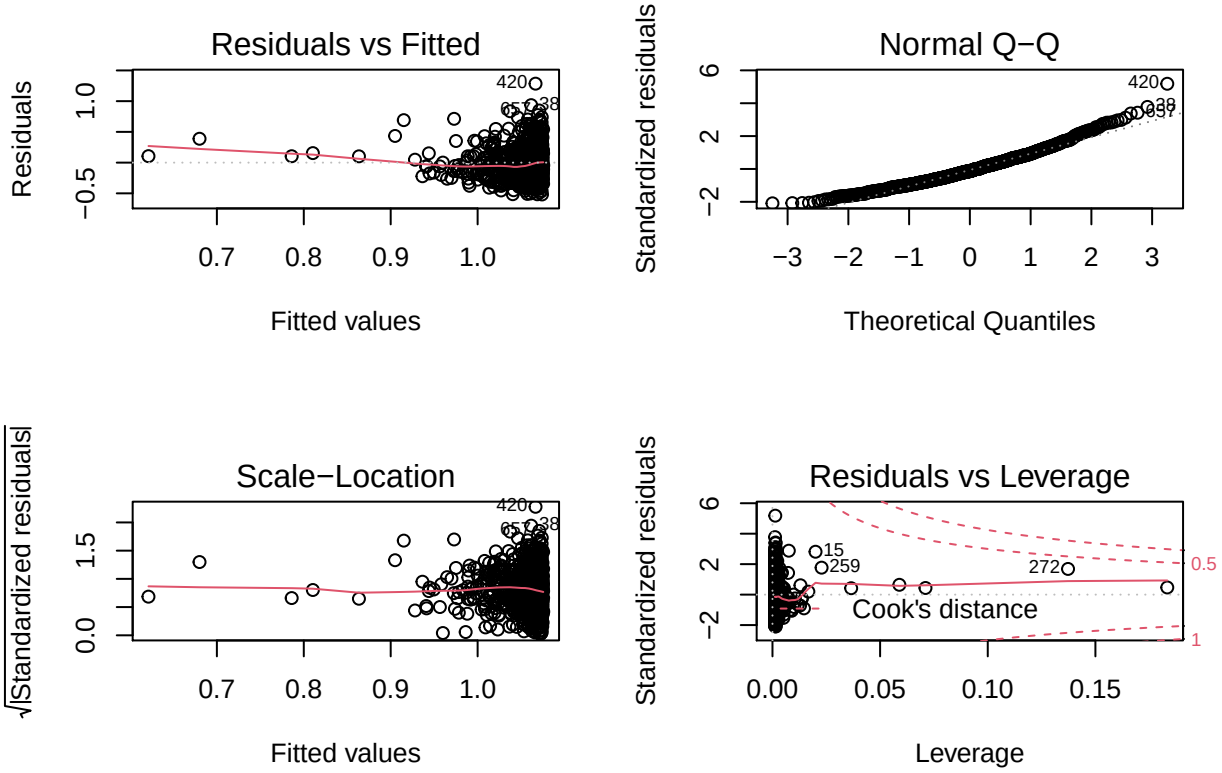
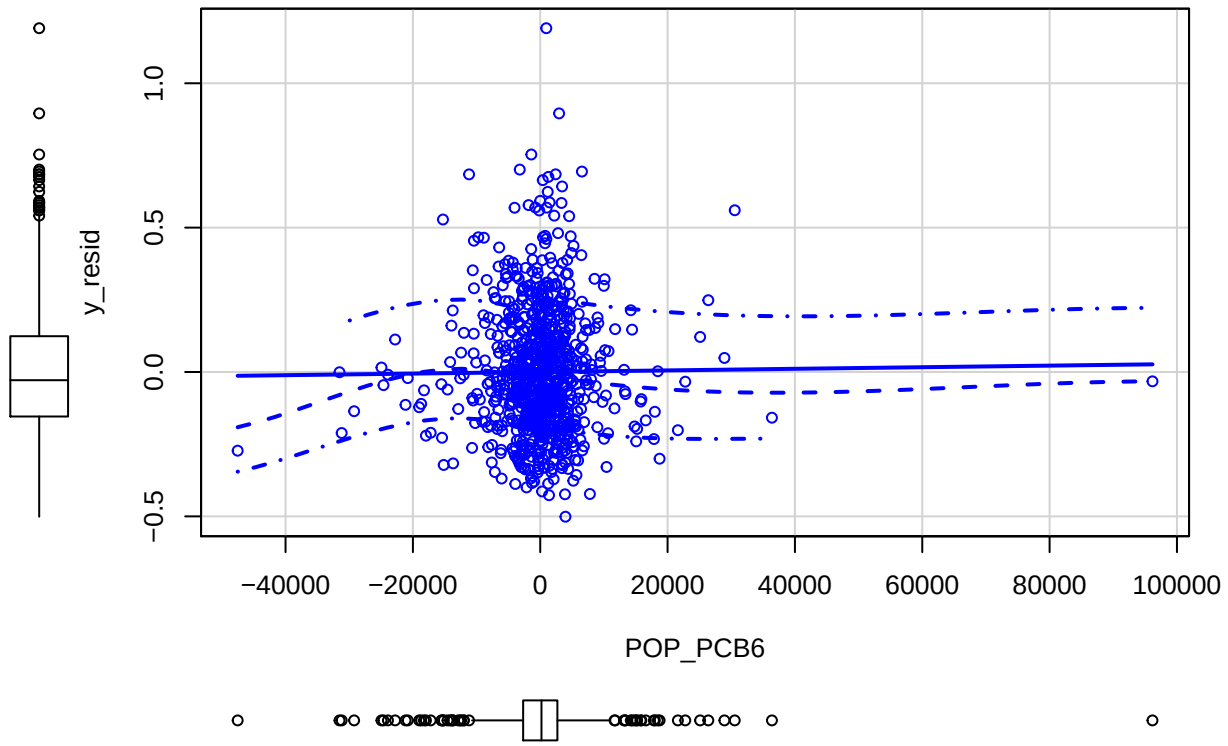
0.5
0.0
−0.5
−40000
−20000
0
20000
40000
POP_PCB5


Residuals vs Fitted
Residuals
Fitted values
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Cook's distance
Leverage
420
15
259
272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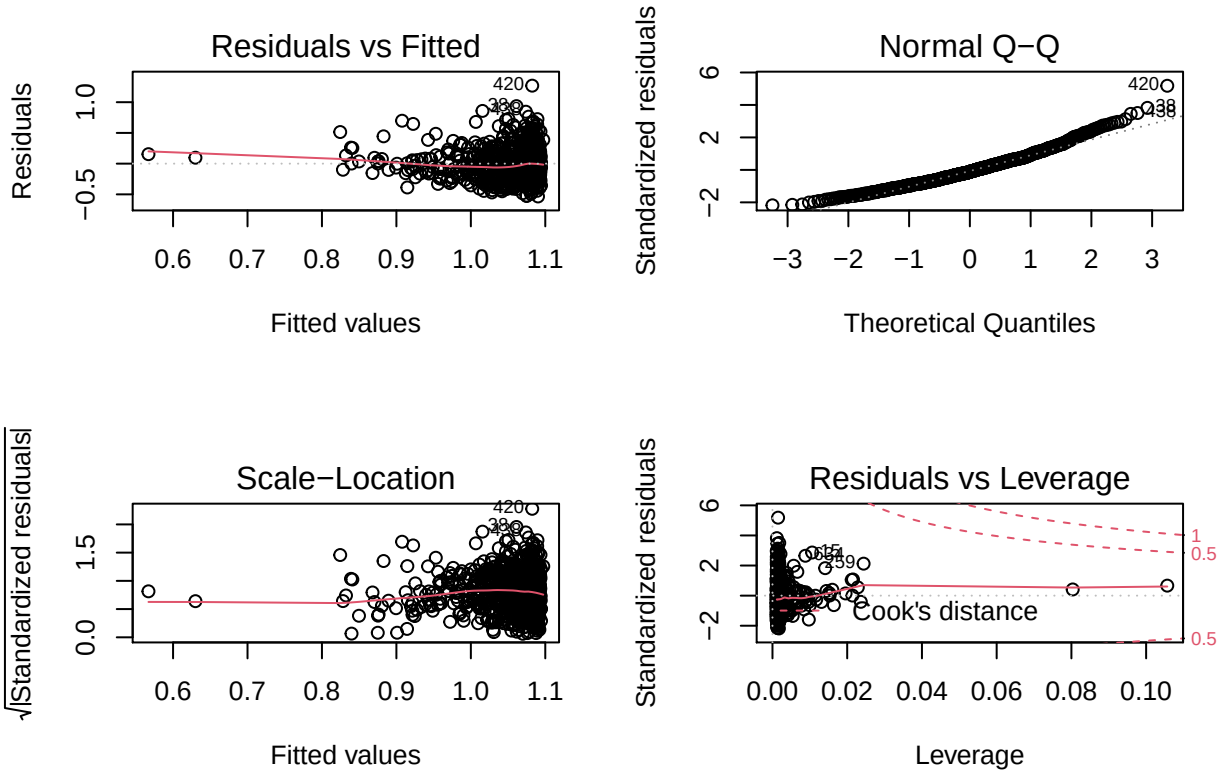
−40000
−20000
0
20000
40000
60000
80000
100000
POP_PCB6


Residuals vs Fitted
Residuals
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Standardized residuals
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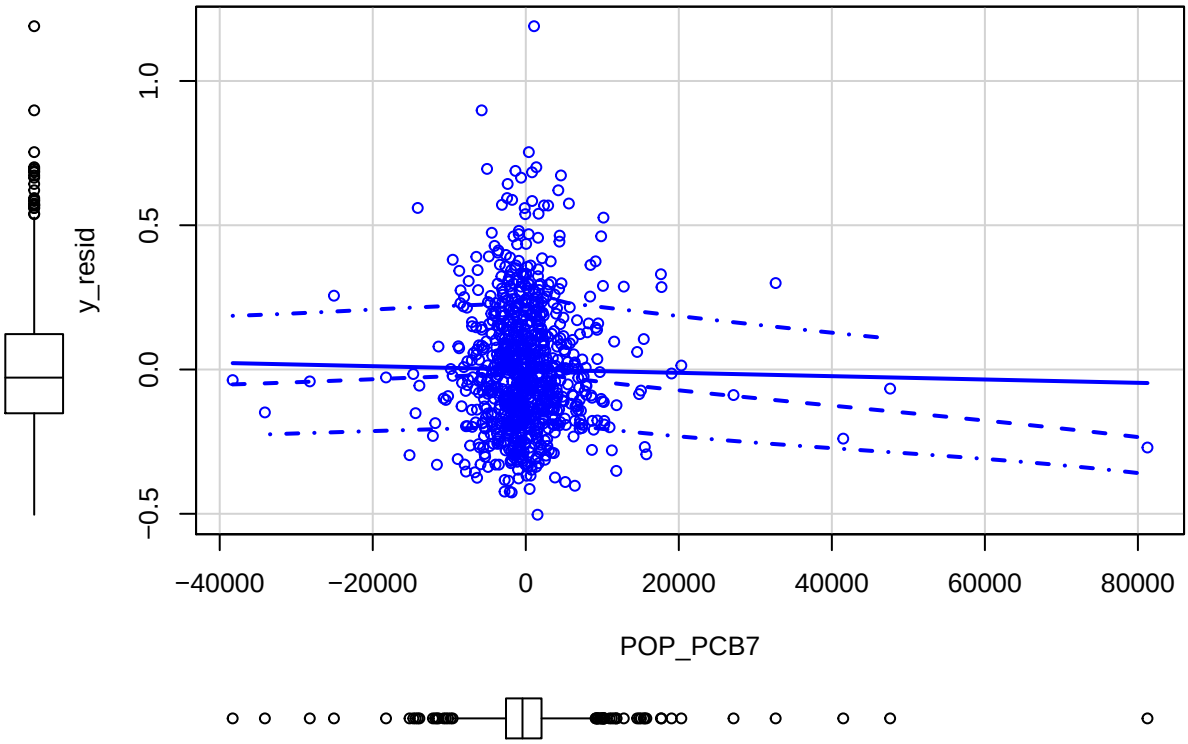
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Cook's distance
Leverage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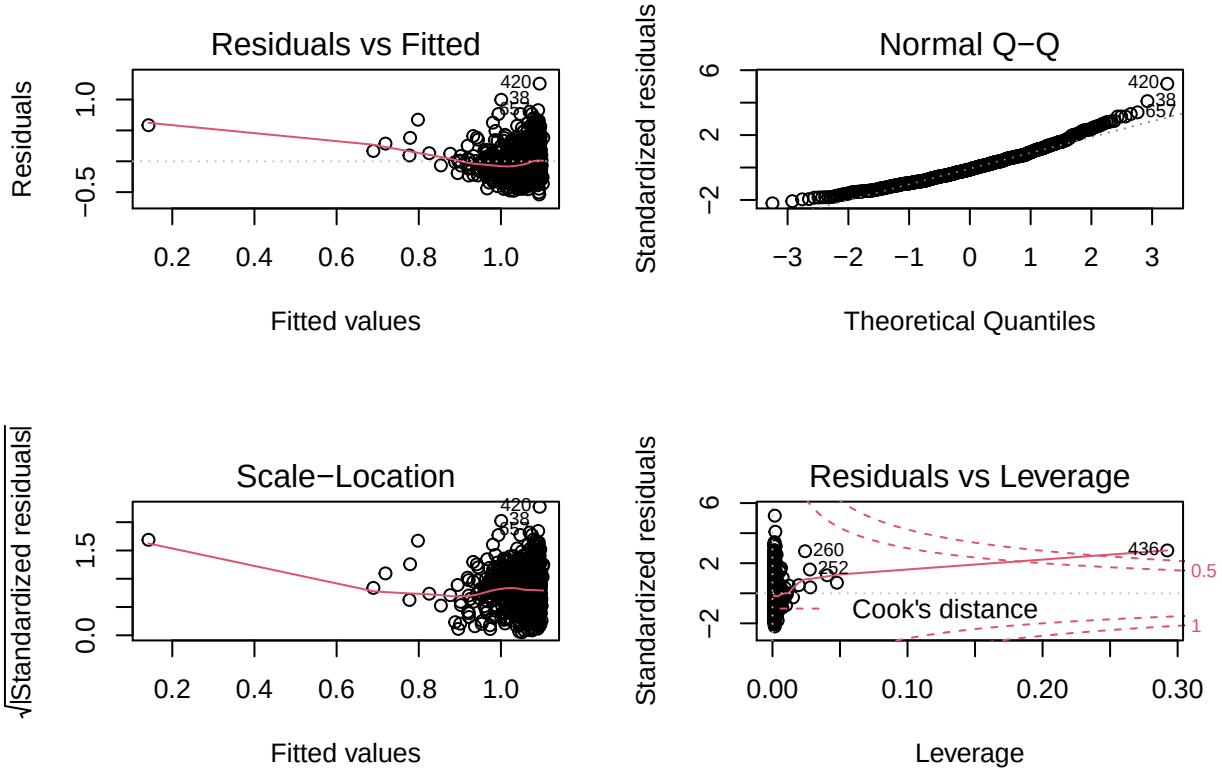
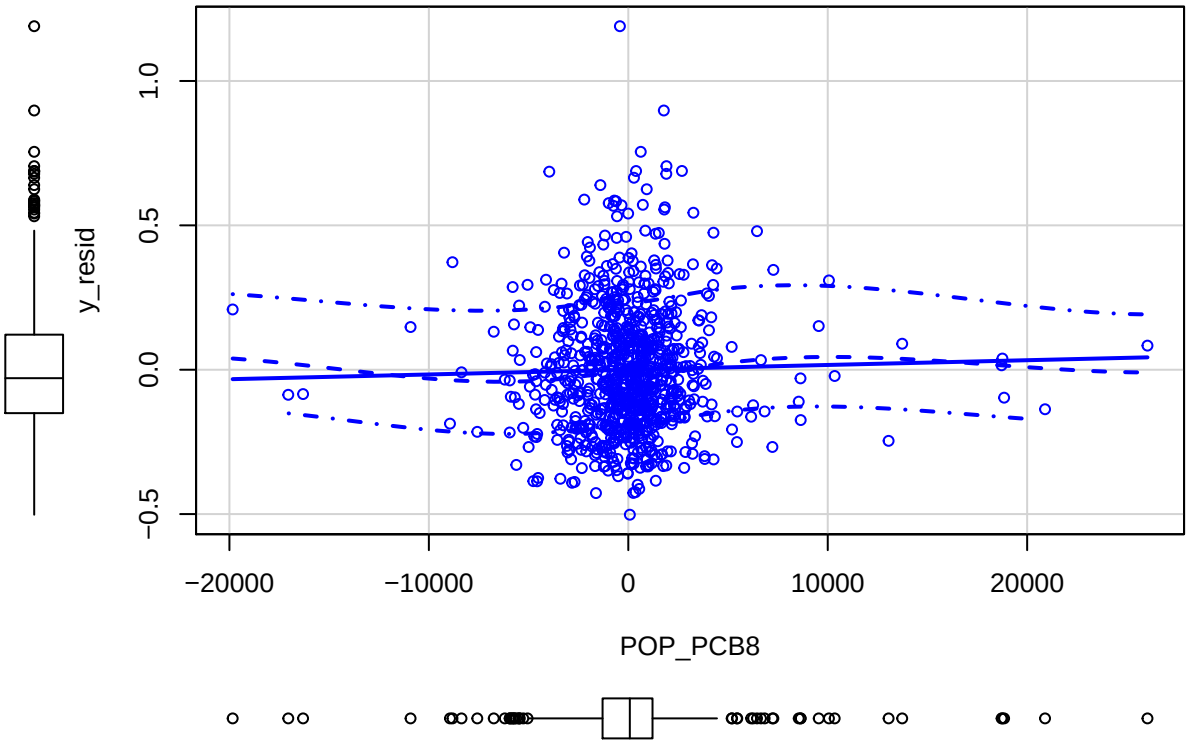
1.0
0.5
0.0
−0.5
−40000
−20000
0
20000
40000
60000
80000
POP_PCB7


Residuals vs Fitted
Residuals
Fitted values
420
38
657
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
260
252
436
0.5
1
Cook's distance
Leverage


y_resid
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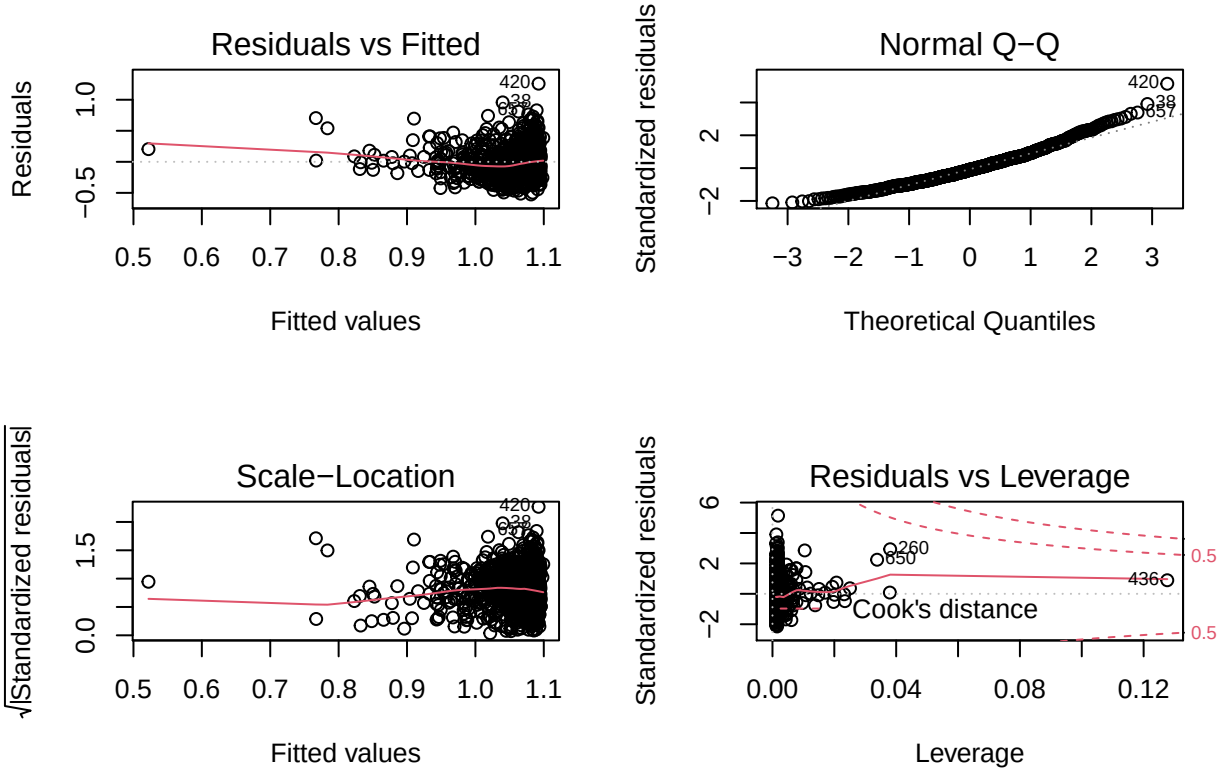
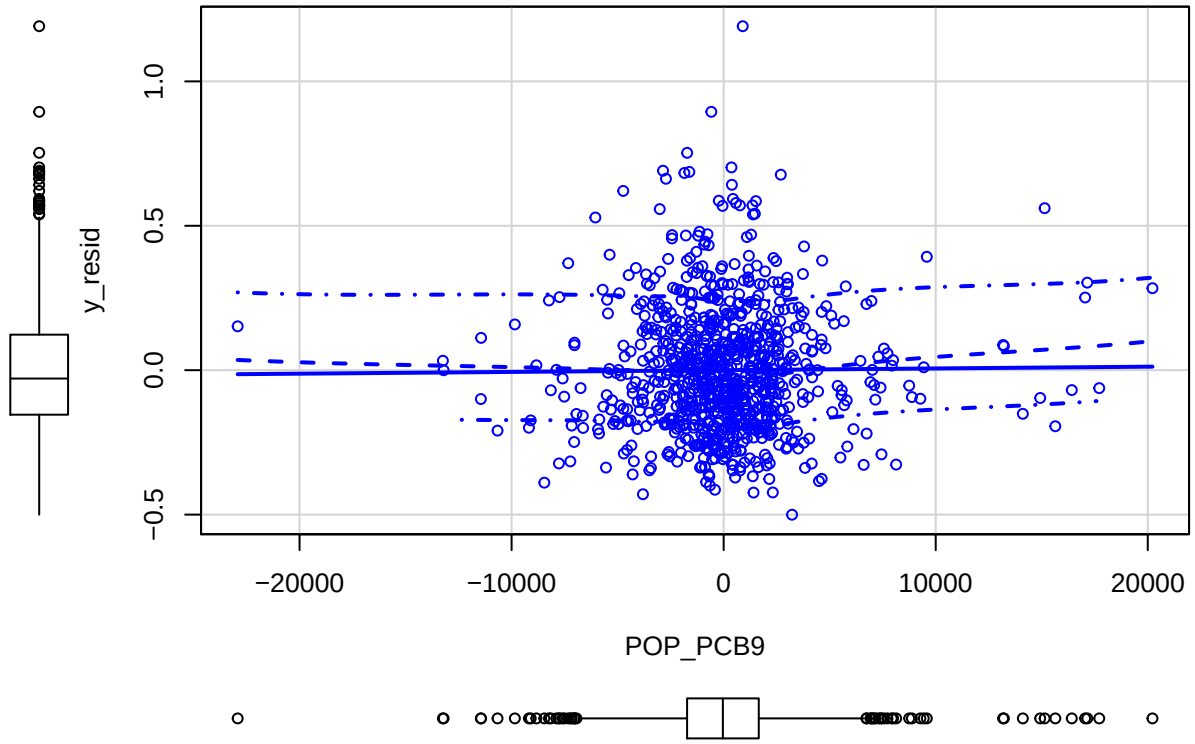
−10000
0
10000
20000
POP_PCB8


Residuals vs Fitted
Residuals
Fitted values
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Cook's distance
Leverage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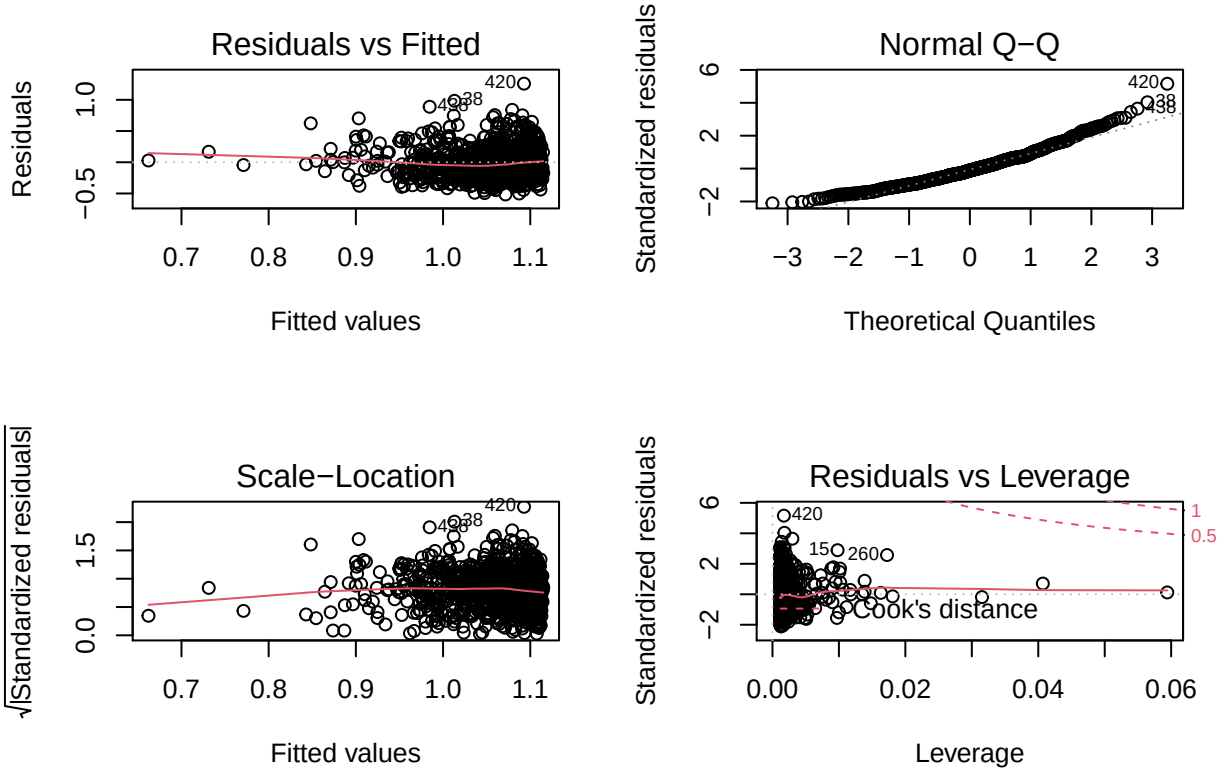
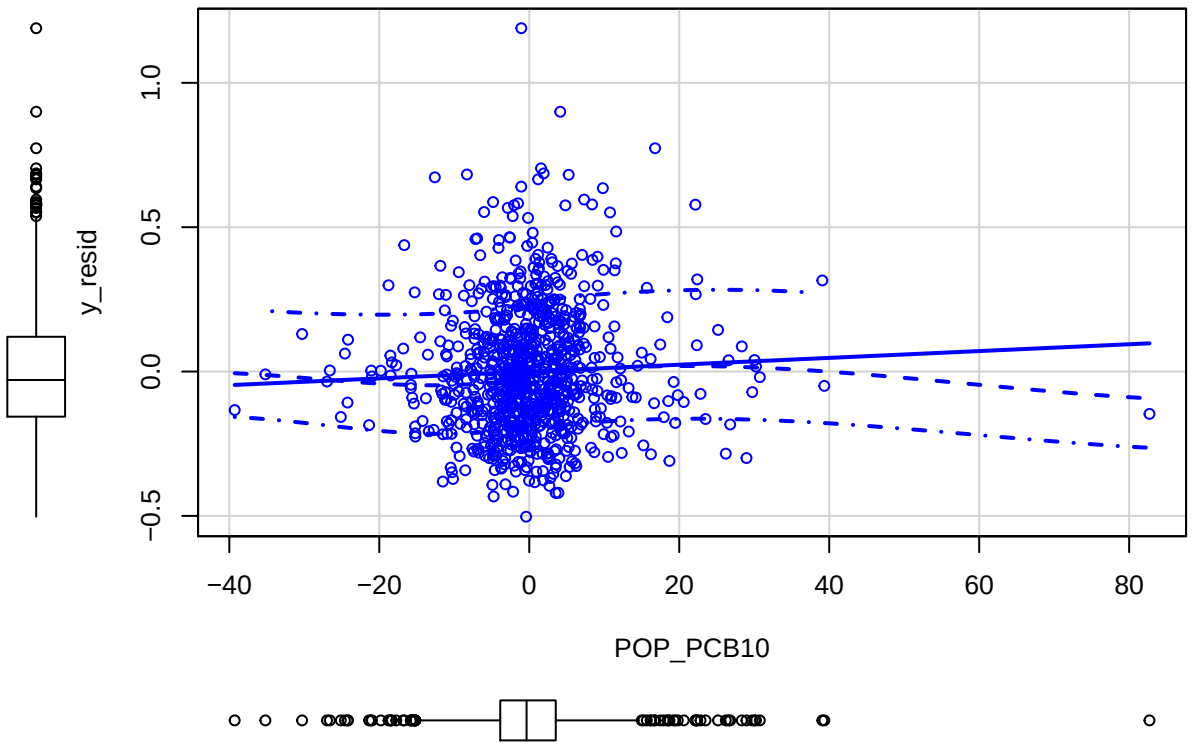
−20000
−10000
0
10000
20000
POP_PCB9


Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
Leverage
15
260
1
0.5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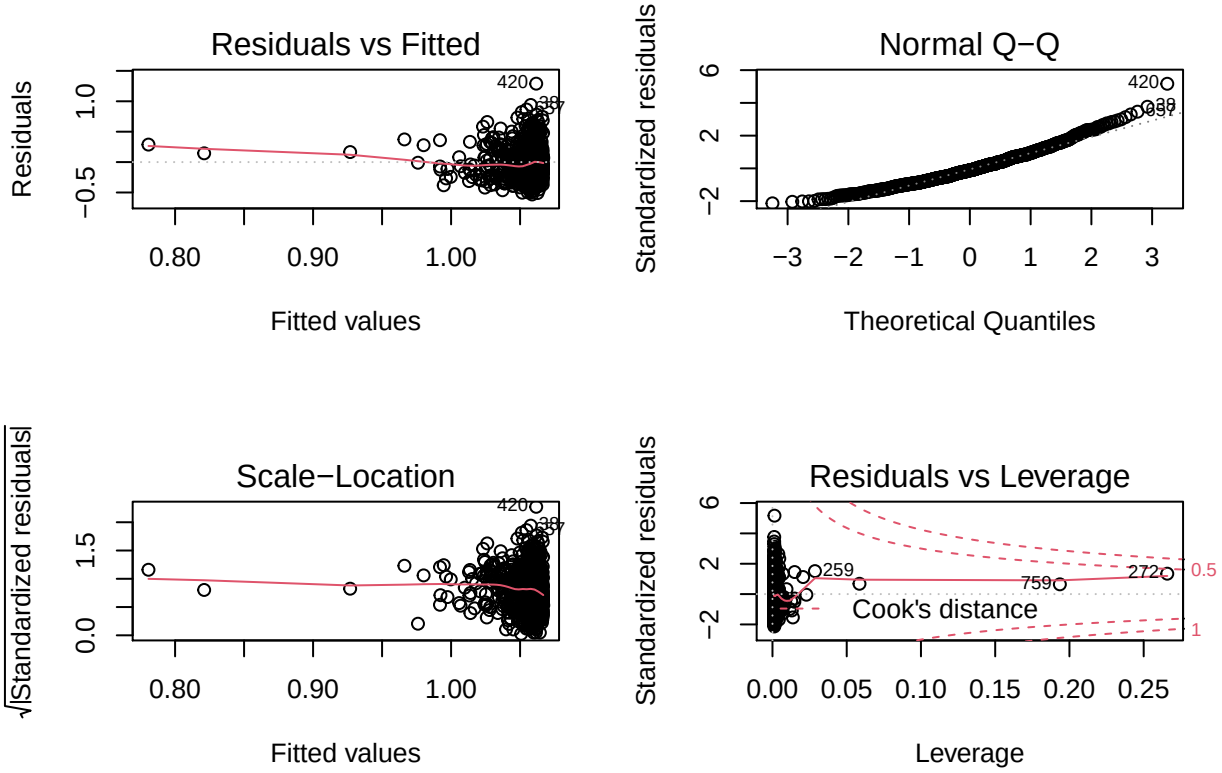
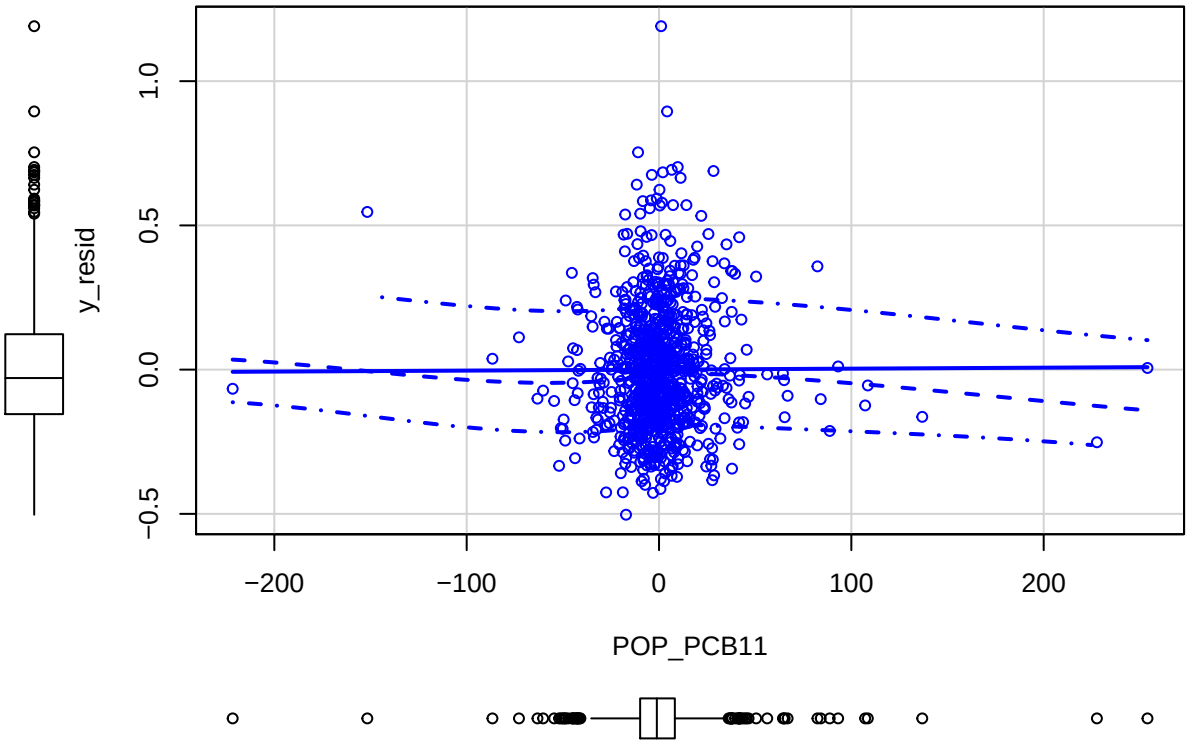
0.0
−0.5
−40
−20
0
20
40
60
80
POP_PCB10


Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
Leverage
259
759
272
0.5
1


y_resid
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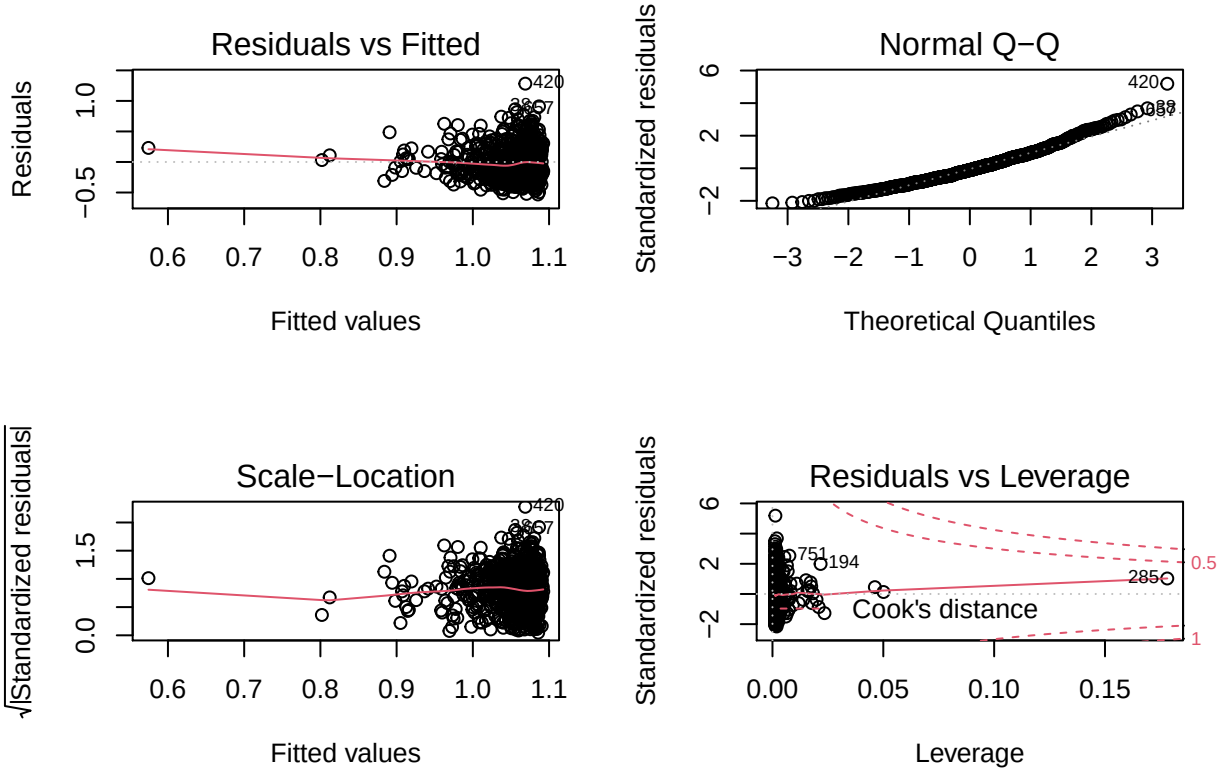
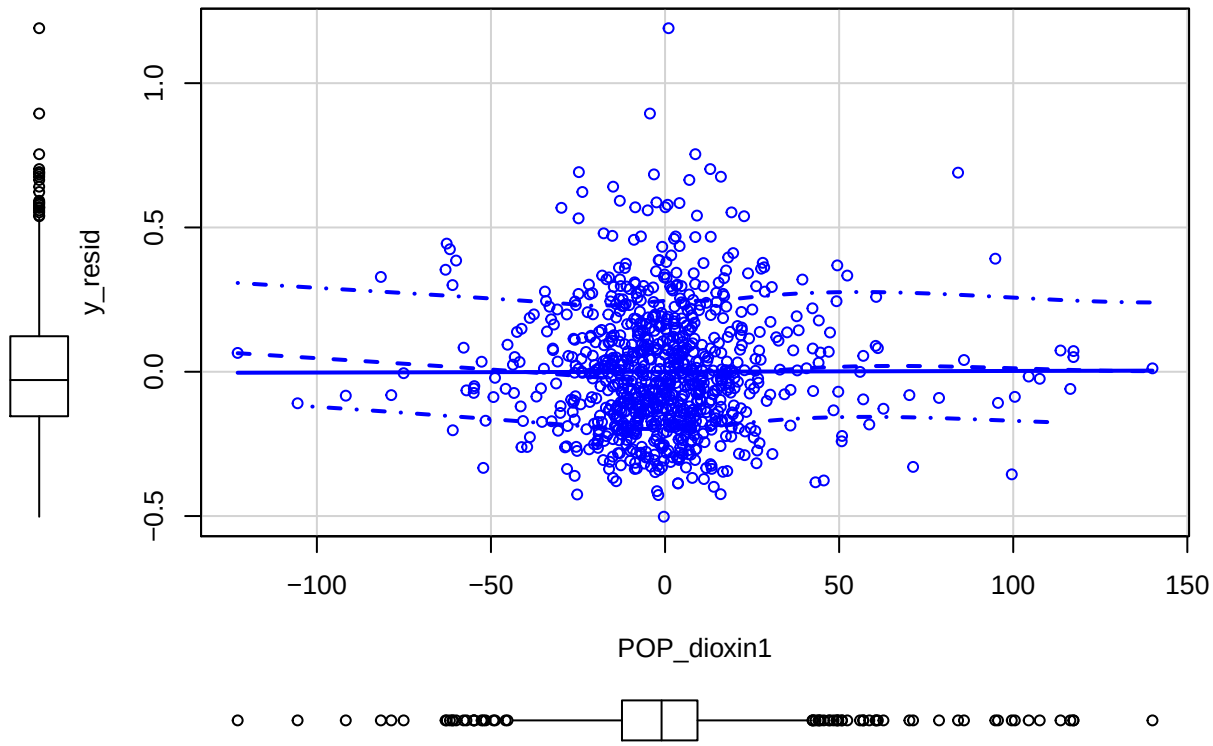
0.5
0.0
−0.5
−200
−100
0
100
200
POP_PCB11


Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
420
Scale−Location
√|Standardized residuals|
Fitted values
420
Residuals vs Leverage
Standardized residuals
Leverage
751
194
285
Cook's distance
0.5
1


y_resid
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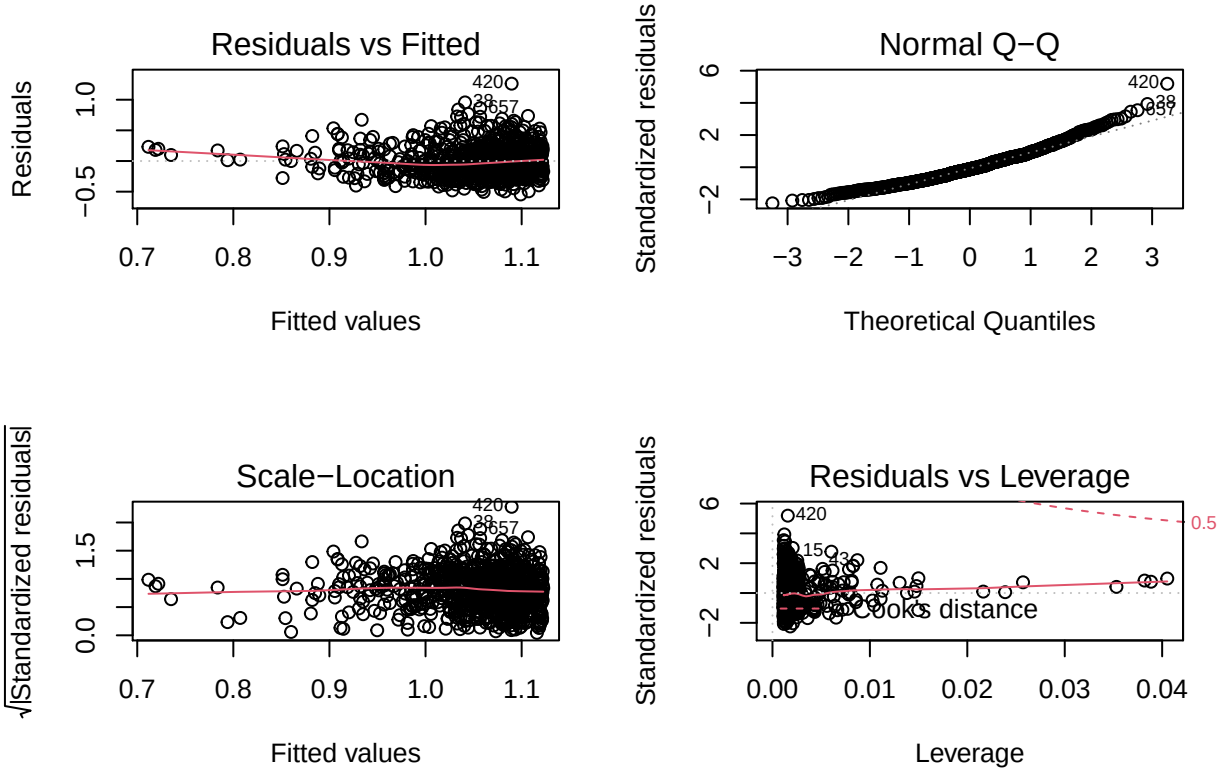
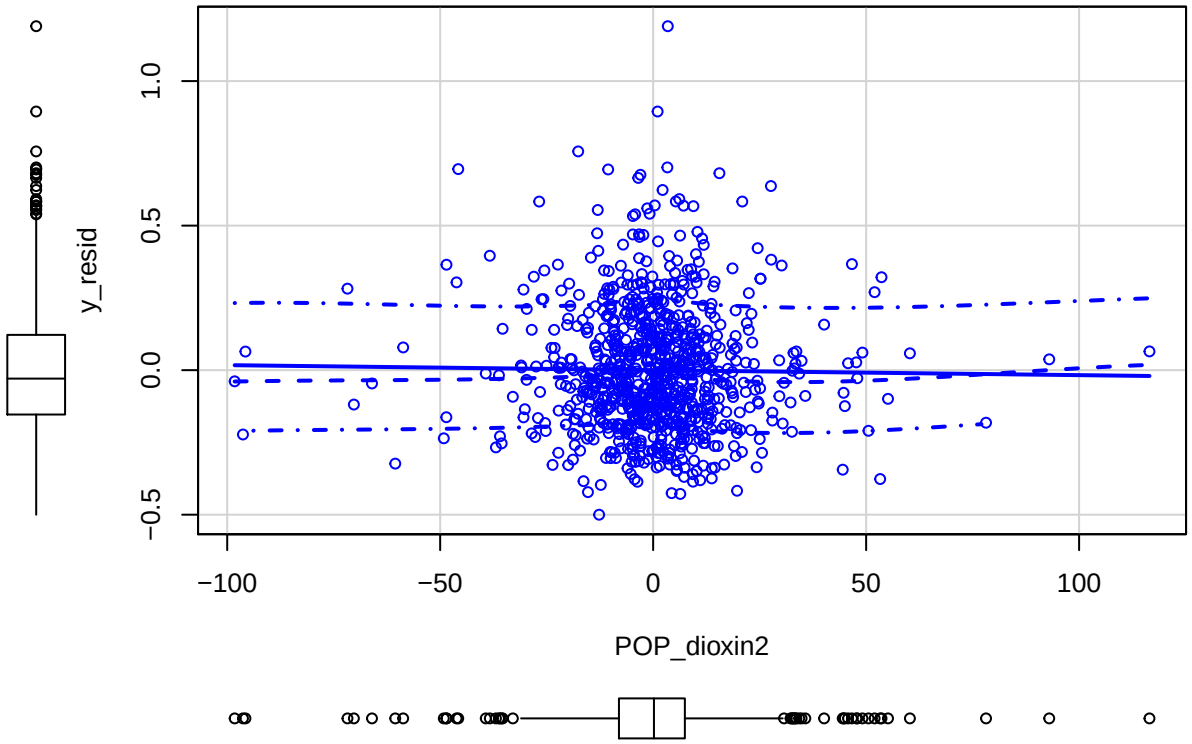
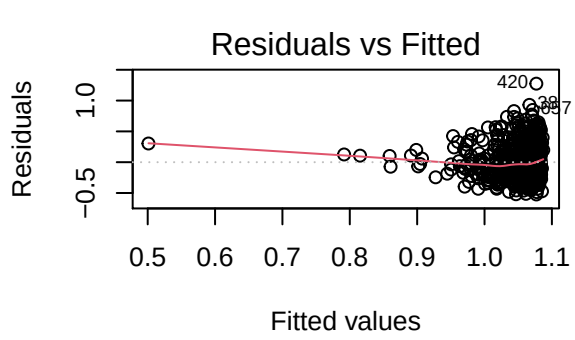
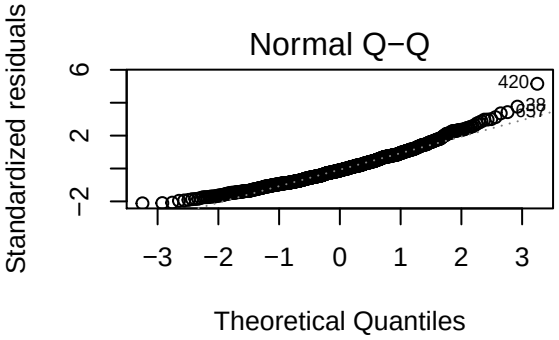
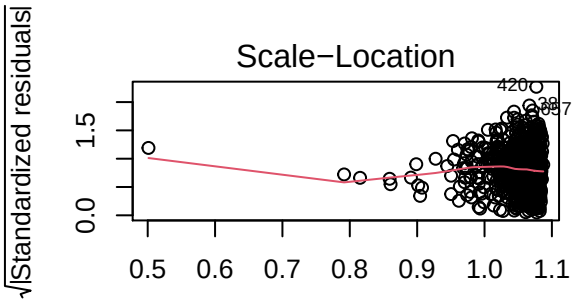
0.5
0.0
−0.5
−100
−50
0
50
100
150
POP_dioxin1

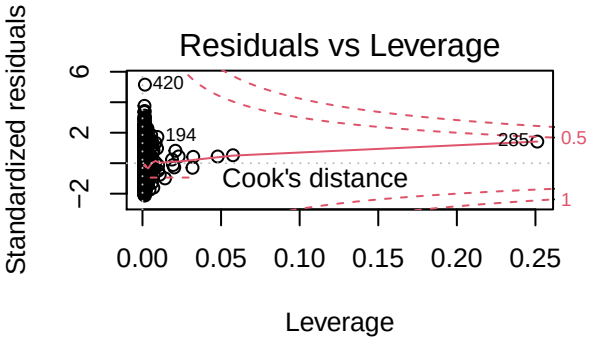

Residuals vs Fitted
Residuals
Fitted values
420
28
657
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
0.5
Leverage
15
43

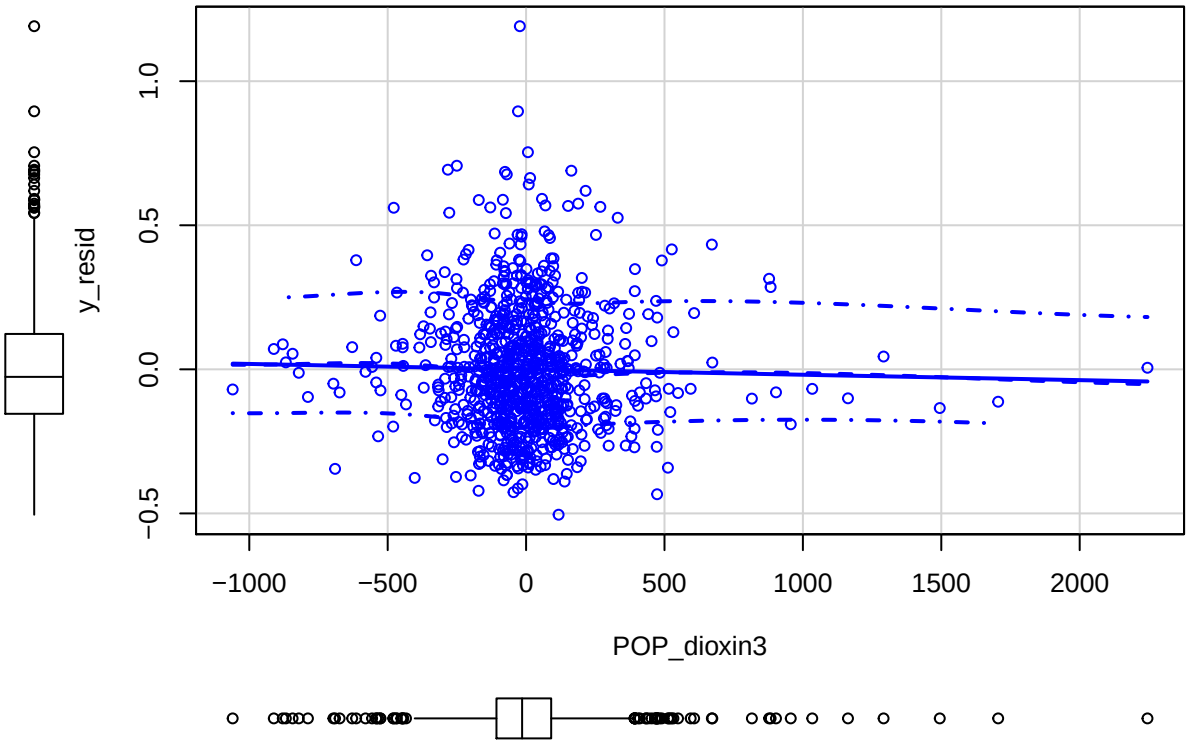

y_resid
1.0
0.5
0.0
−0.5
−100
−50
0
50
100
POP_dioxin2

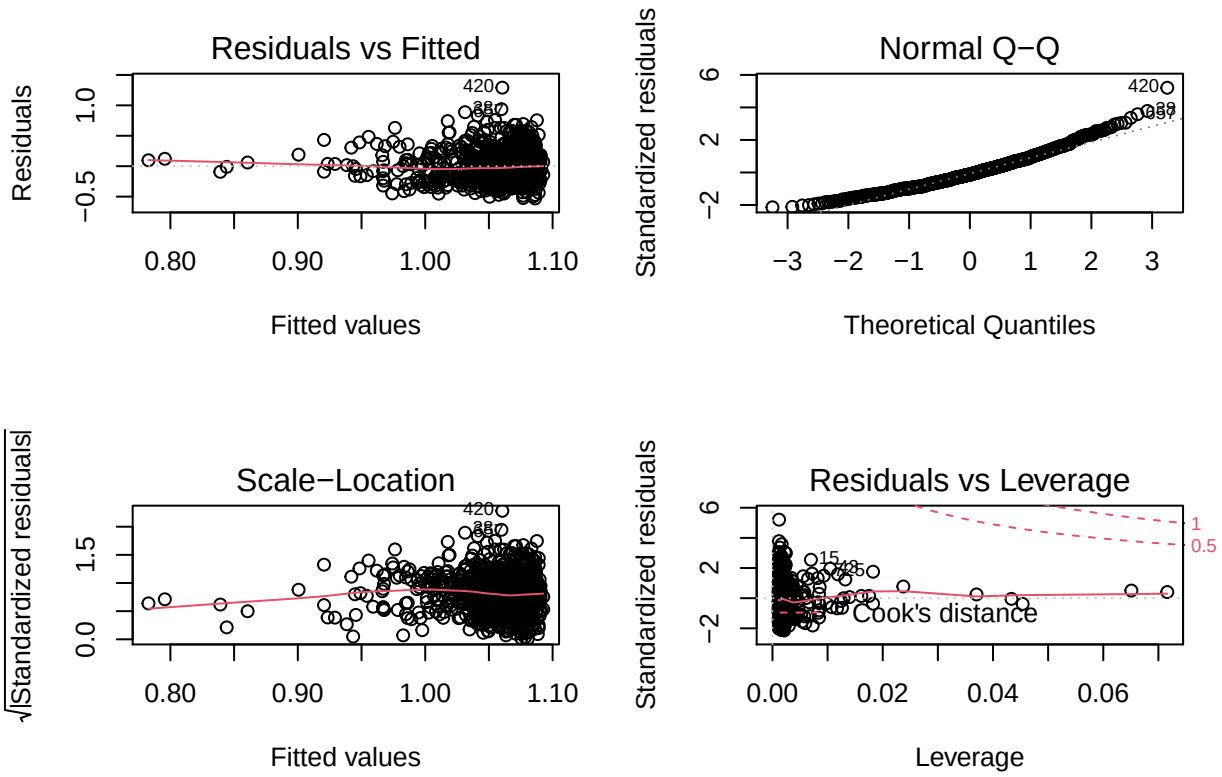

Residuals vs Fitted
Residuals
Fitted values
420

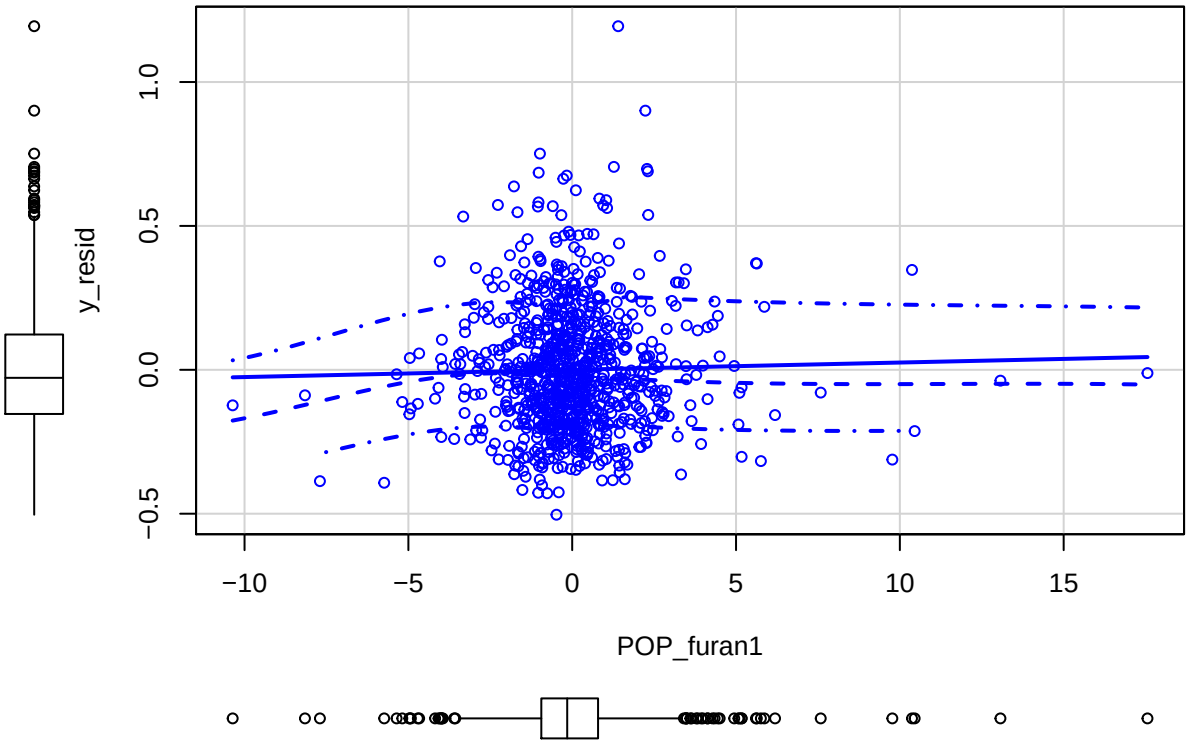

Normal Q−Q
Standardized residuals
Theoretical Quantiles
420

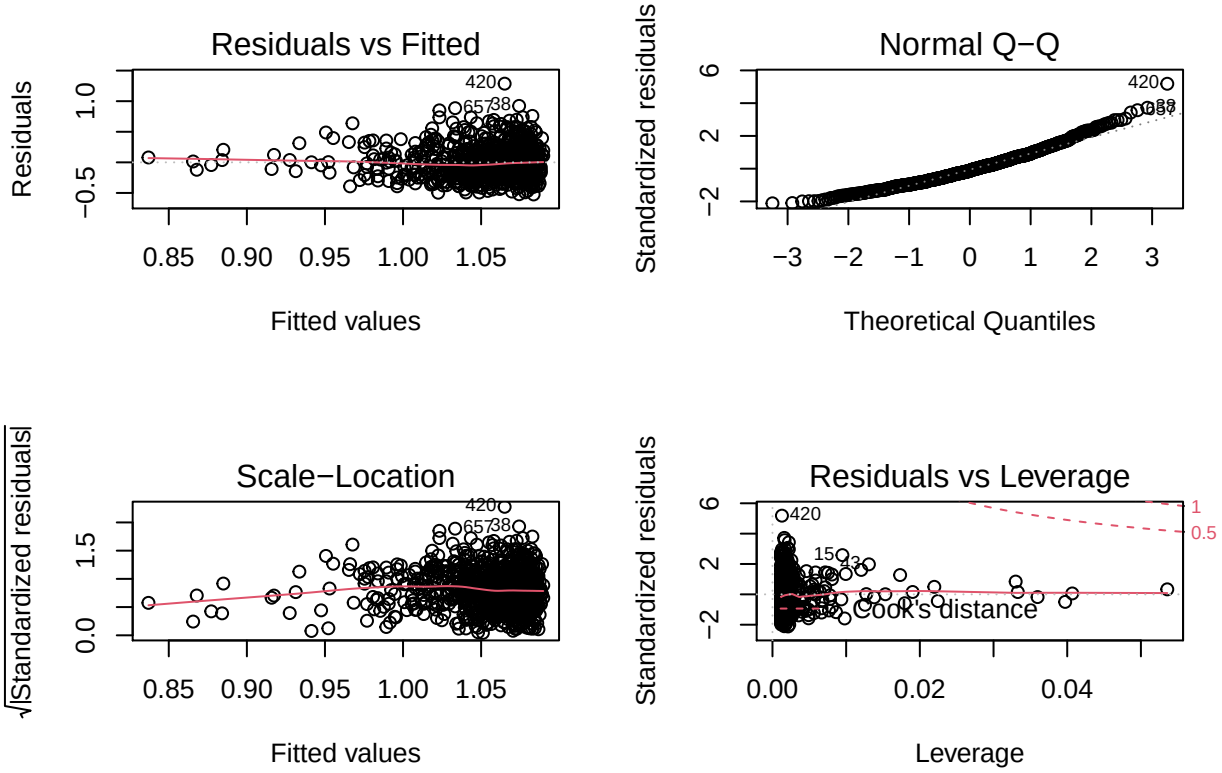

Scale−Location
√|Standardized residuals|
Fitted values
420

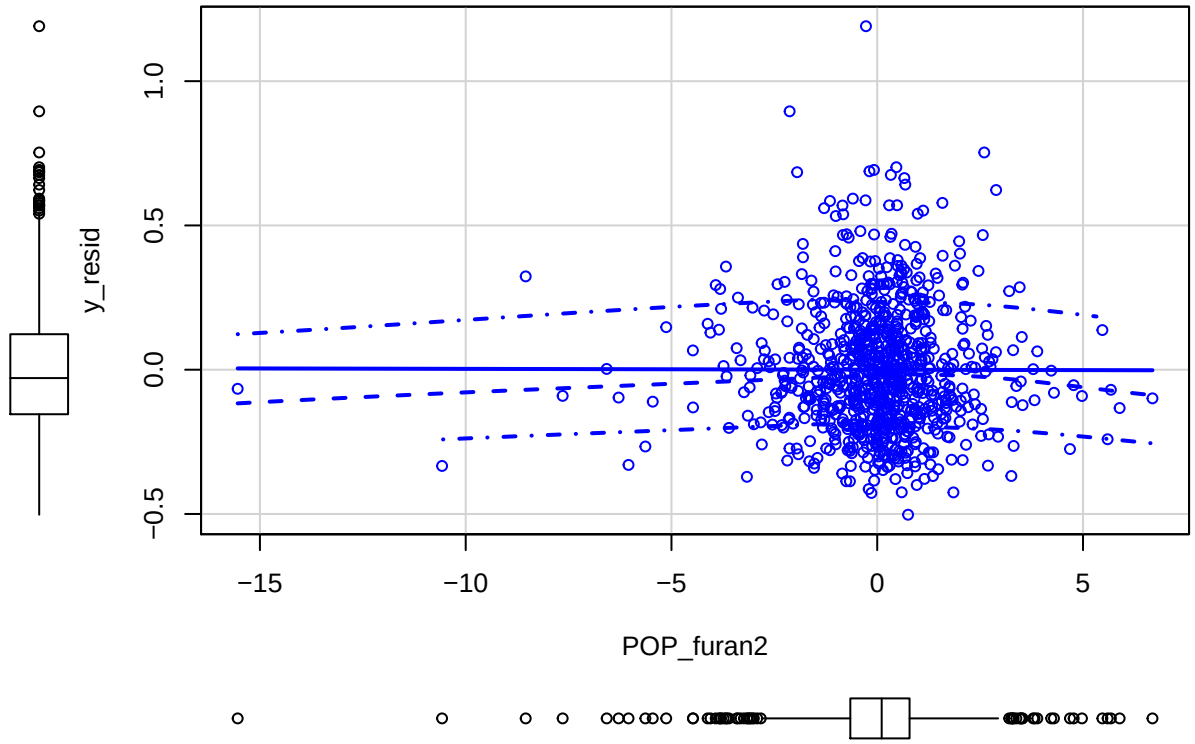

Residuals vs Leverage
Standardized residuals
Leverage
Cook's distance
420
194
285
0.5
1

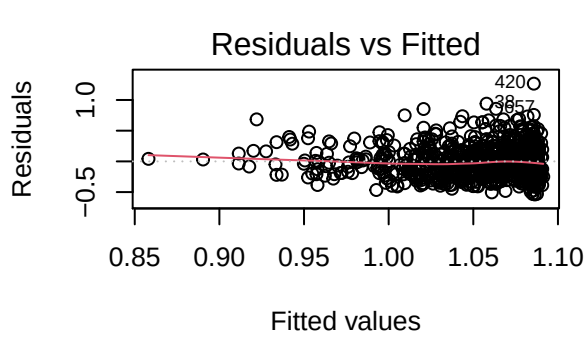

y_resid
1.0
0.5
0.0
−0.5
−1000
−500
0
500
1000
1500
2000
POP_dioxin3

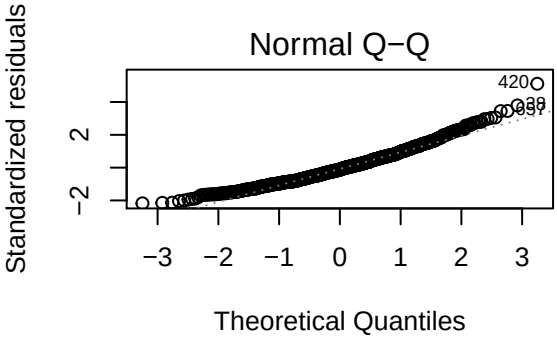

Residuals vs Fitted
Residuals
Fitted values
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Cook's distance
Leverage

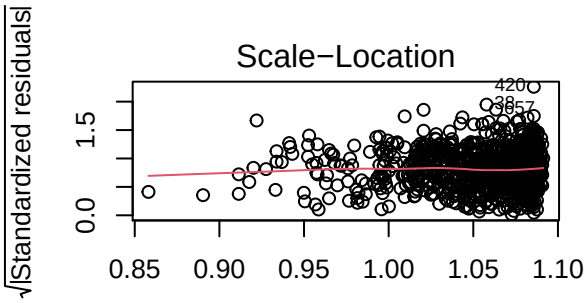

y_resid
1.0
0.5
0.0
−0.5
−10
−5
0
5
10
15
POP_furan1

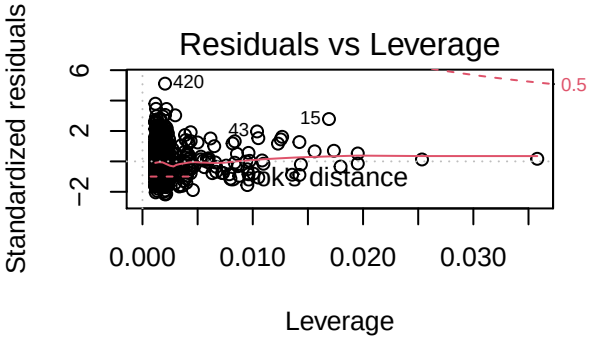

Residuals vs Fitted
Residuals
Fitted values
420
657
38
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
Leverage
1
0.5
15
43

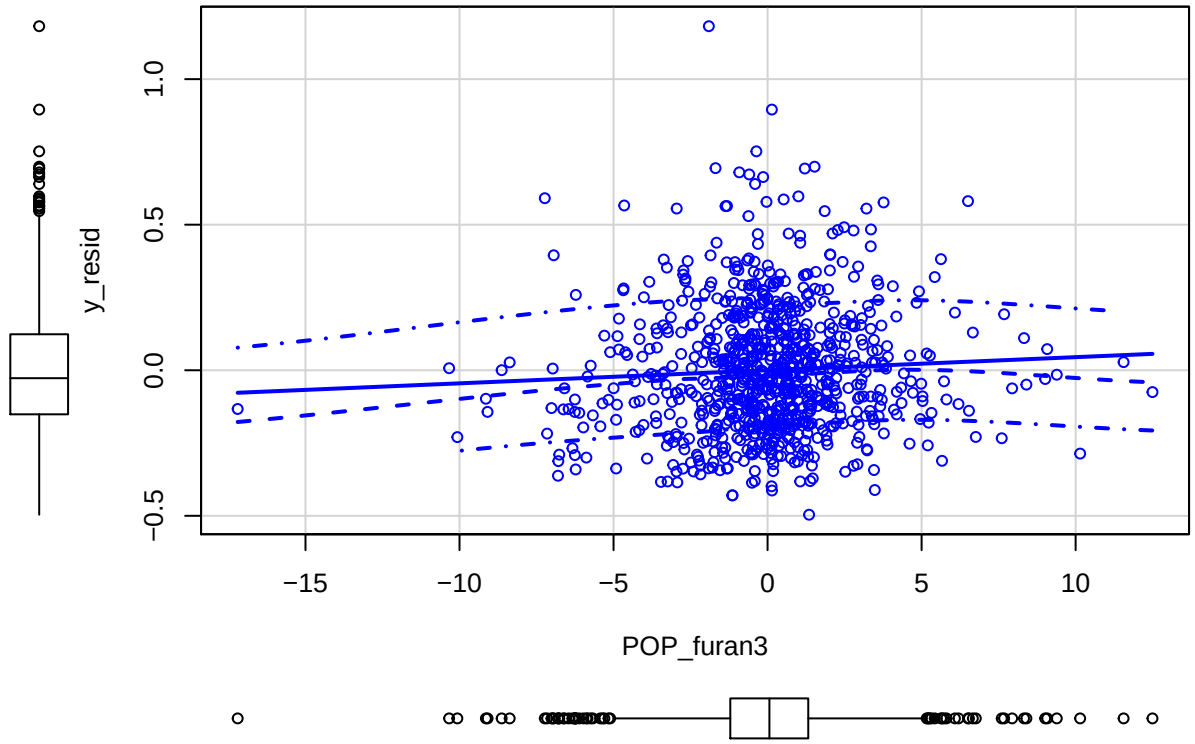

y_resid
1.0
0.5
0.0
−0.5
−15
−10
−5
0
5
POP_furan2

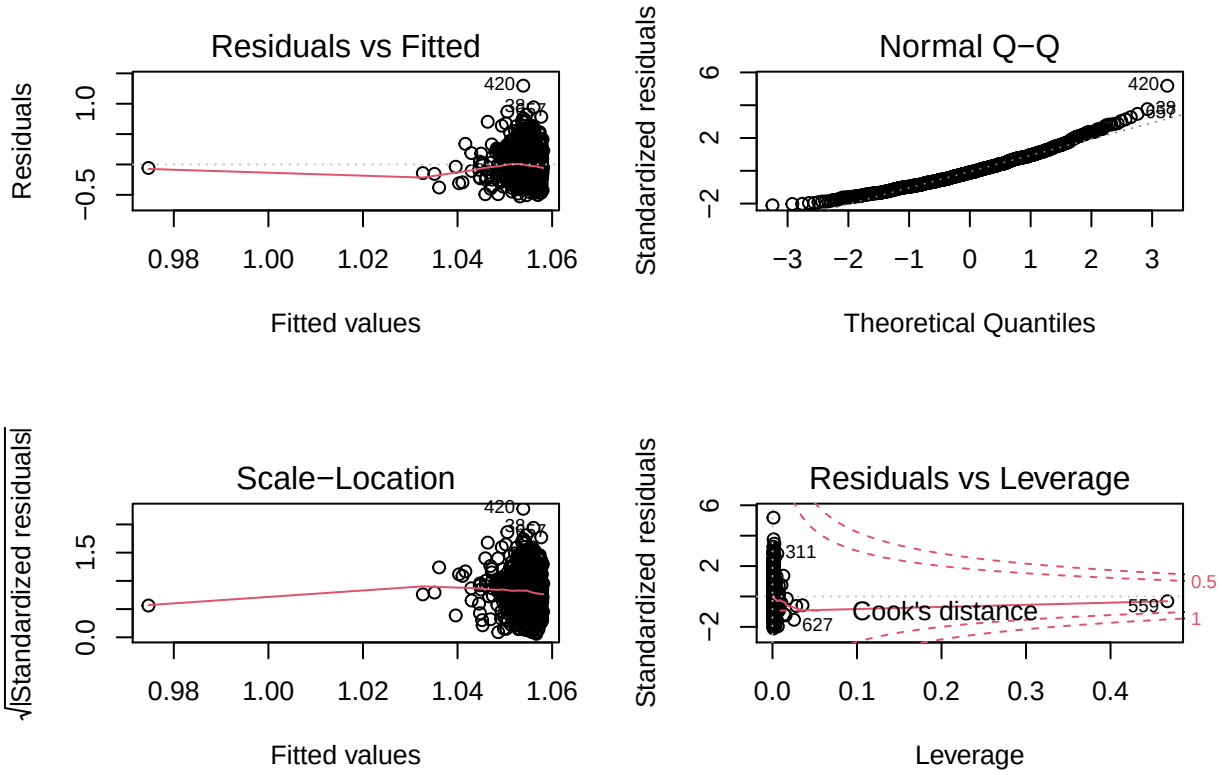

Residuals vs Fitted
Residuals
Fitted values
420
38
57
0.85
0.90
0.95
1.00
1.05
1.10
−0.5
1.0

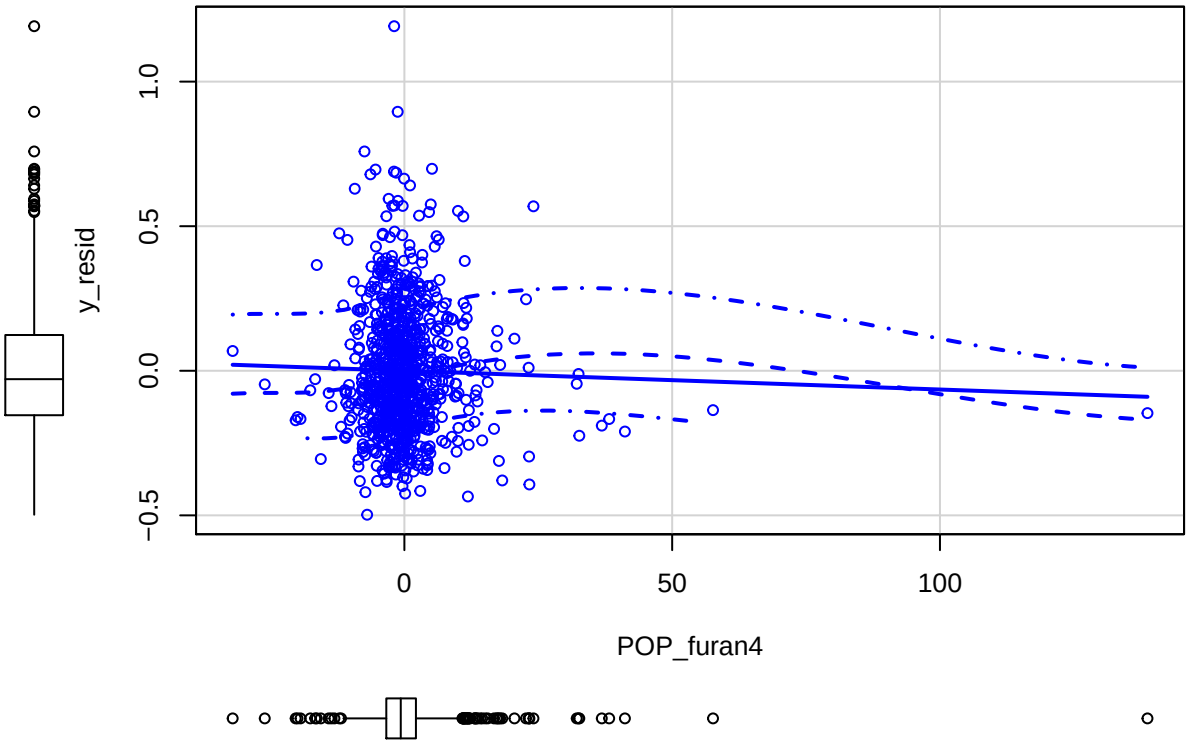

Normal Q−Q
Standardized residuals
Theoretical Quantiles
420
−3
−2
−1
0
1
2
3

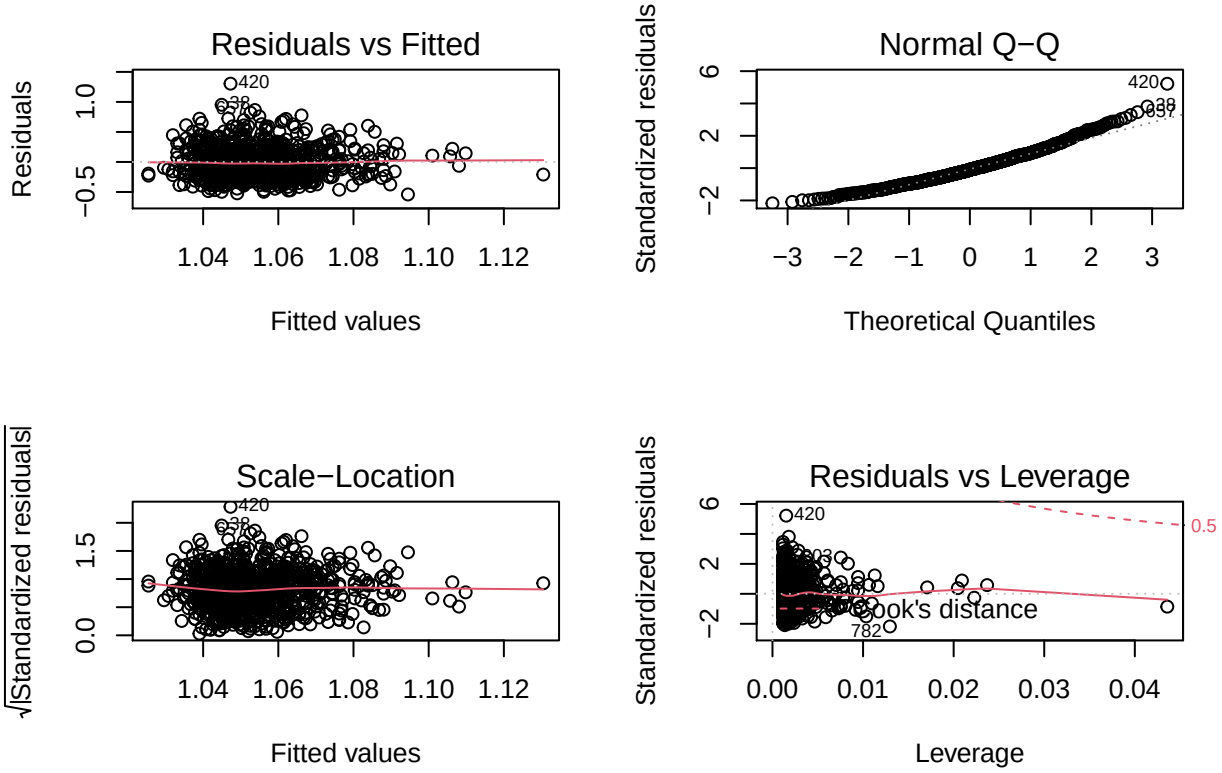

Scale−Location
√|Standardized residuals|
Fitted values
420
38
57
0.85
0.90
0.95
1.00
1.05
1.10
0.0
1.5

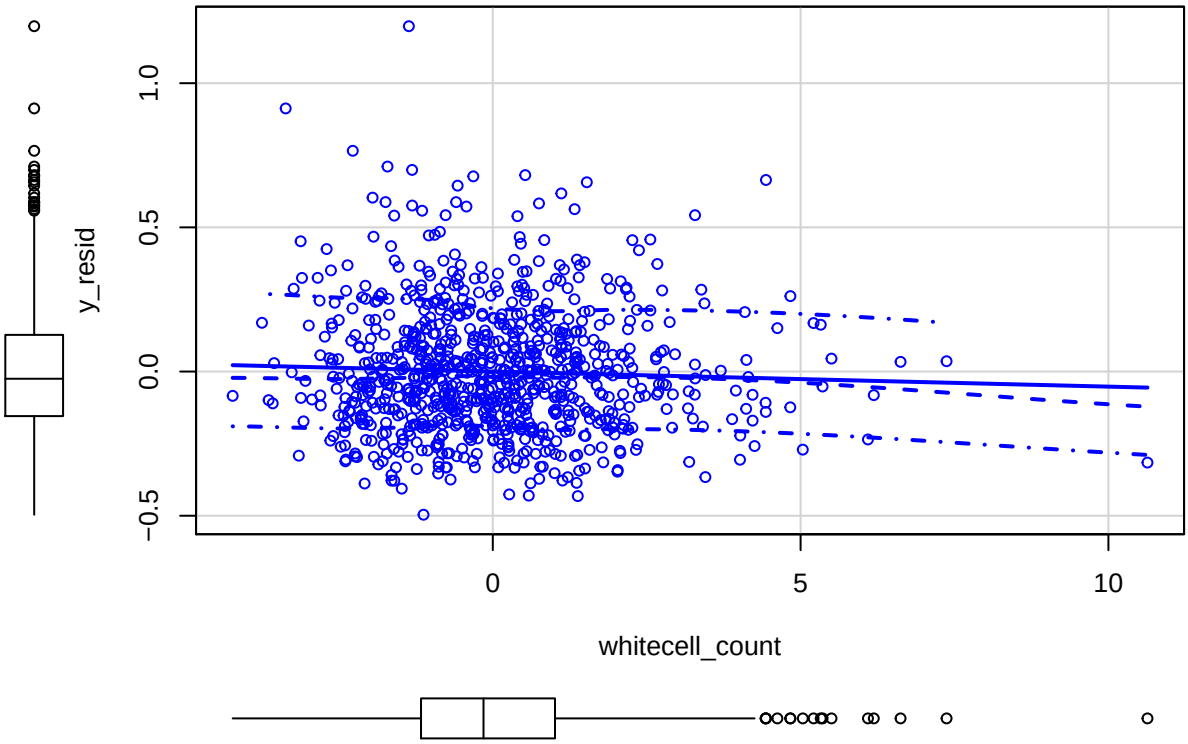

Residuals vs Leverage
Standardized residuals
Leverage
Cook's distance
420
15
43
0.5
0.000
0.010
0.020
0.030
−2
2
6


y_resid
1.0
0.5
0.0
−0.5
−15
−10
−5
0
5
10
POP_furan3


Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
Leverage
311
627
559
0.5
1


y_resid
1.0
0.5
0.0
−0.5
0
50
100
POP_furan4


Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
Leverage
0.5
782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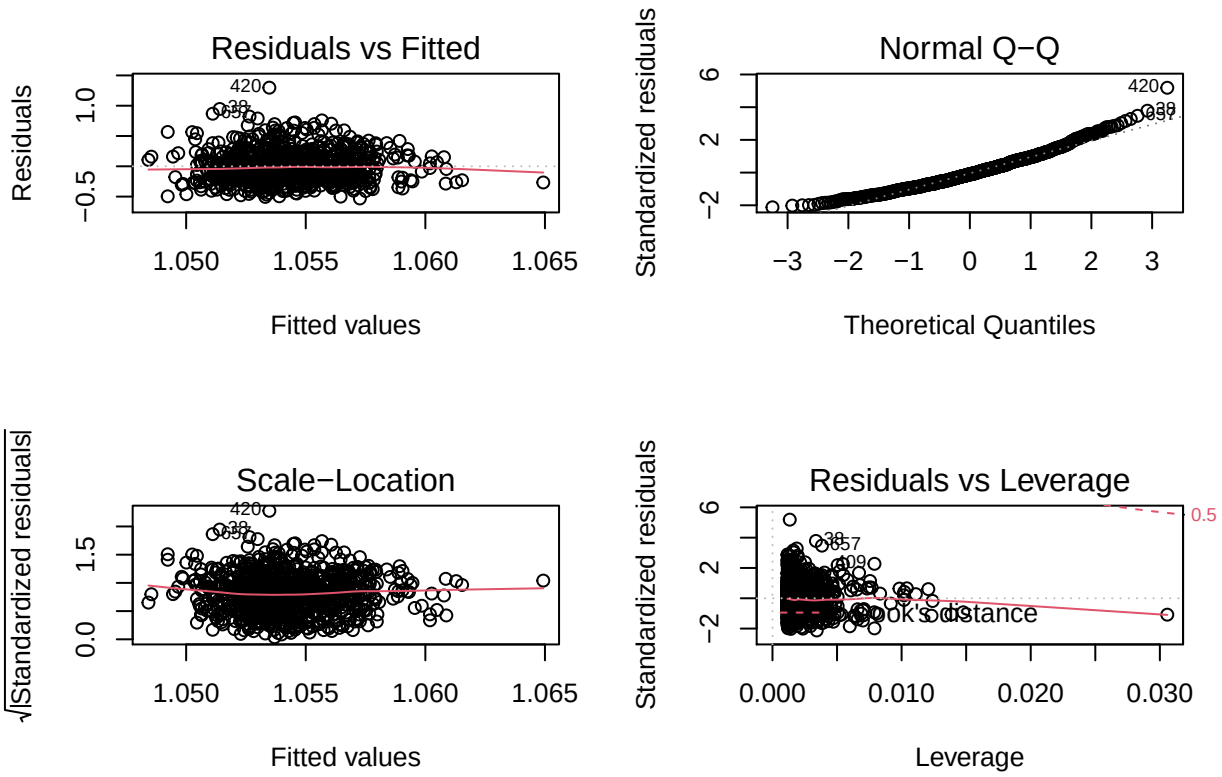
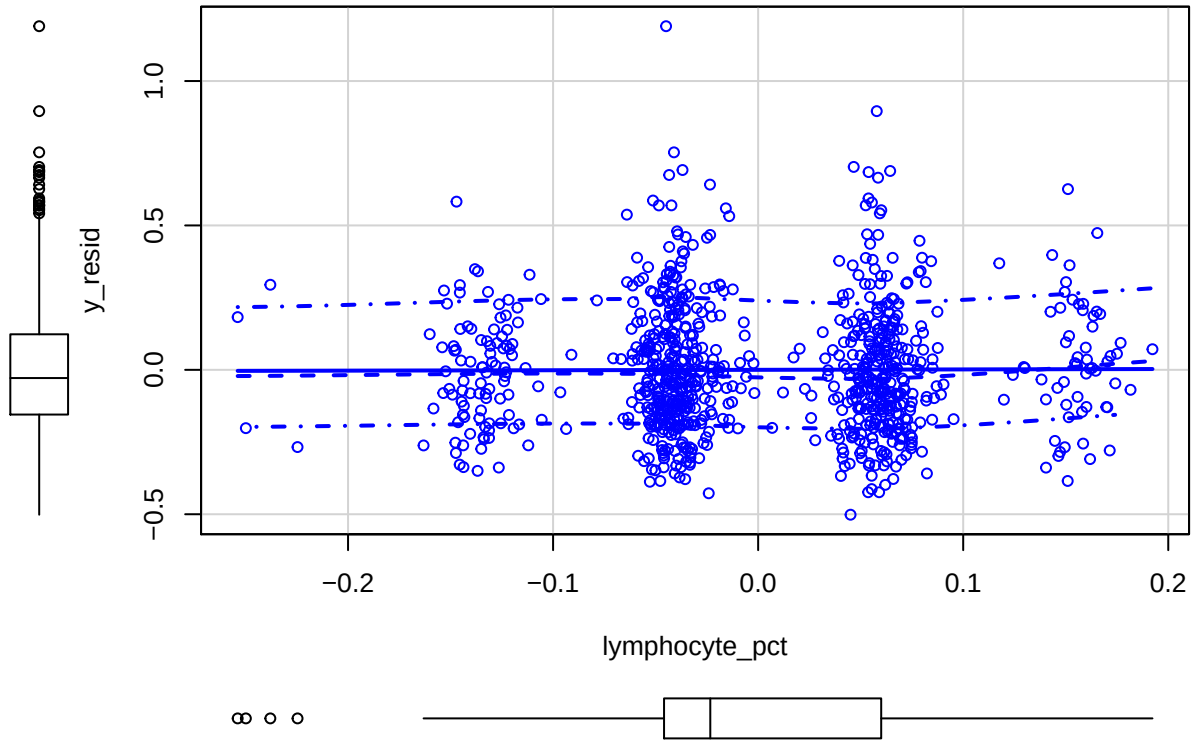
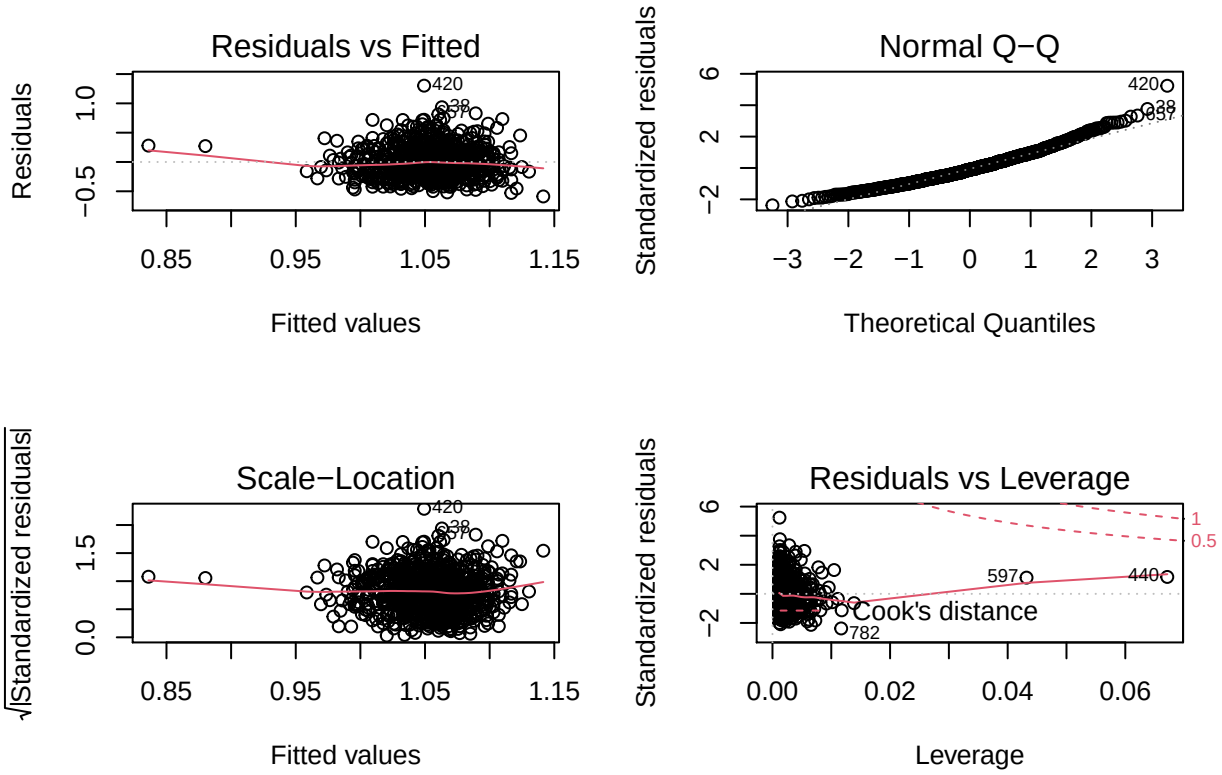
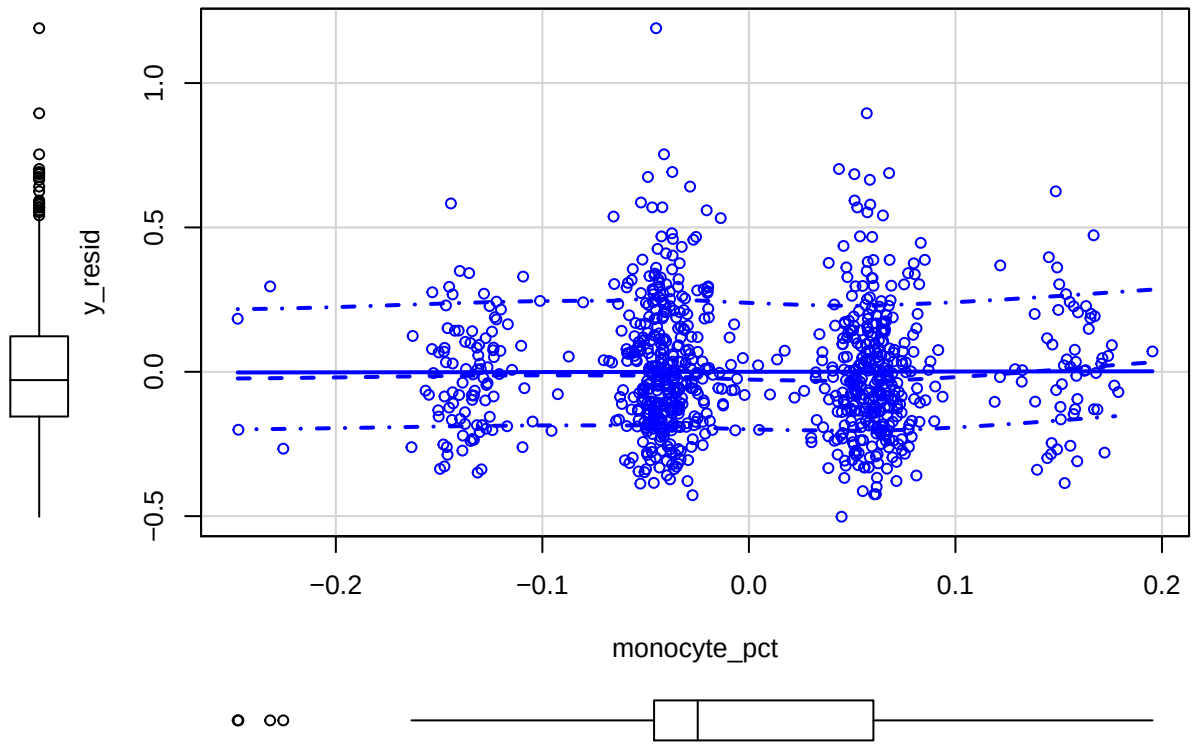
1.0
0.5
0.0
−0.5
0
5
10
whitecell_count


Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
0.5
Leverage


y_resid
1.0
0.5
0.0
−0.5
−0.2
−0.1
0.0
0.1
0.2
lymphocyte_pct


Residuals vs Fitted
Residuals
Fitted values
420
38
37
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
Leverage
597
440
782
1
0.5


y_resid
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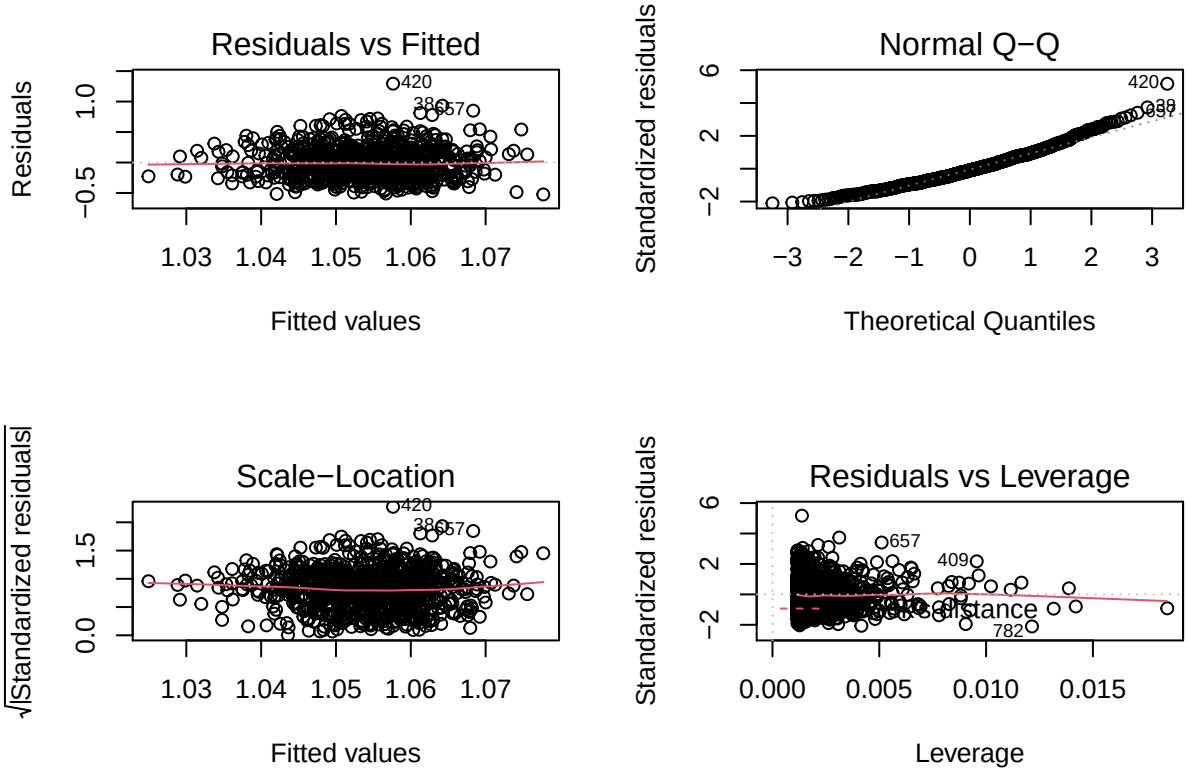
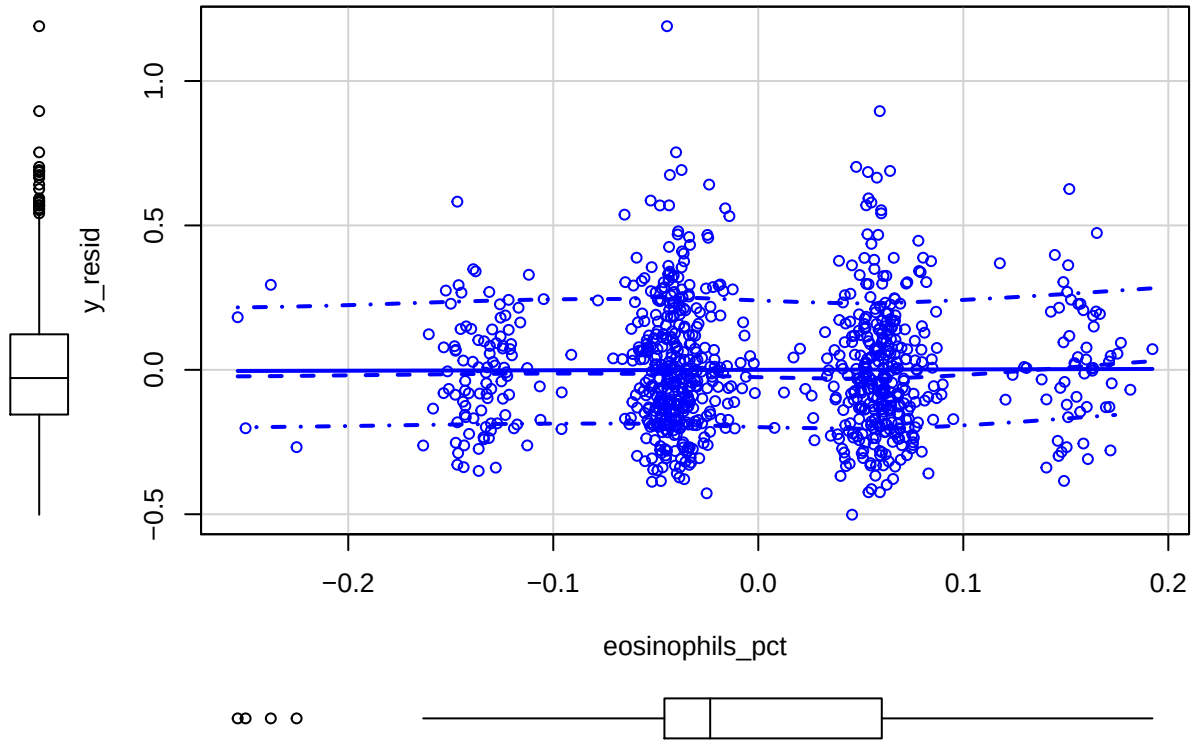
0.5
0.0
−0.5
−0.2
−0.1
0.0
0.1
0.2
monocyte_pct


Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
657
409
782
Leverage


y_resid
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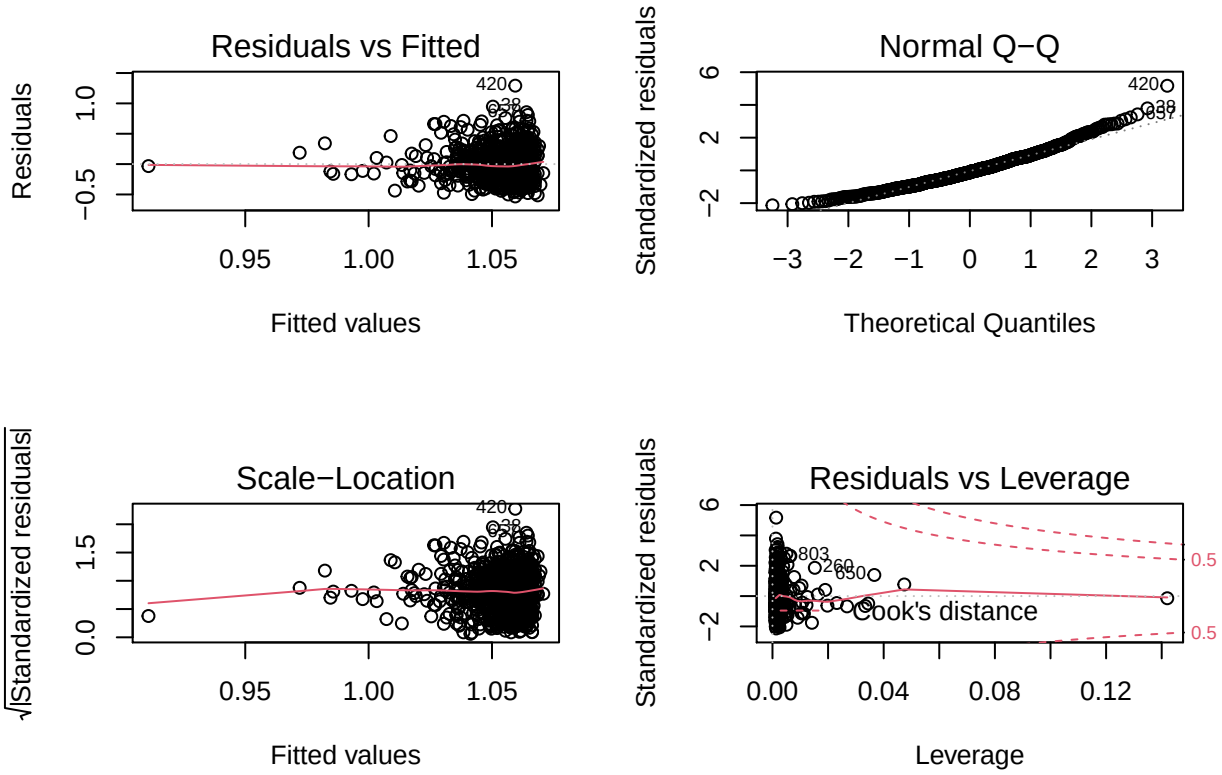
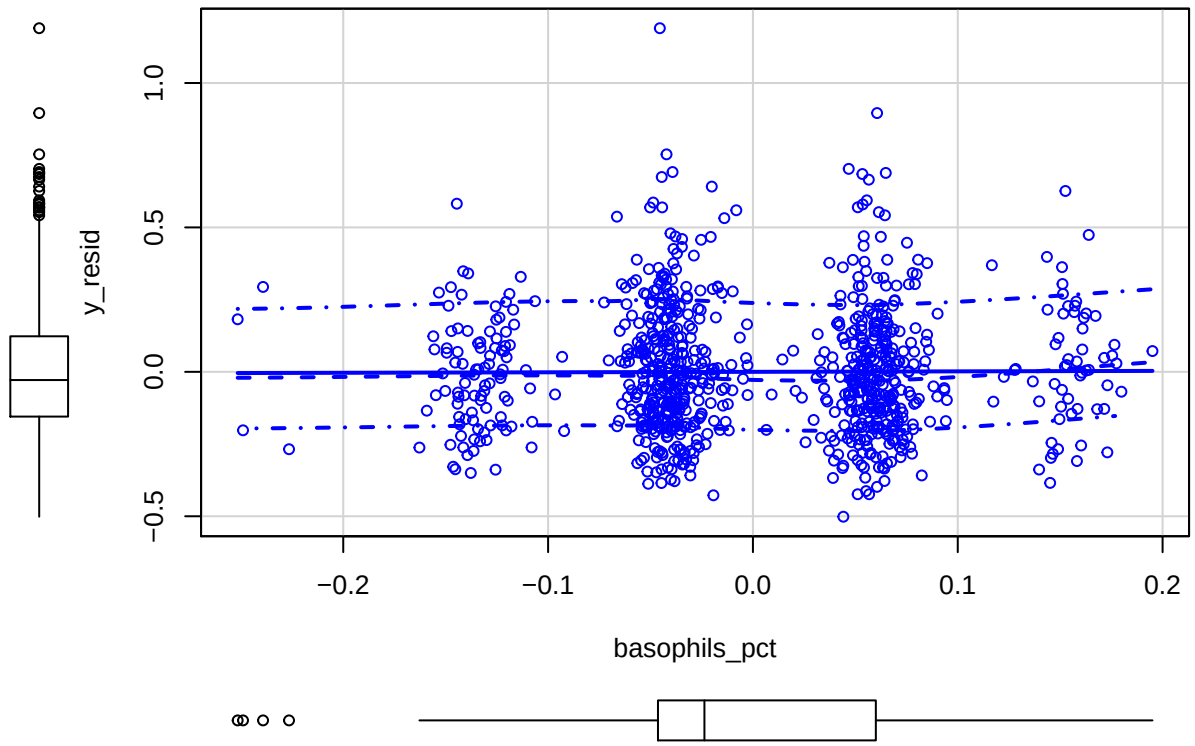
0.5
0.0
−0.5
−0.2
−0.1
0.0
0.1
0.2
eosinophils_pct


Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
Leverage
803
260
650
0.5


y_resid
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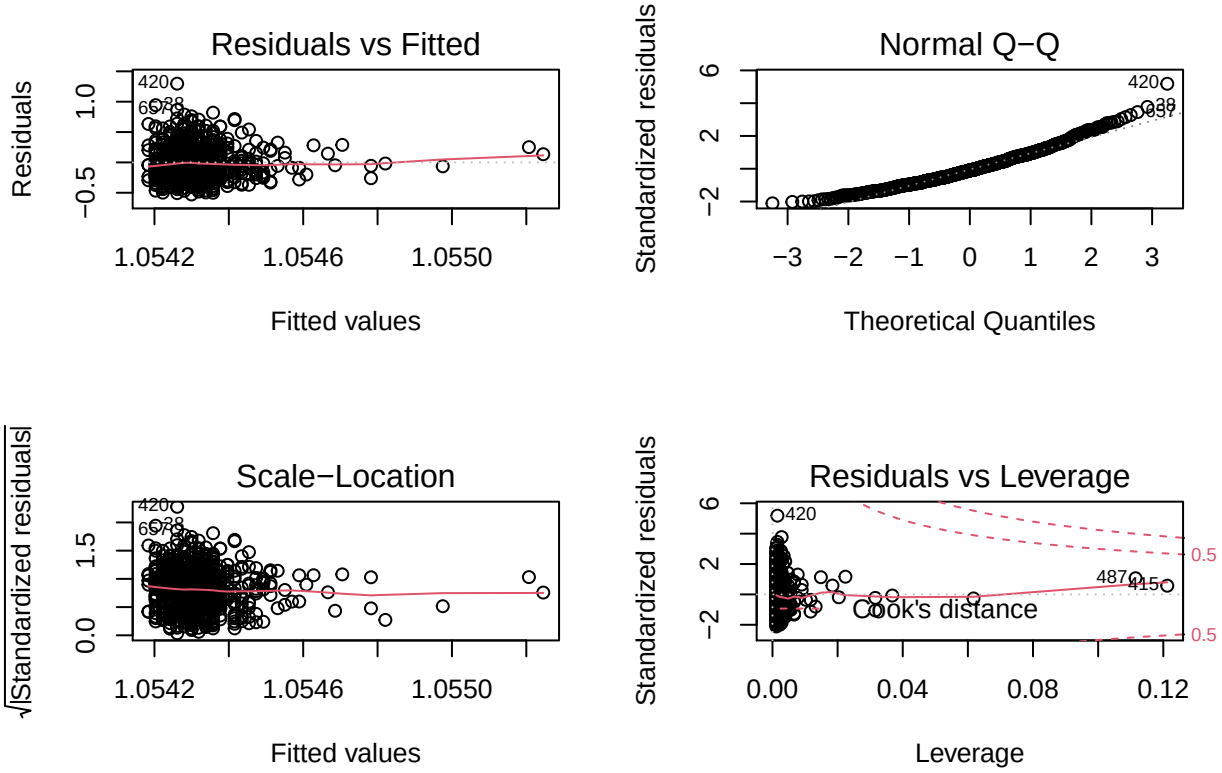
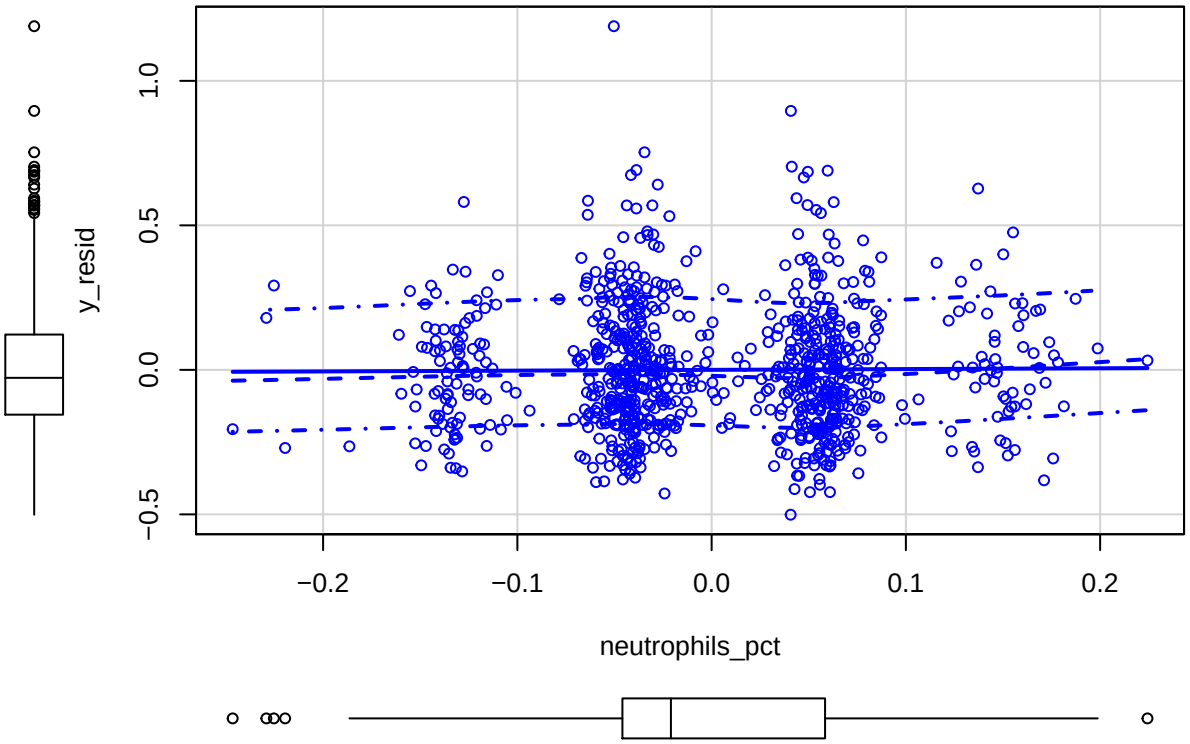
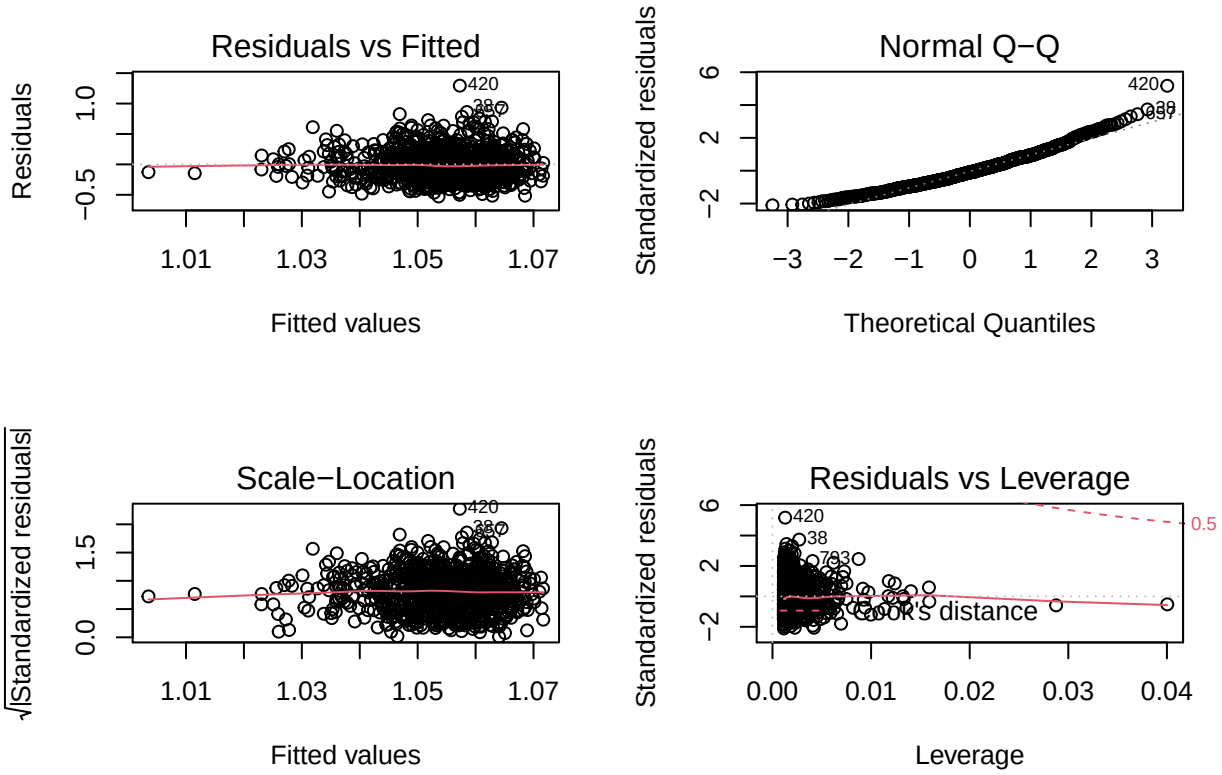
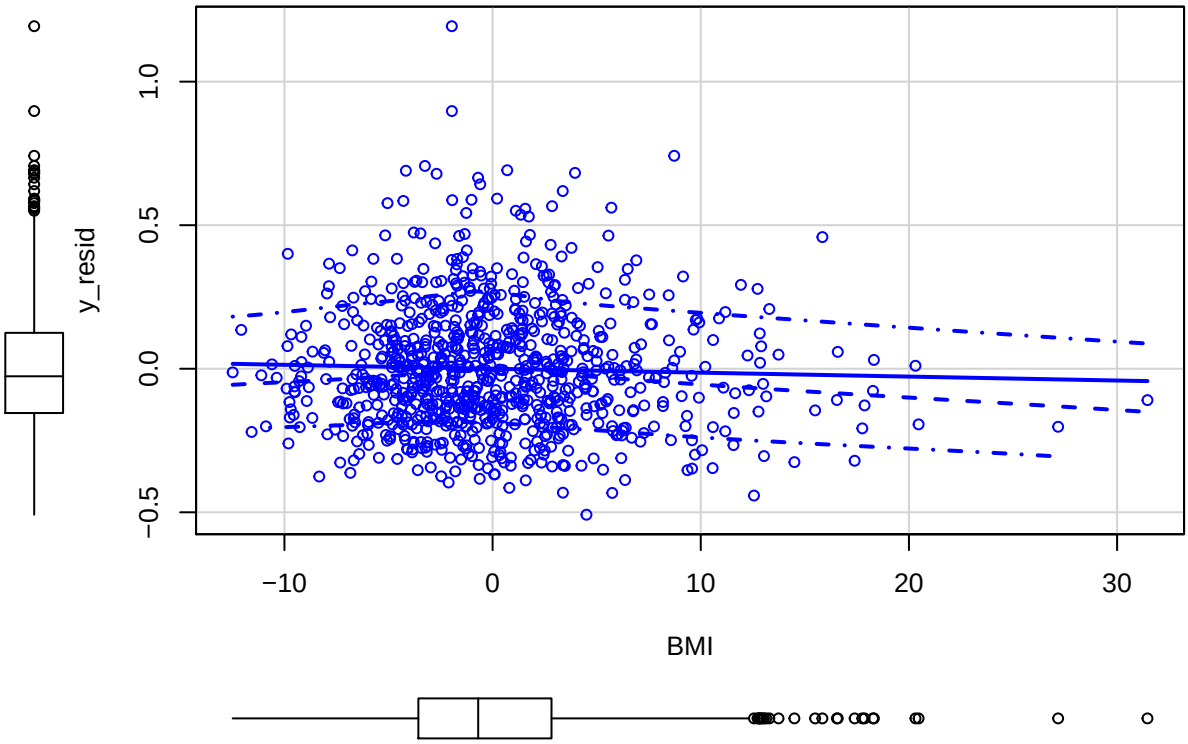
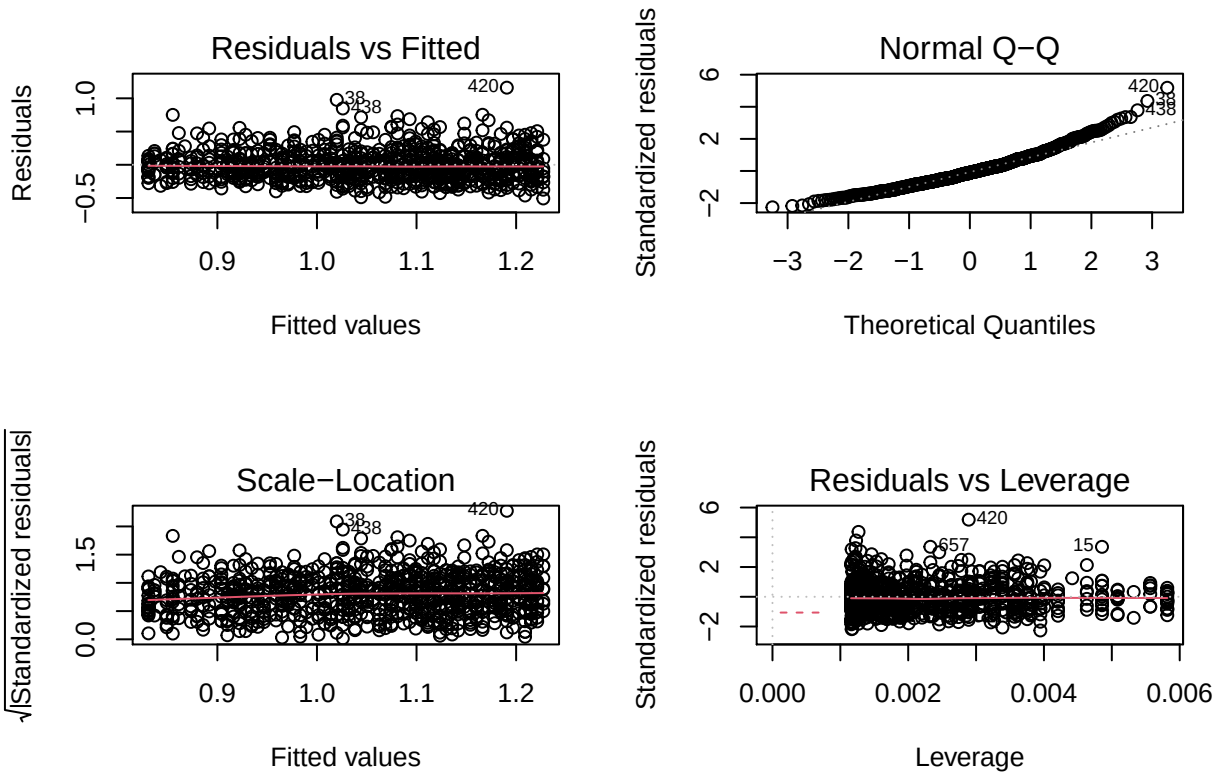
0.5
0.0
−0.5
−0.2
−0.1
0.0
0.1
0.2
basophils_pct

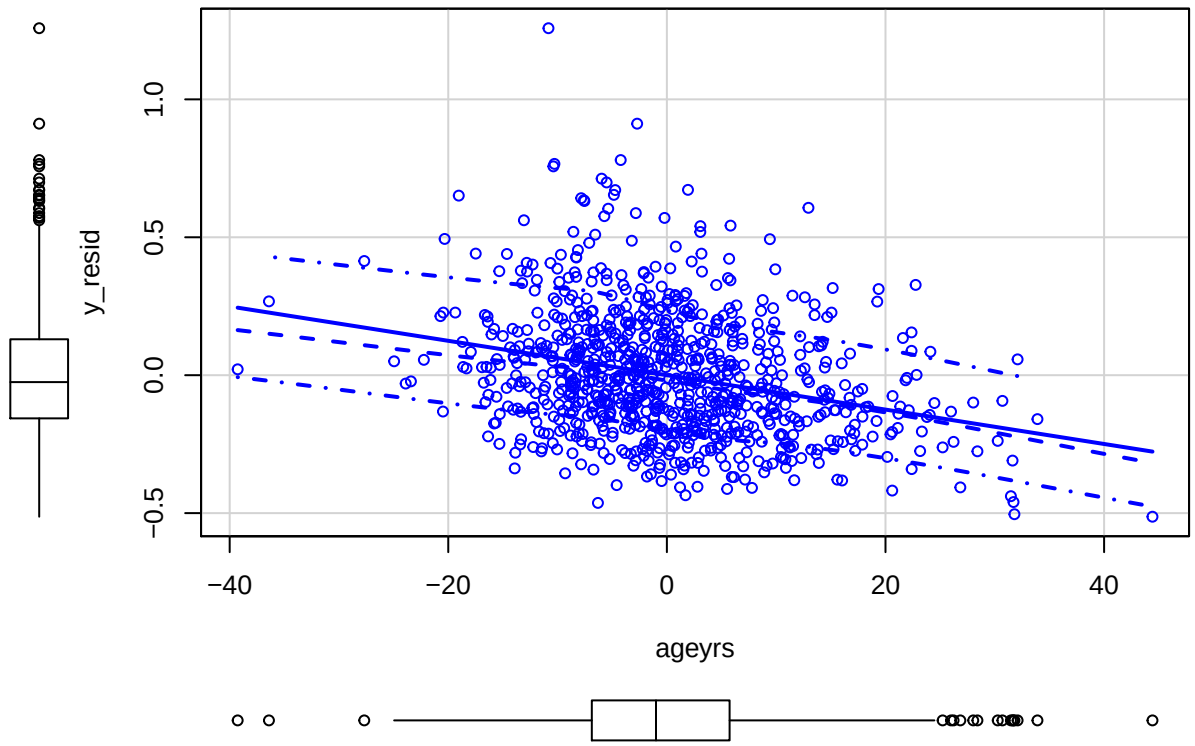

Residuals vs Fitted
Residuals
Fitted values
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Cook's distance
Leverage

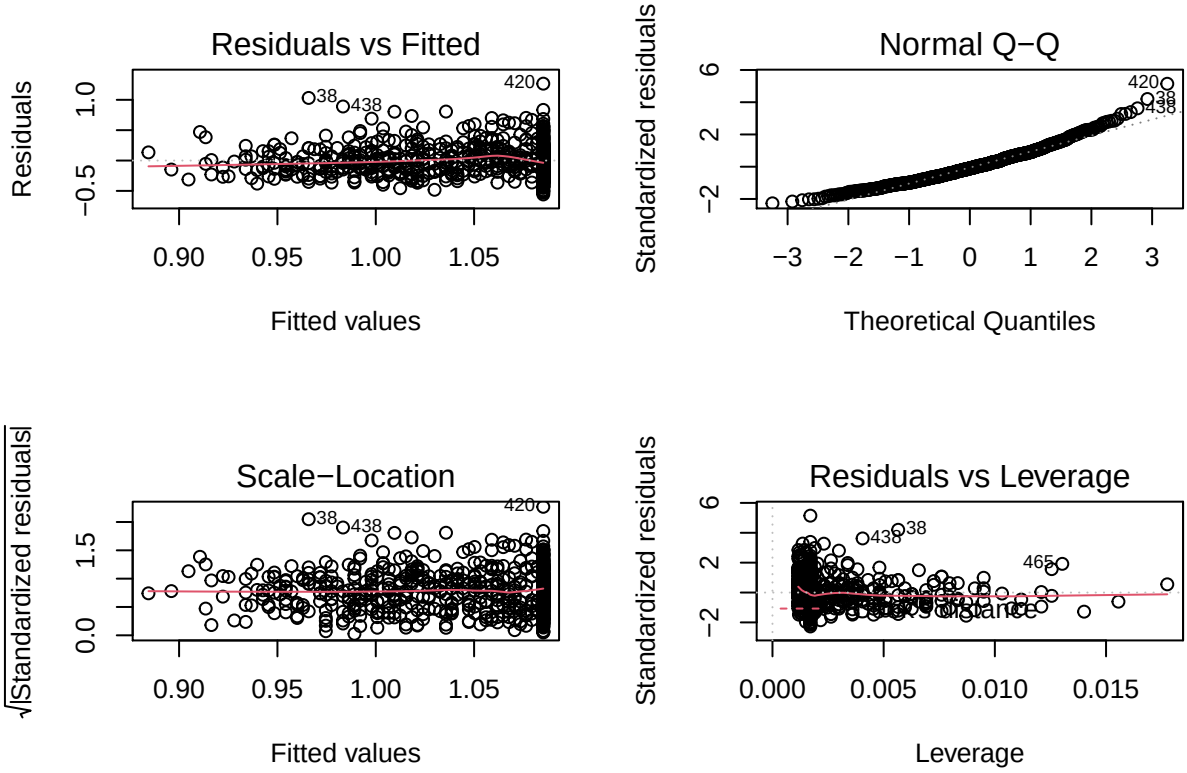

y_resid
1.0
0.5
0.0
−0.5
−0.2
−0.1
0.0
0.1
0.2
neutrophils_pct

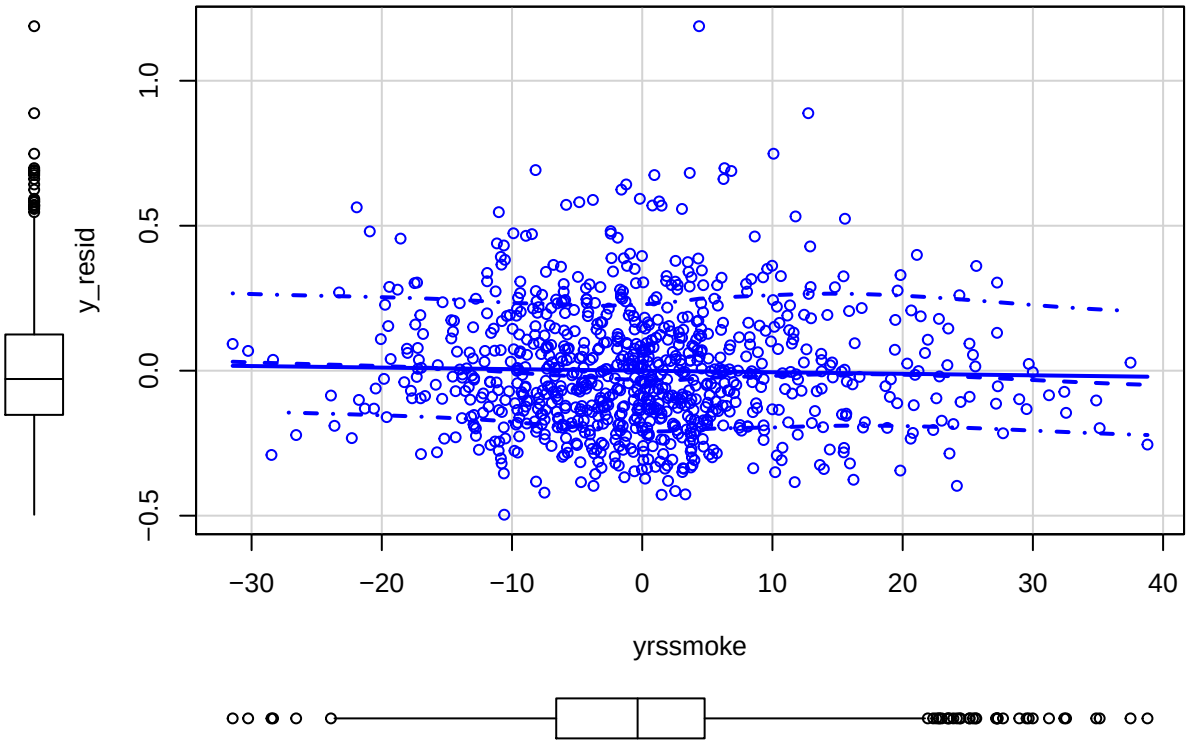

Residuals vs Fitted
Residuals
Fitted values
420
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
0.5
Leverage

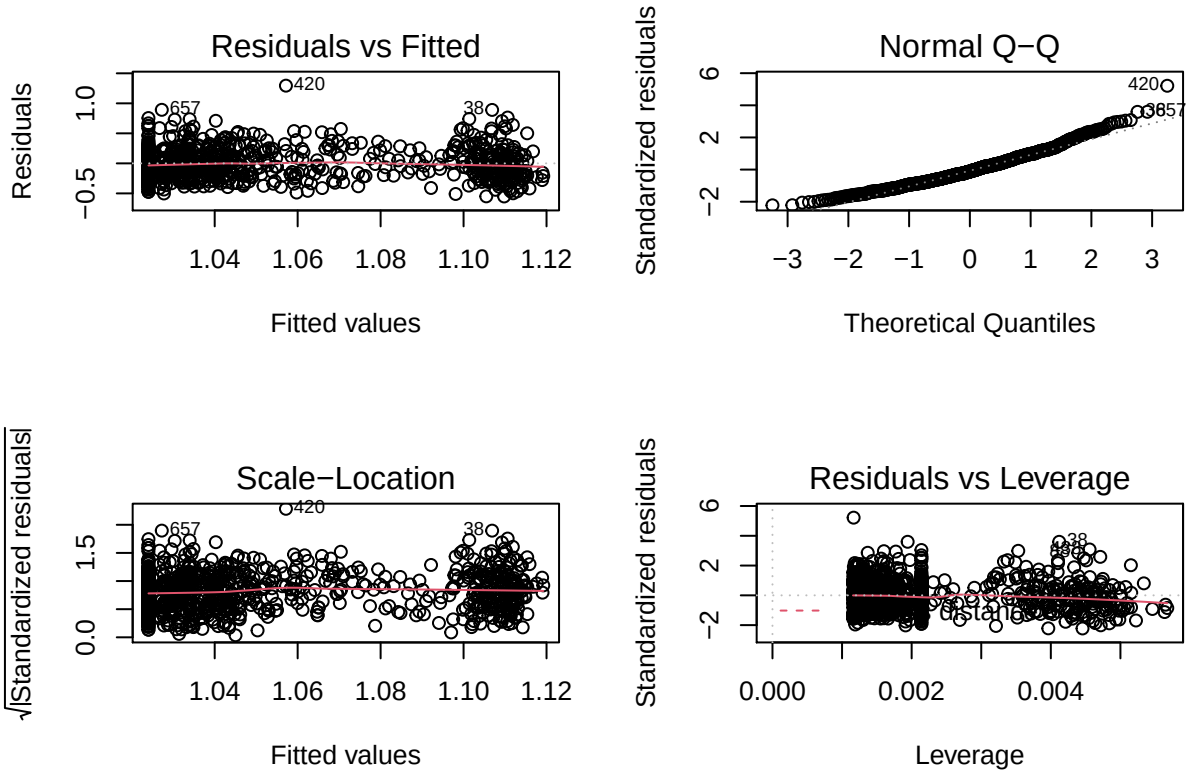

y_resid
1.0
0.5
0.0
−0.5
−10
0
10
20
30
BMI

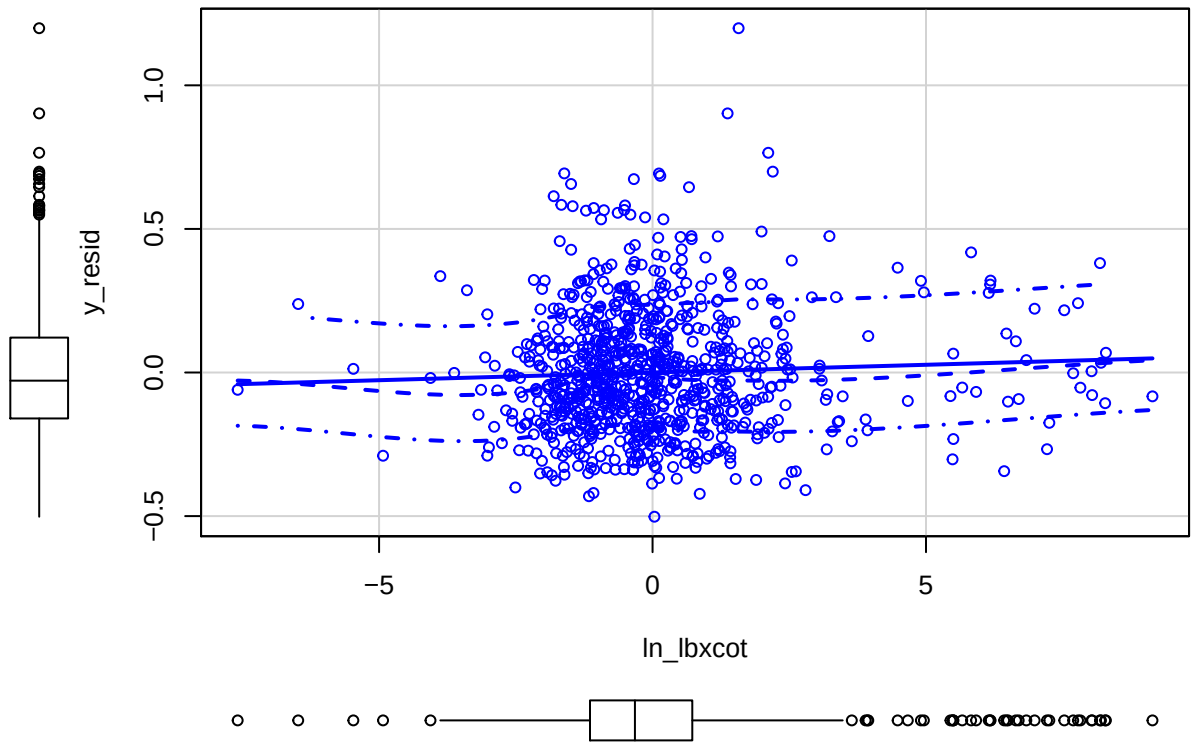

Residuals vs Fitted
Residuals
Fitted values
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
420
38
438
657
15


y_resid
1.0
0.5
0.0
−0.5
−40
−20
0
20
40
ageyrs


Residuals vs Fitted
Residuals
Fitted values
420
38
438
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Leverage
465


y_resid
1.0
0.5
0.0
−0.5
−30
−20
−10
0
10
20
30
40
yrssmoke


Residuals vs Fitted
Residuals
Fitted values
420
657
38
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Cook's distance
Leverage




```
#remove covariates with VIF > 10 below:

#remove highest vif ~ 15047
pollutants$eosinophils_pct = NULL
#fit new model
model = lm(length ~ .,data = pollutants)
#summary
summary(model)
```

```
##
## Call:
## lm(formula = length ~ ., data = pollutants)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.50160 -0.15463 -0.02843  0.12293  1.18974
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.491e+00  8.425e-02  17.693  < 2e-16 ***
## POP_PCB1        -1.606e-06  1.075e-06  -1.494   0.1355
## POP_PCB2         7.294e-07  3.021e-06   0.241   0.8093
## POP_PCB3         1.191e-06  2.156e-06   0.552   0.5809
## POP_PCB4        -1.774e-07  1.025e-06  -0.173   0.8627
## POP_PCB5         1.403e-07  1.068e-06   0.131   0.8955
## POP_PCB6         2.765e-07  1.058e-06   0.261   0.7939
```

```
## POP_PCB7        -5.739e-07  1.206e-06  -0.476   0.6343
## POP_PCB8         1.644e-06  2.446e-06   0.672   0.5016
## POP_PCB9         6.194e-07  2.111e-06   0.293   0.7693
## POP_PCB10        1.191e-03  8.890e-04   1.340   0.1806
## POP_PCB11        3.449e-05  3.078e-04   0.112   0.9108
## POP_dioxin1      3.072e-05  3.048e-04   0.101   0.9198
## POP_dioxin2     -1.744e-04  4.394e-04  -0.397   0.6916
## POP_dioxin3     -1.908e-05  3.018e-05  -0.632   0.5274
## POP_furan1       2.522e-03  3.844e-03   0.656   0.5119
## POP_furan2      -2.799e-04  4.500e-03  -0.062   0.9504
## POP_furan3       4.473e-03  2.756e-03   1.623   0.1049
## POP_furan4      -6.496e-04  9.195e-04  -0.706   0.4801
## whitecell_count -5.261e-03  4.404e-03  -1.195   0.2326
## lymphocyte_pct  -1.255e-03  1.030e-03  -1.219   0.2234
## monocyte_pct    -5.993e-03  4.041e-03  -1.483   0.1384
## basophils_pct    1.051e-03  3.475e-03   0.302   0.7624
## neutrophils_pct  1.213e-02  1.662e-02   0.730   0.4657
## BMI             -1.359e-03  1.409e-03  -0.964   0.3352
## edu_cat2         2.452e-02  2.215e-02   1.107   0.2687
## edu_cat3         4.787e-02  2.164e-02   2.212   0.0272 *
## edu_cat4         3.265e-02  2.555e-02   1.278   0.2016
## race_cat2       -2.195e-02  3.265e-02  -0.672   0.5016
## race_cat3        2.475e-02  3.370e-02   0.735   0.4628
## race_cat4       -3.473e-02  2.991e-02  -1.161   0.2460
## male1           -3.944e-02  1.771e-02  -2.227   0.0262 *
## ageyrs          -6.236e-03  7.442e-04  -8.380 2.25e-16 ***
## yrssmoke        -5.323e-04  7.271e-04  -0.732   0.4643
## smokenow1        2.172e-03  3.581e-02   0.061   0.9516
## ln_lbxcot        5.341e-03  3.922e-03   1.362   0.1736
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.222 on 828 degrees of freedom
## Multiple R-squared:  0.2448, Adjusted R-squared:  0.2129
## F-statistic: 7.668 on 35 and 828 DF,  p-value: < 2.2e-16
```

```
#show the VIF
vif(model)
```

```
##                     GVIF Df GVIF^(1/(2*Df))
## POP_PCB1       33.040956  1        5.748126
## POP_PCB2       34.276806  1        5.854640
## POP_PCB3        9.350969  1        3.057935
## POP_PCB4       31.734341  1        5.633324
## POP_PCB5       59.718357  1        7.727765
## POP_PCB6       11.386137  1        3.374335
## POP_PCB7        4.868942  1        2.206568
## POP_PCB8       12.982530  1        3.603128
## POP_PCB9       12.416573  1        3.523716
## POP_PCB10       5.988829  1        2.447208
## POP_PCB11       4.725385  1        2.173795
## POP_dioxin1     5.256334  1        2.292670
## POP_dioxin2     5.411476  1        2.326258
## POP_dioxin3     4.378774  1        2.092552
## POP_furan1      6.154213  1        2.480769
```

```
## POP_furan2       6.193725  1        2.488720
## POP_furan3       4.450557  1        2.109634
## POP_furan4       1.821773  1        1.349731
## whitecell_count  1.545798  1        1.243301
## lymphocyte_pct   1.382541  1        1.175815
## monocyte_pct     1.263611  1        1.124105
## basophils_pct    1.113199  1        1.055082
## neutrophils_pct  1.090031  1        1.044046
## BMI              1.261934  1        1.123358
## edu_cat          1.541083  3        1.074742
## race_cat         2.051619  3        1.127239
## male             1.350208  1        1.161984
## ageyrs           3.237762  1        1.799378
## yrssmoke         2.204134  1        1.484633
## smokenow         3.998531  1        1.999633
## ln_lbxcot        3.954234  1        1.988526
```

```
#remove highest vif eosinophils_pct ~ 15047 then POP_PCB5 ~ 59.718357
pollutants$POP_PCB5 = NULL
#fit new model
model = lm(length ~ .,data = pollutants)
#summary
summary(model)
```

```
##
## Call:
## lm(formula = length ~ ., data = pollutants)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.50233 -0.15456 -0.02848  0.12242  1.19007
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.491e+00  8.419e-02  17.706   <2e-16 ***
## POP_PCB1        -1.584e-06  1.061e-06  -1.493   0.1359
## POP_PCB2         8.659e-07  2.835e-06   0.305   0.7601
## POP_PCB3         1.229e-06  2.135e-06   0.575   0.5652
## POP_PCB4        -9.537e-08  8.129e-07  -0.117   0.9066
## POP_PCB6         3.209e-07  1.002e-06   0.320   0.7489
## POP_PCB7        -5.874e-07  1.201e-06  -0.489   0.6248
## POP_PCB8         1.574e-06  2.386e-06   0.660   0.5095
## POP_PCB9         7.223e-07  1.960e-06   0.369   0.7125
## POP_PCB10        1.211e-03  8.759e-04   1.382   0.1672
## POP_PCB11        2.293e-05  2.947e-04   0.078   0.9380
## POP_dioxin1      2.999e-05  3.046e-04   0.098   0.9216
## POP_dioxin2     -1.693e-04  4.374e-04  -0.387   0.6989
## POP_dioxin3     -1.949e-05  3.001e-05  -0.650   0.5161
## POP_furan1       2.449e-03  3.801e-03   0.644   0.5196
## POP_furan2      -2.463e-04  4.490e-03  -0.055   0.9563
## POP_furan3       4.477e-03  2.754e-03   1.626   0.1044
## POP_furan4      -6.429e-04  9.176e-04  -0.701   0.4837
## whitecell_count -5.303e-03  4.390e-03  -1.208   0.2274
## lymphocyte_pct  -1.254e-03  1.029e-03  -1.219   0.2233
## monocyte_pct    -5.978e-03  4.037e-03  -1.481   0.1390
```

```
## basophils_pct    1.012e-03  3.460e-03   0.292   0.7700
## neutrophils_pct  1.213e-02  1.661e-02   0.731   0.4653
## BMI             -1.357e-03  1.408e-03  -0.964   0.3356
## edu_cat2         2.450e-02  2.214e-02   1.107   0.2688
## edu_cat3         4.786e-02  2.163e-02   2.213   0.0272 *
## edu_cat4         3.284e-02  2.550e-02   1.288   0.1981
## race_cat2       -2.186e-02  3.263e-02  -0.670   0.5030
## race_cat3        2.503e-02  3.361e-02   0.745   0.4566
## race_cat4       -3.460e-02  2.988e-02  -1.158   0.2472
## male1           -3.945e-02  1.770e-02  -2.228   0.0261 *
## ageyrs          -6.237e-03  7.437e-04  -8.387   <2e-16 ***
## yrssmoke        -5.391e-04  7.248e-04  -0.744   0.4572
## smokenow1        2.165e-03  3.579e-02   0.061   0.9518
## ln_lbxcot        5.346e-03  3.919e-03   1.364   0.1729
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2219 on 829 degrees of freedom
## Multiple R-squared:  0.2448, Adjusted R-squared:  0.2138
## F-statistic: 7.902 on 34 and 829 DF,  p-value: < 2.2e-16
```

```
#show the VIF
vif(model)
```

```
##                     GVIF Df GVIF^(1/(2*Df))
## POP_PCB1       32.255513  1        5.679394
## POP_PCB2       30.220860  1        5.497350
## POP_PCB3        9.182804  1        3.030314
## POP_PCB4       19.965194  1        4.468243
## POP_PCB6       10.226099  1        3.197827
## POP_PCB7        4.833396  1        2.198498
## POP_PCB8       12.363256  1        3.516142
## POP_PCB9       10.707771  1        3.272273
## POP_PCB10       5.820661  1        2.412605
## POP_PCB11       4.338648  1        2.082942
## POP_dioxin1     5.254606  1        2.292293
## POP_dioxin2     5.368810  1        2.317069
## POP_dioxin3     4.332013  1        2.081349
## POP_furan1      6.023932  1        2.454370
## POP_furan2      6.173626  1        2.484678
## POP_furan3      4.450098  1        2.109526
## POP_furan4      1.816182  1        1.347658
## whitecell_count 1.537750  1        1.240060
## lymphocyte_pct  1.382511  1        1.175802
## monocyte_pct    1.262603  1        1.123656
## basophils_pct   1.105130  1        1.051251
## neutrophils_pct 1.090023  1        1.044042
## BMI             1.261809  1        1.123303
## edu_cat         1.533185  3        1.073822
## race_cat        2.042113  3        1.126367
## male            1.350206  1        1.161984
## ageyrs          3.237570  1        1.799325
## yrssmoke        2.192917  1        1.480850
## smokenow        3.998522  1        1.999630
## ln_lbxcot       3.953781  1        1.988412
```

```r
#remove highest vif eosinophils_pct ~ 15047 then POP_PCB5 ~ 59.718357 then POP_PCB1 ~ 32.255513
pollutants$POP_PCB1 = NULL
#fit new model
model = lm(length ~ .,data = pollutants)
#summary
summary(model)
```

```
##
## Call:
## lm(formula = length ~ ., data = pollutants)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.49329 -0.15025 -0.02981  0.12229  1.18766
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       1.505e+00  8.371e-02  17.977   <2e-16 ***
## POP_PCB2         -1.264e-06  2.451e-06  -0.516   0.6062
## POP_PCB3          1.587e-06  2.123e-06   0.747   0.4551
## POP_PCB4         -2.160e-07  8.094e-07  -0.267   0.7896
## POP_PCB6          1.820e-07  9.987e-07   0.182   0.8555
## POP_PCB7         -6.786e-07  1.200e-06  -0.565   0.5719
## POP_PCB8         -1.708e-07  2.081e-06  -0.082   0.9346
## POP_PCB9         -8.899e-09  1.899e-06  -0.005   0.9963
## POP_PCB10         1.035e-03  8.686e-04   1.192   0.2337
## POP_PCB11         9.381e-05  2.911e-04   0.322   0.7473
## POP_dioxin1       3.693e-05  3.048e-04   0.121   0.9036
## POP_dioxin2      -1.018e-04  4.354e-04  -0.234   0.8152
## POP_dioxin3      -1.942e-05  3.003e-05  -0.647   0.5179
## POP_furan1        2.488e-03  3.804e-03   0.654   0.5132
## POP_furan2       -5.409e-04  4.489e-03  -0.120   0.9041
## POP_furan3        4.497e-03  2.756e-03   1.632   0.1032
## POP_furan4       -6.516e-04  9.182e-04  -0.710   0.4781
## whitecell_count  -5.516e-03  4.391e-03  -1.256   0.2094
## lymphocyte_pct   -1.382e-03  1.026e-03  -1.347   0.1784
## monocyte_pct     -5.839e-03  4.039e-03  -1.446   0.1486
## basophils_pct     1.159e-03  3.462e-03   0.335   0.7377
## neutrophils_pct   1.127e-02  1.661e-02   0.678   0.4978
## BMI              -1.358e-03  1.409e-03  -0.964   0.3354
## edu_cat2          2.226e-02  2.211e-02   1.007   0.3143
## edu_cat3          4.353e-02  2.145e-02   2.030   0.0427 *
## edu_cat4          2.960e-02  2.542e-02   1.164   0.2447
## race_cat2        -2.335e-02  3.263e-02  -0.716   0.4744
## race_cat3         2.489e-02  3.363e-02   0.740   0.4596
## race_cat4        -3.529e-02  2.990e-02  -1.181   0.2381
## male1            -3.992e-02  1.771e-02  -2.254   0.0245 *
## ageyrs           -6.298e-03  7.431e-04  -8.476   <2e-16 ***
## yrssmoke         -4.629e-04  7.236e-04  -0.640   0.5225
## smokenow1         7.390e-04  3.580e-02   0.021   0.9835
## ln_lbxcot         5.387e-03  3.922e-03   1.374   0.1699
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 0.222 on 830 degrees of freedom
## Multiple R-squared:  0.2427, Adjusted R-squared:  0.2126
## F-statistic: 8.062 on 33 and 830 DF,  p-value: < 2.2e-16
```

```
#show the VIF
vif(model)
```

```
##                      GVIF Df GVIF^(1/(2*Df))
## POP_PCB2        22.564616  1        4.750223
## POP_PCB3         9.066898  1        3.011129
## POP_PCB4        19.767850  1        4.446105
## POP_PCB6        10.137933  1        3.184012
## POP_PCB7         4.820891  1        2.195653
## POP_PCB8         9.395135  1        3.065148
## POP_PCB9        10.038785  1        3.168404
## POP_PCB10        5.715628  1        2.390738
## POP_PCB11        4.226036  1        2.055733
## POP_dioxin1      5.253381  1        2.292026
## POP_dioxin2      5.311508  1        2.304671
## POP_dioxin3      4.332003  1        2.081346
## POP_furan1       6.023639  1        2.454310
## POP_furan2       6.161696  1        2.482276
## POP_furan3       4.449999  1        2.109502
## POP_furan4       1.816107  1        1.347630
## whitecell_count  1.536123  1        1.239404
## lymphocyte_pct   1.372891  1        1.171704
## monocyte_pct     1.261930  1        1.123356
## basophils_pct    1.104229  1        1.050823
## neutrophils_pct  1.088688  1        1.043402
## BMI              1.261809  1        1.123303
## edu_cat          1.504890  3        1.070494
## race_cat         2.039232  3        1.126102
## male             1.349779  1        1.161800
## ageyrs           3.227727  1        1.796588
## yrssmoke         2.182035  1        1.477171
## smokenow         3.995671  1        1.998918
## ln_lbxcot        3.953587  1        1.988363
```

```
#remove highest vif eosinophils_pct ~ 15047 then POP_PCB5 ~ 59.718357 then POP_PCB1 ~ 32.255513 then PO
pollutants$POP_PCB2 = NULL
#fit new model
model = lm(length ~ .,data = pollutants)
#summary
summary(model)
```

```
##
## Call:
## lm(formula = length ~ ., data = pollutants)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.49387 -0.15104 -0.02904  0.12181  1.18897
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.502e+00  8.354e-02  17.985   <2e-16 ***
```

```
## POP_PCB3         1.846e-06  2.062e-06   0.895   0.3709
## POP_PCB4        -4.363e-07  6.872e-07  -0.635   0.5256
## POP_PCB6         3.180e-07  9.628e-07   0.330   0.7413
## POP_PCB7        -7.809e-07  1.183e-06  -0.660   0.5094
## POP_PCB8        -8.255e-07  1.648e-06  -0.501   0.6166
## POP_PCB9        -3.387e-07  1.787e-06  -0.190   0.8497
## POP_PCB10        9.249e-04  8.414e-04   1.099   0.2720
## POP_PCB11        9.491e-05  2.909e-04   0.326   0.7444
## POP_dioxin1      1.933e-05  3.028e-04   0.064   0.9491
## POP_dioxin2     -1.104e-04  4.349e-04  -0.254   0.7997
## POP_dioxin3     -1.856e-05  2.997e-05  -0.619   0.5359
## POP_furan1       2.570e-03  3.799e-03   0.677   0.4989
## POP_furan2      -6.152e-04  4.485e-03  -0.137   0.8909
## POP_furan3       4.443e-03  2.753e-03   1.614   0.1069
## POP_furan4      -6.314e-04  9.170e-04  -0.689   0.4913
## whitecell_count -5.469e-03  4.388e-03  -1.246   0.2130
## lymphocyte_pct  -1.364e-03  1.025e-03  -1.330   0.1838
## monocyte_pct    -5.733e-03  4.032e-03  -1.422   0.1554
## basophils_pct    1.182e-03  3.460e-03   0.342   0.7326
## neutrophils_pct  1.103e-02  1.660e-02   0.664   0.5066
## BMI             -1.332e-03  1.408e-03  -0.946   0.3445
## edu_cat2         2.268e-02  2.208e-02   1.027   0.3046
## edu_cat3         4.375e-02  2.143e-02   2.041   0.0416 *
## edu_cat4         2.929e-02  2.541e-02   1.153   0.2494
## race_cat2       -2.311e-02  3.262e-02  -0.709   0.4788
## race_cat3        2.558e-02  3.359e-02   0.761   0.4466
## race_cat4       -3.492e-02  2.987e-02  -1.169   0.2428
## male1           -3.975e-02  1.770e-02  -2.246   0.0250 *
## ageyrs          -6.308e-03  7.425e-04  -8.495   <2e-16 ***
## yrssmoke        -4.532e-04  7.230e-04  -0.627   0.5310
## smokenow1       -5.910e-04  3.569e-02  -0.017   0.9868
## ln_lbxcot        5.473e-03  3.917e-03   1.397   0.1626
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2219 on 831 degrees of freedom
## Multiple R-squared:  0.2425, Adjusted R-squared:  0.2133
## F-statistic: 8.313 on 32 and 831 DF,  p-value: < 2.2e-16
```

```
#show the VIF
vif(model)
```

```
##                     GVIF Df GVIF^(1/(2*Df))
## POP_PCB3        8.558618  1        2.925512
## POP_PCB4       14.260201  1        3.776268
## POP_PCB6        9.430583  1        3.070925
## POP_PCB7        4.689281  1        2.165475
## POP_PCB8        5.899020  1        2.428790
## POP_PCB9        8.900140  1        2.983310
## POP_PCB10       5.368201  1        2.316938
## POP_PCB11       4.225811  1        2.055678
## POP_dioxin1     5.187456  1        2.277599
## POP_dioxin2     5.303754  1        2.302988
## POP_dioxin3     4.318541  1        2.078110
## POP_furan1      6.013167  1        2.452176
```

```
## POP_furan2       6.155357  1        2.480999
## POP_furan3       4.443638  1        2.107994
## POP_furan4       1.812808  1        1.346405
## whitecell_count  1.535444  1        1.239130
## lymphocyte_pct   1.371183  1        1.170975
## monocyte_pct     1.258625  1        1.121885
## basophils_pct    1.104048  1        1.050737
## neutrophils_pct  1.087848  1        1.042999
## BMI              1.260084  1        1.122535
## edu_cat          1.499070  3        1.069803
## race_cat         2.035520  3        1.125760
## male             1.349340  1        1.161611
## ageyrs           3.225616  1        1.796000
## yrssmoke         2.180551  1        1.476669
## smokenow         3.974936  1        1.993724
## ln_lbxcot        3.946444  1        1.986566
```

```
#remove highest vif eosinophils_pct ~ 15047 then POP_PCB5 ~ 59.718357 then POP_PCB1 ~ 32.255513 then PO
# then POP_PCB4 ~ 14.260201
pollutants$POP_PCB4 = NULL
#fit new model
model = lm(length ~ .,data = pollutants)
#summary
summary(model)
```

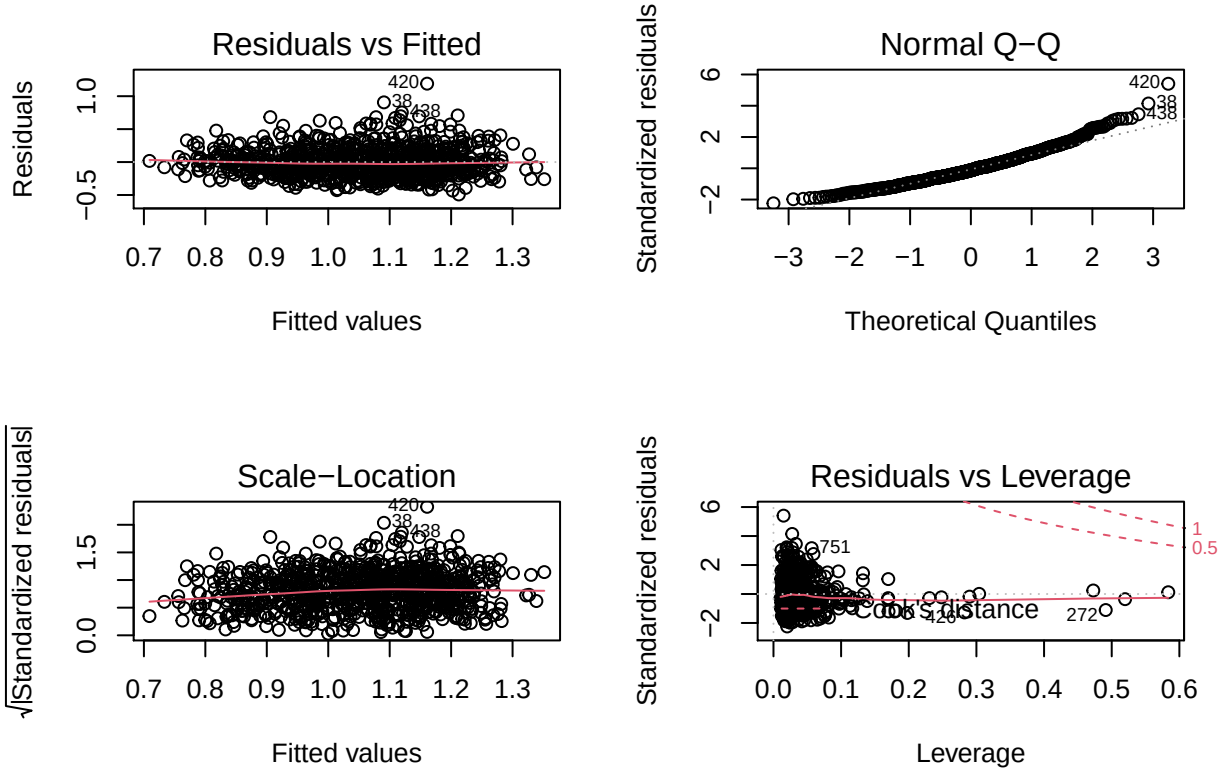
```
##
## Call:
## lm(formula = length ~ ., data = pollutants)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.49174 -0.15062 -0.02829  0.12117  1.19031
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.505e+00  8.339e-02  18.048   <2e-16 ***
## POP_PCB3         1.039e-06  1.624e-06   0.640   0.5223
## POP_PCB6         2.008e-07  9.446e-07   0.213   0.8317
## POP_PCB7        -7.992e-07  1.182e-06  -0.676   0.4993
## POP_PCB8        -7.951e-07  1.647e-06  -0.483   0.6294
## POP_PCB9        -7.655e-07  1.655e-06  -0.463   0.6438
## POP_PCB10        8.170e-04  8.238e-04   0.992   0.3216
## POP_PCB11        8.365e-05  2.903e-04   0.288   0.7733
## POP_dioxin1      2.403e-05  3.026e-04   0.079   0.9367
## POP_dioxin2     -1.306e-04  4.336e-04  -0.301   0.7633
## POP_dioxin3     -1.933e-05  2.993e-05  -0.646   0.5185
## POP_furan1       2.682e-03  3.793e-03   0.707   0.4797
## POP_furan2      -5.840e-04  4.483e-03  -0.130   0.8964
## POP_furan3       4.589e-03  2.742e-03   1.673   0.0946 .
## POP_furan4      -6.331e-04  9.166e-04  -0.691   0.4900
## whitecell_count -5.564e-03  4.384e-03  -1.269   0.2047
## lymphocyte_pct  -1.355e-03  1.025e-03  -1.323   0.1863
## monocyte_pct    -5.859e-03  4.025e-03  -1.456   0.1459
## basophils_pct    1.356e-03  3.448e-03   0.393   0.6941
## neutrophils_pct  1.038e-02  1.656e-02   0.627   0.5311
```

```
## BMI             -1.292e-03  1.406e-03  -0.919   0.3585
## edu_cat2         2.258e-02  2.207e-02   1.023   0.3066
## edu_cat3         4.383e-02  2.143e-02   2.046   0.0411 *
## edu_cat4         2.954e-02  2.539e-02   1.163   0.2450
## race_cat2       -2.332e-02  3.260e-02  -0.715   0.4746
## race_cat3        2.375e-02  3.346e-02   0.710   0.4780
## race_cat4       -3.549e-02  2.985e-02  -1.189   0.2348
## male1           -4.034e-02  1.767e-02  -2.282   0.0227 *
## ageyrs          -6.317e-03  7.421e-04  -8.512   <2e-16 ***
## yrssmoke        -5.096e-04  7.173e-04  -0.710   0.4776
## smokenow1        4.148e-04  3.564e-02   0.012   0.9907
## ln_lbxcot        5.455e-03  3.915e-03   1.393   0.1639
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2219 on 832 degrees of freedom
## Multiple R-squared:  0.2421, Adjusted R-squared:  0.2139
## F-statistic: 8.574 on 31 and 832 DF,  p-value: < 2.2e-16
```

```
#show the VIF
vif(model)
```

```
##                     GVIF Df GVIF^(1/(2*Df))
## POP_PCB3        5.310340  1        2.304417
## POP_PCB6        9.083828  1        3.013939
## POP_PCB7        4.686485  1        2.164829
## POP_PCB8        5.894052  1        2.427767
## POP_PCB9        7.640480  1        2.764142
## POP_PCB10       5.149483  1        2.269247
## POP_PCB11       4.210120  1        2.051858
## POP_dioxin1     5.184345  1        2.276916
## POP_dioxin2     5.275271  1        2.296796
## POP_dioxin3     4.311410  1        2.076394
## POP_furan1      6.000097  1        2.449509
## POP_furan2      6.154621  1        2.480851
## POP_furan3      4.412739  1        2.100652
## POP_furan4      1.812793  1        1.346400
## whitecell_count 1.533642  1        1.238403
## lymphocyte_pct  1.370966  1        1.170882
## monocyte_pct    1.255543  1        1.120510
## basophils_pct   1.097132  1        1.047441
## neutrophils_pct 1.083675  1        1.040997
## BMI             1.257562  1        1.121411
## edu_cat         1.498239  3        1.069704
## race_cat        2.012804  3        1.123657
## male            1.345703  1        1.160045
## ageyrs          3.224432  1        1.795670
## yrssmoke        2.147610  1        1.465473
## smokenow        3.967106  1        1.991759
## ln_lbxcot       3.946223  1        1.986510
```

```
#find the model fit for homoscedasticity before remove multicolinearity
par(mfrow=c(2,2))
plot(model)
```



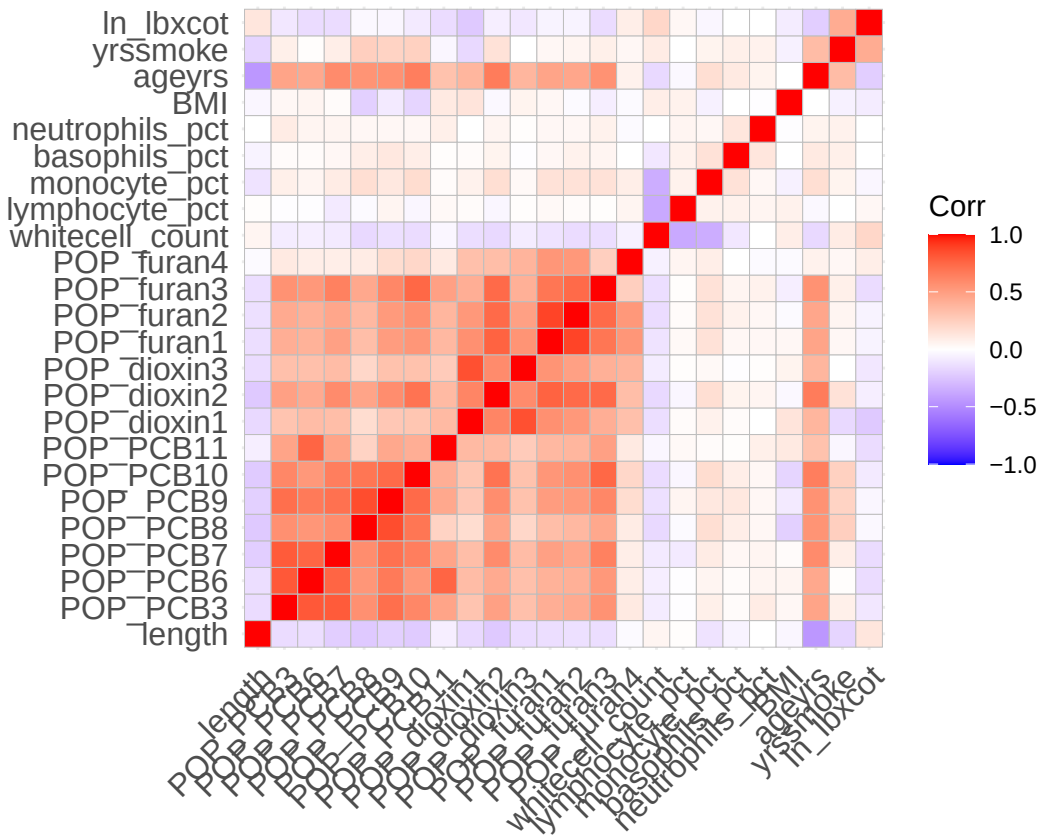

```
par(mfrow=c(1,1))

#get set a dataset with no categorical covariates
no_cat = pollutants
no_cat$edu_cat = NULL
no_cat$race_cat = NULL
no_cat$male = NULL
no_cat$smokenow = NULL
#summary of the dataset
summary(no_cat)
```

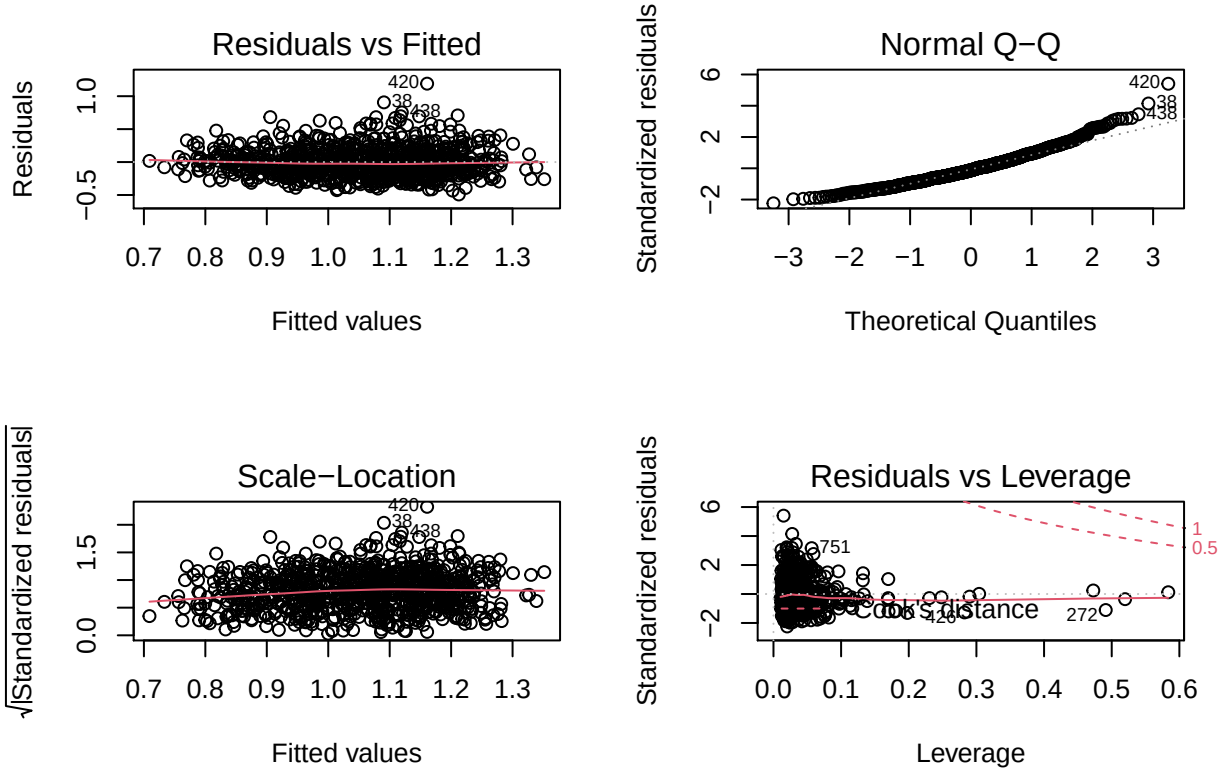
```
##      length          POP_PCB3         POP_PCB6         POP_PCB7
##  Min.   :0.5266   Min.   :  2000   Min.   :  2000   Min.   :  1100
##  1st Qu.:0.8754   1st Qu.:  3700   1st Qu.:  4400   1st Qu.:  4000
##  Median :1.0286   Median :  6200   Median :  9400   Median :  7450
##  Mean   :1.0543   Mean   : 10158   Mean   : 16820   Mean   : 12682
##  3rd Qu.:1.2095   3rd Qu.: 12000   3rd Qu.: 19500   3rd Qu.: 15625
##  Max.   :2.3512   Max.   :123000   Max.   :319000   Max.   :144000
##     POP_PCB8         POP_PCB9        POP_PCB10        POP_PCB11
##  Min.   :  1100   Min.   :  1100   Min.   :  1.70   Min.   :  1.30
##  1st Qu.:  3800   1st Qu.:  3900   1st Qu.:  9.10   1st Qu.: 14.80
##  Median :  6950   Median :  8050   Median : 18.35   Median : 24.50
##  Mean   : 10530   Mean   : 12220   Mean   : 24.49   Mean   : 38.15
##  3rd Qu.: 14425   3rd Qu.: 16025   3rd Qu.: 34.90   3rd Qu.: 42.95
##  Max.   :187000   Max.   :144000   Max.   :172.00   Max.   :845.00
##   POP_dioxin1      POP_dioxin2      POP_dioxin3      POP_furan1
```

```
##  Min.   :  1.90   Min.   :  1.40   Min.   :  36.8   Min.   : 1.000
##  1st Qu.: 23.90   1st Qu.: 21.27   1st Qu.: 197.0   1st Qu.: 3.200
##  Median : 41.35   Median : 37.80   Median : 342.5   Median : 5.200
##  Mean   : 57.65   Mean   : 47.81   Mean   : 494.4   Mean   : 6.371
##  3rd Qu.: 71.62   3rd Qu.: 62.42   3rd Qu.: 603.0   3rd Qu.: 7.700
##  Max.   :760.00   Max.   :281.00   Max.   :8190.0   Max.   :44.400
##    POP_furan2       POP_furan3       POP_furan4     whitecell_count
##  Min.   : 0.800   Min.   : 0.700   Min.   :  0.90   Min.   : 2.300
##  1st Qu.: 2.600   1st Qu.: 2.200   1st Qu.:  6.40   1st Qu.: 5.600
##  Median : 4.200   Median : 5.050   Median :  9.65   Median : 6.900
##  Mean   : 5.390   Mean   : 6.669   Mean   : 11.54   Mean   : 7.191
##  3rd Qu.: 6.825   3rd Qu.: 9.300   3rd Qu.: 14.00   3rd Qu.: 8.300
##  Max.   :33.500   Max.   :38.300   Max.   :234.00   Max.   :20.100
##  lymphocyte_pct   monocyte_pct    basophils_pct    neutrophils_pct
##  Min.   : 5.80   Min.   : 1.600   Min.   : 0.000   Min.   :0.0000
##  1st Qu.:24.00   1st Qu.: 6.600   1st Qu.: 1.500   1st Qu.:0.4000
##  Median :28.95   Median : 7.700   Median : 2.300   Median :0.6000
##  Mean   :29.92   Mean   : 7.936   Mean   : 2.903   Mean   :0.6669
##  3rd Qu.:35.42   3rd Qu.: 9.100   3rd Qu.: 3.700   3rd Qu.:0.8000
##  Max.   :73.40   Max.   :23.800   Max.   :28.200   Max.   :5.5000
##       BMI            ageyrs         yrssmoke      ln_lbxcot
##  Min.   :16.16   Min.   :20.00   Min.   : 0.0   Min.   :-4.5099
##  1st Qu.:23.88   1st Qu.:34.00   1st Qu.: 0.0   1st Qu.:-4.0745
##  Median :27.38   Median :46.00   Median : 0.0   Median :-2.7334
##  Mean   :28.09   Mean   :48.36   Mean   :10.6   Mean   :-0.9804
##  3rd Qu.:31.17   3rd Qu.:63.00   3rd Qu.:20.0   3rd Qu.: 2.8000
##  Max.   :62.99   Max.   :85.00   Max.   :69.0   Max.   : 6.5848
```

```
#calculate correlation matrix
corr_matrix = cor(no_cat)
#graph colored corr matrix
ggcorrplot(corr_matrix)
```




```
#find the model fit for homoscedasticity after removing multicolinearity
par(mfrow=c(2,2))
plot(model)
```




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

#set up train and test model
data = model.matrix(length ~ ., data = pollutants)
n = nrow(data)
#set seed for sample and
set.seed(331)
#get index for random train and test index (90% train, 10% test)
train_row = sample(1:n, 0.9*n)
#train set
x_matrix = data[,-1]
y_matrix = pollutants$length

#get the y values
train_y = y_matrix[train_row]
#get the x values
train_x = x_matrix[train_row,]
#get the y values
test_y = y_matrix[-train_row]
#get the x values
test_x = x_matrix[-train_row,]

eval_results <- function(true, predicted, df){
  SSE <- sum((predicted - true)^2)
  SST <- sum((true - mean(true))^2)
  R_square <- 1 - SSE / SST
```

```
  RMSE = sqrt(SSE/nrow(df))


  # Model performance metrics
  data.frame(
    RMSE = RMSE,
    Rsquare = R_square)
}

#k fold lasso
lambdas <- 10^seq(2, -4, by = -.0001)
lasso = cv.glmnet(train_x, train_y, alpha = 1, lambda = lambdas)
best_lam = lasso$lambda.min
best_lam
```

```
## [1] 0.008386872
```

```
#use lasso with best lambda
best_lasso = glmnet(train_x, train_y, alpha = 1, lambda = best_lam)
#predict with lasso result with training set
pred_train = predict(best_lasso, s = best_lam, newx = train_x)
eval_results(train_y, pred_train, train_x)
```

```
##        RMSE   Rsquare
## 1 0.2201948 0.2180372
```

```
#predict with lasso result with test set
pred_train = predict(best_lasso, s = best_lam, newx = test_x)
eval_results(test_y, pred_train, test_x)
```

```
##        RMSE   Rsquare
## 1 0.2303651 0.2104174
```

```
#training data set
train_data = pollutants[train_row,]
#training model
train_model = lm(length ~ ., data = train_data)

#step wise AIC on training data
step_aic = step(train_model, direction = "both", trace = FALSE)
summary(step_aic)
```

```
##
## Call:
## lm(formula = length ~ POP_furan3 + male + ageyrs + ln_lbxcot,
##     data = train_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5045 -0.1510 -0.0268  0.1211  1.1946
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.3701058  0.0232028  59.049  < 2e-16 ***
## POP_furan3   0.0058730  0.0016414   3.578 0.000368 ***
## male1       -0.0421775  0.0161389  -2.613 0.009139 **
```

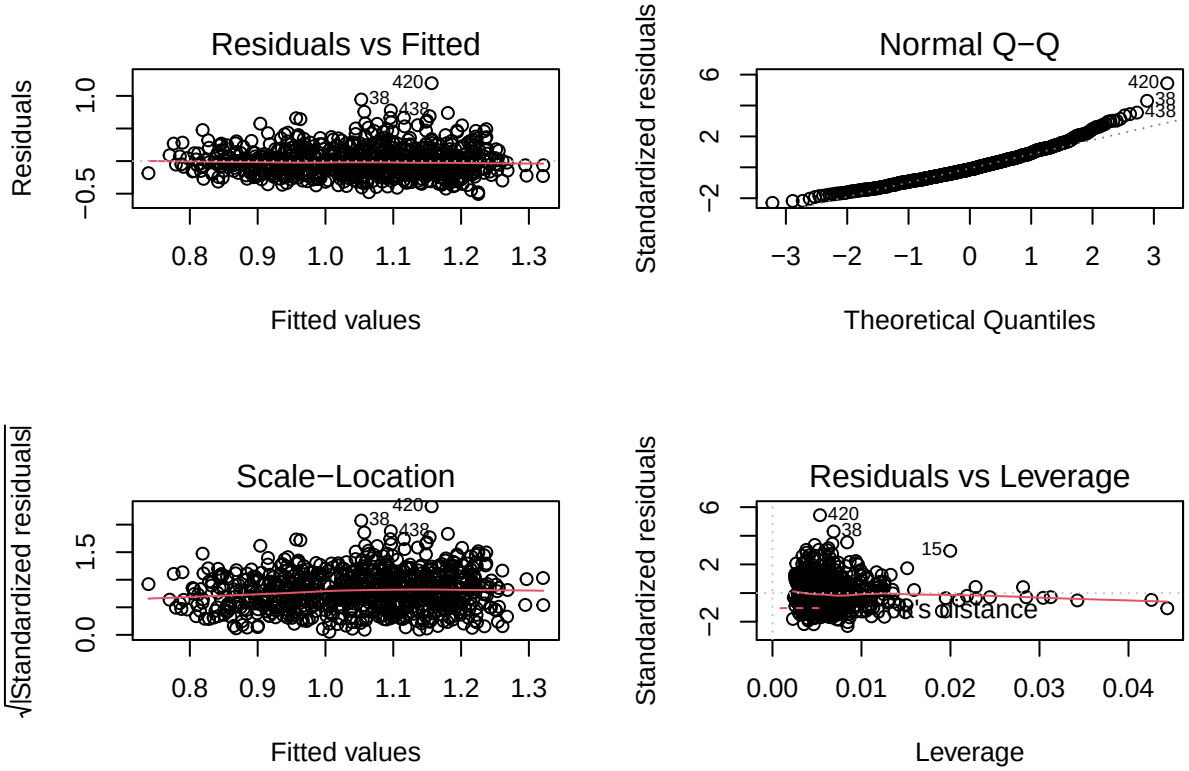
```
## ageyrs      -0.0068654  0.0005261 -13.049  < 2e-16 ***
## ln_lbxcot    0.0034173  0.0021327   1.602 0.109501
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2203 on 772 degrees of freedom
## Multiple R-squared:  0.2223, Adjusted R-squared:  0.2183
## F-statistic: 55.17 on 4 and 772 DF,  p-value: < 2.2e-16
```

```
aic_pred = predict(step_aic, newdata = pollutants[-train_row,])

#RMSE AIC
aic_true = pollutants$length[-train_row]
aic_sd = sum((aic_true - aic_pred)^2)
msd_aic = aic_sd / length(aic_true)
rmse_aic = sqrt(msd_aic)
rmse_aic
```

```
## [1] 0.2295366
```

```
#find the AIC model fit for homoscedasticity after removing multicolinearity
par(mfrow=c(2,2))
plot(step_aic)
```




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

#step wise BIC on training data
step_bic = step(train_model, direction = "both", trace = FALSE, k = log(nrow(train_x)))
```

```r
summary(step_bic)
```

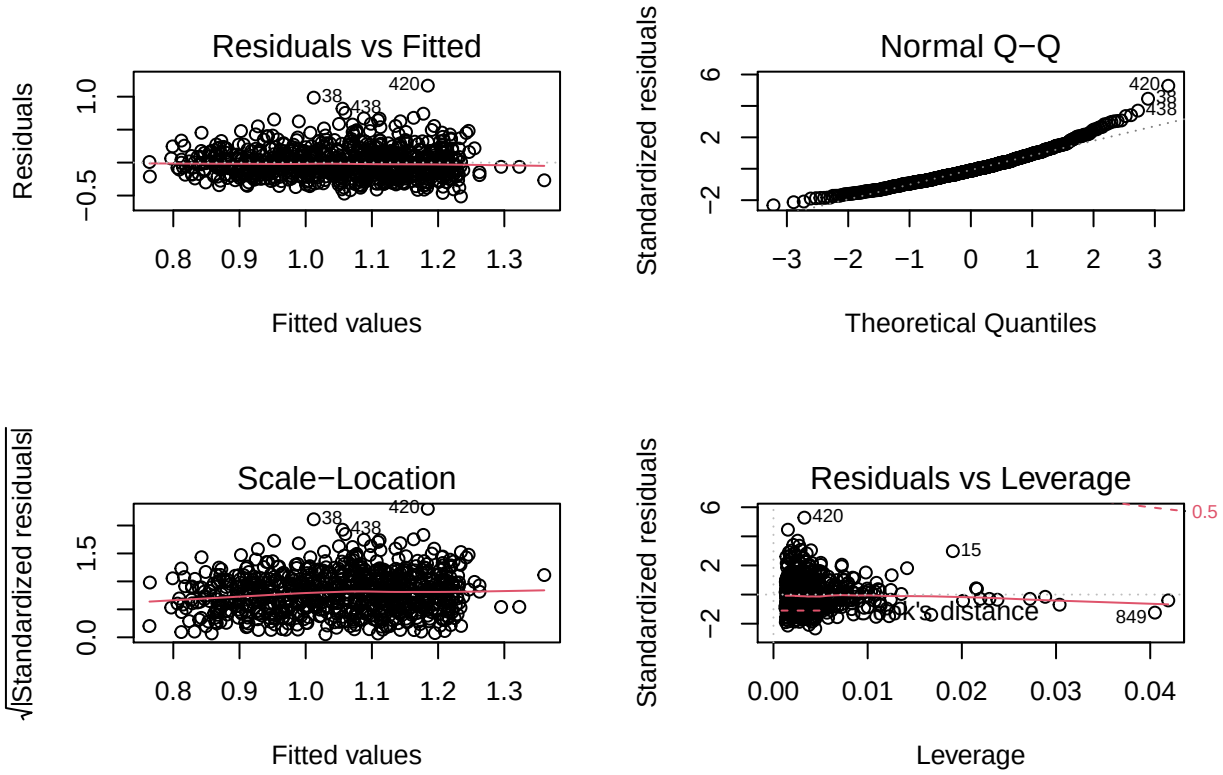
```
##
## Call:
## lm(formula = length ~ POP_furan3 + ageyrs, data = train_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.51364 -0.15642 -0.02609  0.12092  1.16684
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.359962   0.022585  60.215  < 2e-16 ***
## POP_furan3   0.006055   0.001644   3.682 0.000247 ***
## ageyrs      -0.007125   0.000518 -13.755  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2212 on 774 degrees of freedom
## Multiple R-squared:  0.2137, Adjusted R-squared:  0.2116
## F-statistic: 105.2 on 2 and 774 DF,  p-value: < 2.2e-16
```

```r
bic_pred = predict(step_bic, newdata = pollutants[-train_row,])

#RMSE AIC
bic_true = pollutants$length[-train_row]
bic_sd = sum((bic_true - bic_pred)^2)
msd_bic = bic_sd / length(bic_true)
rmse_bic = sqrt(msd_bic)
rmse_bic
```

```
## [1] 0.2298015
```

```r
#find the BIC model fit for homoscedasticity after removing multicolinearity
par(mfrow=c(2,2))
plot(step_bic)
```




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