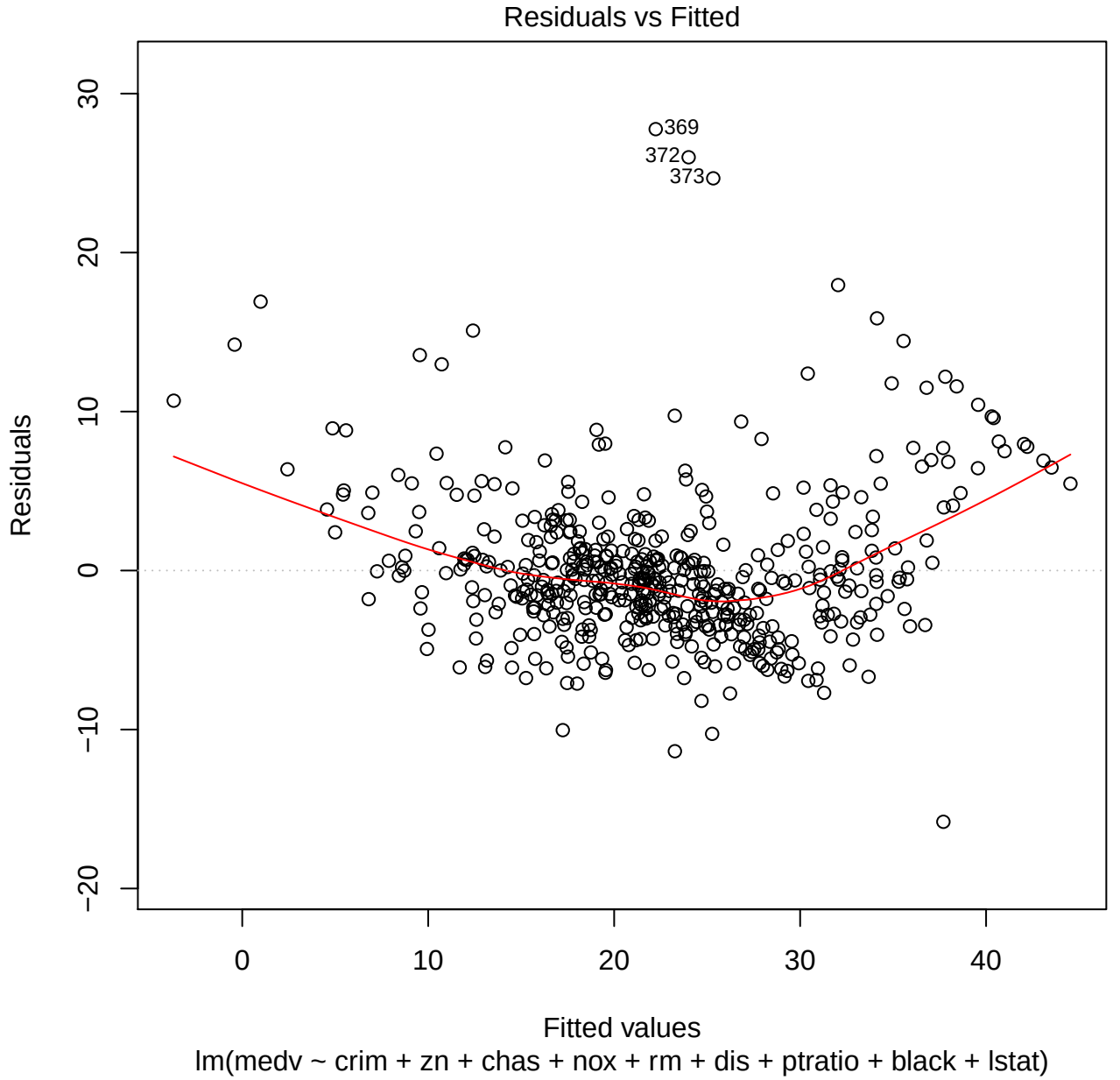
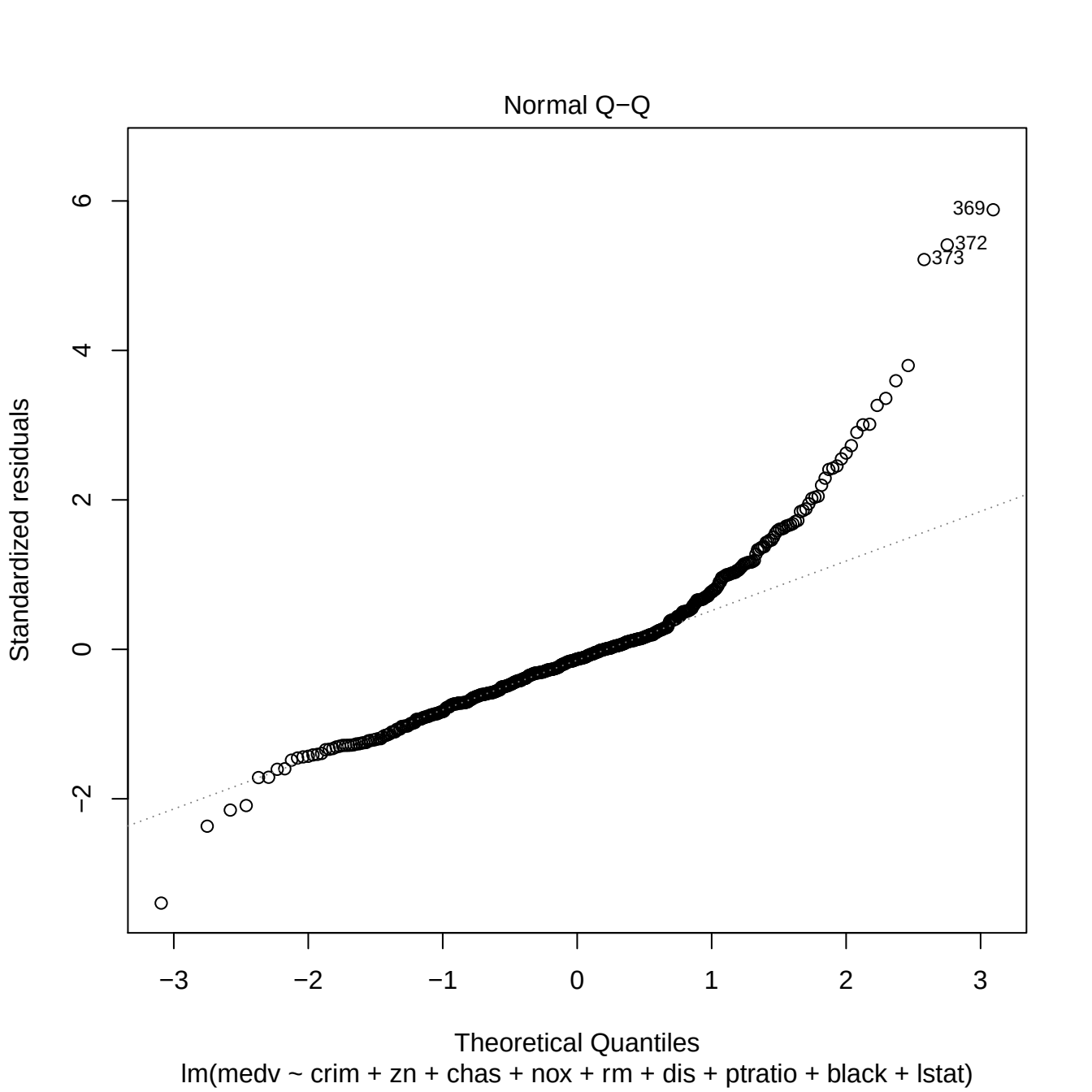
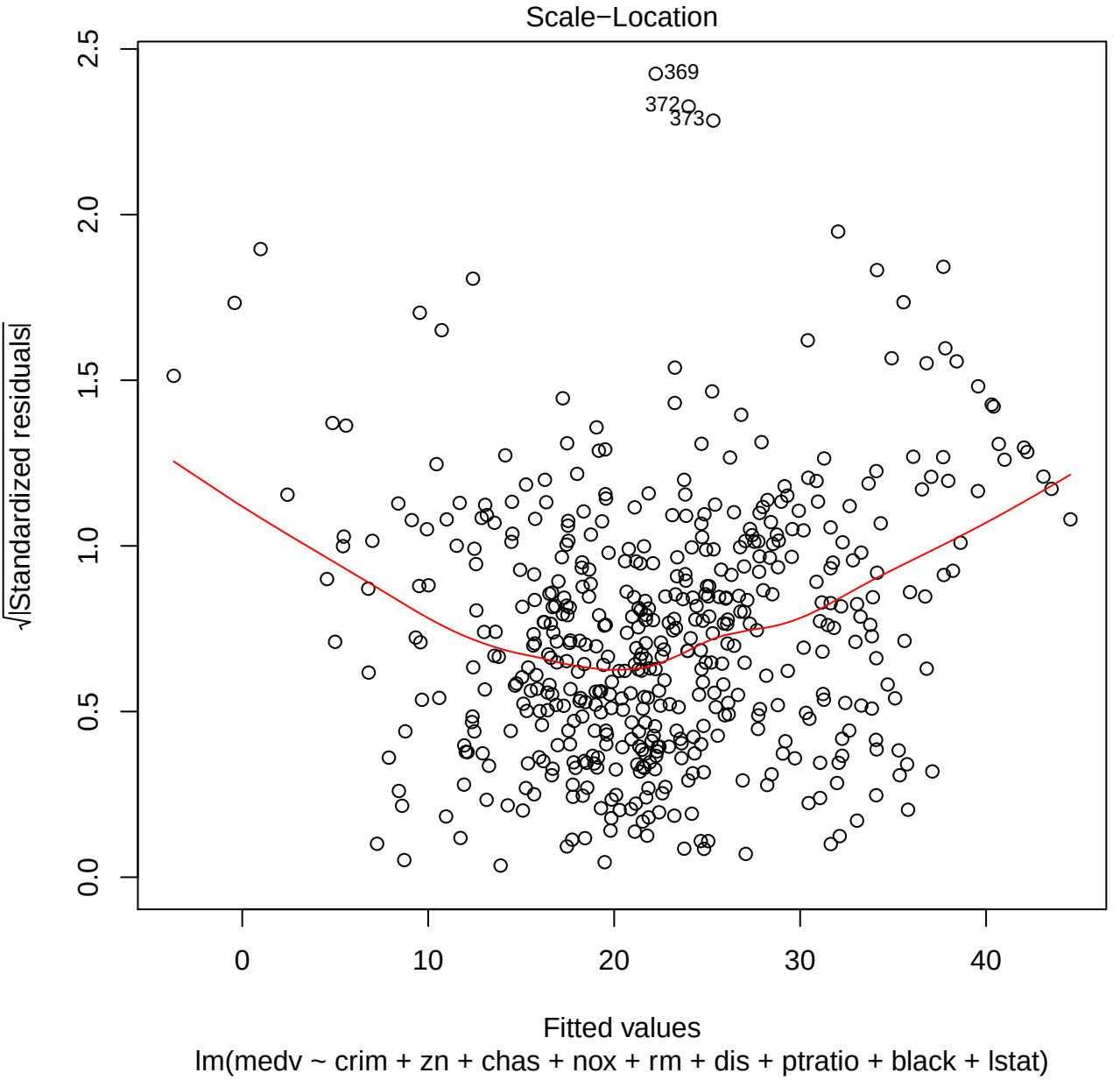
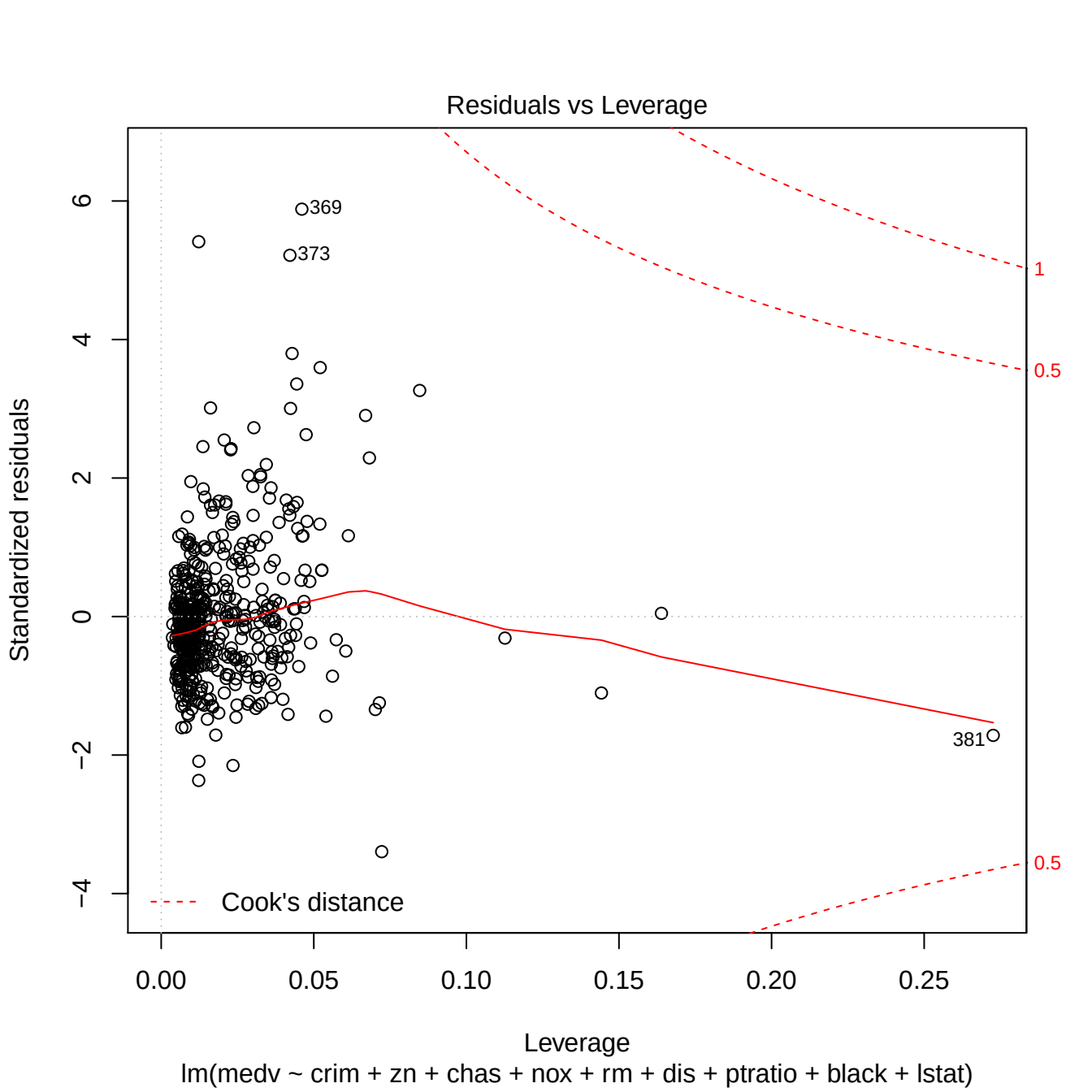
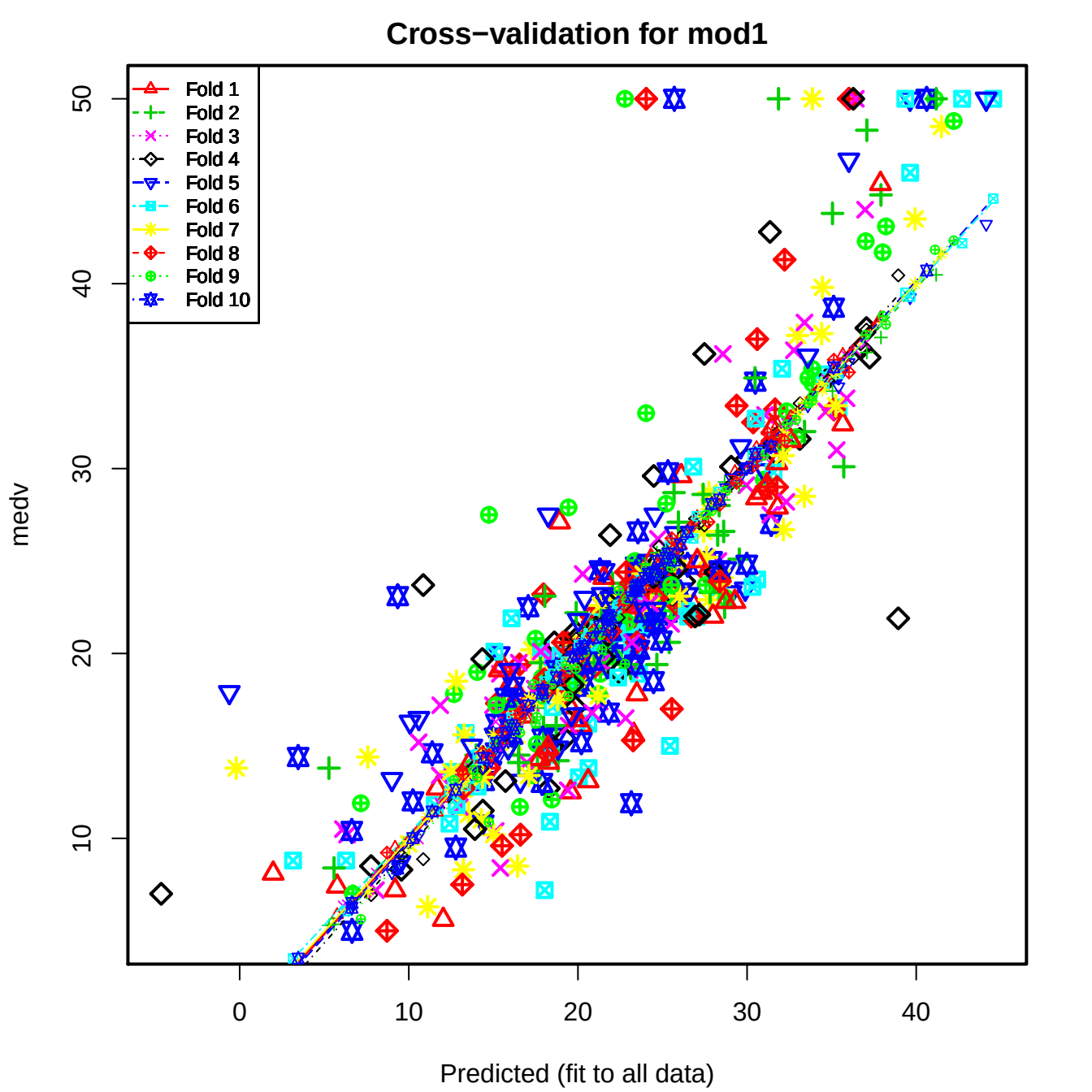
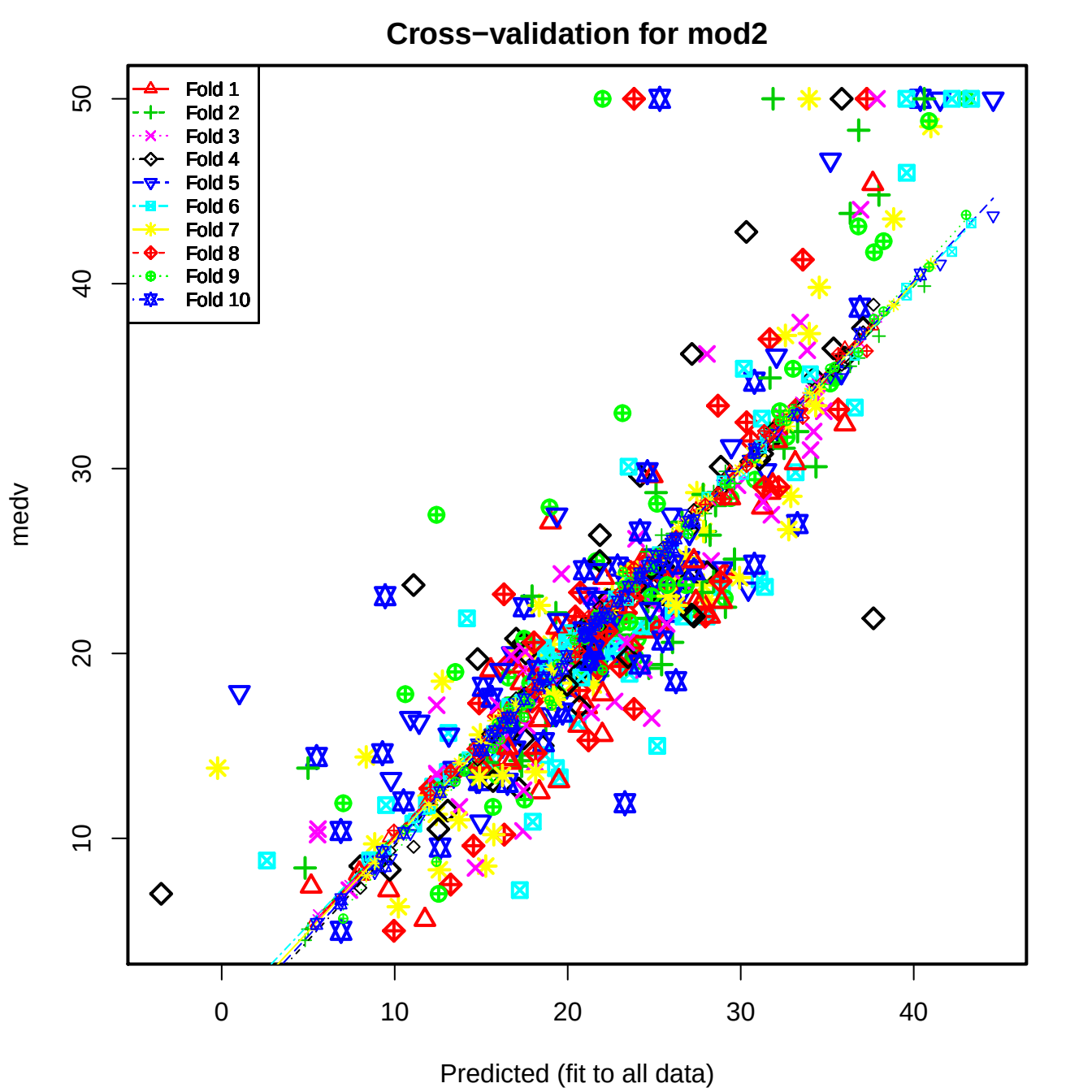

Residuals vs Fitted
369
372
373
Residuals
30
20
10
0
−10
−20
0
10
20
30
40
Fitted values
lm(medv ~ crim + zn + chas + nox + rm + dis + ptratio + black + lstat)

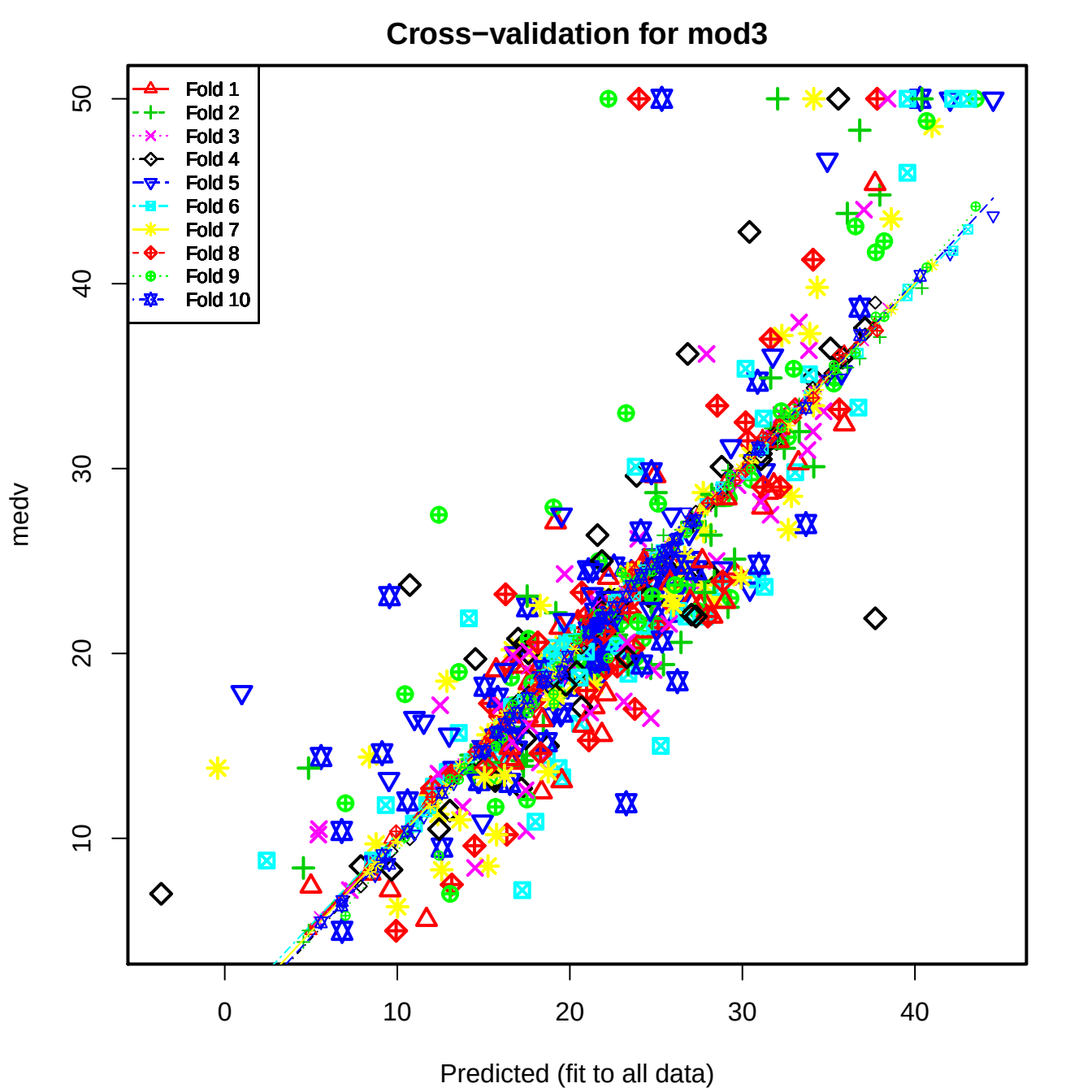

Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(medv ~ crim + zn + chas + nox + rm + dis + ptratio + black + lstat)
369
372
373
6
4
2
0
−2
−3
−2
−1
0
1
2
3


Scale−Location
369
372
373
2.5
2.0
1.5
1.0
0.5
0.0
√|Standardized residuals|
0
10
20
30
40
Fitted values
lm(medv ~ crim + zn + chas + nox + rm + dis + ptratio + black + lstat)


Residuals vs Leverage
Standardized residuals
Leverage
lm(medv ~ crim + zn + chas + nox + rm + dis + ptratio + black + lstat)
Cook's distance
1
0.5
0.5
369
373
381
6
4
2
0
−2
−4
0.00
0.05
0.10
0.15
0.20
0.25


Cross−validation for mod1
Fold 1
Fold 2
Fold 3
Fold 4
Fold 5
Fold 6
Fold 7
Fold 8
Fold 9
Fold 10
medv
Predicted (fit to all data)
0
10
20
30
40
10
20
30
40
50


Cross−validation for mod2
Fold 1
Fold 2
Fold 3
Fold 4
Fold 5
Fold 6
Fold 7
Fold 8
Fold 9
Fold 10
medv
Predicted (fit to all data)
0
10
20
30
40
10
20
30
40
50


Cross−validation for mod3
Fold 1
Fold 2
Fold 3
Fold 4
Fold 5
Fold 6
Fold 7
Fold 8
Fold 9
Fold 10
medv
Predicted (fit to all data)
0
10
20
30
40
10
20
30
40
50