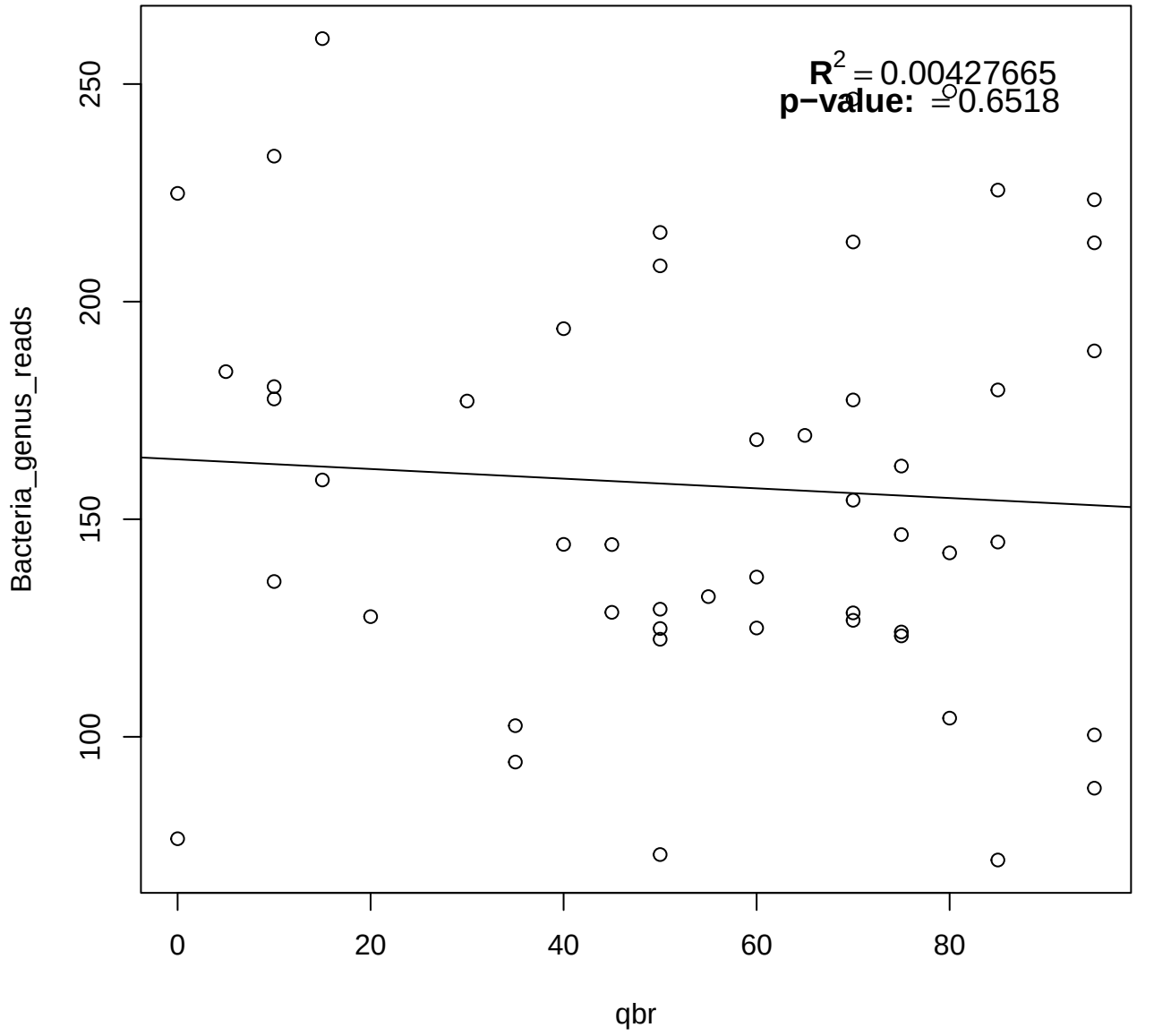
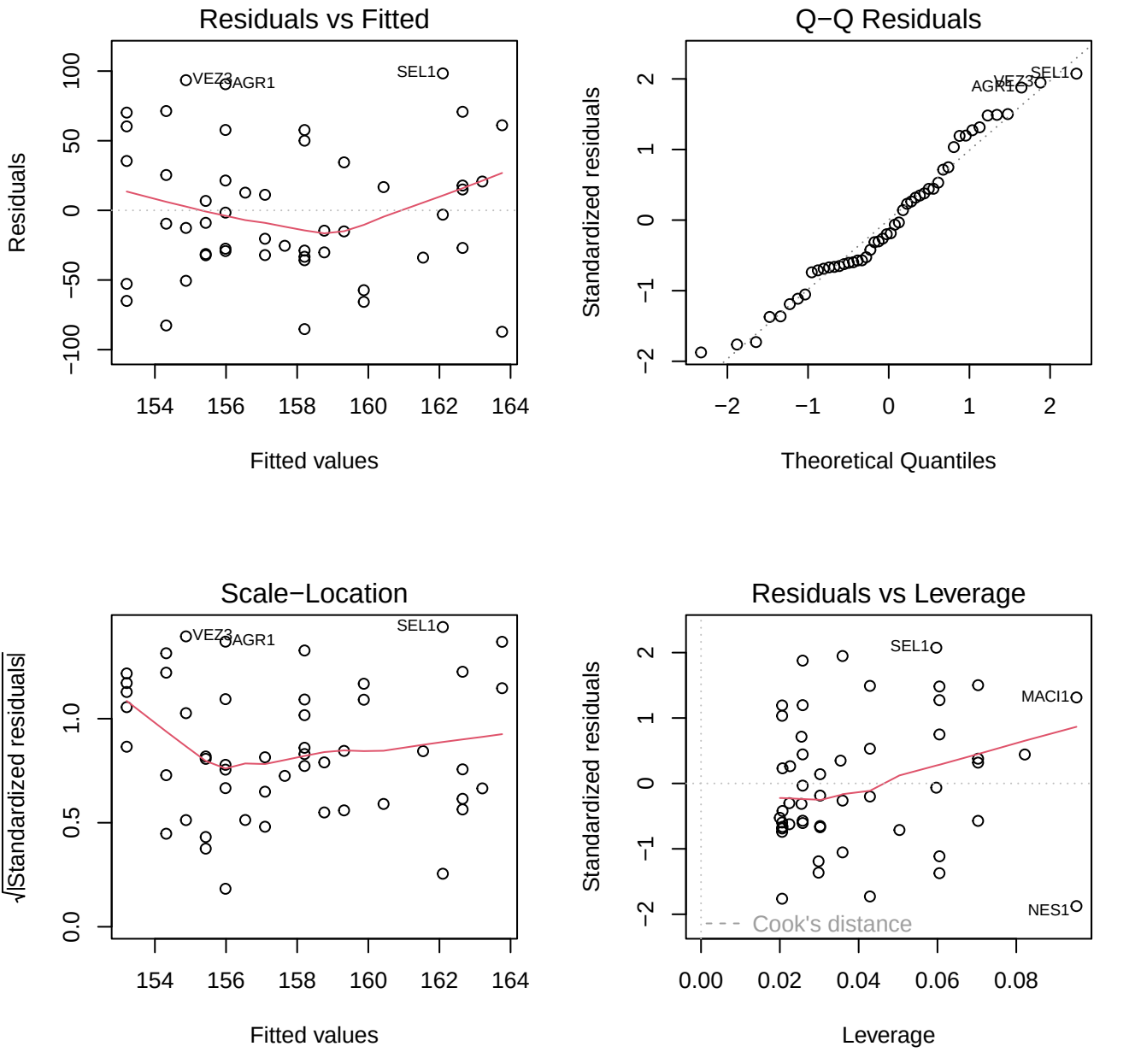
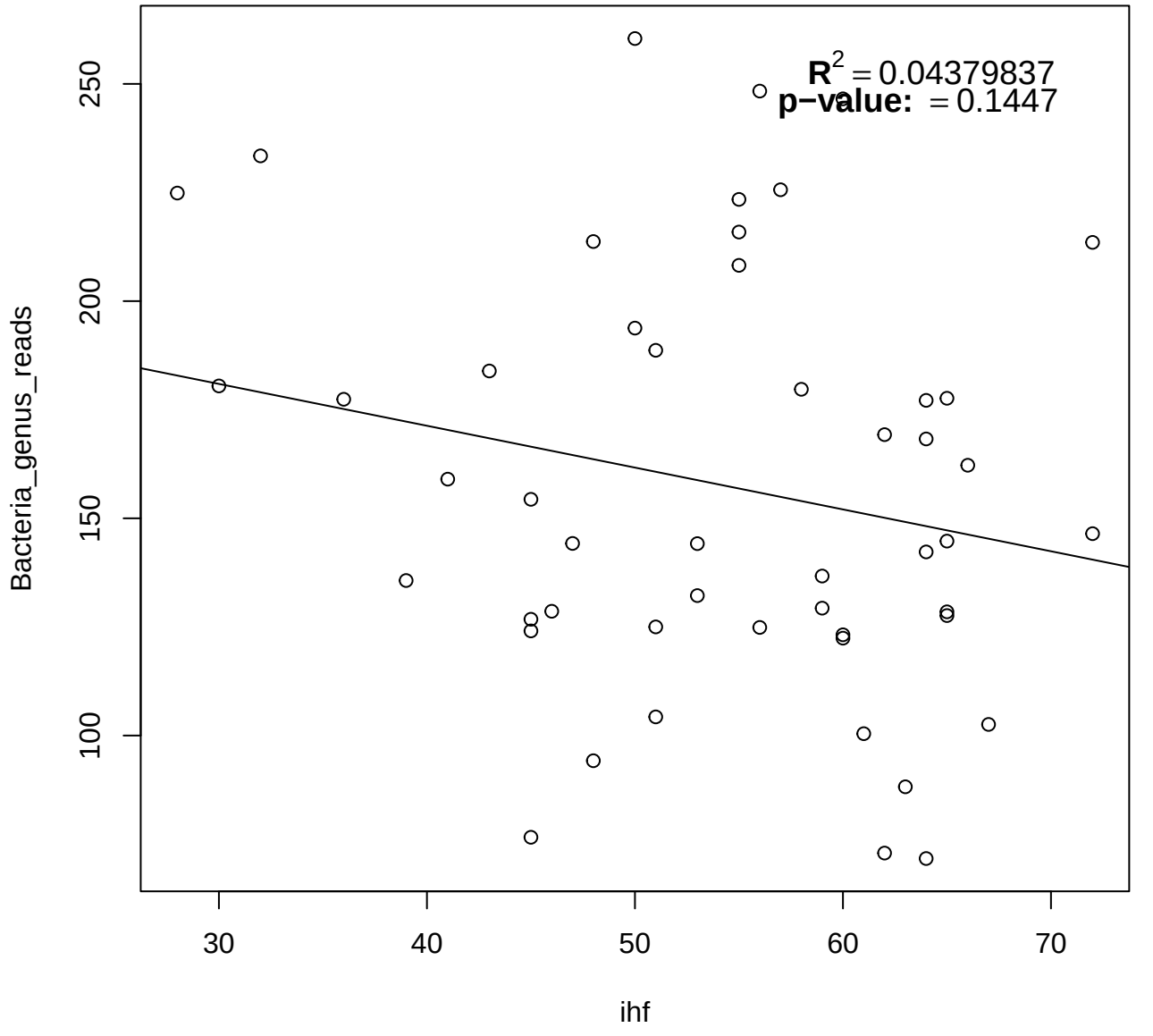
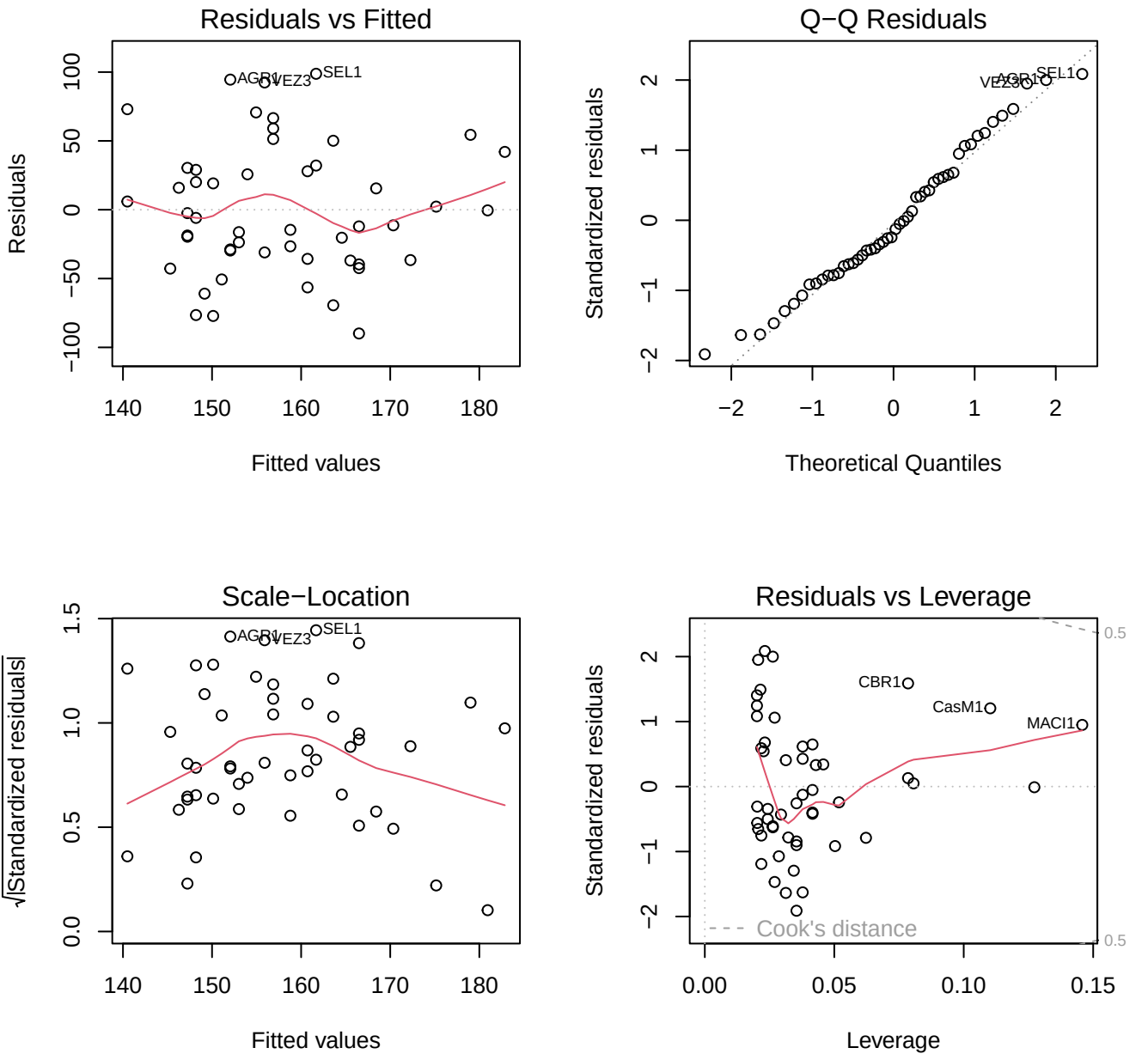
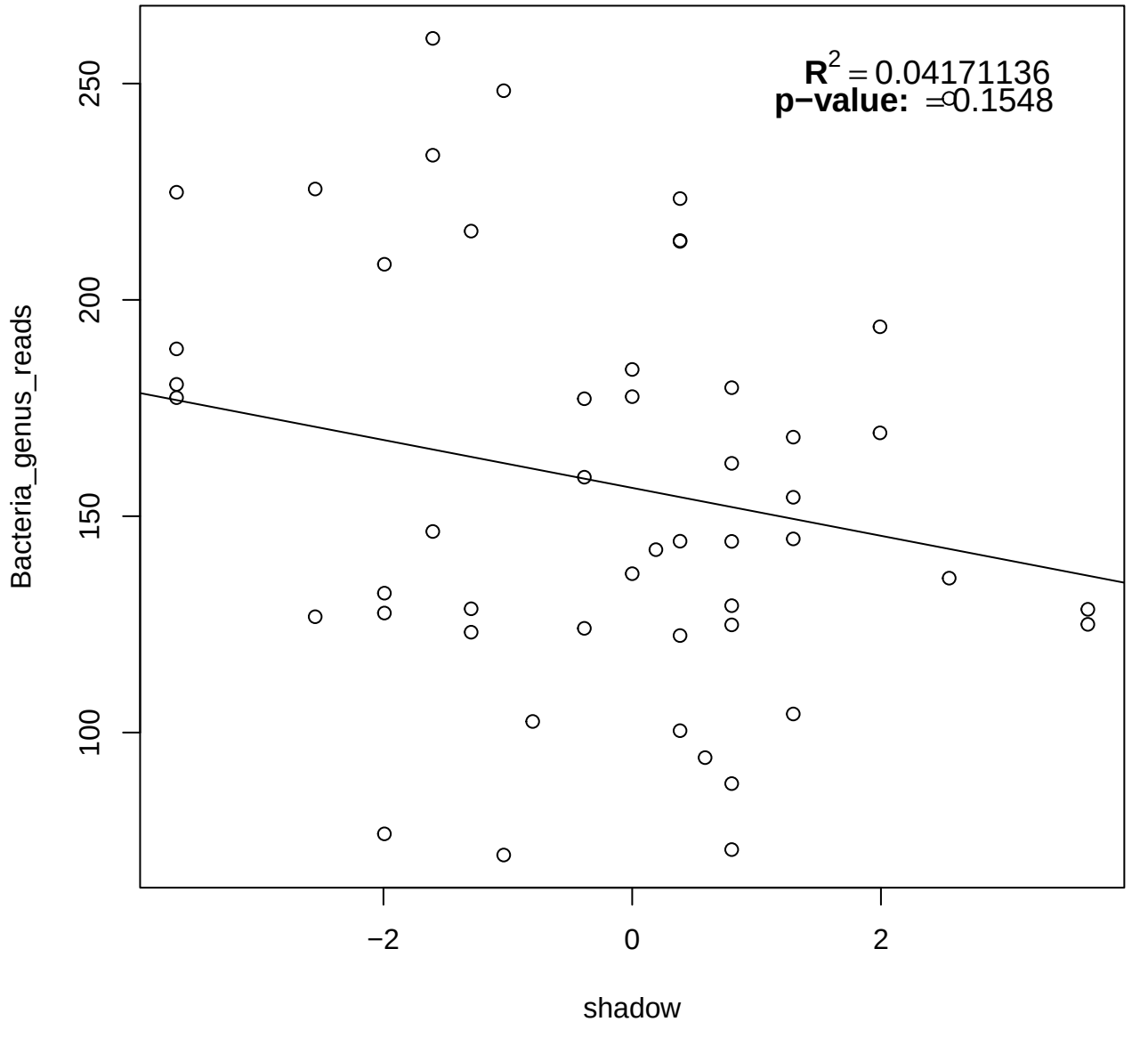
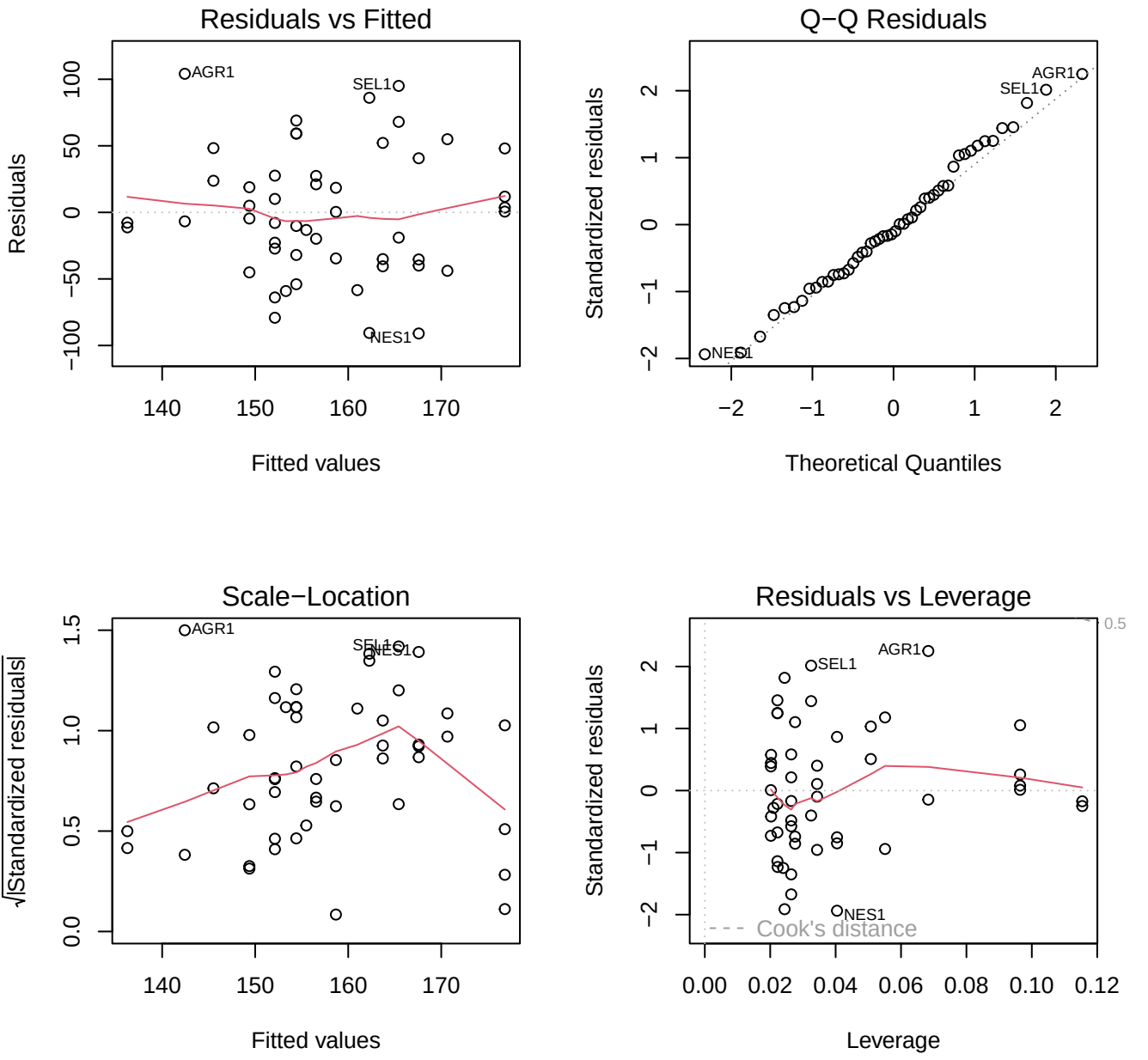

$R^2 = 0.00427665$
p−value: = 0.6518
Bacteria_genus_reads
100
150
200
250
0
20
40
60
80
qbr

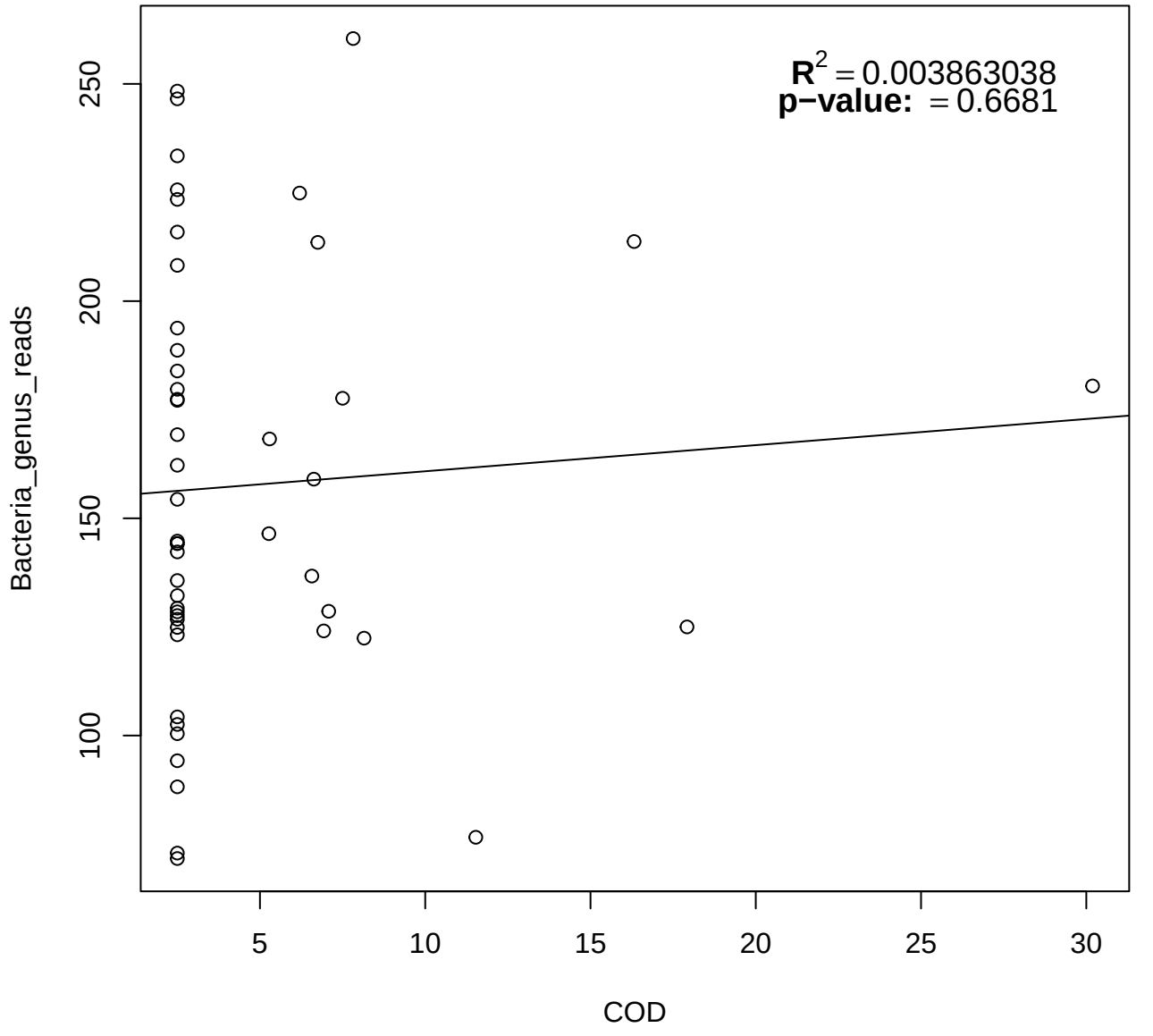

Residuals vs Fitted
Residuals
Fitted values
VEZ3
AGR1
SEL1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
VEZ3
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
VEZ3
AGR1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
MACI1
NES1
Cook's distance

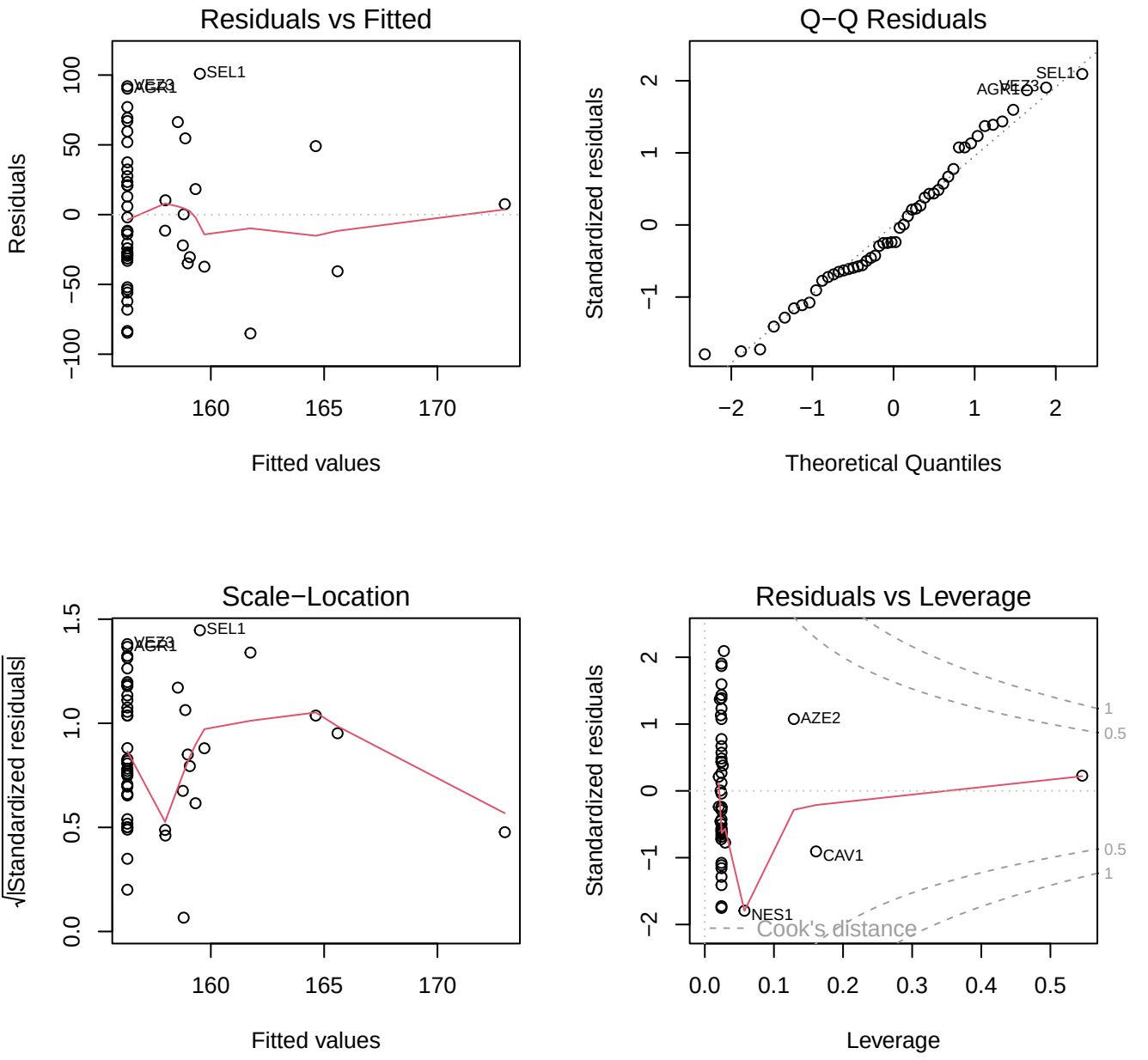

$R^2 = 0.04379837$
p−value: = 0.1447
Bacteria_genus_reads
ihf
100
150
200
250
30
40
50
60
70

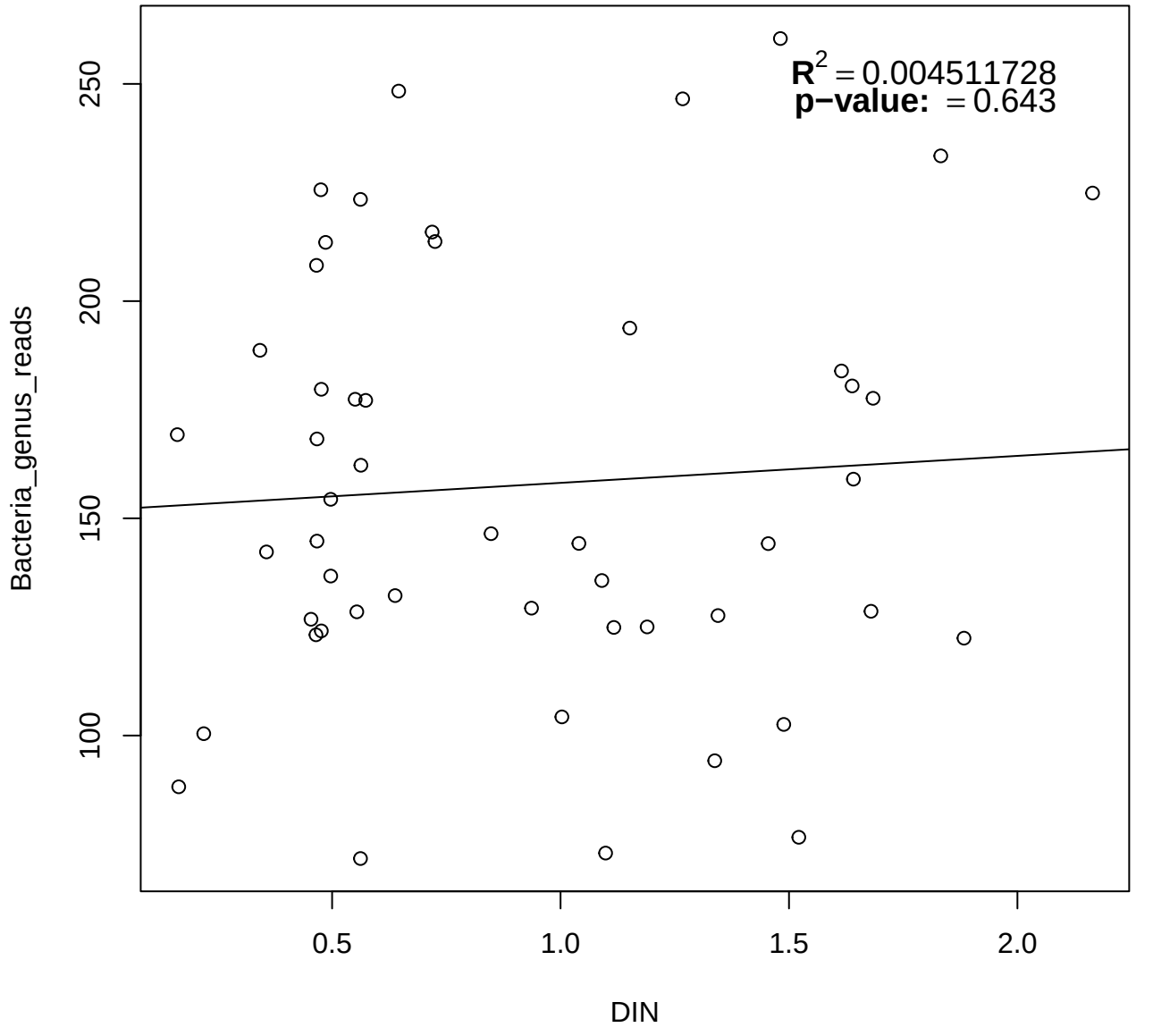

Residuals vs Fitted
Residuals
Fitted values
AGR1
VEZ3
SEL1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
CBR1
CasM1
MACI1
Cook's distance
0.5

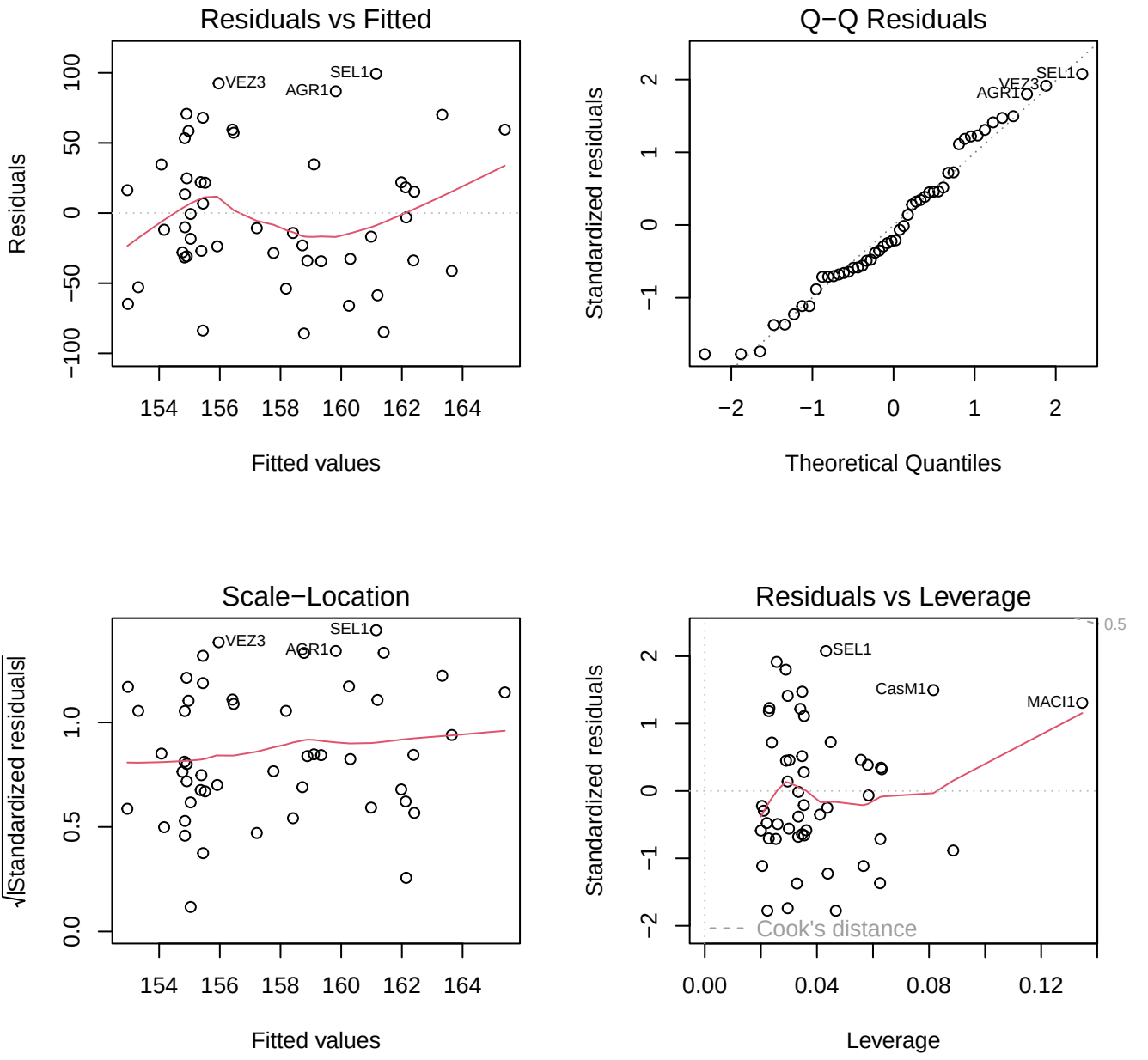

$R^2 = 0.04171136$
p−value: =0.1548
Bacteria_genus_reads
250
200
150
100
−2
0
2
shadow

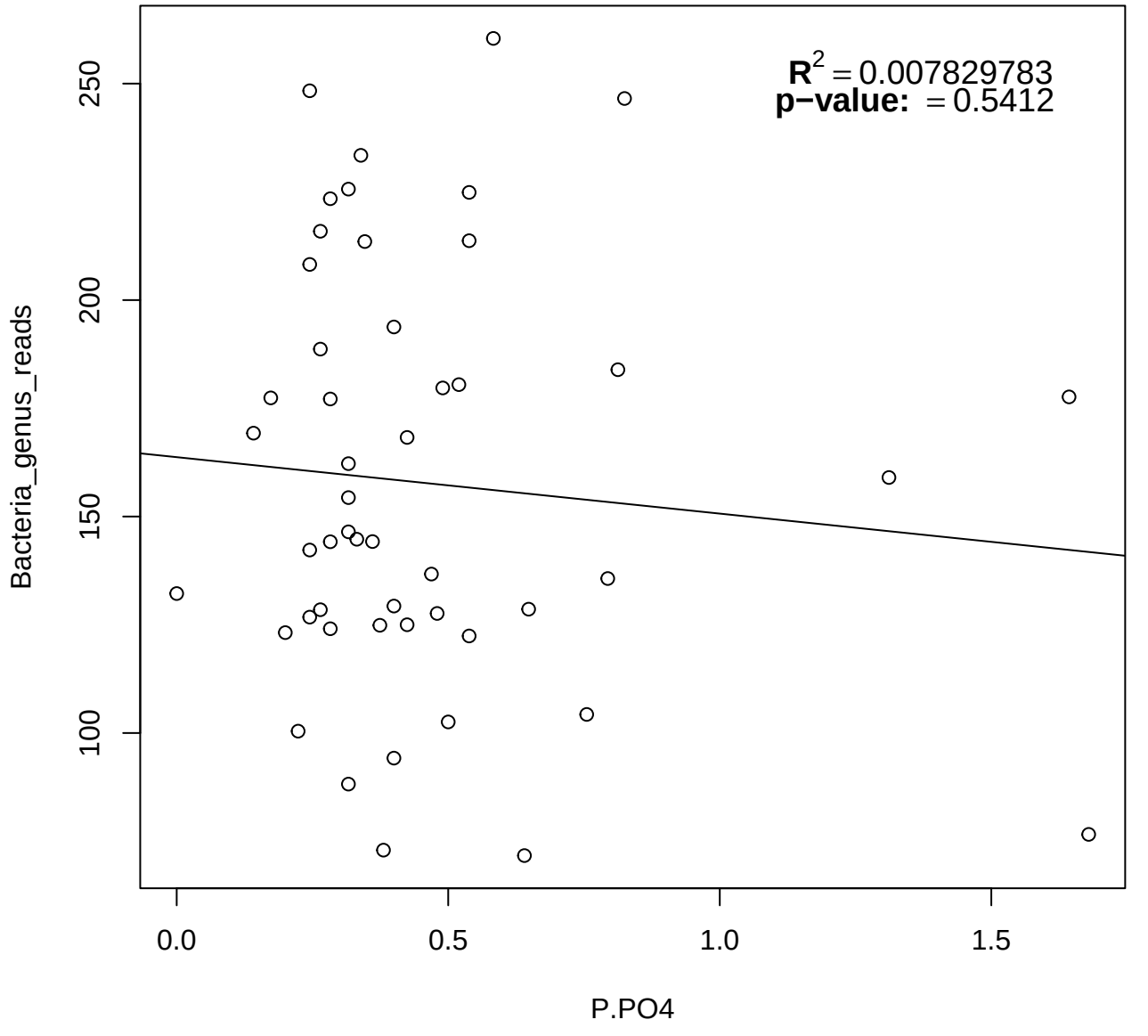

Residuals vs Fitted
Residuals
Fitted values
AGR1
SEL1
NES1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
AGR1
SEL1
NES1
Scale−Location
√|Standardized residuals|
Fitted values
AGR1
SEL1
NES1
Residuals vs Leverage
Standardized residuals
Leverage
AGR1
SEL1
NES1
Cook's distance
0.5

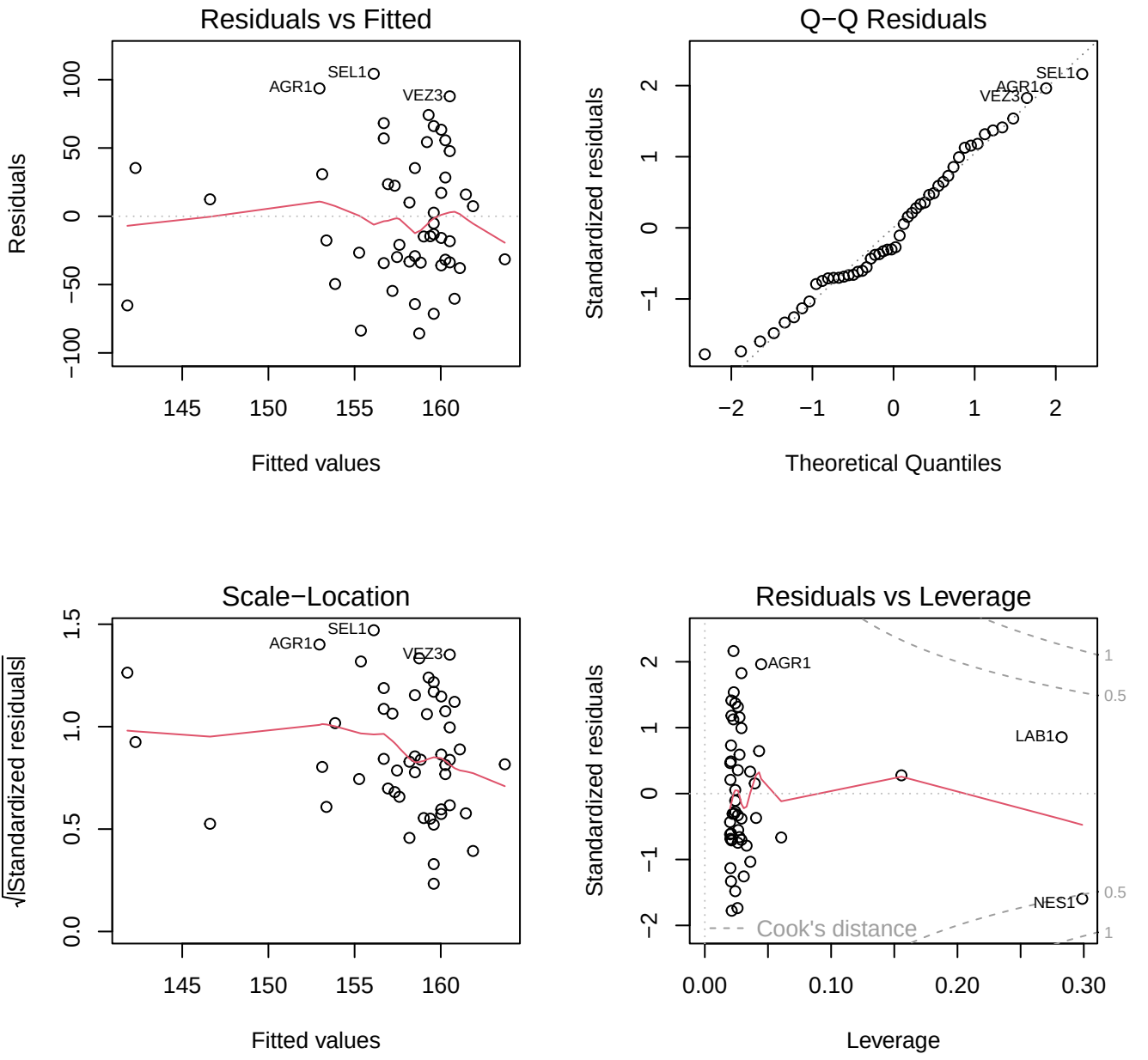

$R^2 = 0.003863038$
p−value: = 0.6681
Bacteria_genus_reads
100
150
200
250
5
10
15
20
25
30
COD

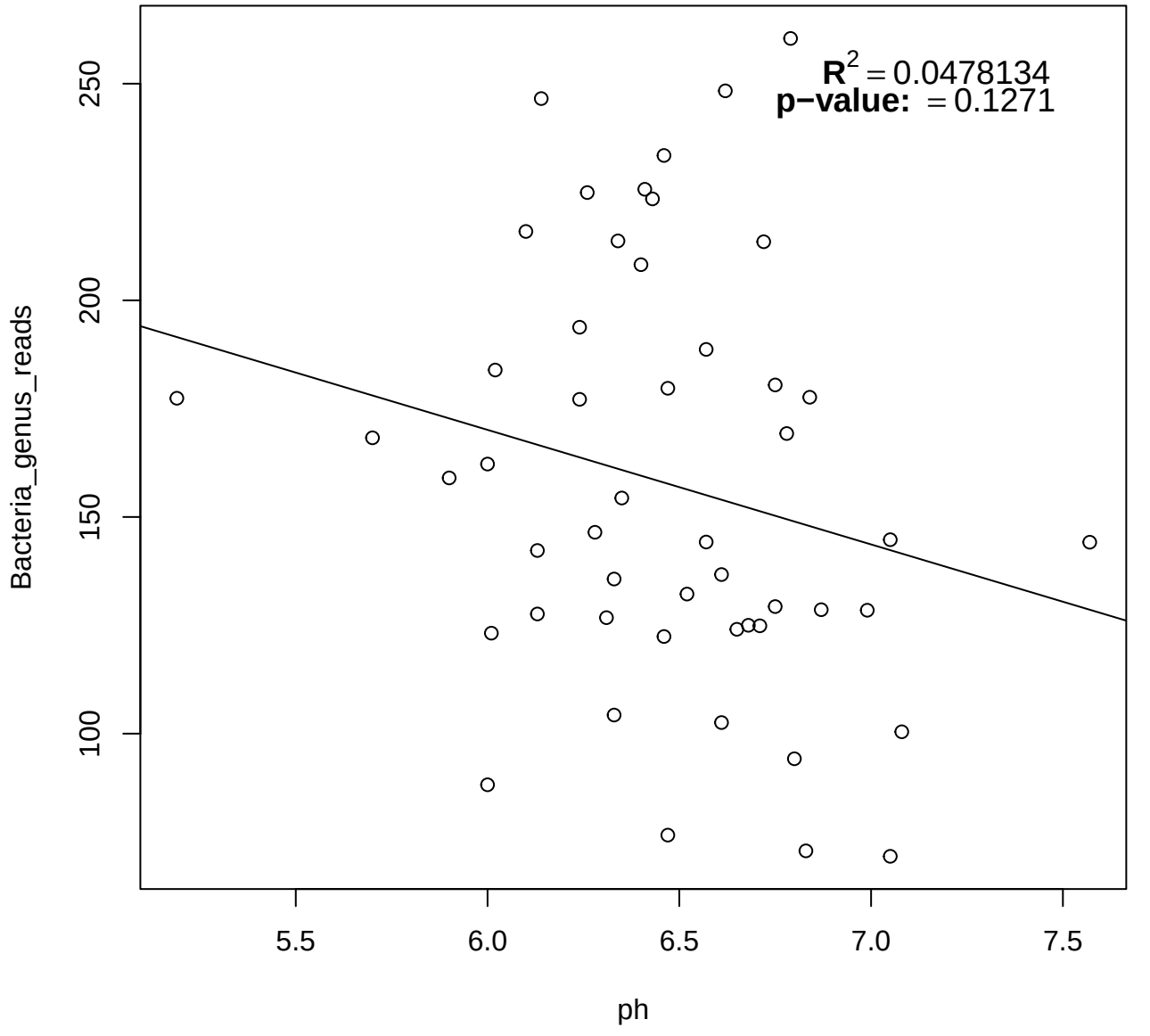

Residuals vs Fitted
Residuals
Fitted values
SEL1
VEZ3
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
VEZ3
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
VEZ3
AGR1
Residuals vs Leverage
Standardized residuals
Leverage
AZE2
CAV1
NES1
Cook's distance

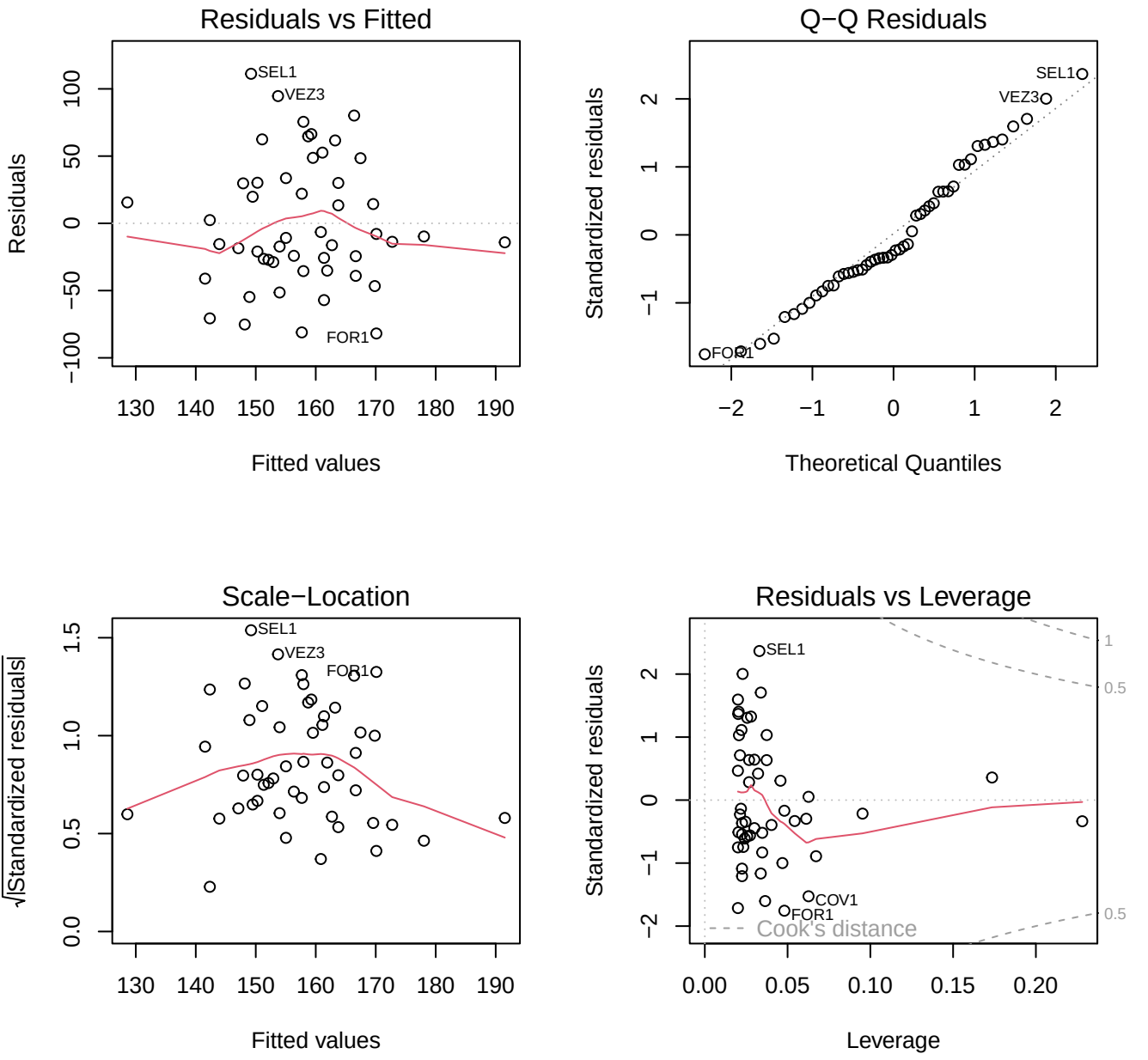

$R^2 = 0.004511728$
p−value: = 0.643
Bacteria_genus_reads
100
150
200
250
0.5
1.0
1.5
2.0
DIN

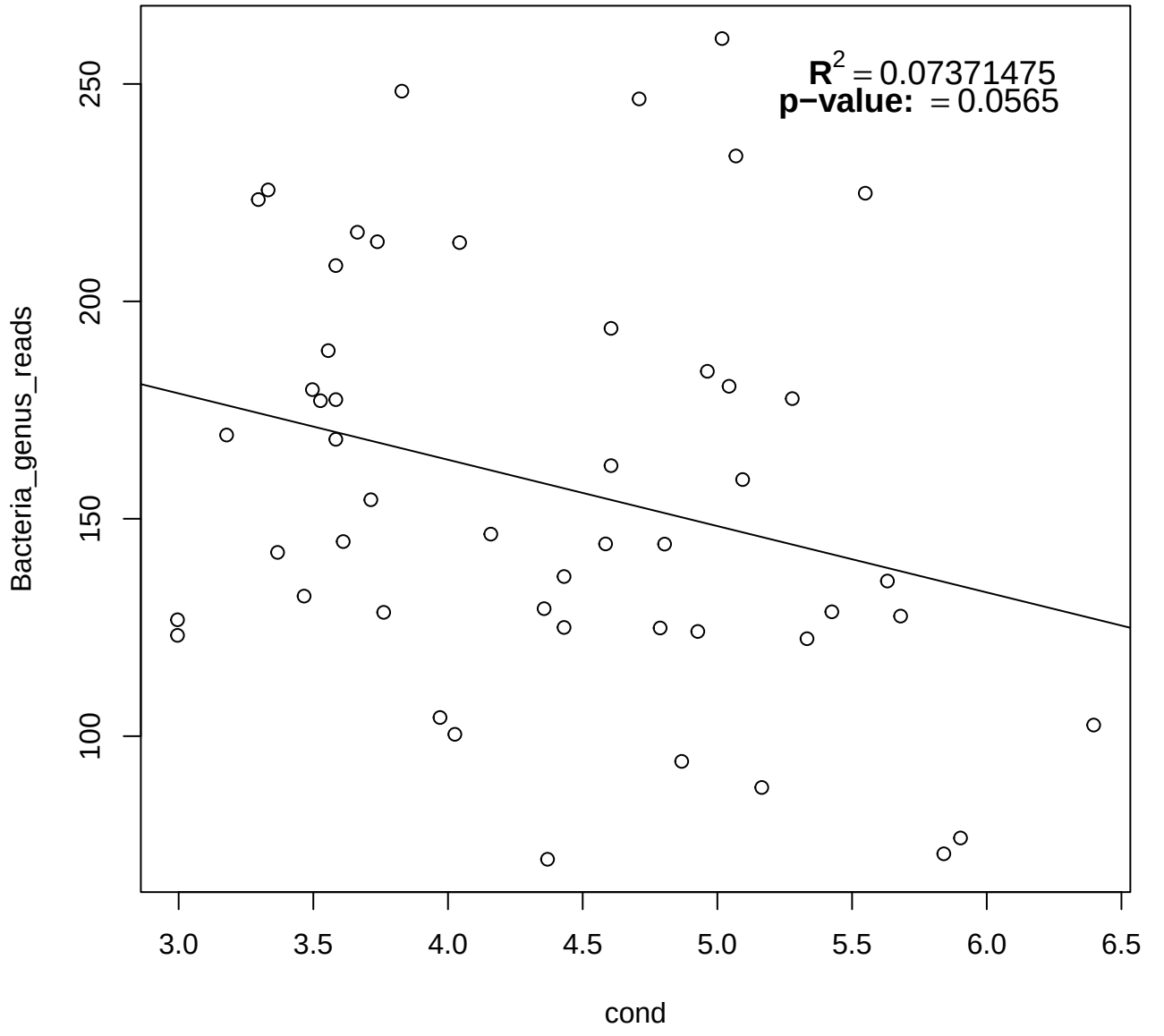

Residuals vs Fitted
Residuals
Fitted values
VEZ3
SEL1
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
VEZ3
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
VEZ3
SEL1
AGR1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
CasM1
MACI1
Cook's distance
0.5

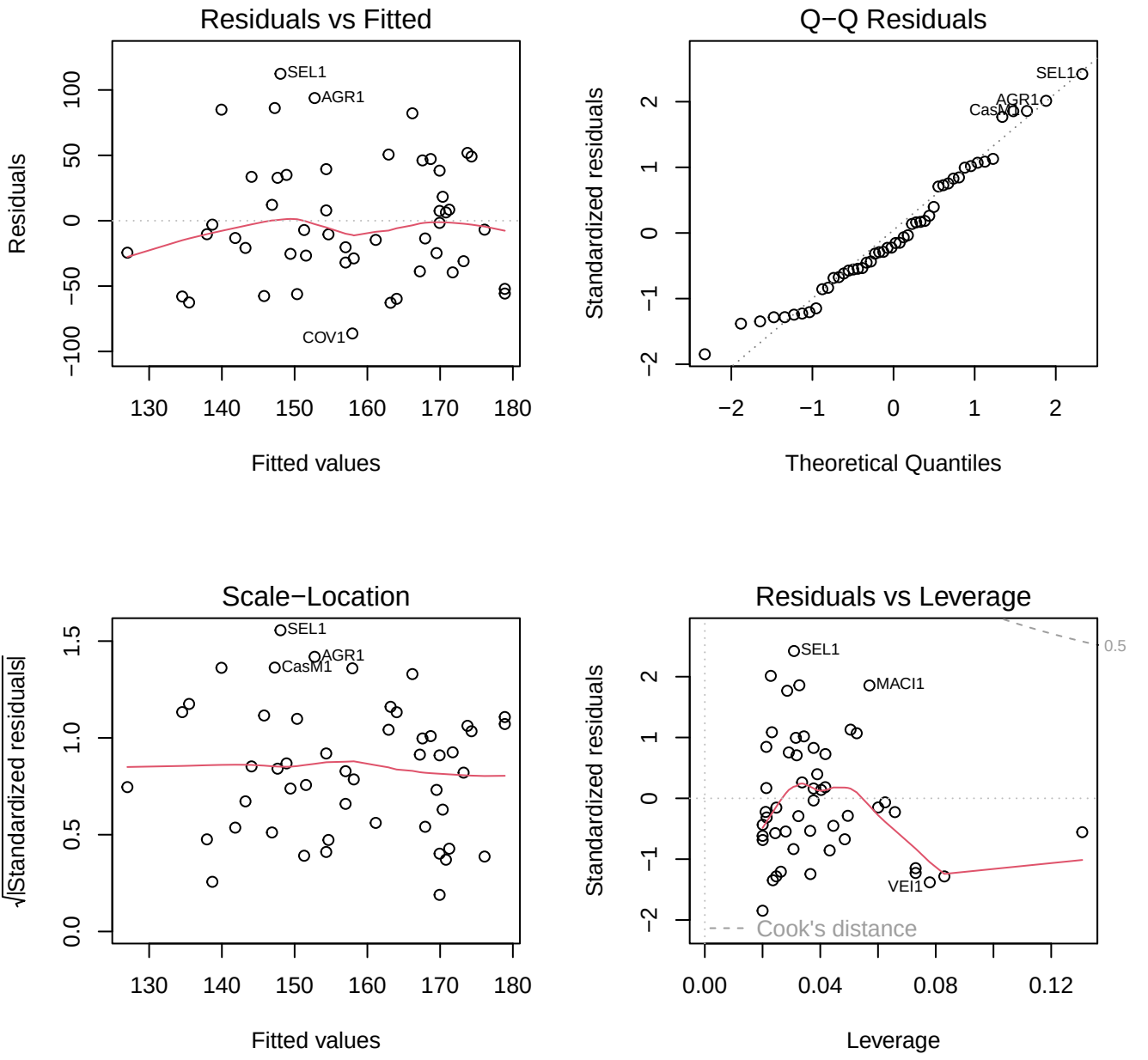

$R^2 = 0.007829783$
p−value: = 0.5412
Bacteria_genus_reads
250
200
150
100
0.0
0.5
1.0
1.5
P.PO4

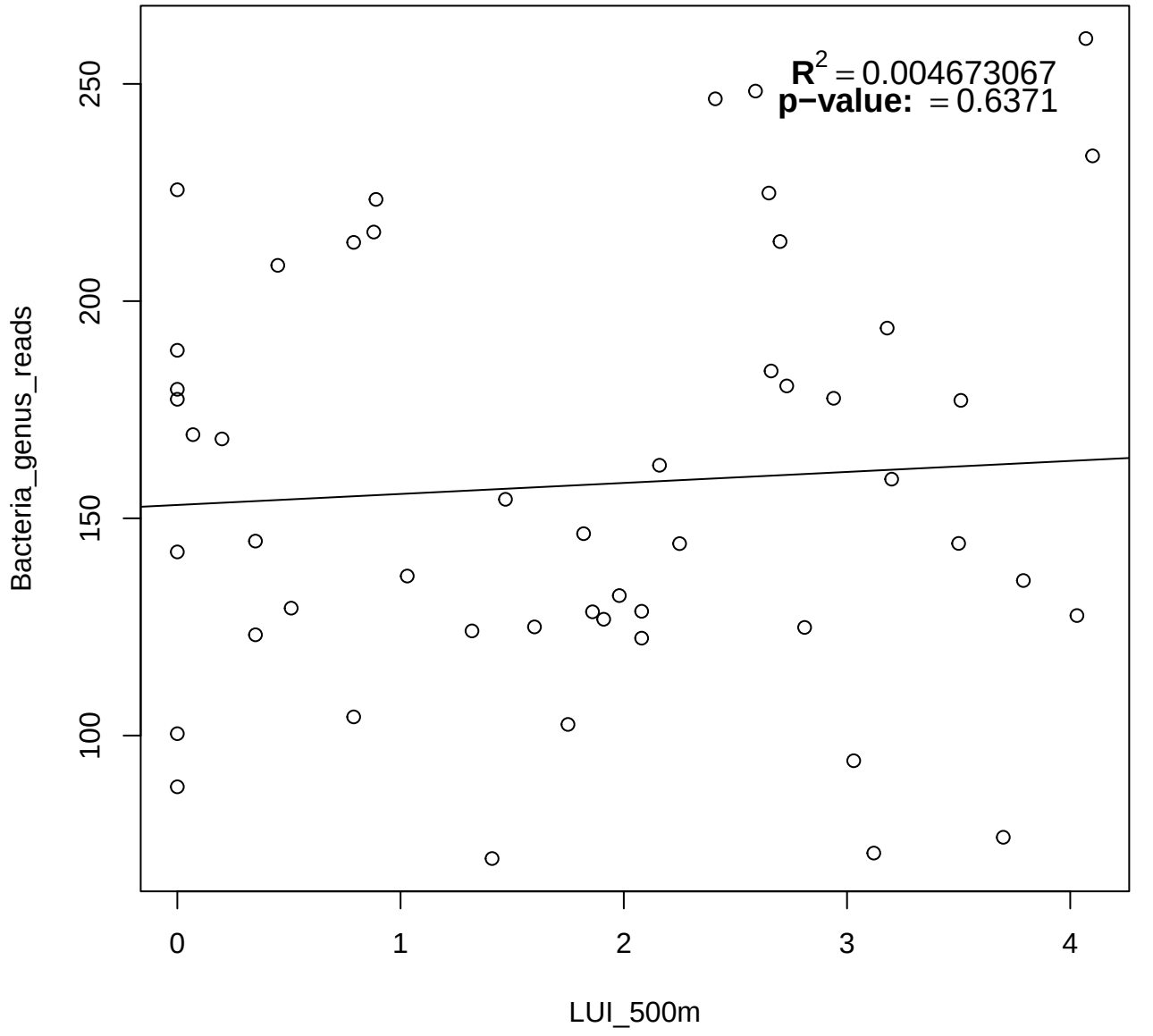

Residuals vs Fitted
Residuals
Fitted values
SEL1
AGR1
VEZ3
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
AGR1
VEZ3
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
AGR1
VEZ3
Residuals vs Leverage
Standardized residuals
Leverage
AGR1
LAB1
NES1
Cook's distance

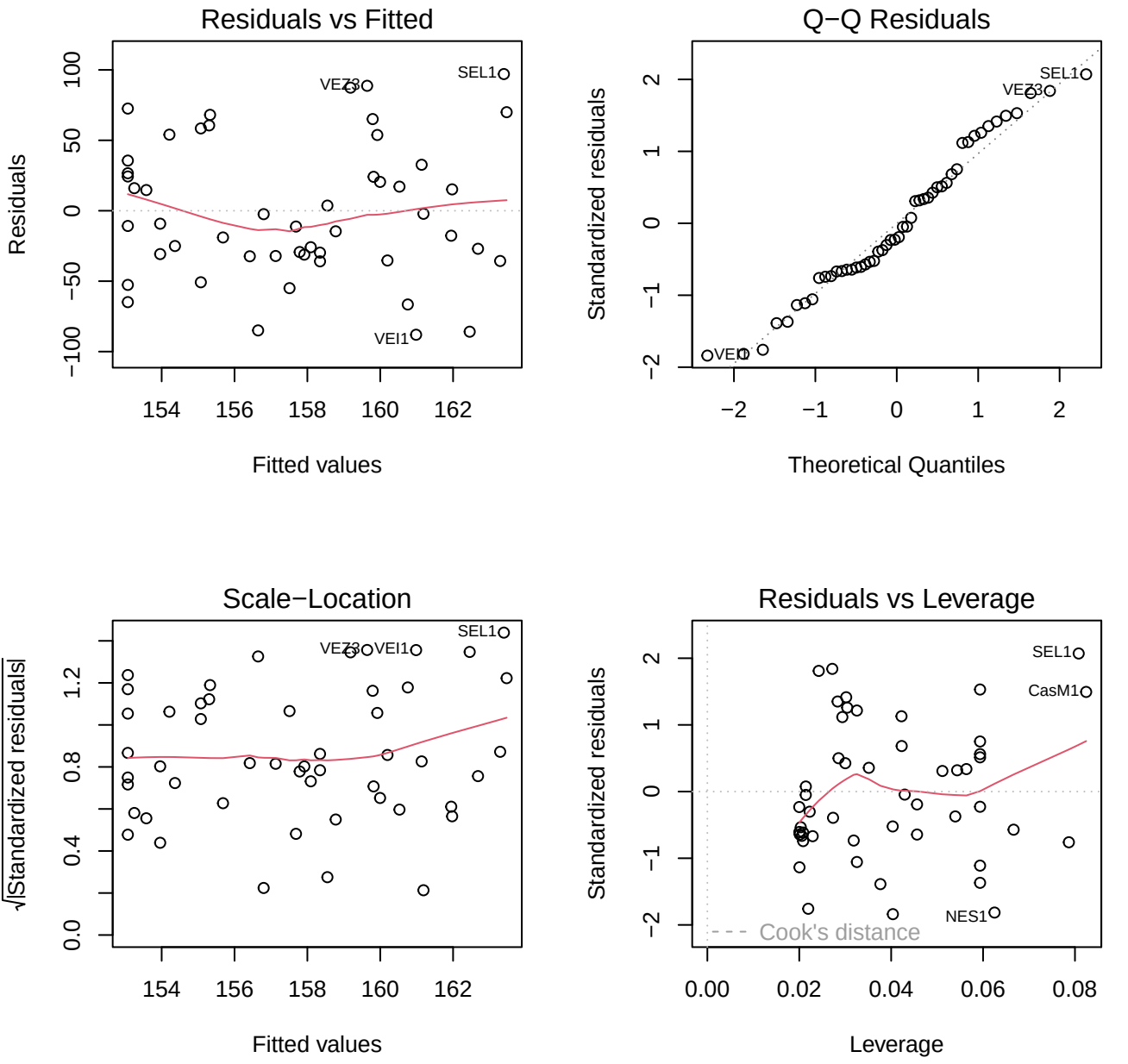

$R^2 = 0.0478134$
p−value: = 0.1271
Bacteria_genus_reads
250
200
150
100
5.5
6.0
6.5
7.0
7.5
ph

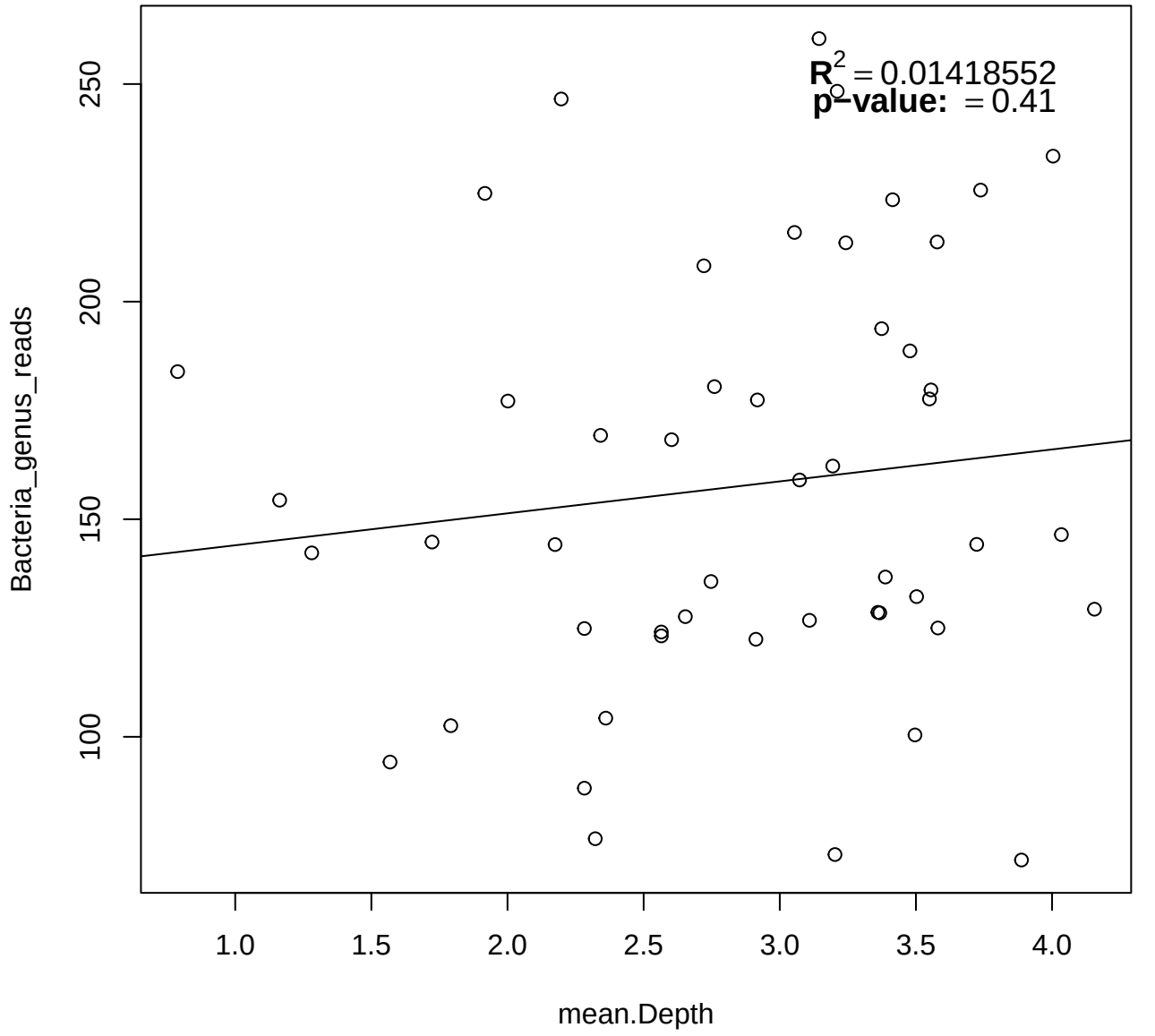

Residuals vs Fitted
Residuals
Fitted values
SEL1
VEZ3
FOR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
VEZ3
FOR1
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
VEZ3
FOR1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
COV1
FOR1
Cook's distance

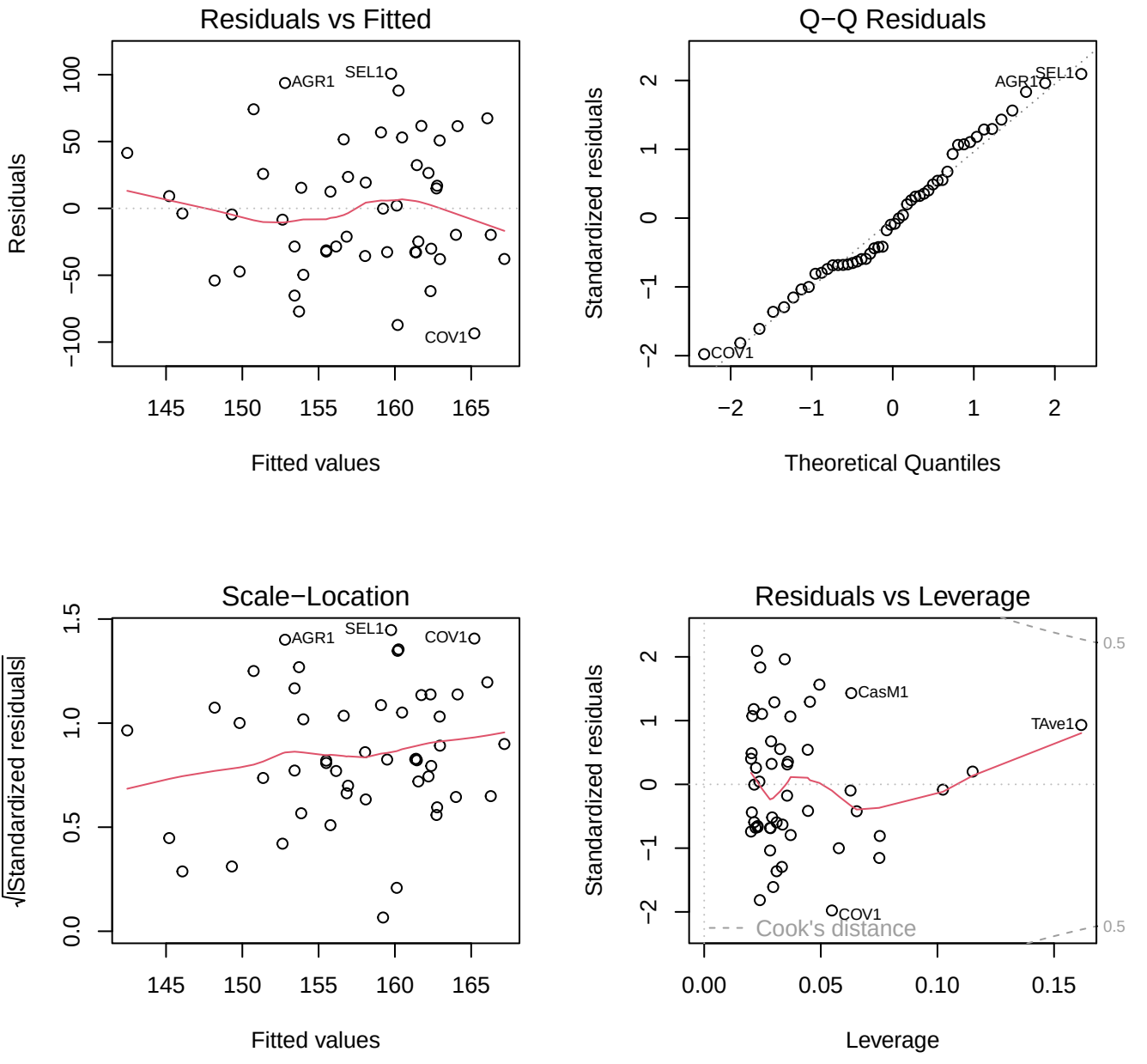

$R^2 = 0.07371475$
p−value: = 0.0565
Bacteria_genus_reads
250
200
150
100
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
cond

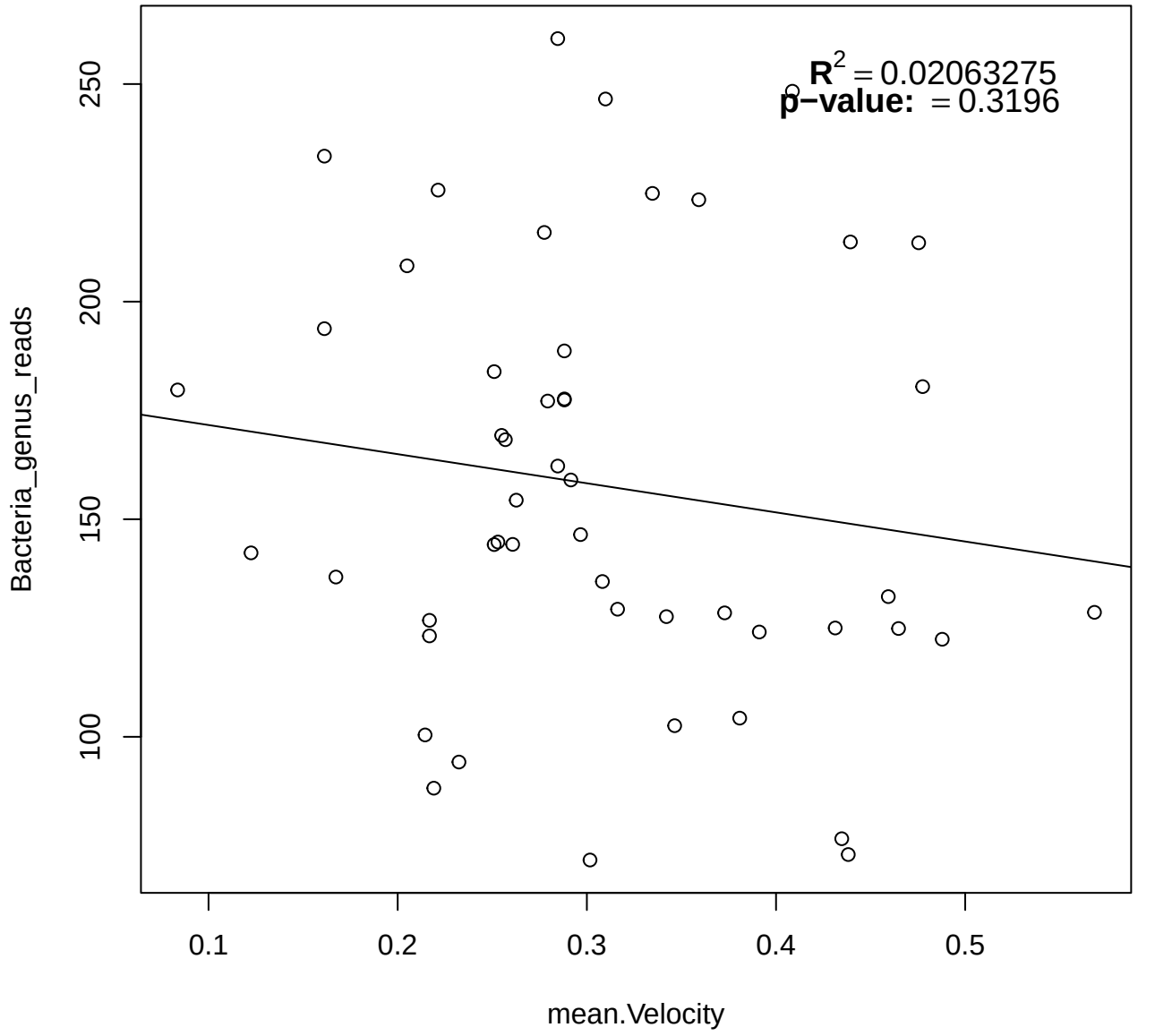

Residuals vs Fitted
Residuals
Fitted values
SEL1
AGR1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
AGR1
CasM1
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
AGR1
CasM1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
MACI1
VEI1
0.5
Cook's distance

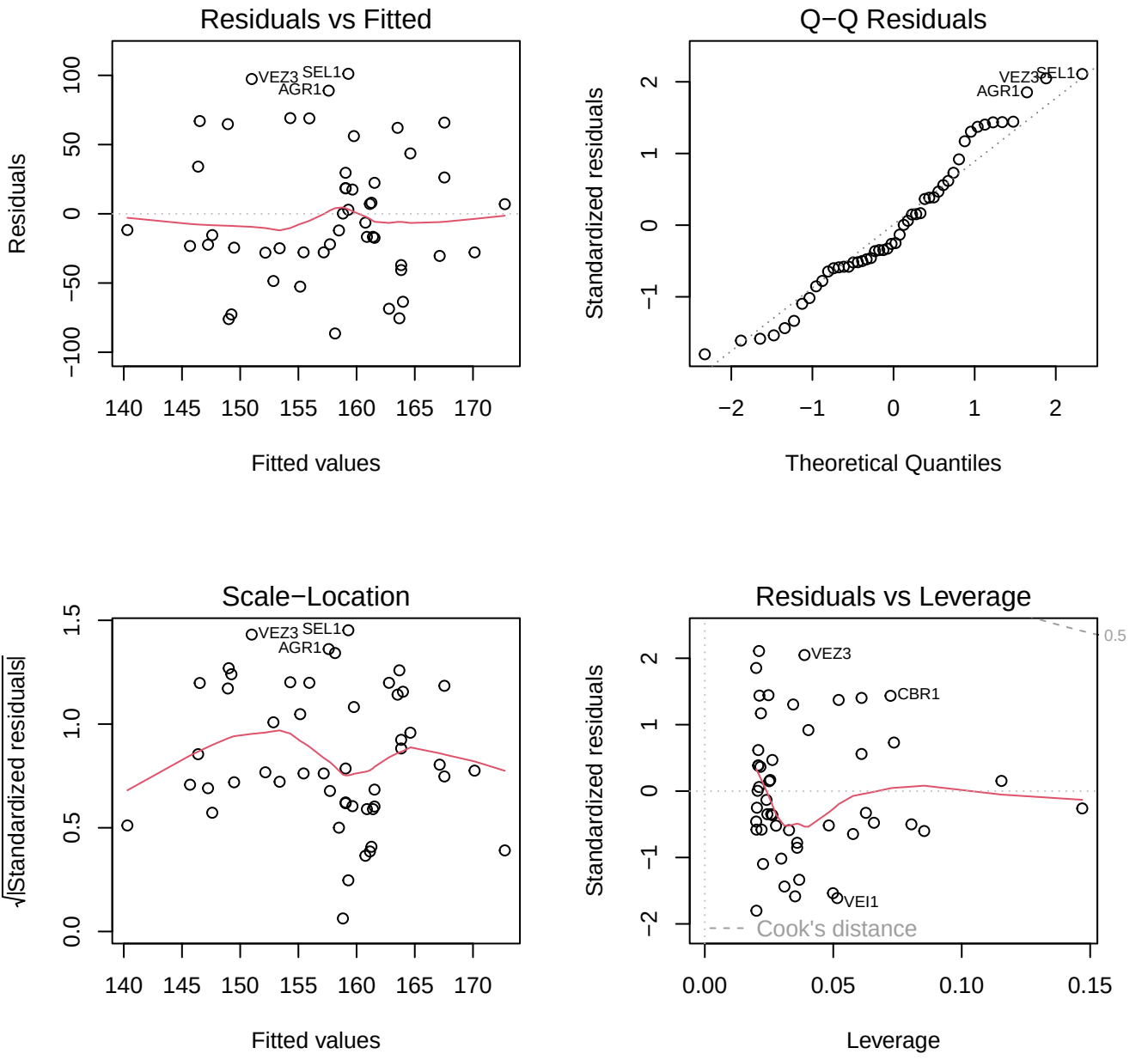

$R^2 = 0.004673067$
p−value: = 0.6371
Bacteria_genus_reads
LUI_500m
100
150
200
250
0
1
2
3
4

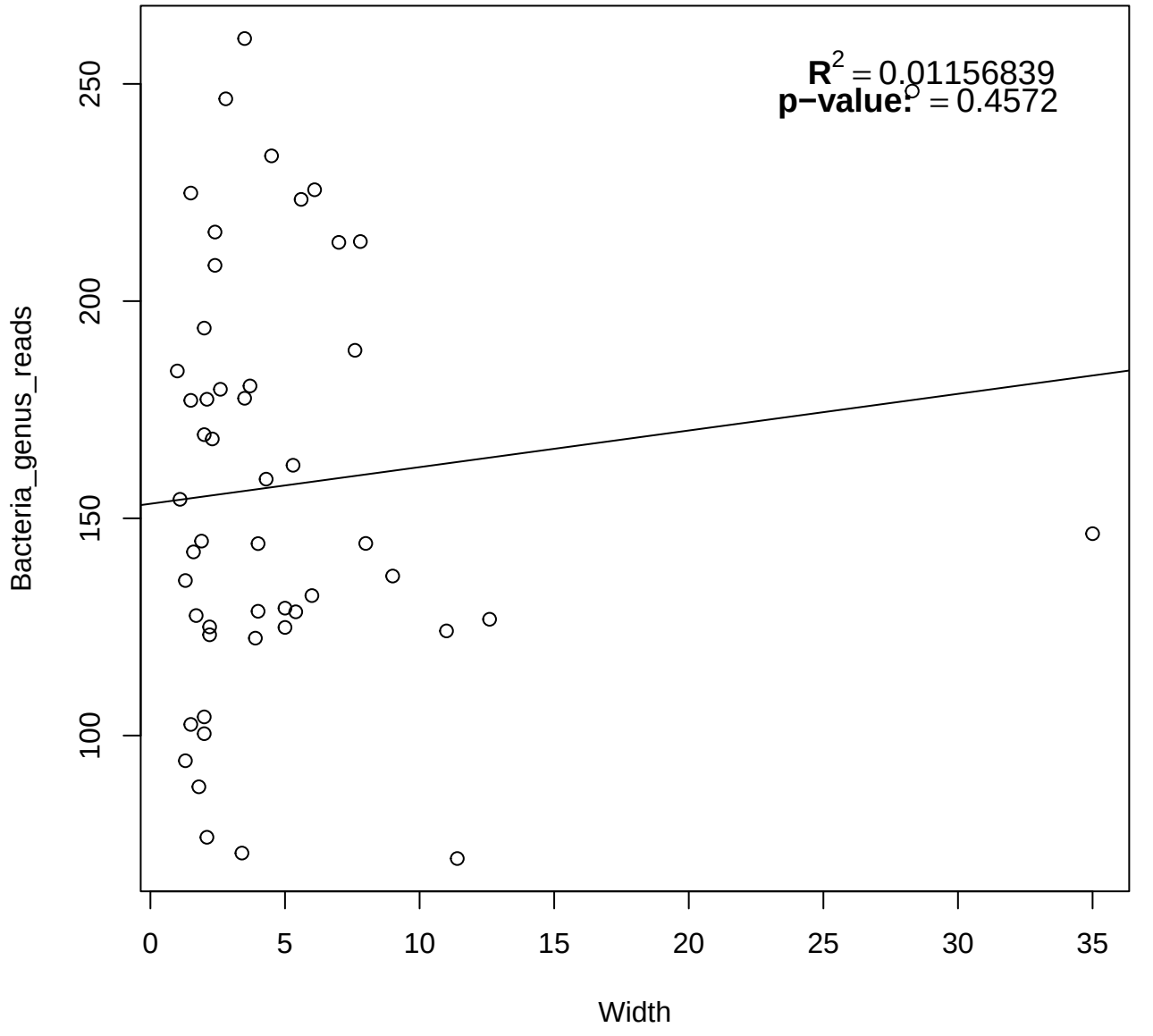

Residuals vs Fitted
Residuals
Fitted values
SEL1
VEZ3
VEI1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
VEZ3
VEI1
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
VEZ3
VEI1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
CasM1
NES1
Cook's distance

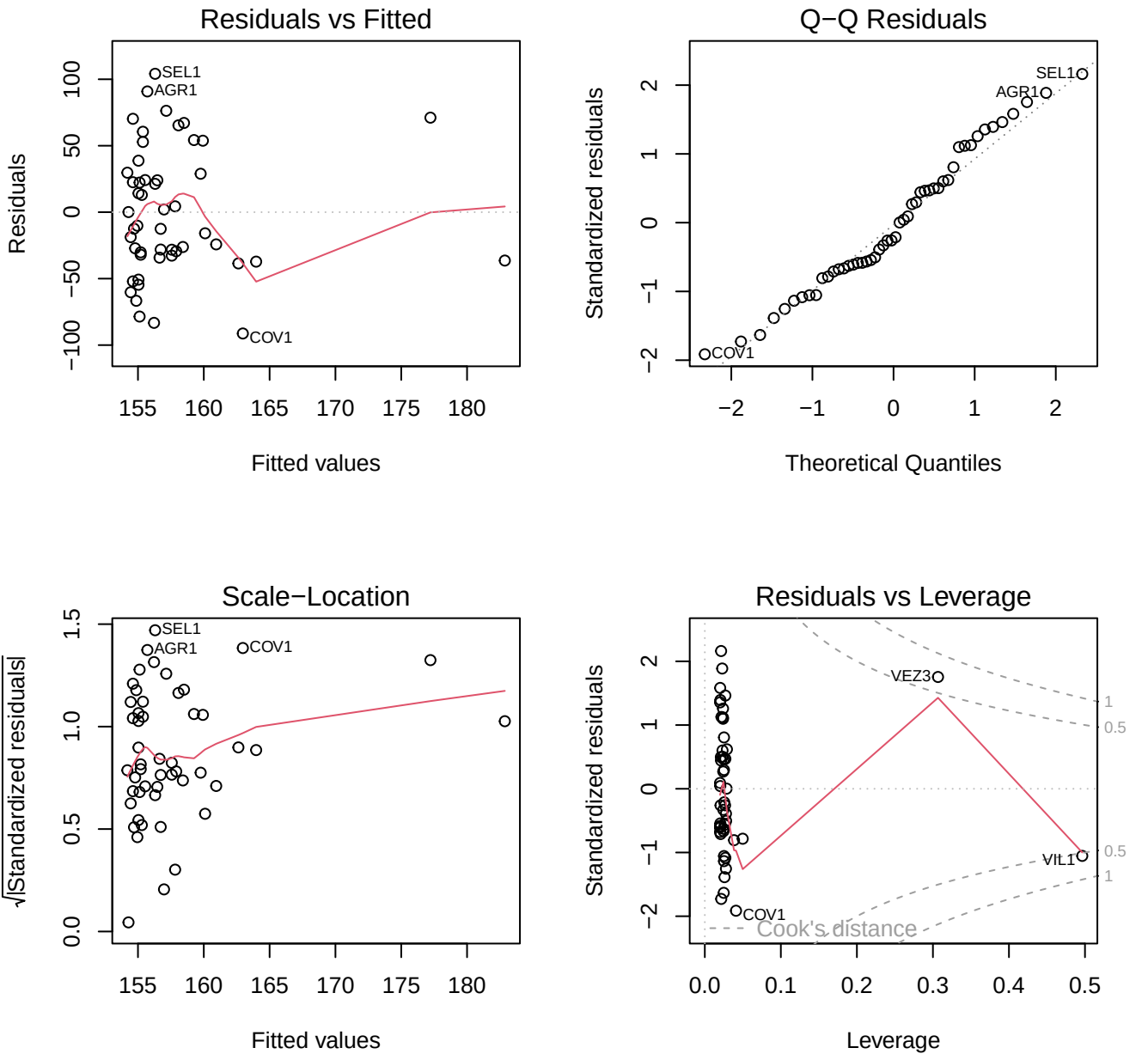

$R^2 = 0.01418552$
p−value: = 0.41
Bacteria_genus_reads
100
150
200
250
1.0
1.5
2.0
2.5
3.0
3.5
4.0
mean.Depth

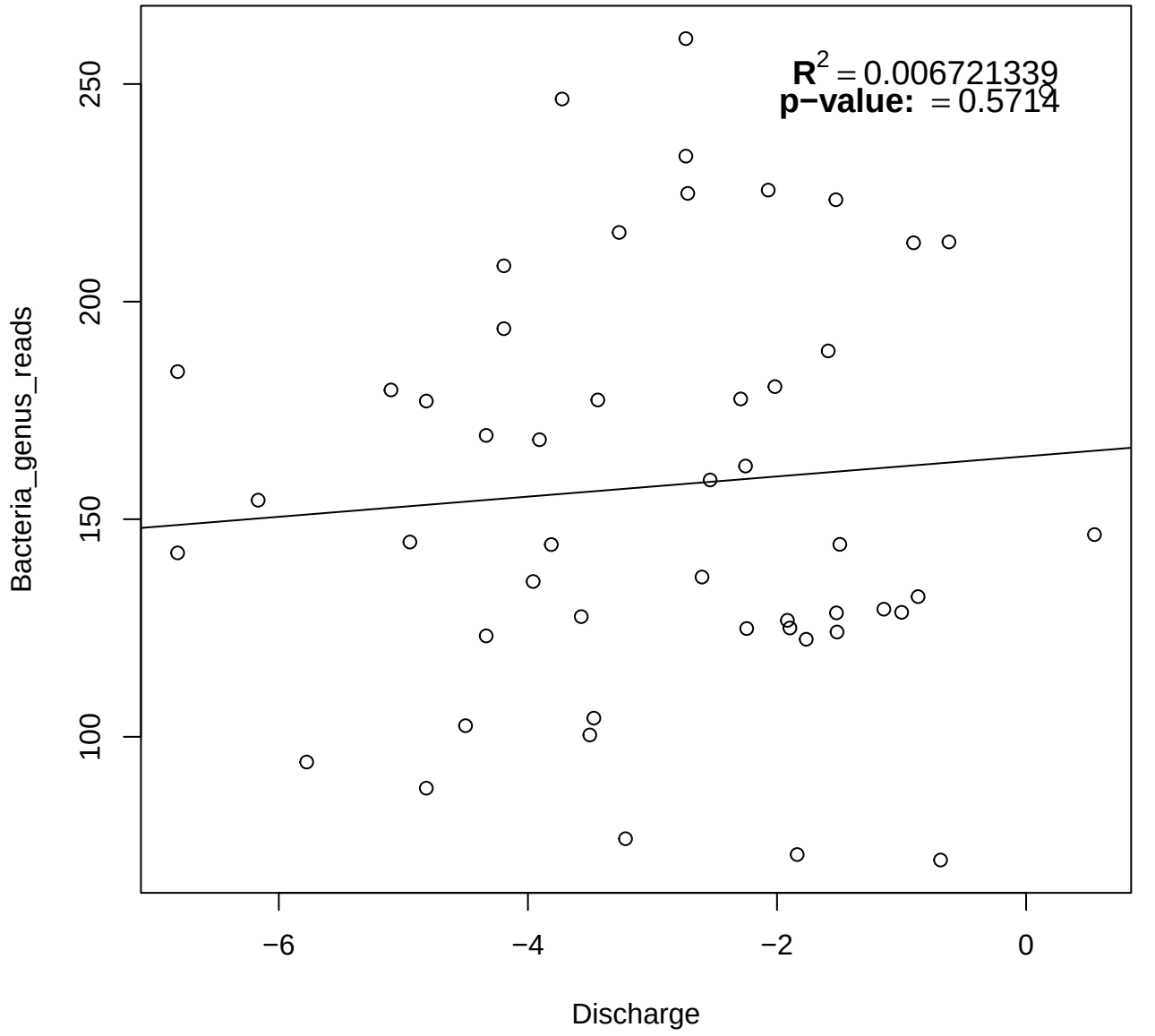

Residuals vs Fitted
Residuals
Fitted values
AGR1
SEL1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
AGR1
SEL1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
AGR1
SEL1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
CasM1
TAve1
COV1
Cook's distance
0.5
0.5

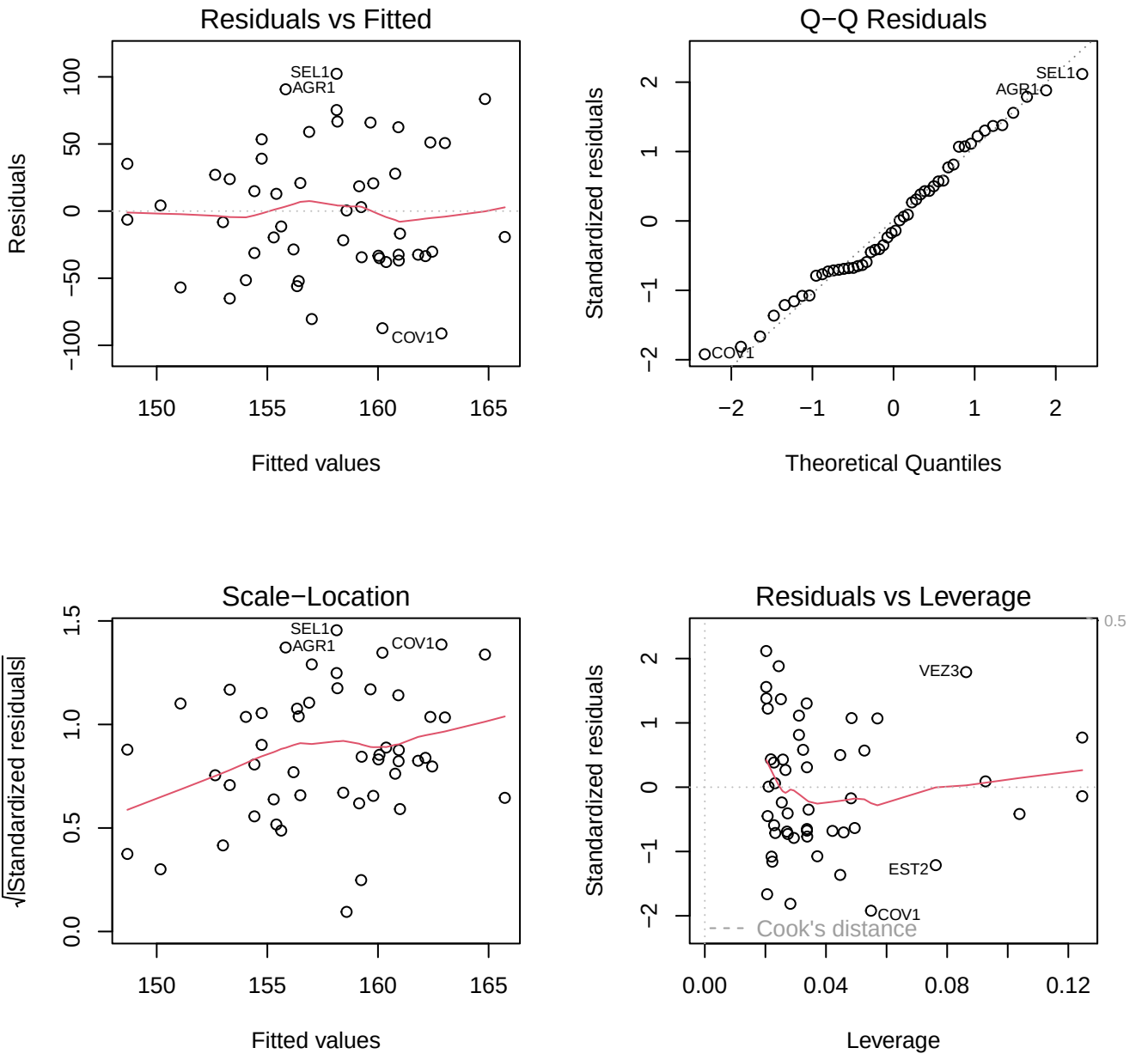

$R^2 = 0.02063275$
p−value: = 0.3196
Bacteria_genus_reads
250
200
150
100
0.1
0.2
0.3
0.4
0.5
mean.Velocity

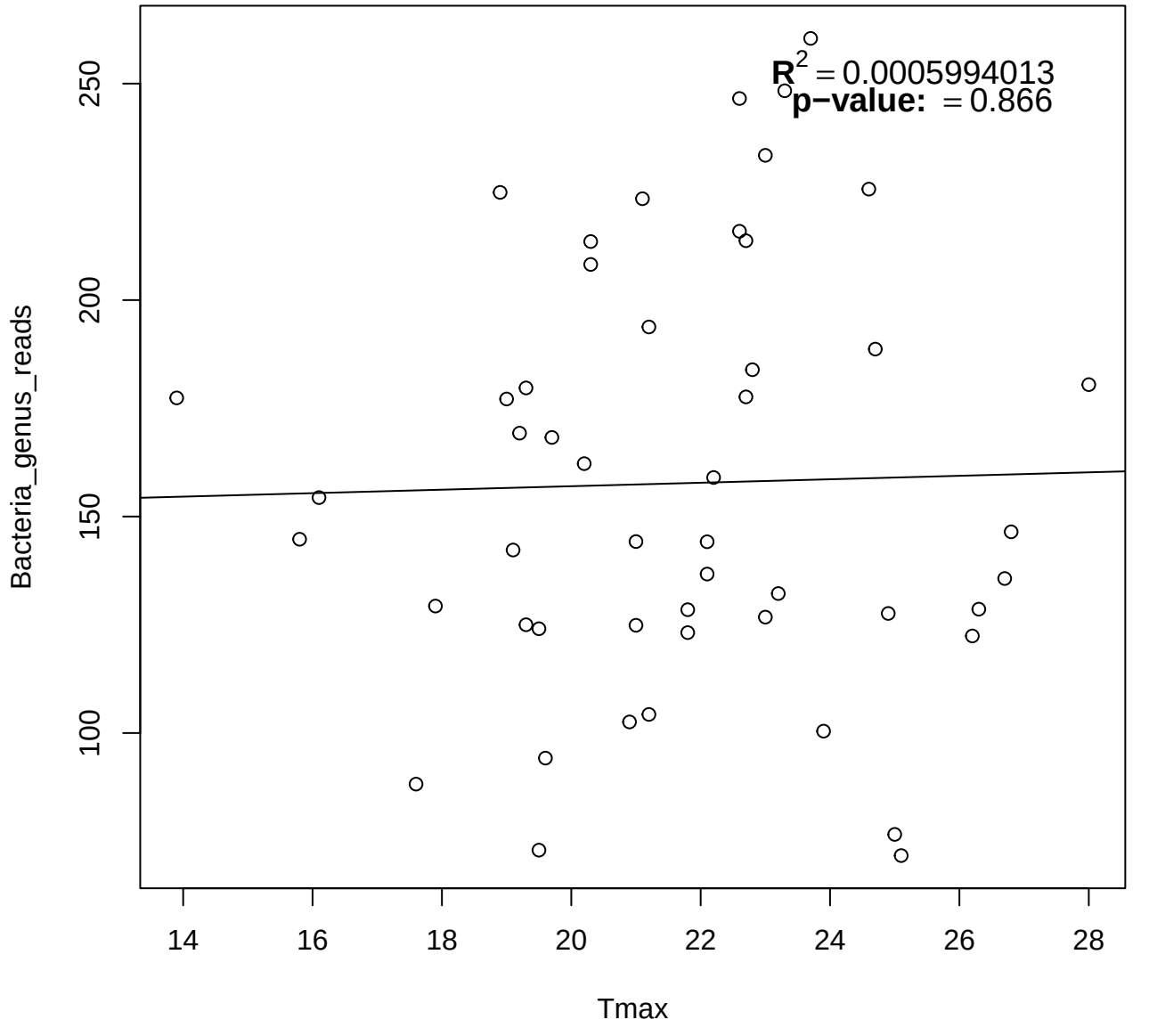

Residuals vs Fitted
Residuals
Fitted values
VEZ3
SEL1
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Standardized residuals
Leverage
VEZ3
CBR1
VEI1
Cook's distance
0.5

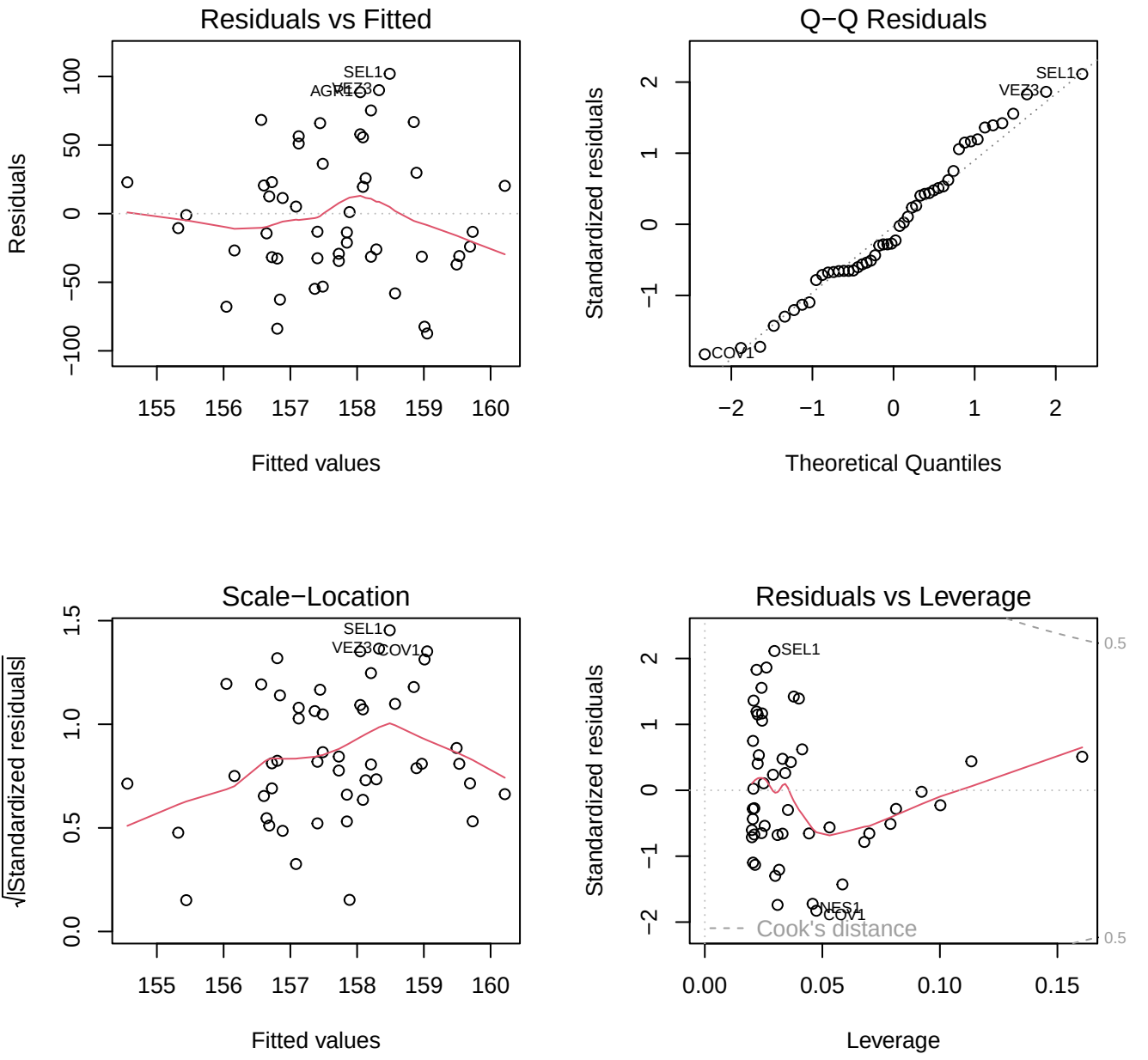

$R^2 = 0.01156839$
p−value: = 0.4572
Bacteria_genus_reads
Width
100
150
200
250
0
5
10
15
20
25
30
35

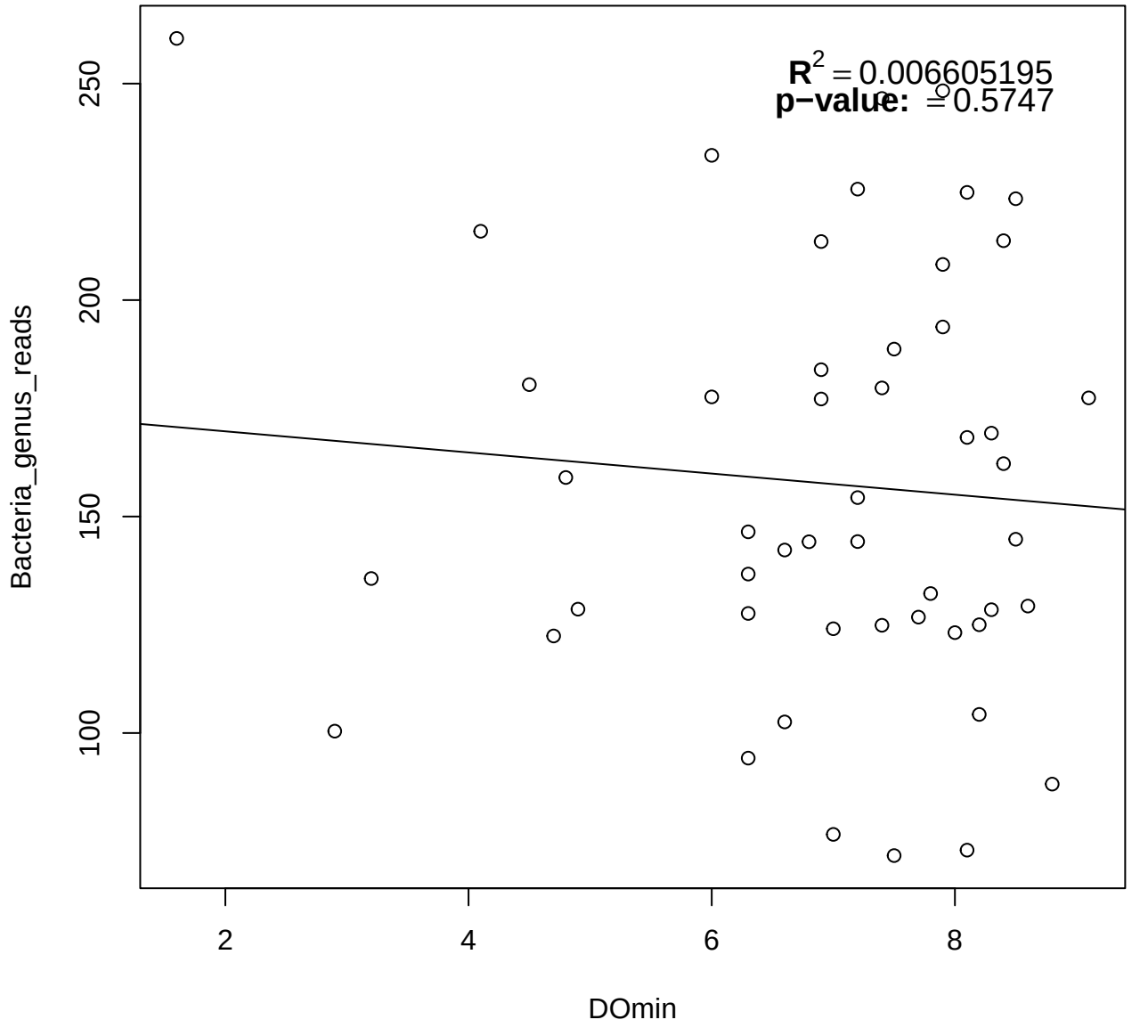

Residuals vs Fitted
Residuals
Fitted values
SEL1
AGR1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
AGR1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
AGR1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
VEZ3
VIL1
COV1
Cook's distance

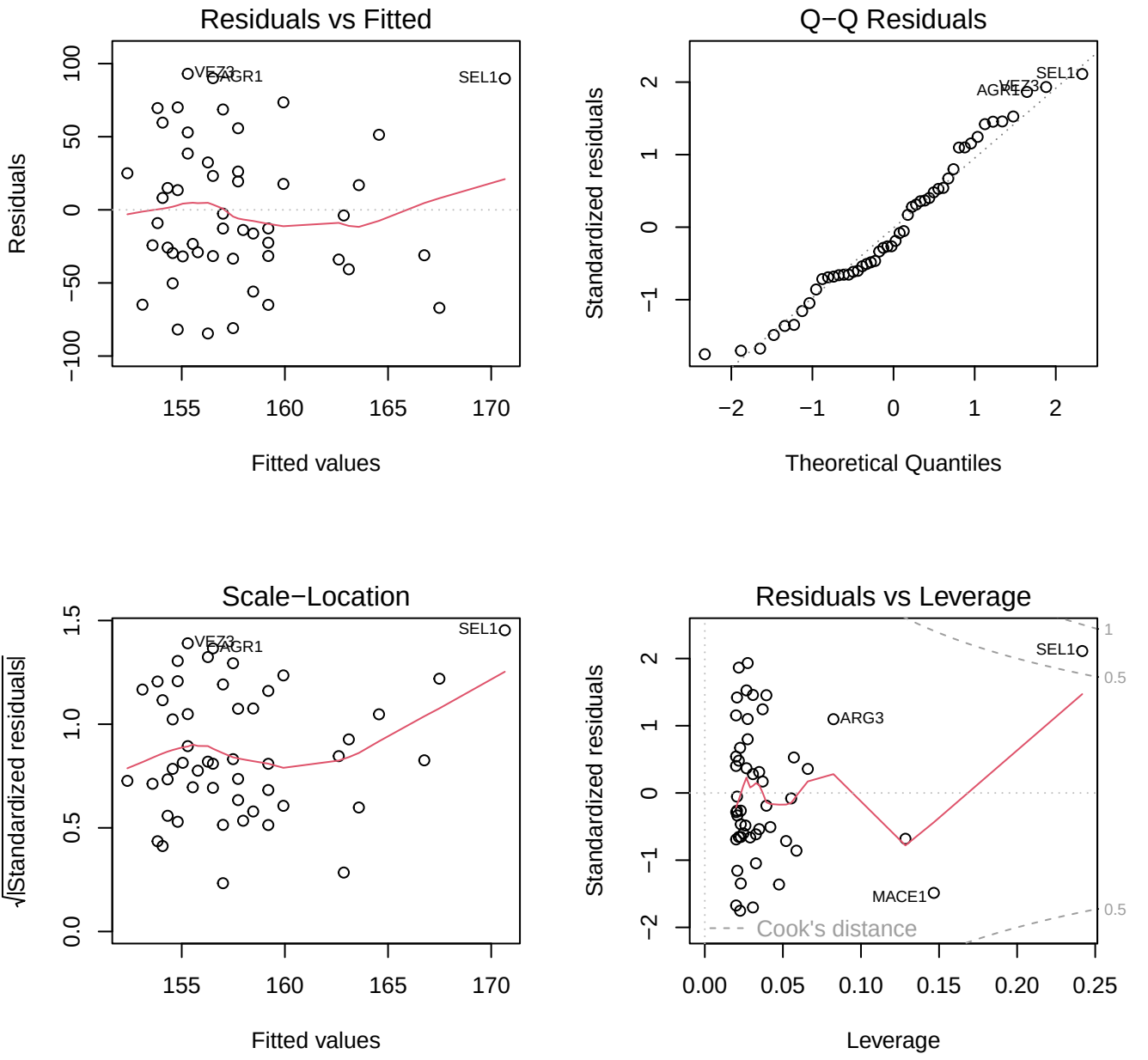

$R^2 = 0.006721339$
p−value: = 0.5714
Bacteria_genus_reads
Discharge
250
200
150
100
−6
−4
−2
0

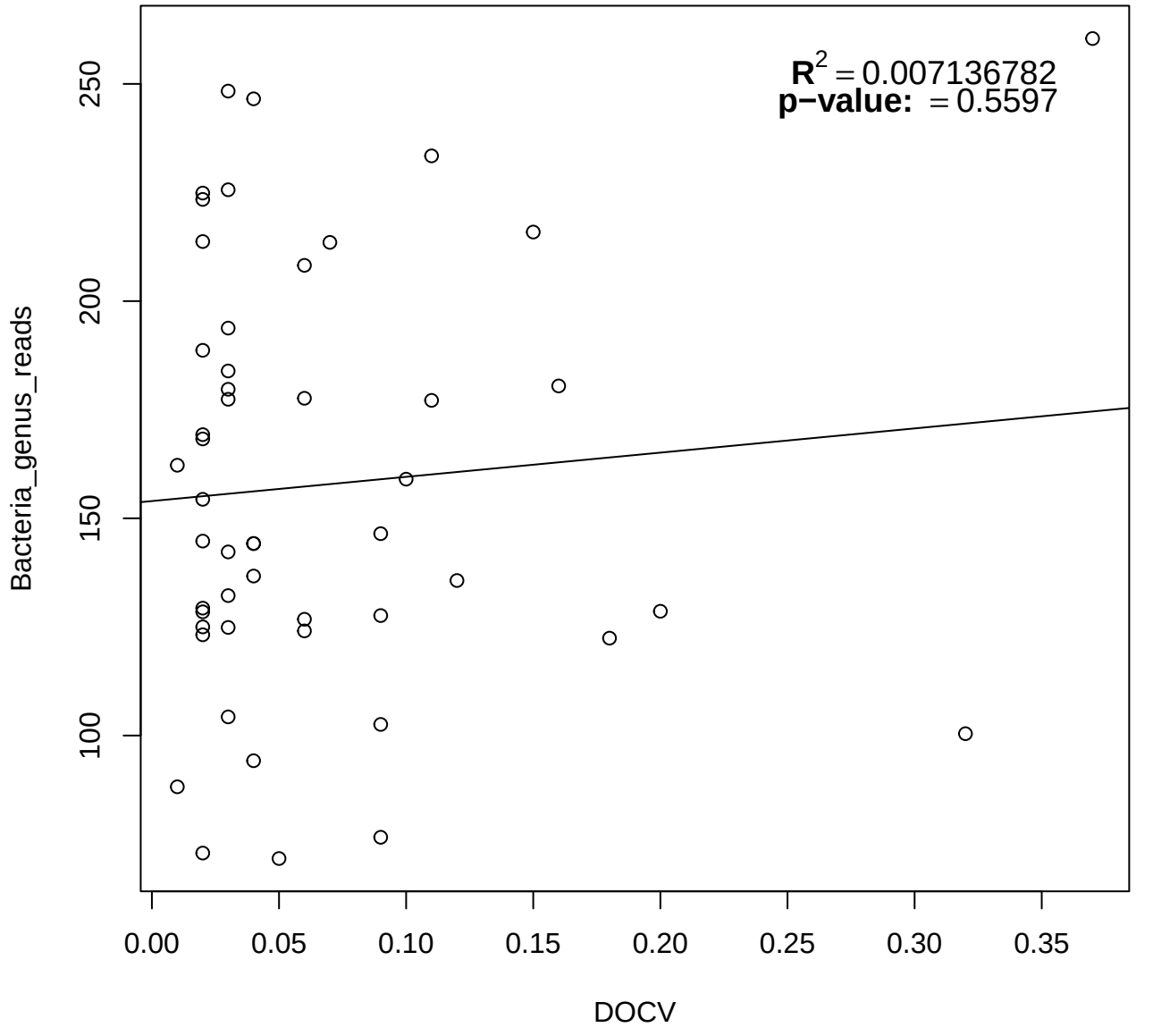

Residuals vs Fitted
Residuals
Fitted values
SEL1
AGR1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
AGR1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
AGR1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
VEZ3
EST2
COV1
Cook's distance
0.5

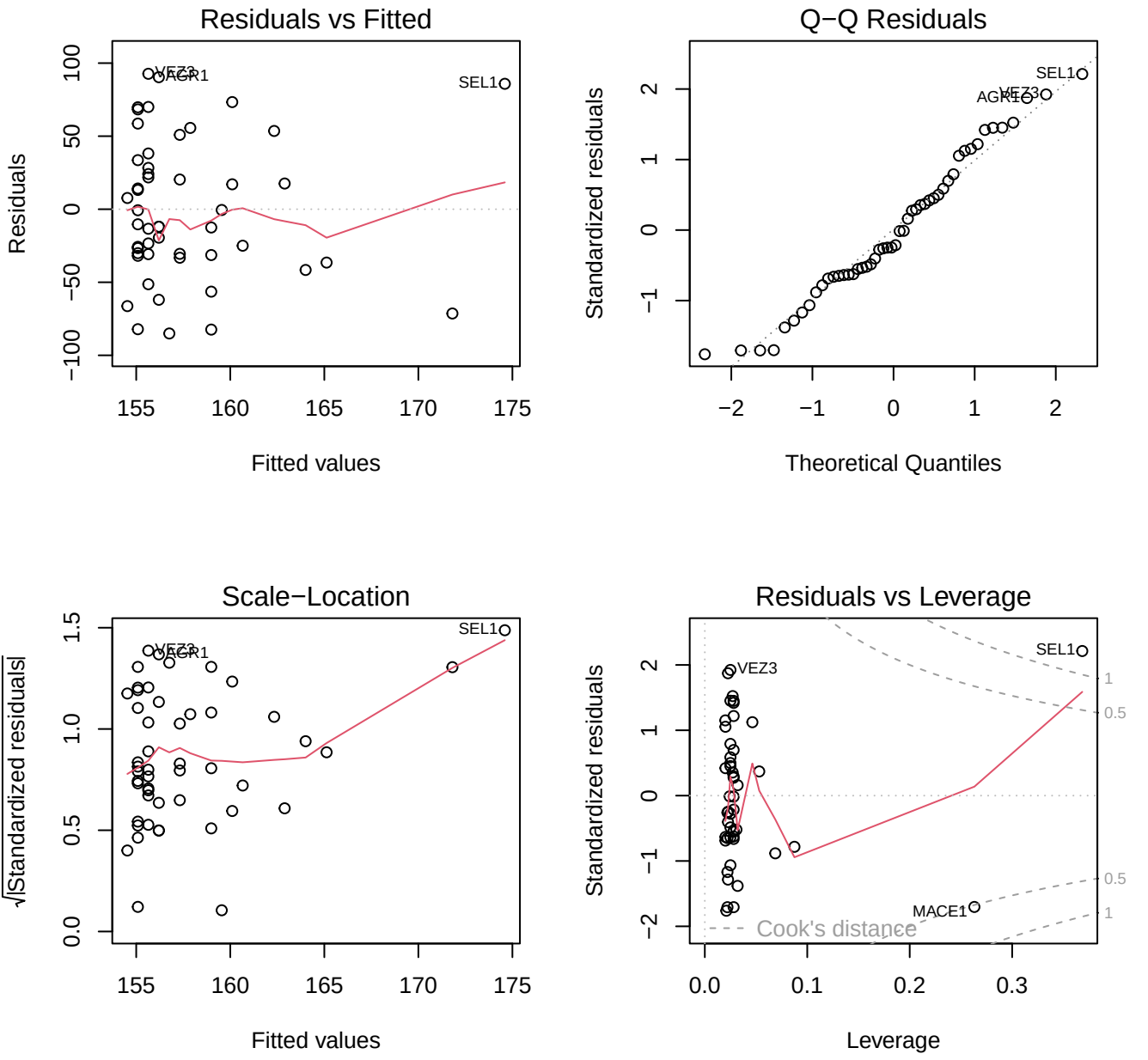

$R^2 = 0.0005994013$
p−value: = 0.866
Bacteria_genus_reads
100
150
200
250
14
16
18
20
22
24
26
28
Tmax

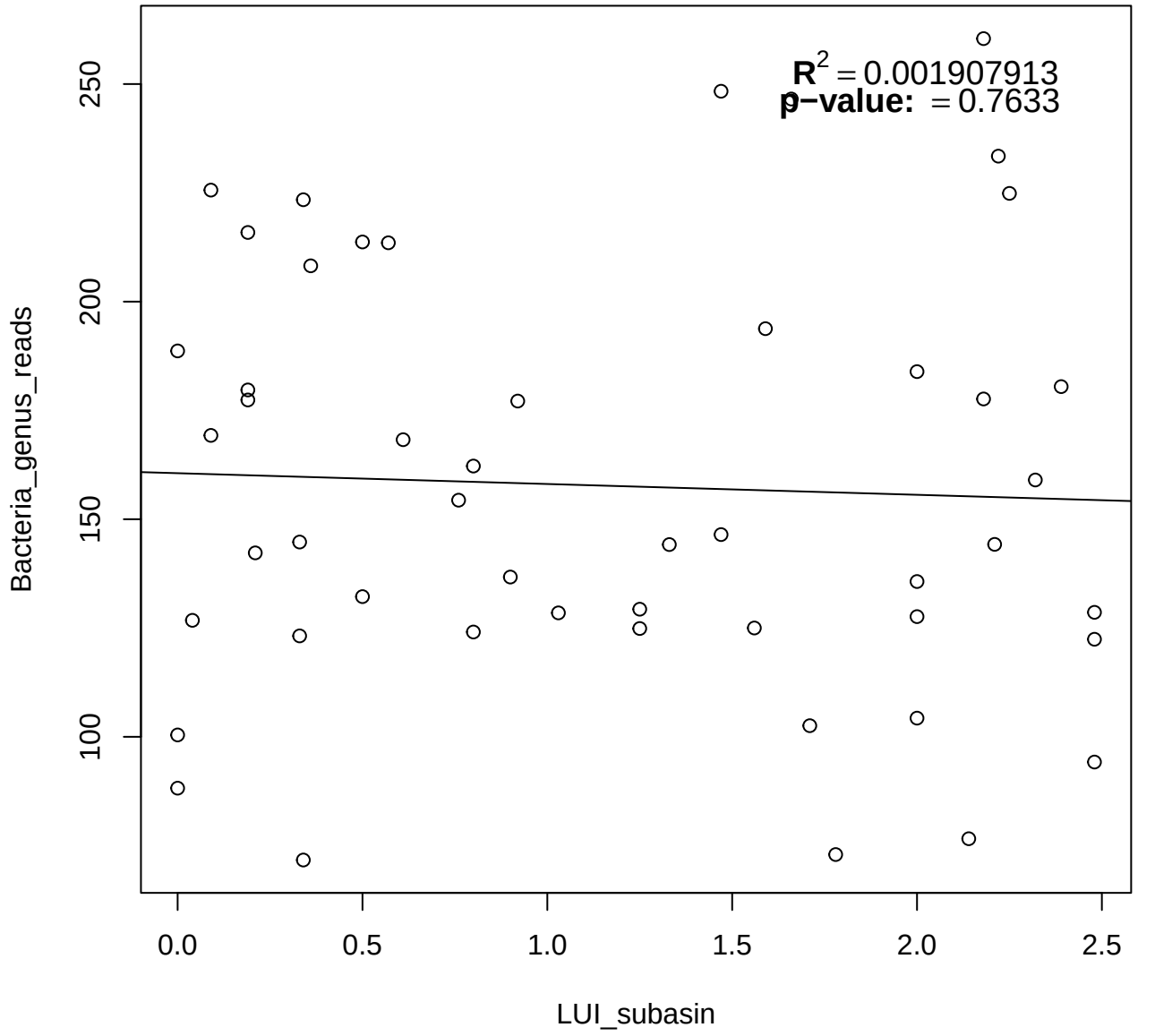

Residuals vs Fitted
Residuals
Fitted values
SEL1
VEZ3
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
VEZ3
COV1
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
VEZ3
COV1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
NES1
COV1
Cook's distance
0.5
0.5

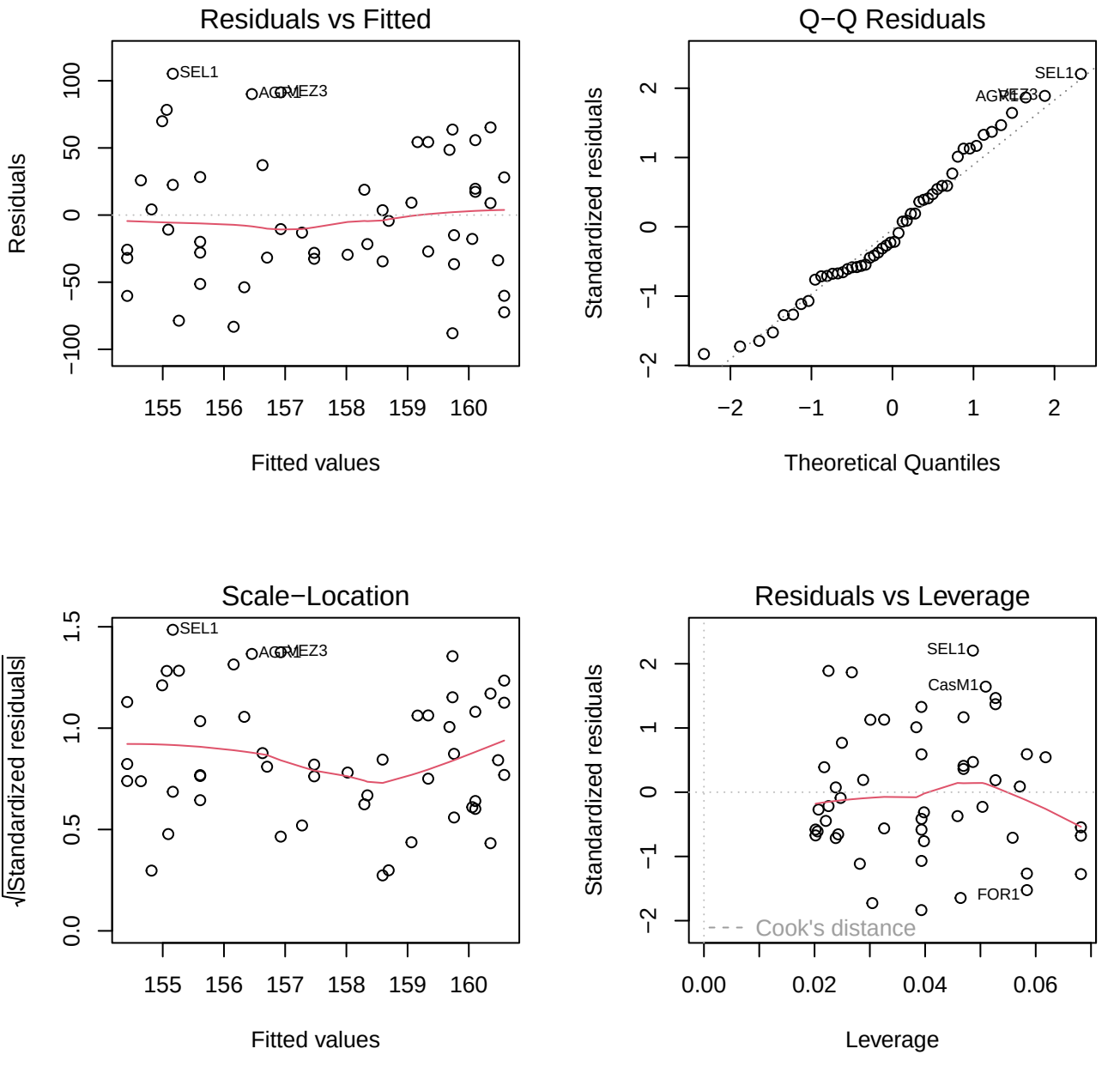

$R^2 = 0.006605195$
p−value: = 0.5747
Bacteria_genus_reads
250
200
150
100
2
4
6
8
DOmin

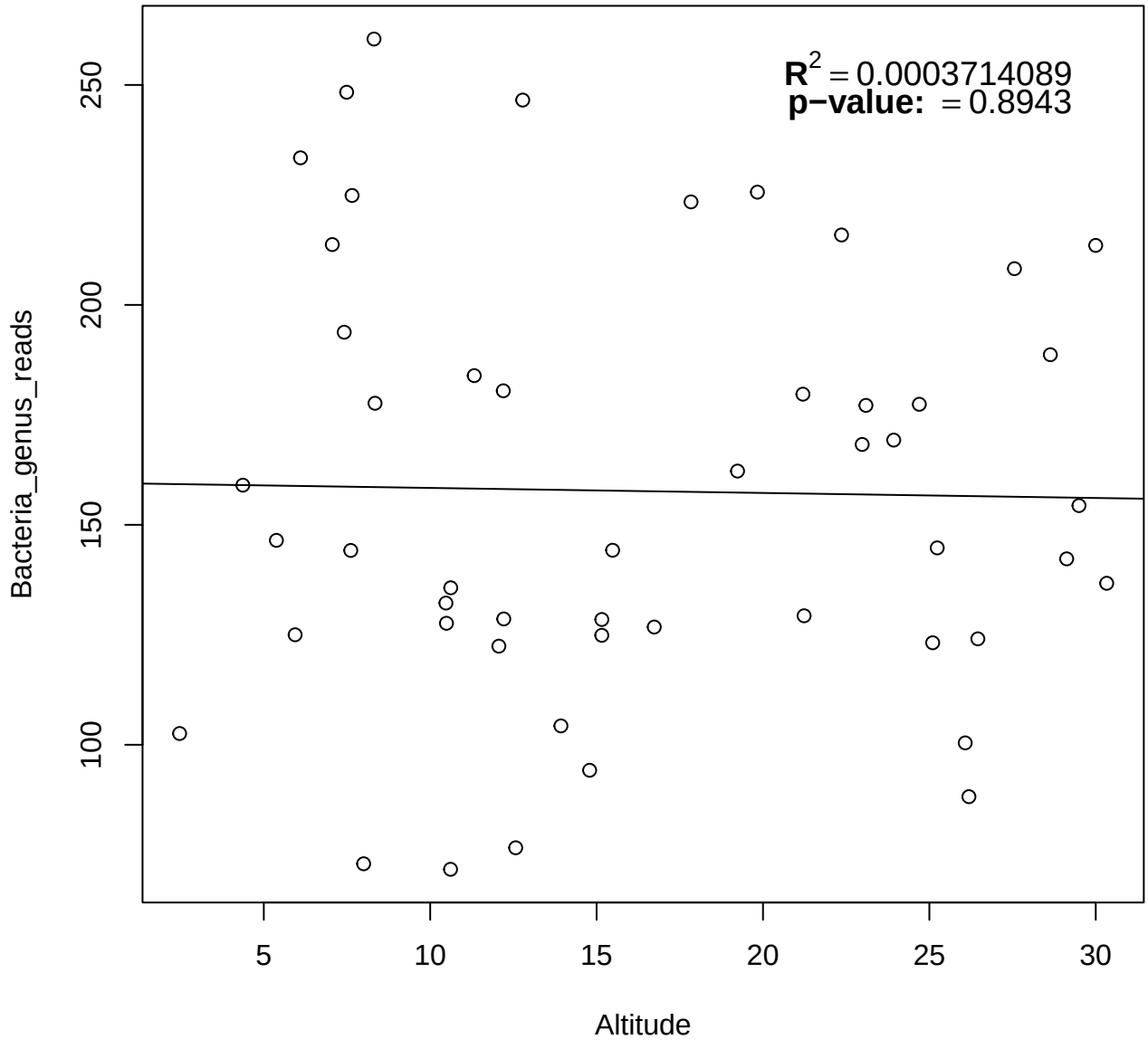

Residuals vs Fitted
Residuals
Fitted values
VEZ3
AGR1
SEL1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
AGR1
VEZ3
Scale−Location
√|Standardized residuals|
Fitted values
VEZ3
AGR1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
ARG3
MACE1
Cook's distance
1
0.5
0.5

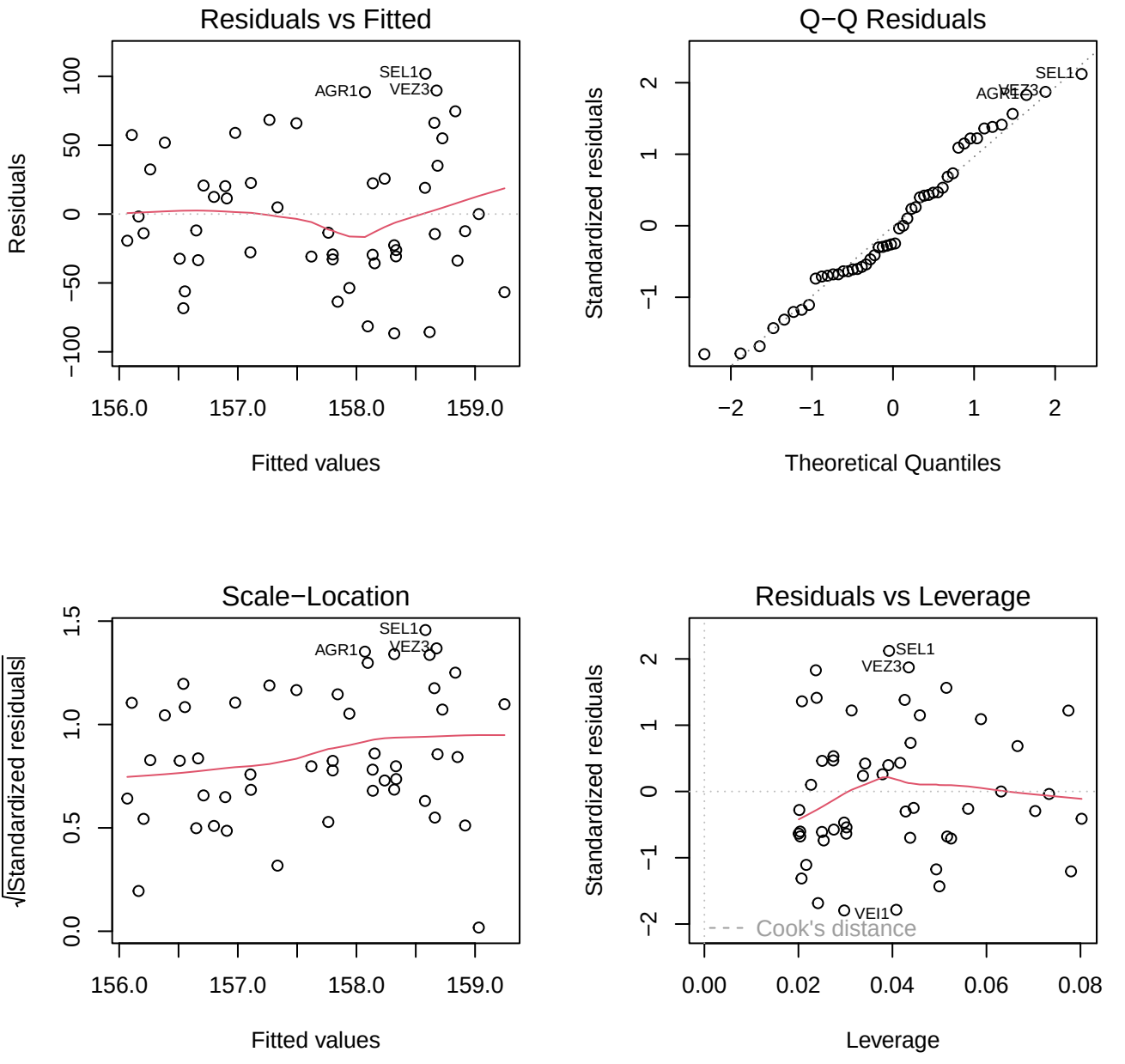

$R^2 = 0.007136782$
p−value: = 0.5597
Bacteria_genus_reads
100
150
200
250
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
DOCV

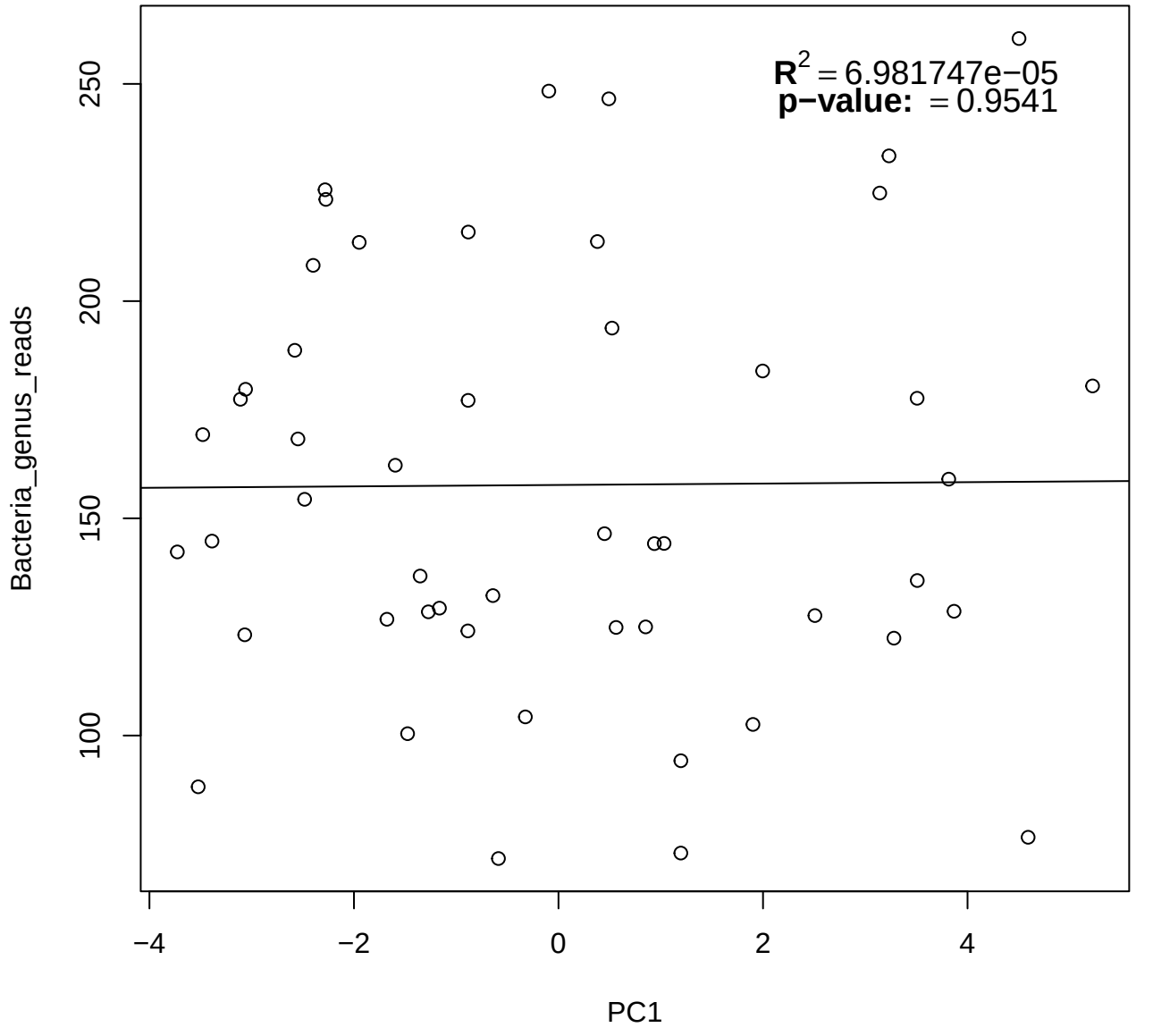

Residuals vs Fitted
Residuals
Fitted values
VEZ3
AGR1
SEL1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
AGR1
VEZ3
Scale−Location
√|Standardized residuals|
Fitted values
VEZ3
AGR1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
VEZ3
MACE1
Cook's distance

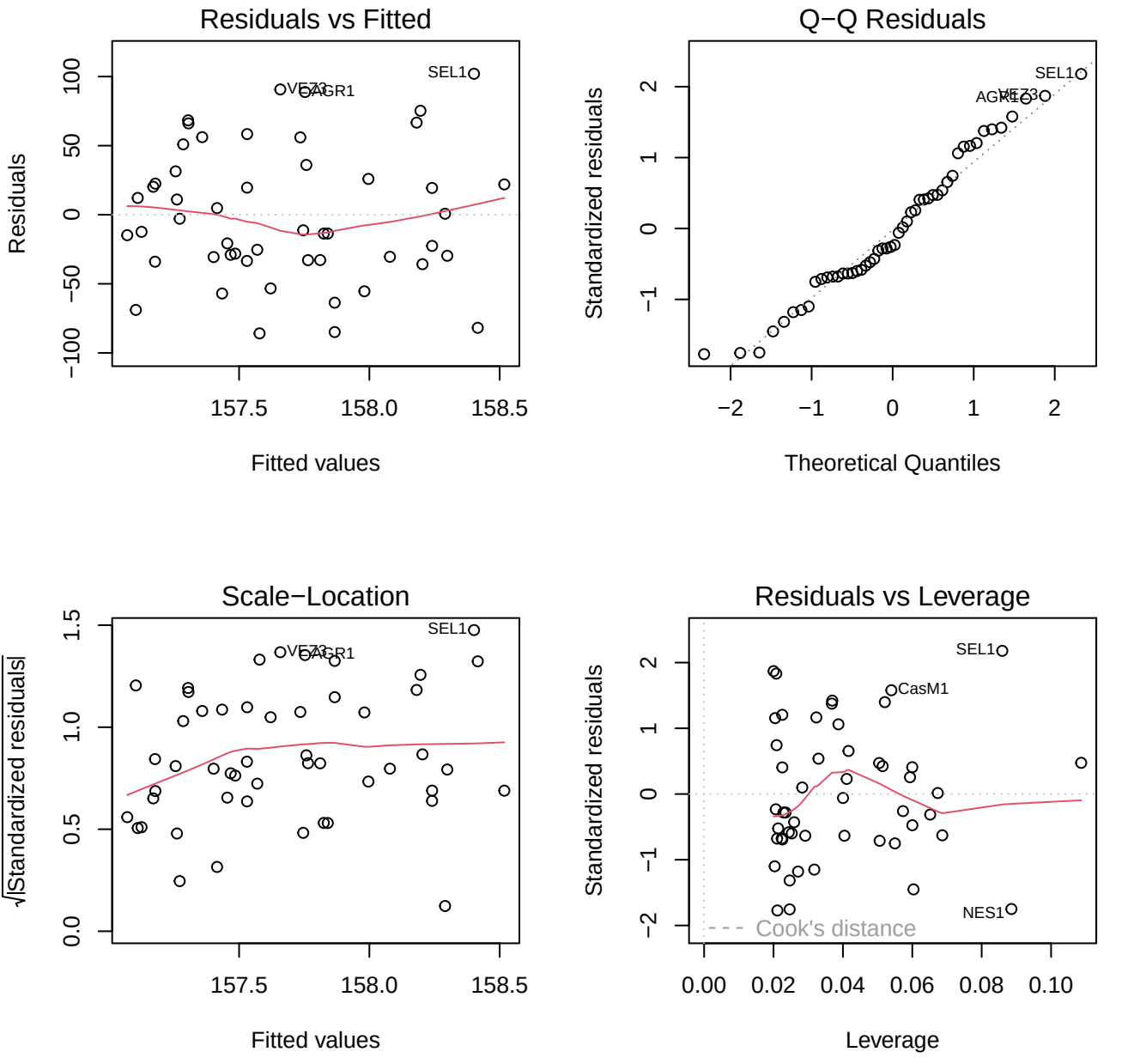

$R^2 = 0.001907913$
p−value: = 0.7633
Bacteria_genus_reads
LUI_subasin
100
150
200
250
0.0
0.5
1.0
1.5
2.0
2.5

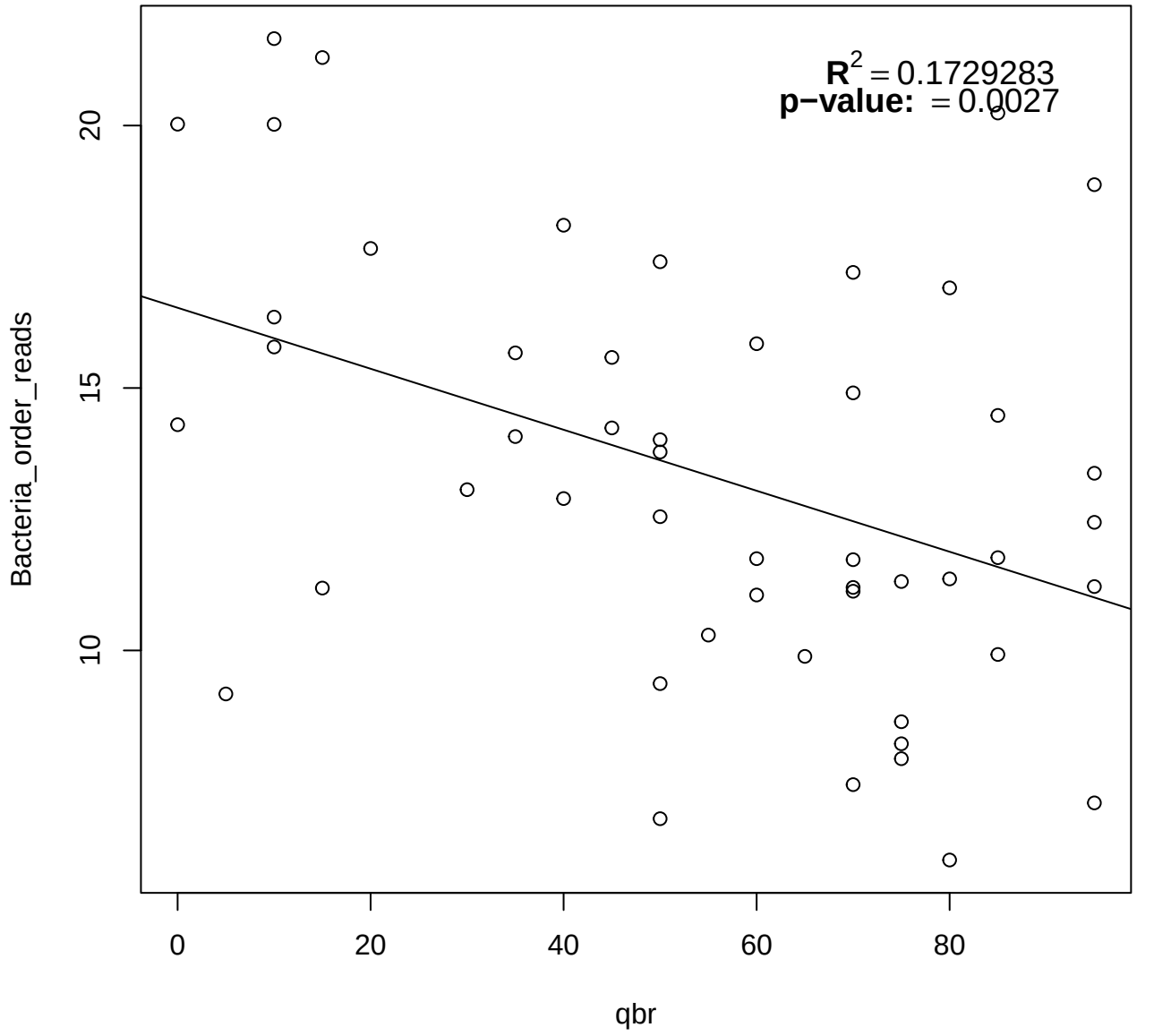

Residuals vs Fitted
Residuals
Fitted values
SEL1
AGRMEZ3
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
AGRMEZ3
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
AGRMEZ3
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
CasM1
FOR1
Cook's distance

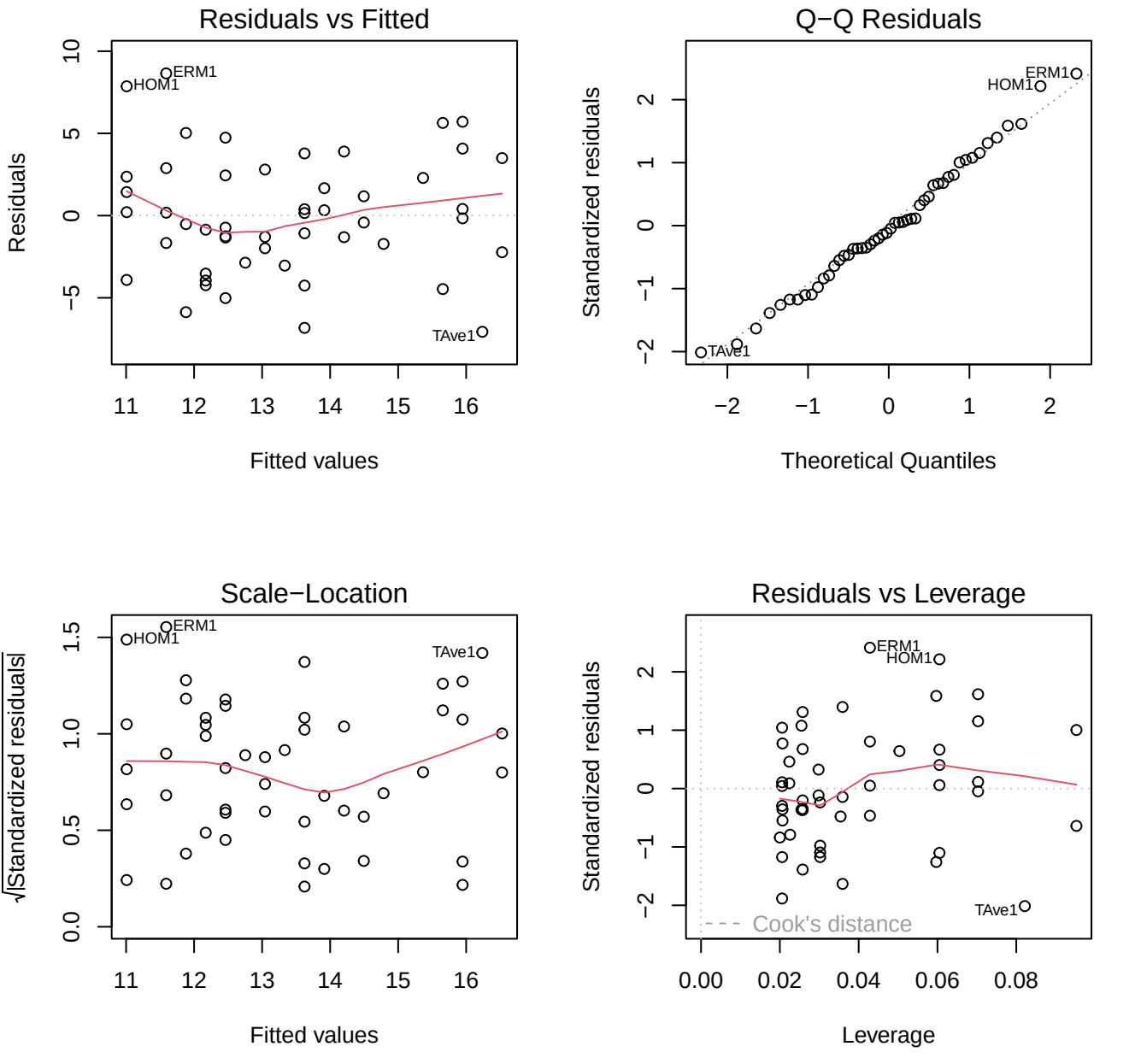

$R^2 = 0.0003714089$
p−value: = 0.8943
Bacteria_genus_reads
100
150
200
250
5
10
15
20
25
30
Altitude

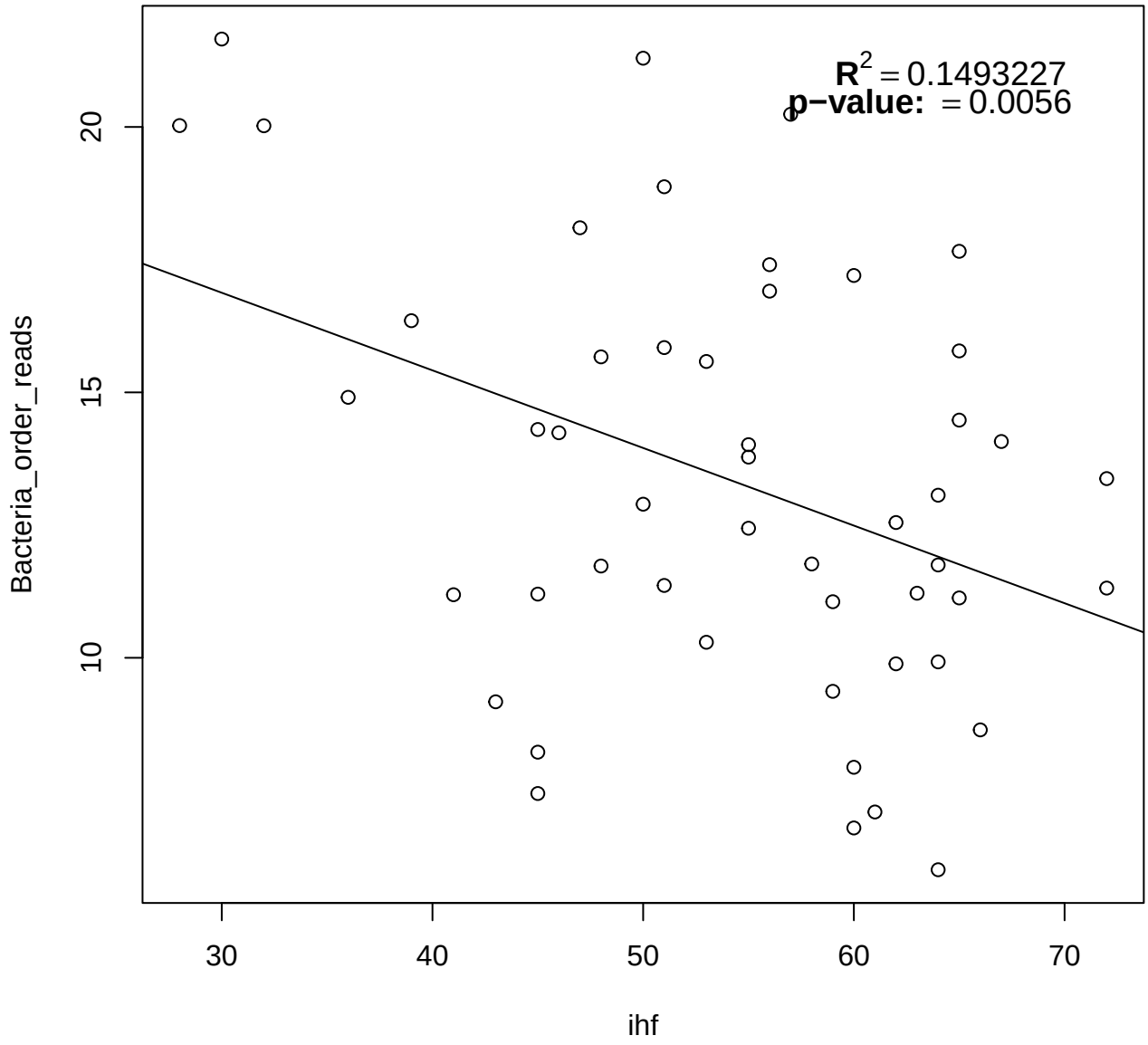

Residuals vs Fitted
Residuals
Fitted values
SEL1
AGR1
VEZ3
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
AGR1
VEZ3
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
AGR1
VEZ3
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
VEZ3
VEI1
Cook's distance

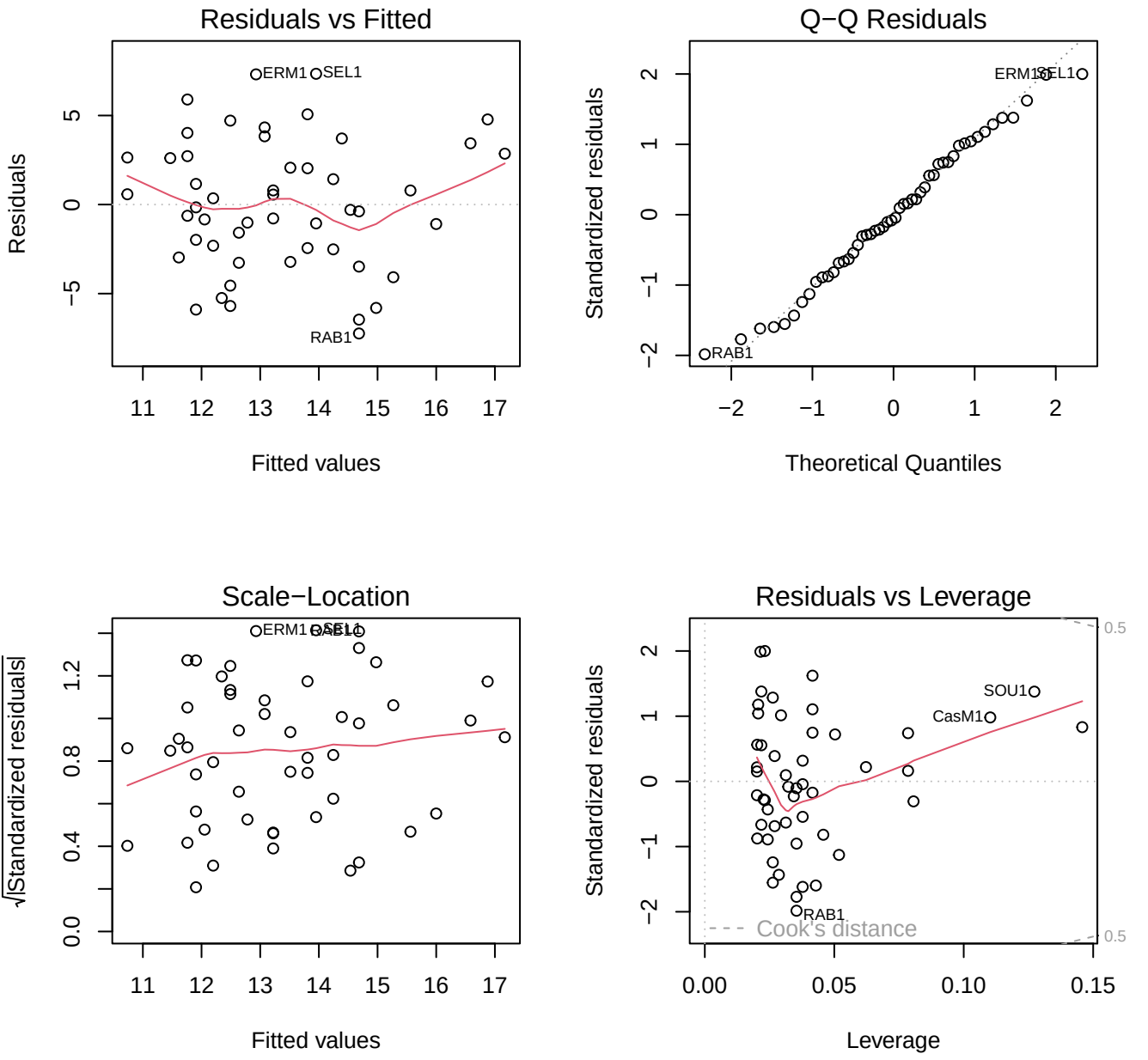

$R^2 = 6.981747e-05$
p−value: = 0.9541
Bacteria_genus_reads
250
200
150
100
−4
−2
0
2
4
PC1

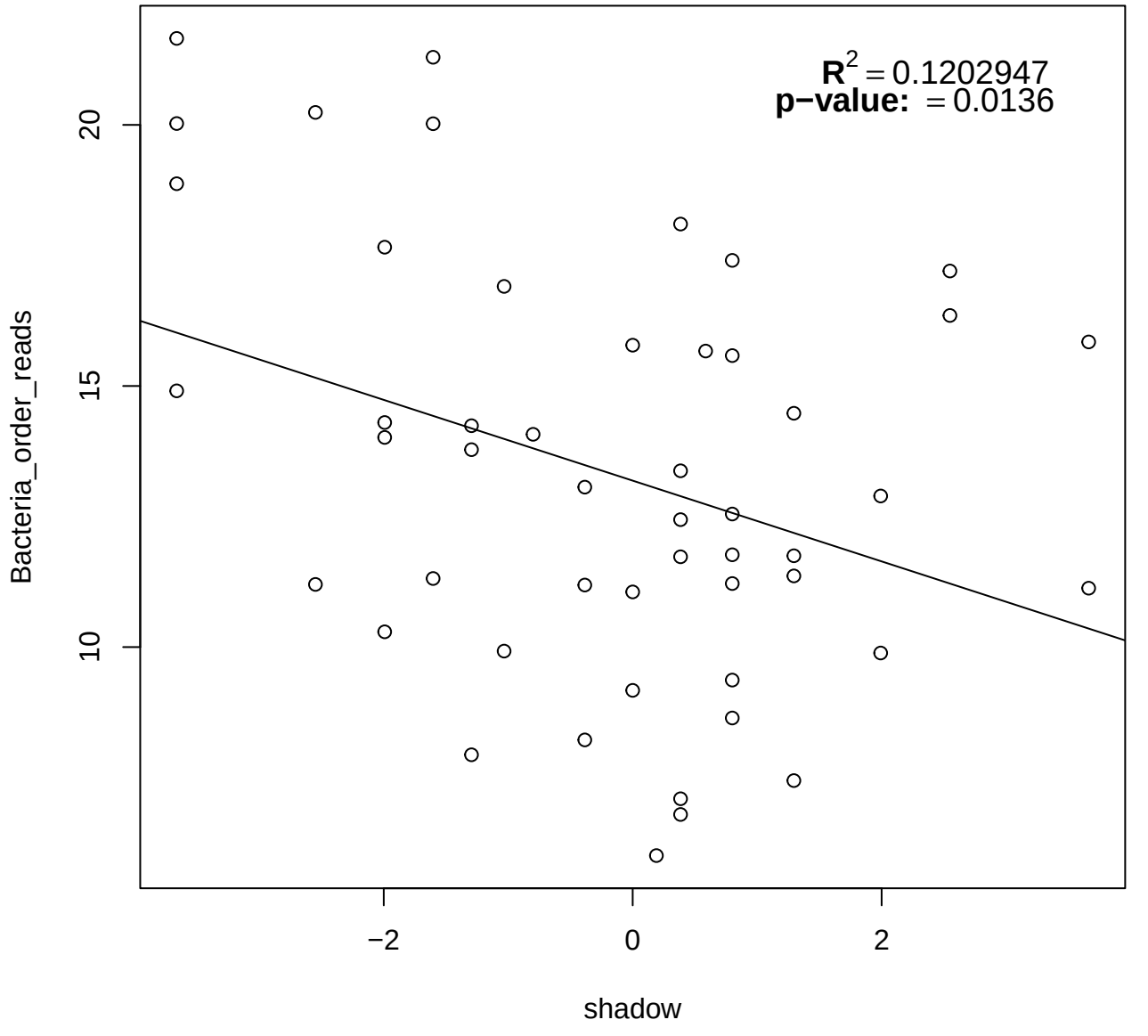

Residuals vs Fitted
Residuals
Fitted values
SEL1
VEZ3
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
AGR1
VEZ3
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
VEZ3
AGR1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
CasM1
NES1
Cook's distance

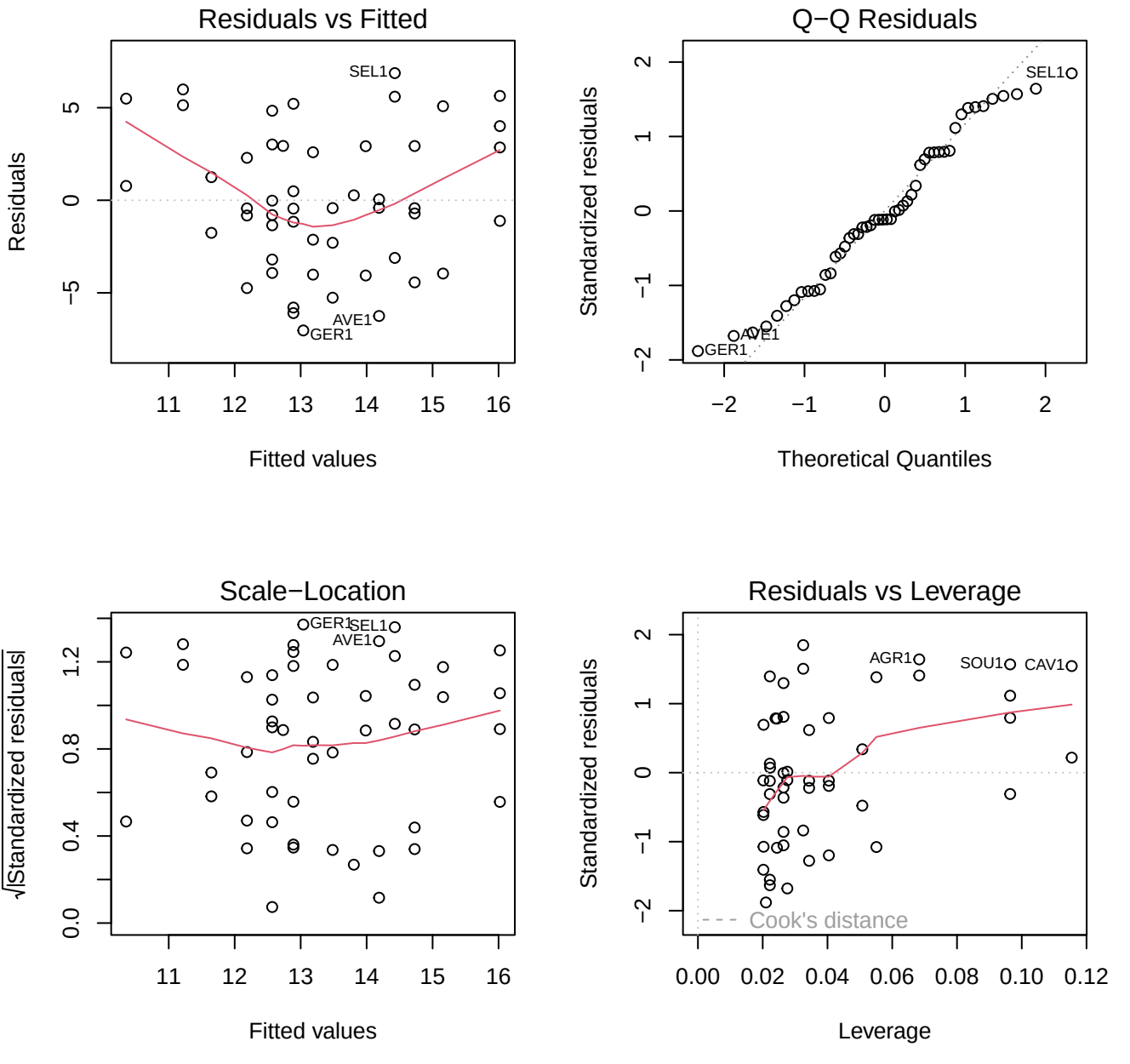

$R^2 = 0.1729283$
p−value: = 0.0027
Bacteria_order_reads
qbr
10
15
20
0
20
40
60
80

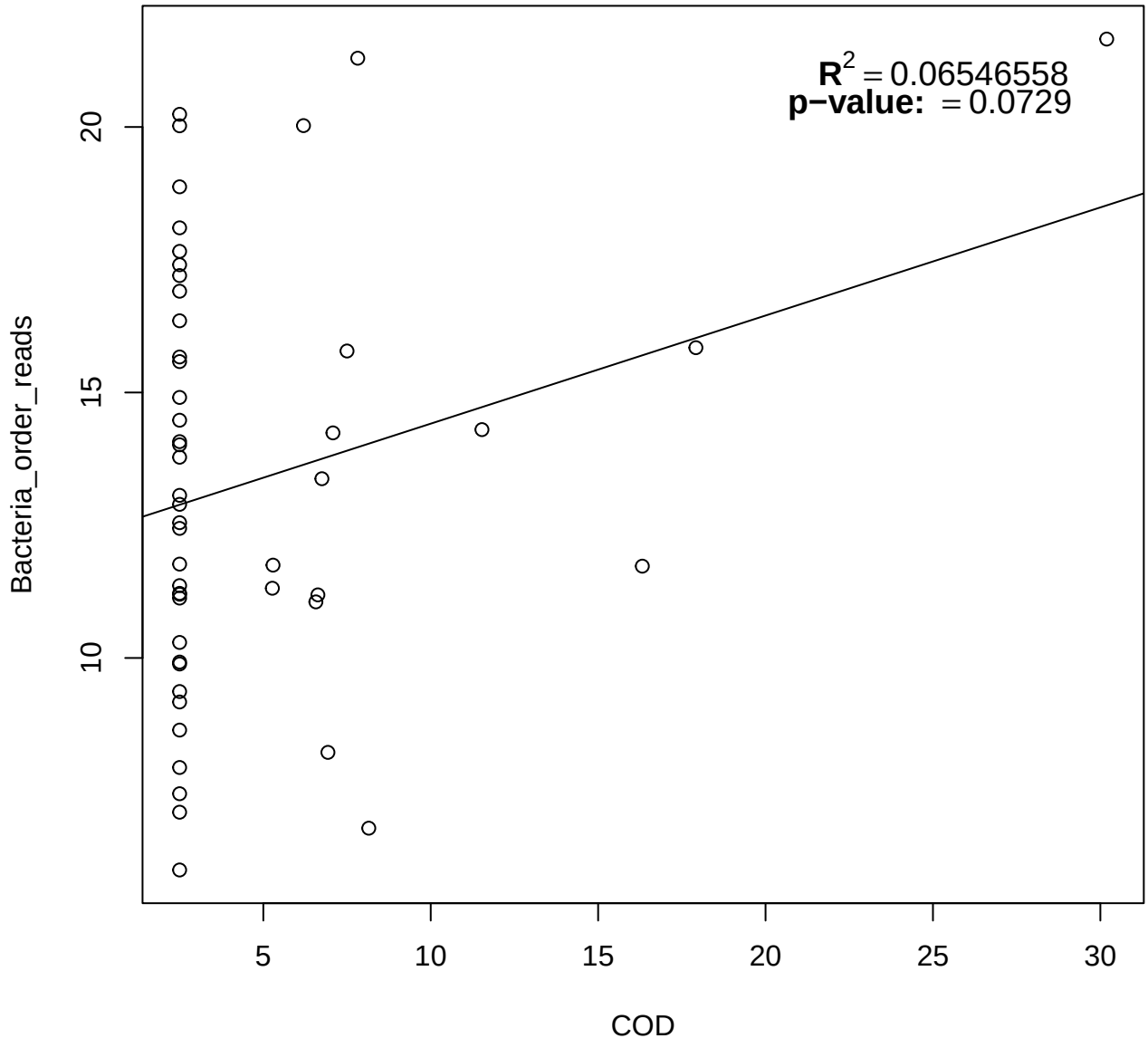

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
TAve1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
TAve1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
TAve1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
HOM1
TAve1
Cook's distance

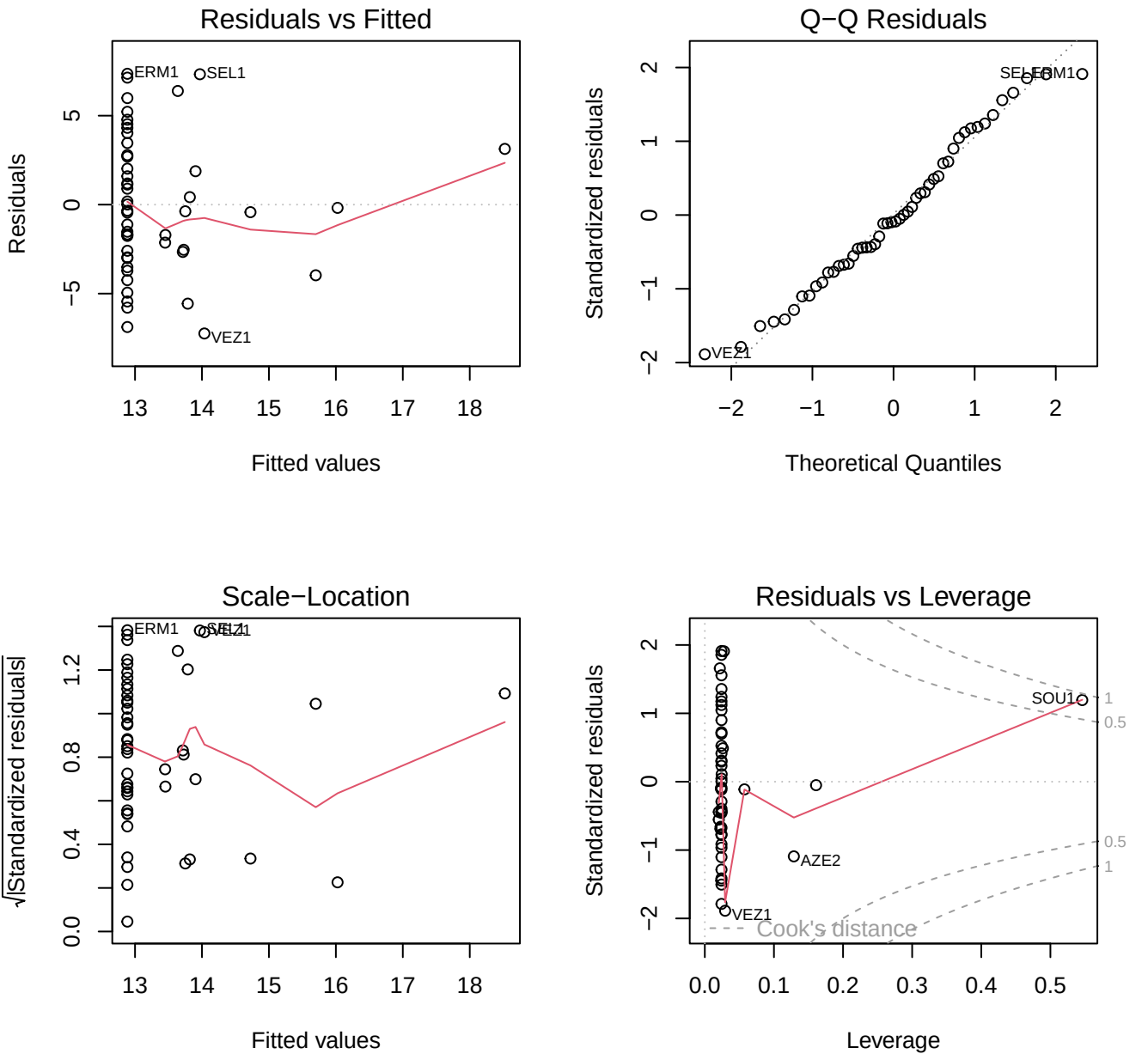

$R^2 = 0.1493227$
p−value: = 0.0056
Bacteria_order_reads
ihf
10
15
20
30
40
50
60
70

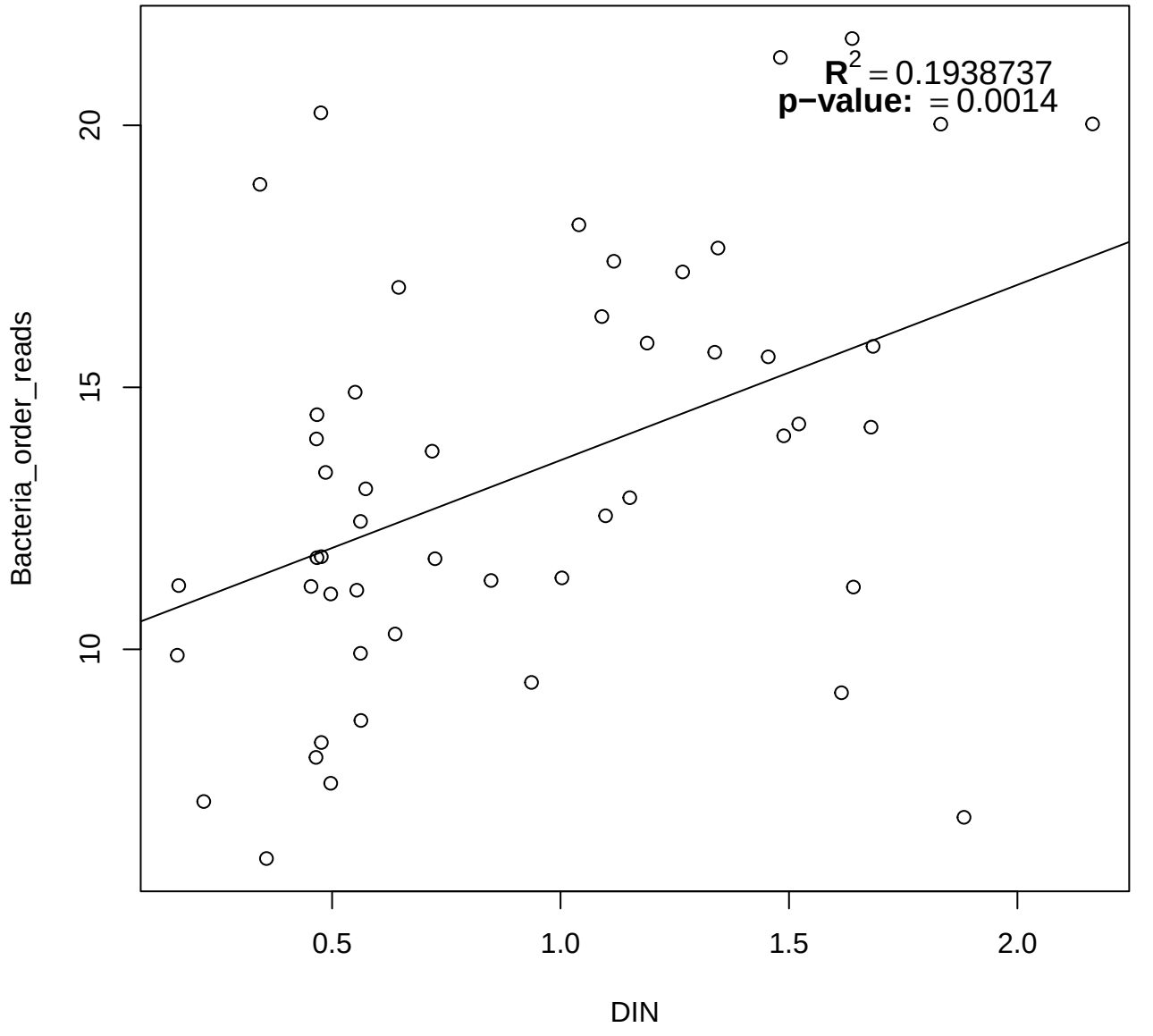

Residuals vs Fitted
Residuals
Fitted values
ERM1
SEL1
RAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
SEL1
RAB1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
SEL1
RAB1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
CasM1
RAB1
Cook's distance
0.5
0.5

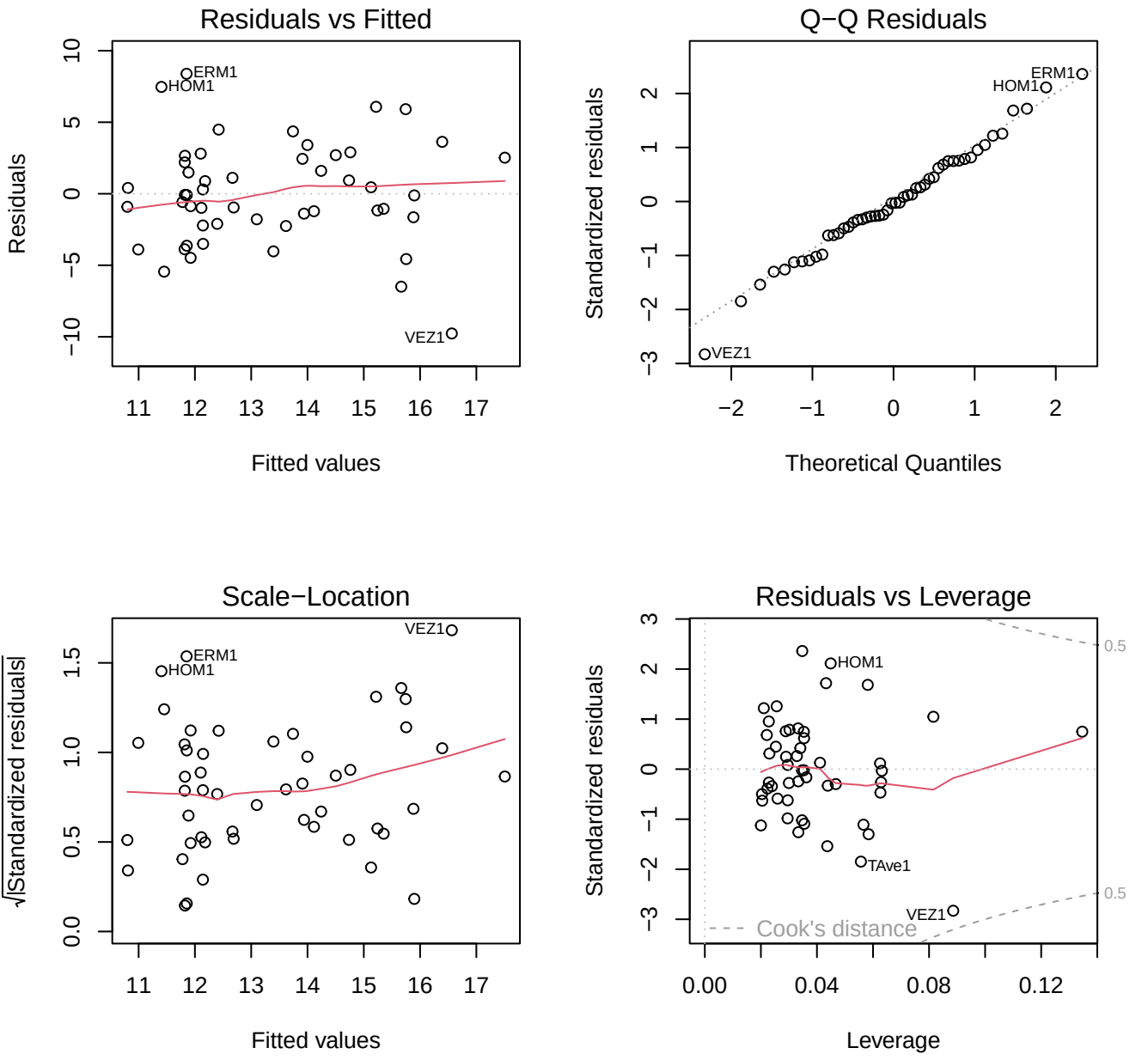

$R^2 = 0.1202947$
p−value: = 0.0136
Bacteria_order_reads
10
15
20
−2
0
2
shadow

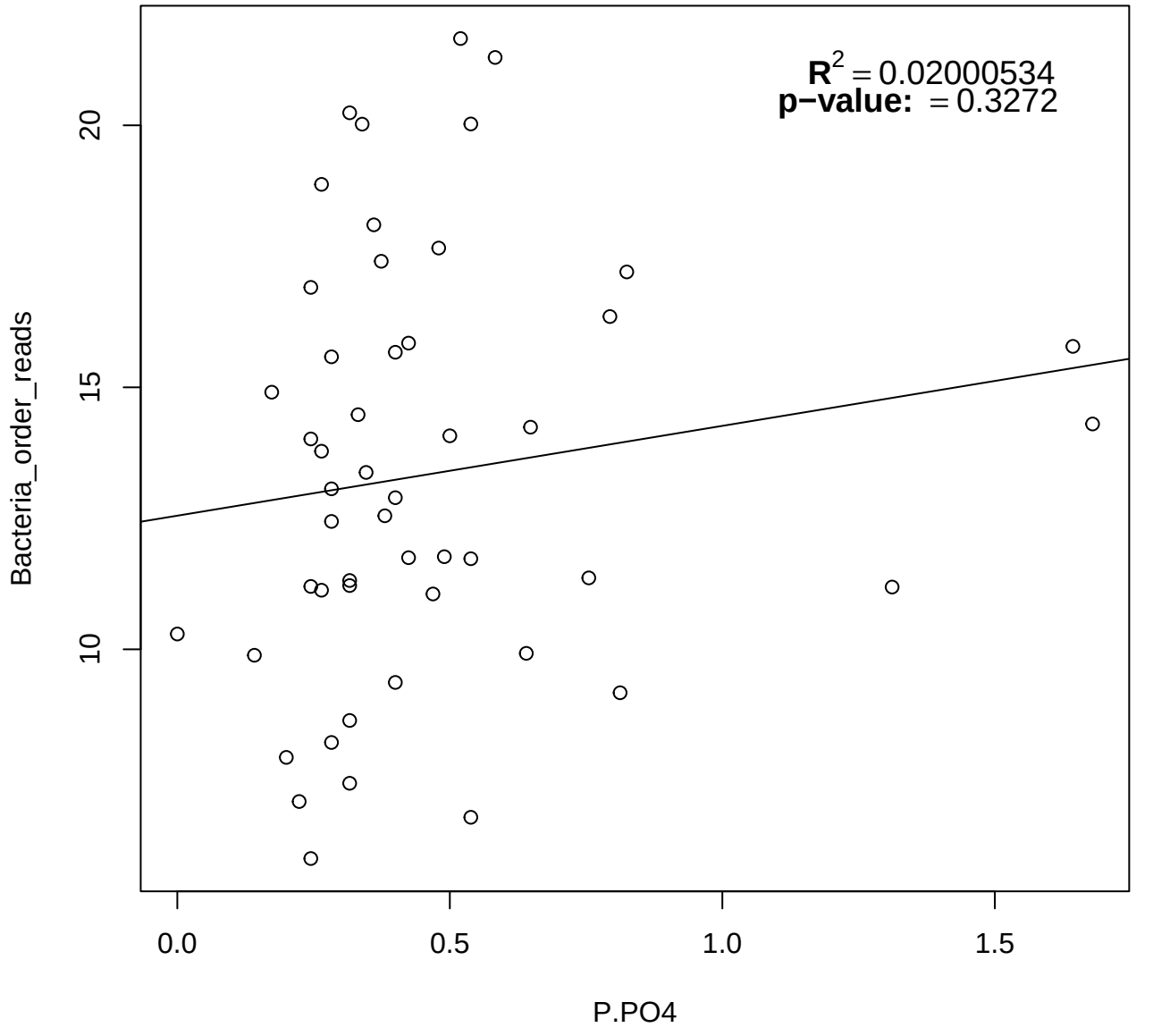

Residuals vs Fitted
Residuals
Fitted values
SEL1
AVE1
GER1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
AVE1
GER1
Scale−Location
√|Standardized residuals|
Fitted values
GER1
SEL1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
AGR1
SOU1
CAV1
Cook's distance

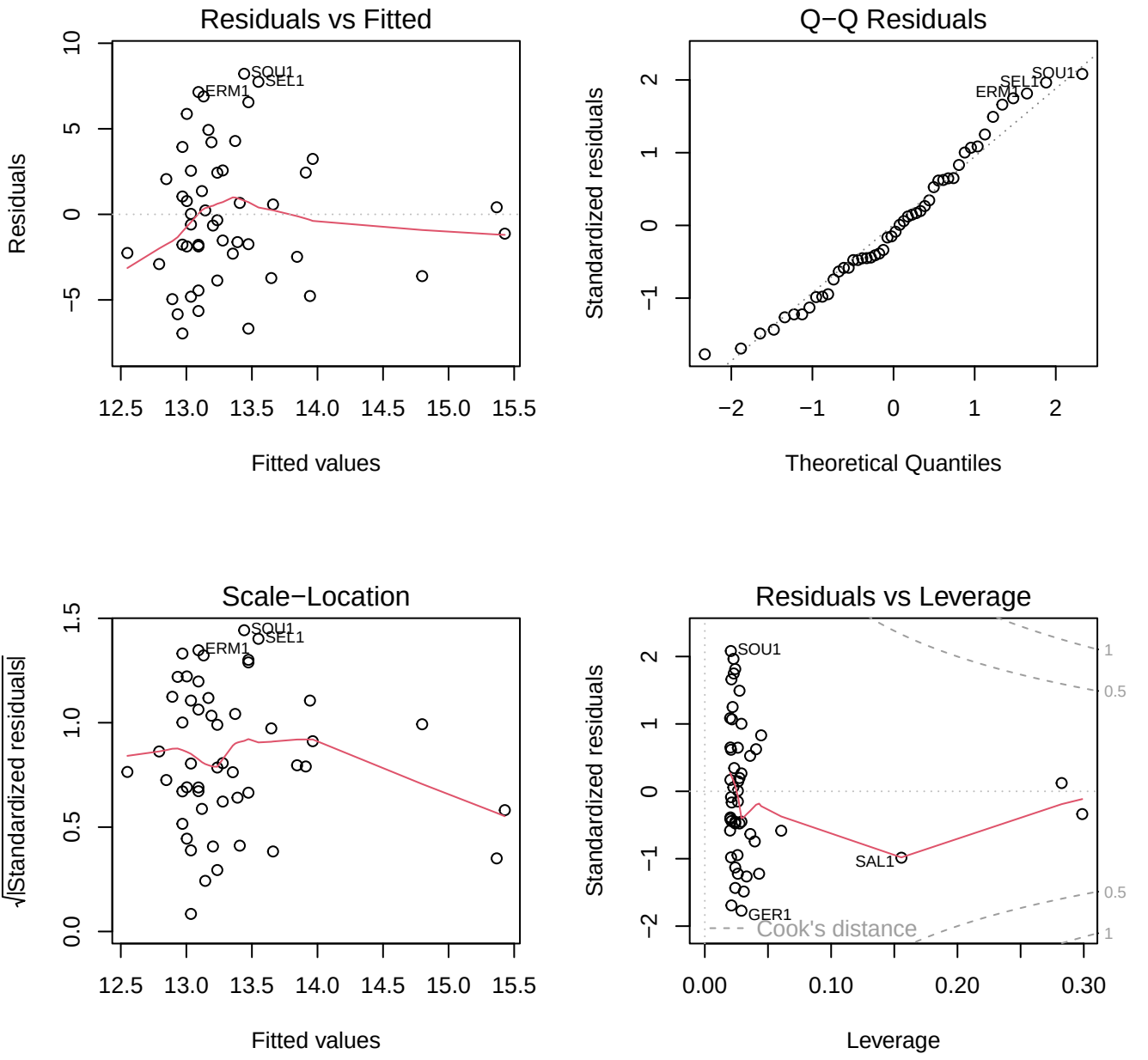

$R^2 = 0.06546558$
p−value: = 0.0729
Bacteria_order_reads
10
15
20
5
10
15
20
25
30
COD

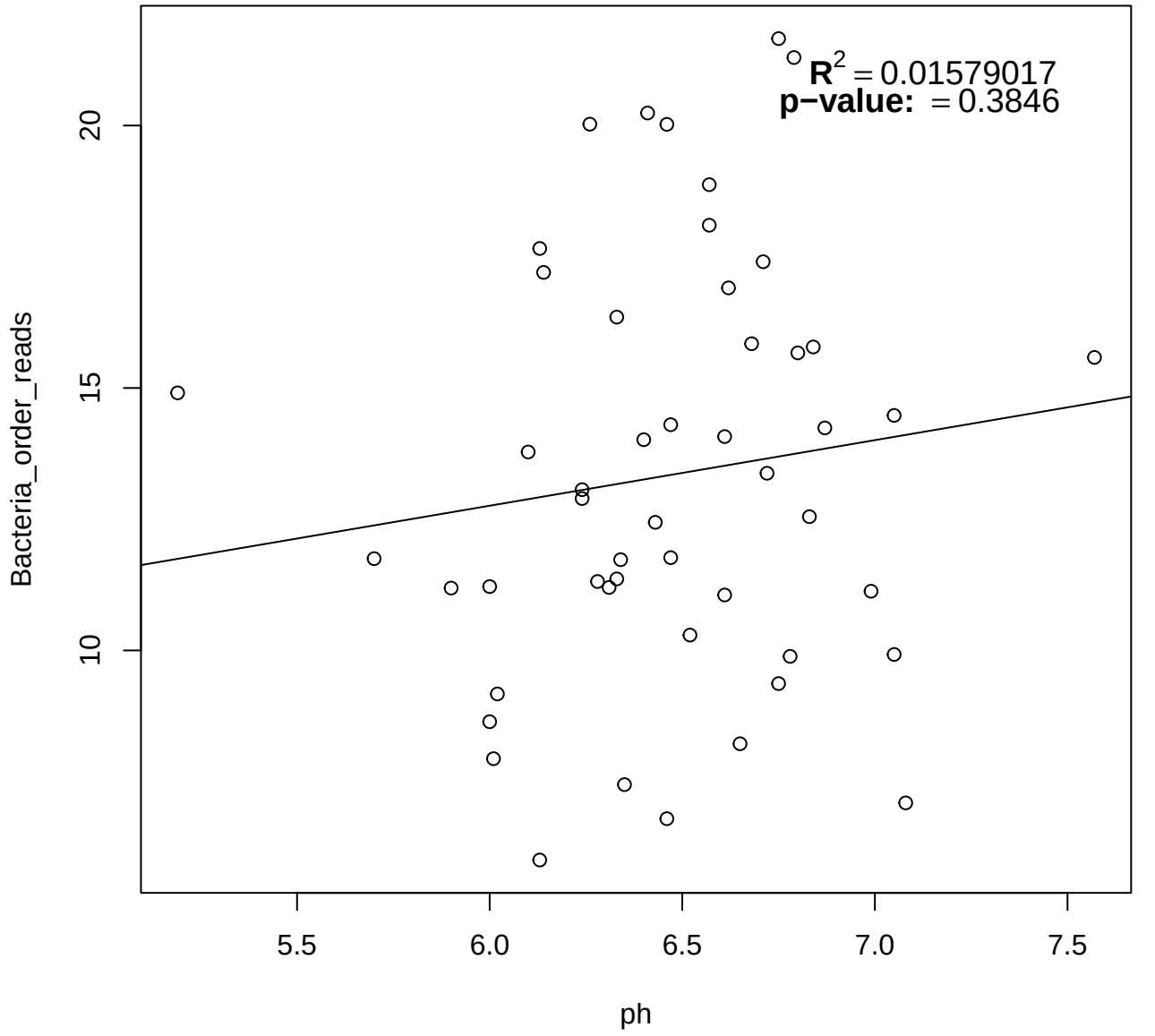

Residuals vs Fitted
Residuals
Fitted values
ERM1
SEL1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
ERM1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
SEL1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
AZE2
VEZ1
Cook's distance

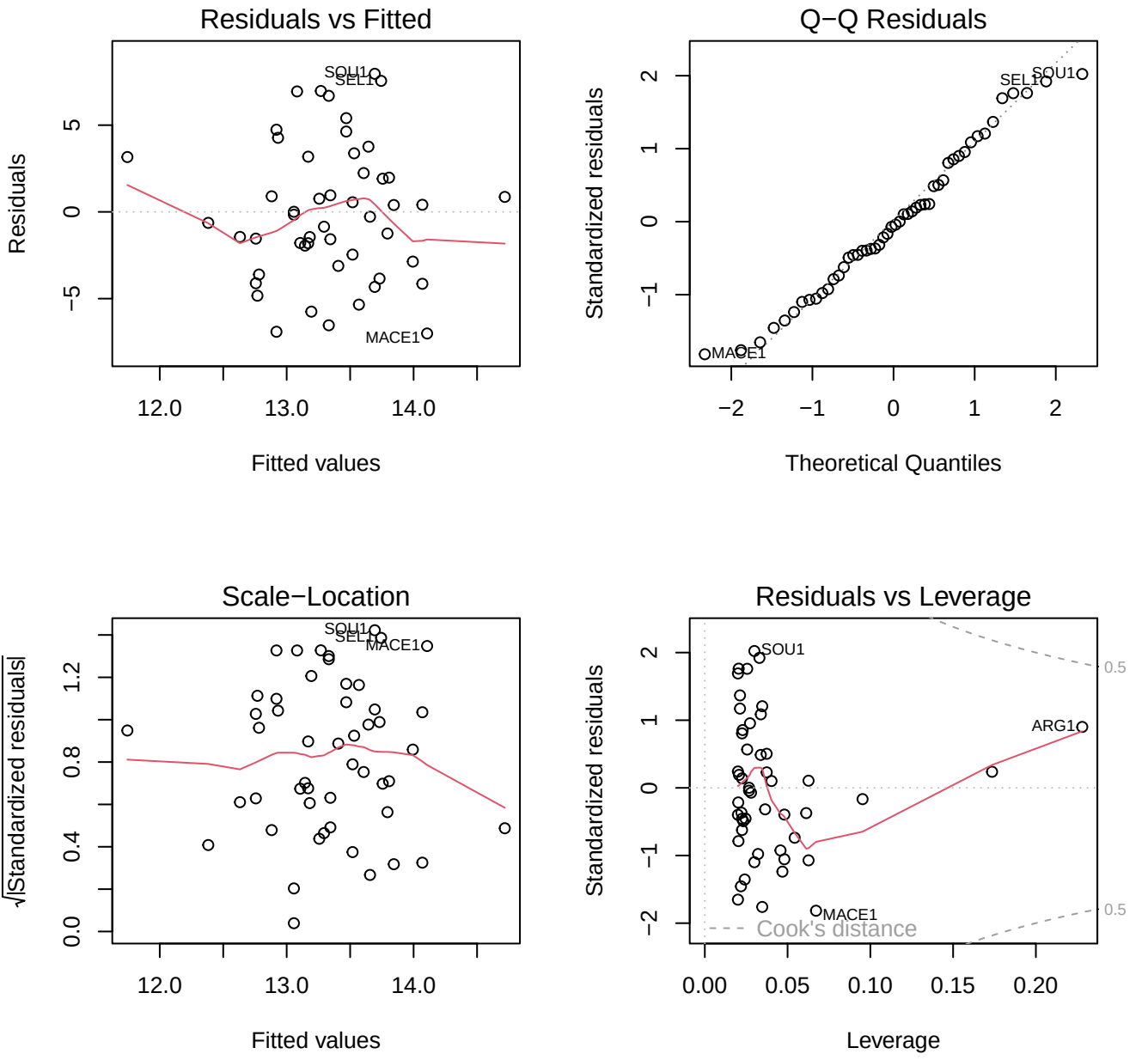

$R^2 = 0.1938737$
p−value: = 0.0014
Bacteria_order_reads
10
15
20
0.5
1.0
1.5
2.0
DIN

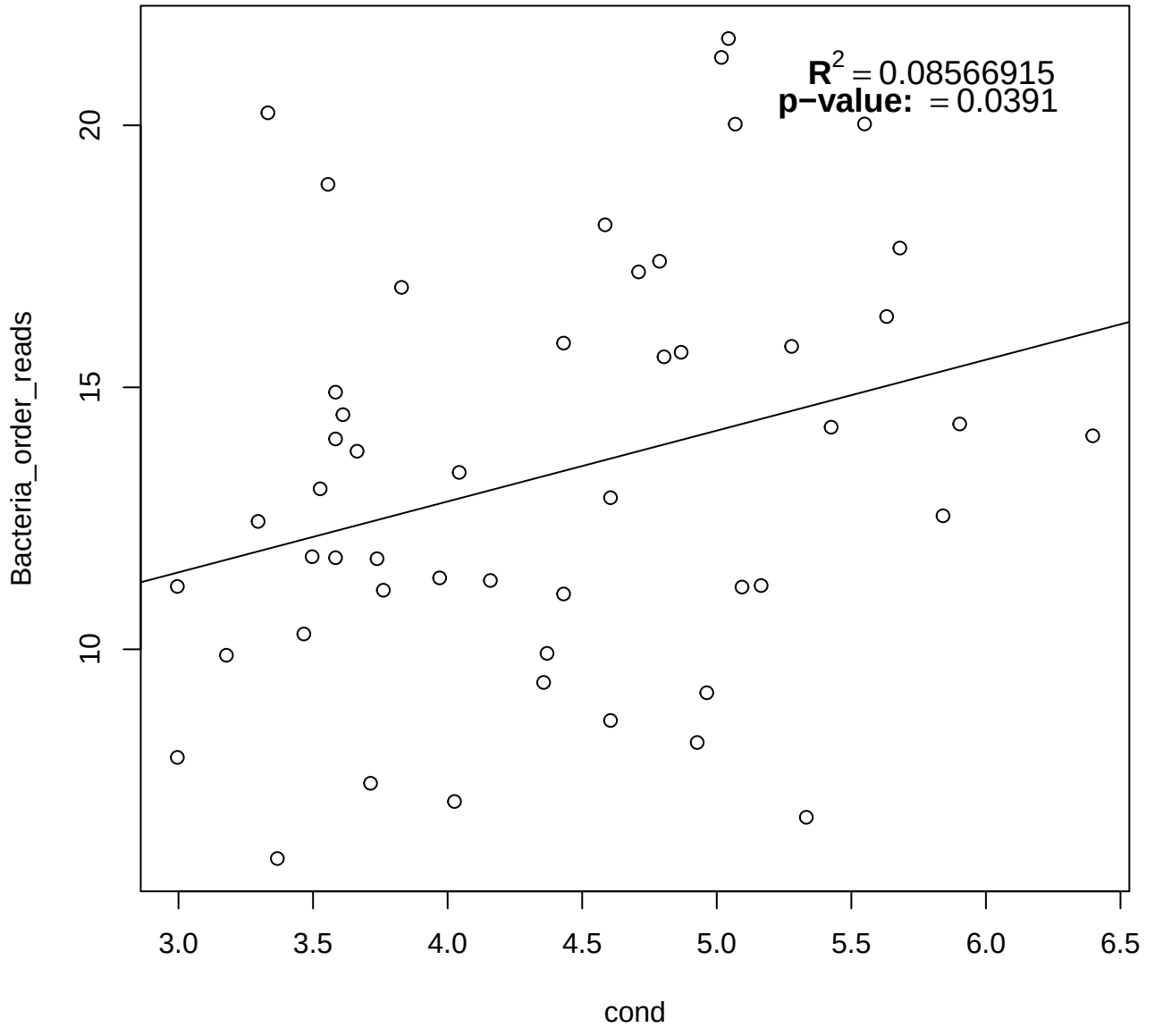

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
VEZ1
ERM1
HOM1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
TAve1
VEZ1
Cook's distance
0.5
0.5

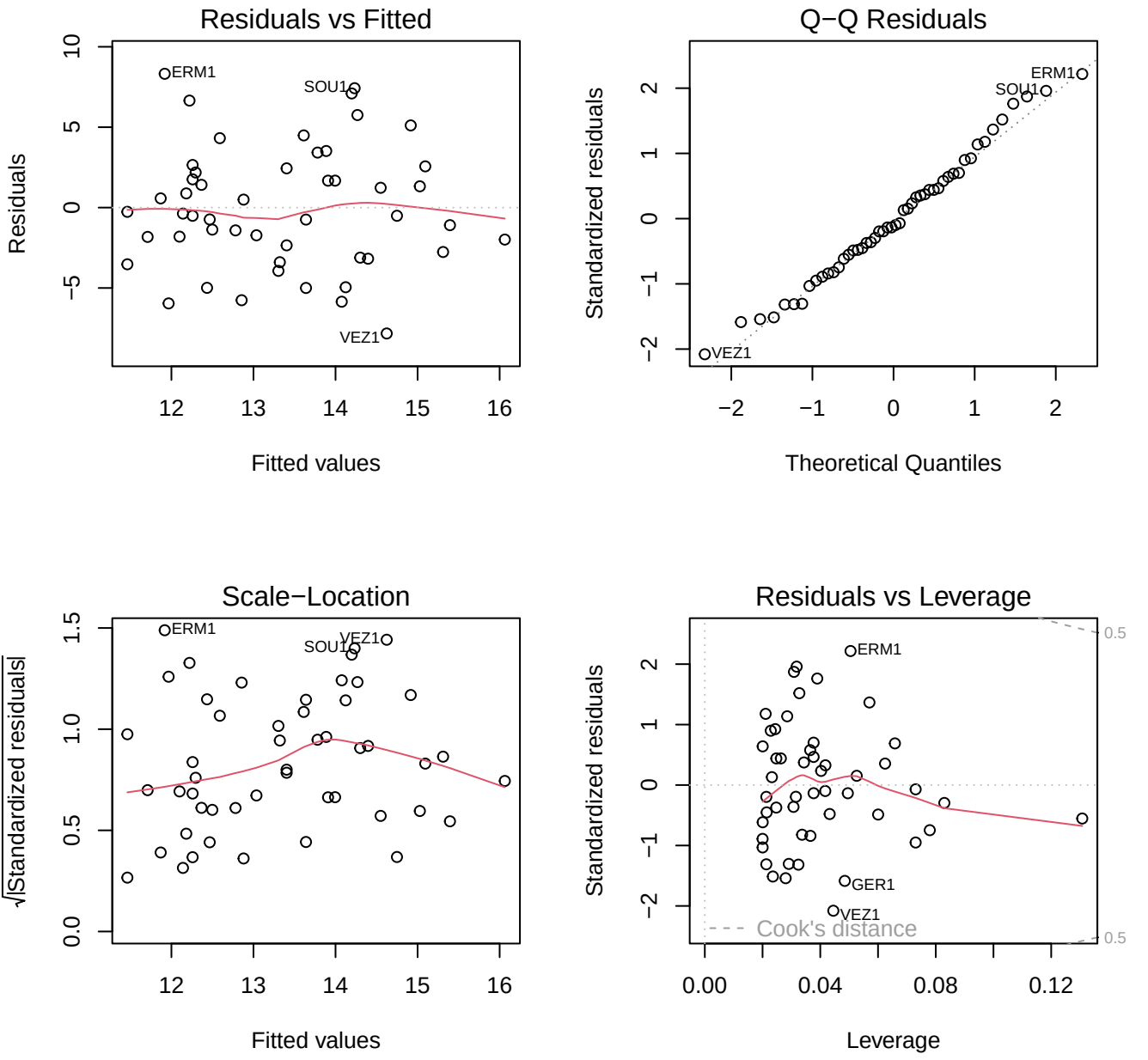

$R^2 = 0.02000534$
p−value: = 0.3272
Bacteria_order_reads
10
15
20
0.0
0.5
1.0
1.5
P.PO4

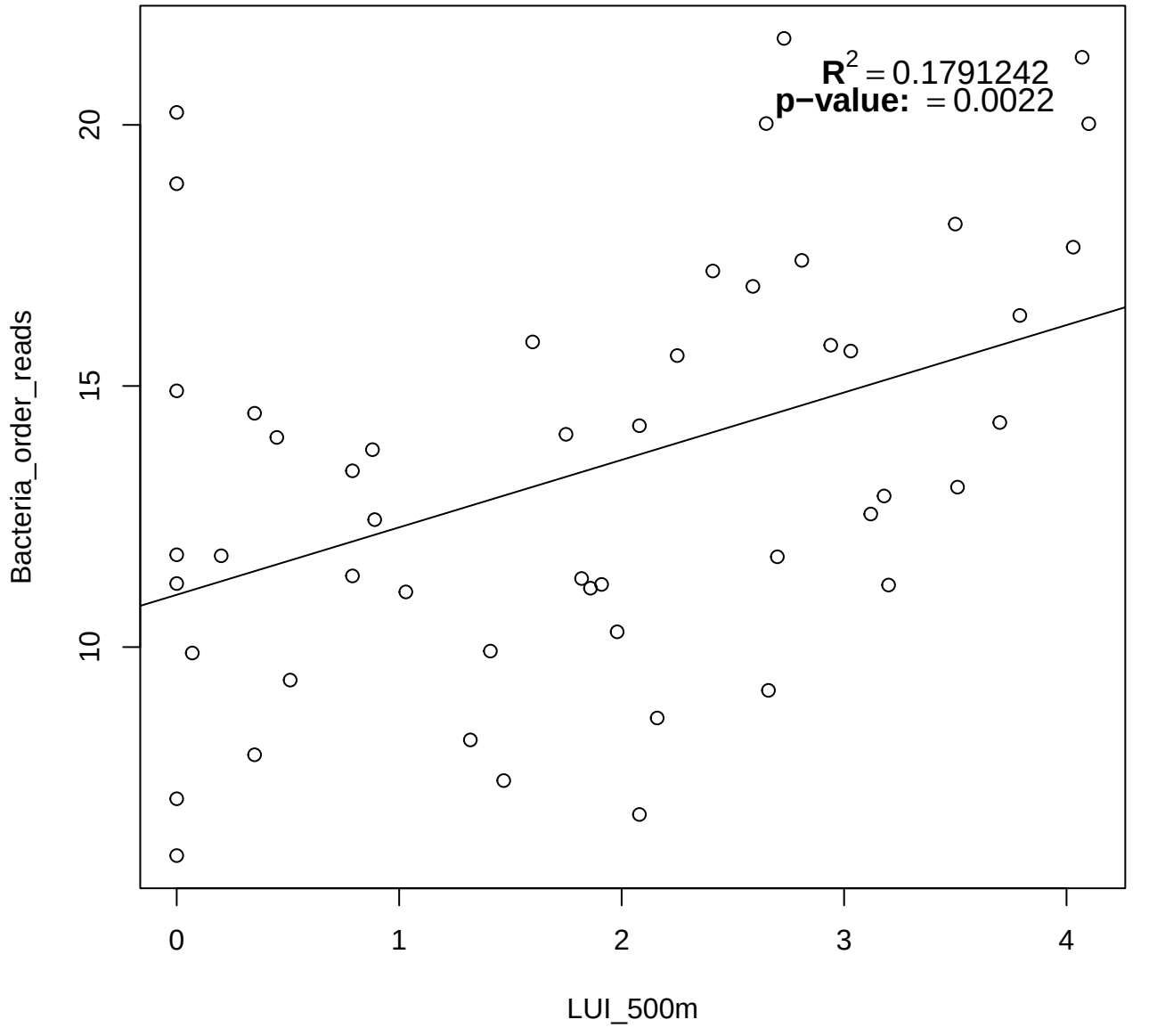

Residuals vs Fitted
Residuals
Fitted values
SOU1
SEL1
ERM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SOU1
SEL1
ERM1
Scale−Location
√|Standardized residuals|
Fitted values
SOU1
SEL1
ERM1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
SAL1
GER1
Cook's distance

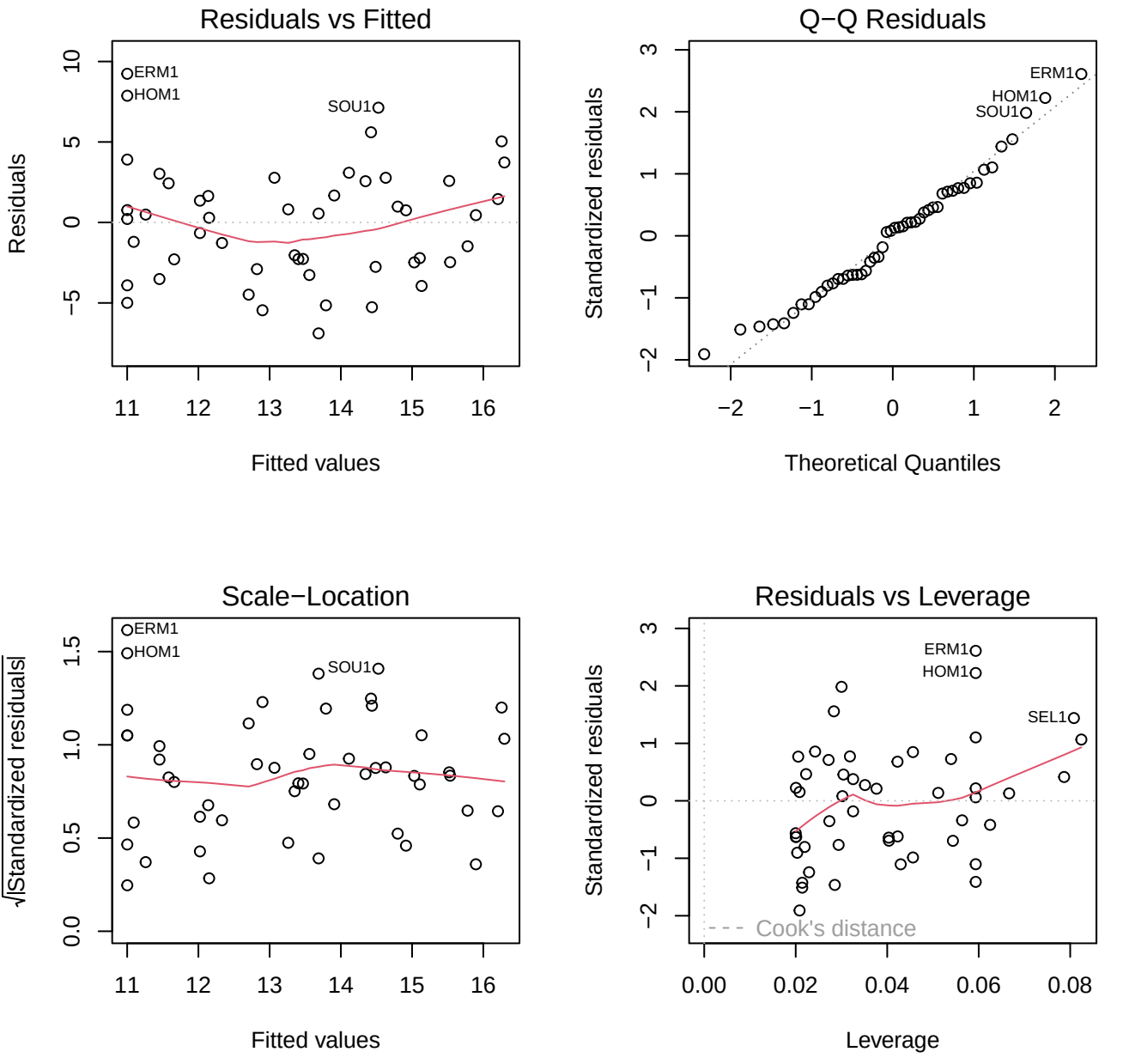

$R^2 = 0.01579017$
p−value: = 0.3846
Bacteria_order_reads
10
15
20
5.5
6.0
6.5
7.0
7.5
ph

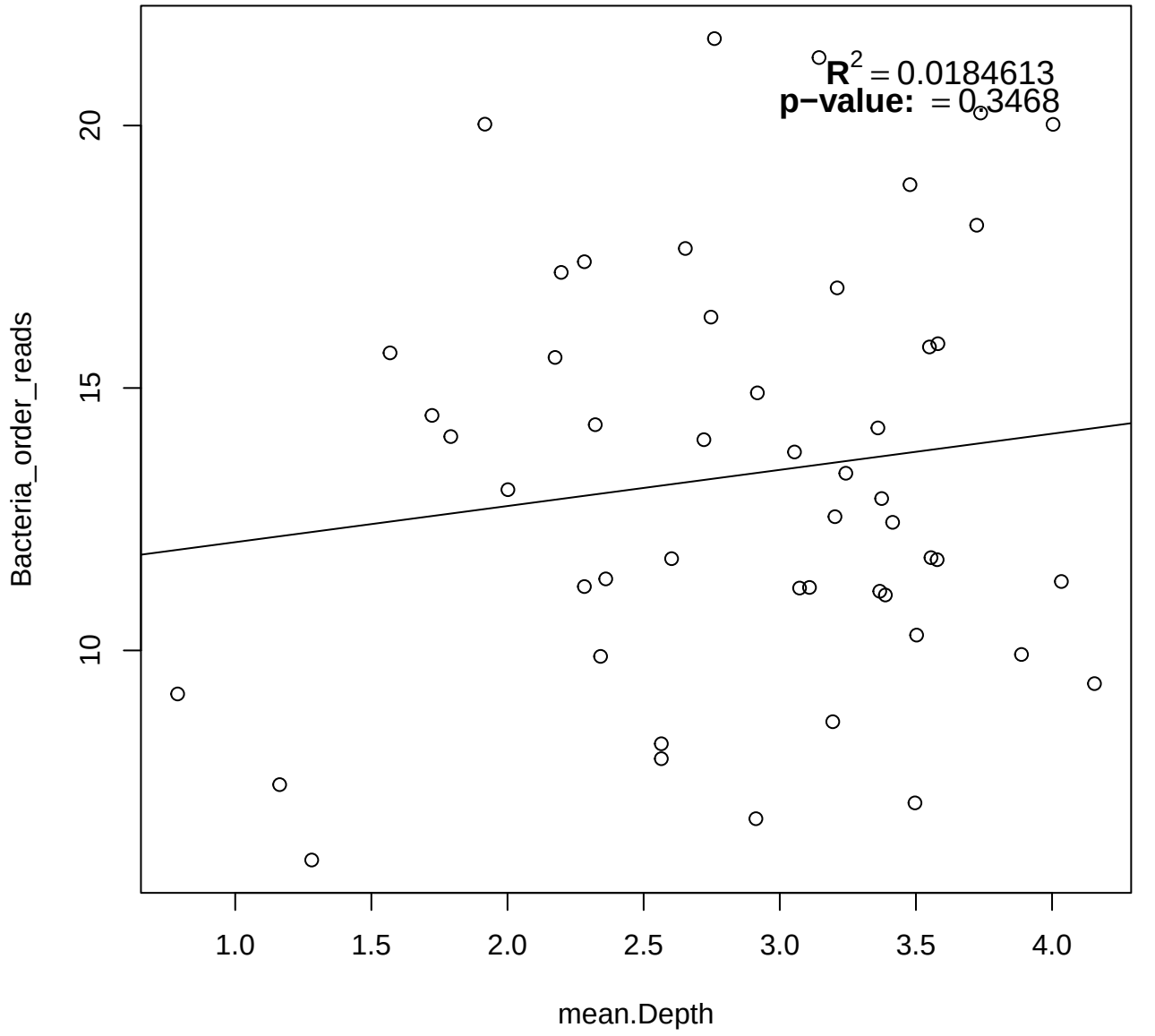

Residuals vs Fitted
Residuals
Fitted values
SOU1
SEL1
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SOU1
SEL1
MACE1
Scale−Location
√|Standardized residuals|
Fitted values
SOU1
SEL1
MACE1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
ARG1
MACE1
Cook's distance
0.5
0.5

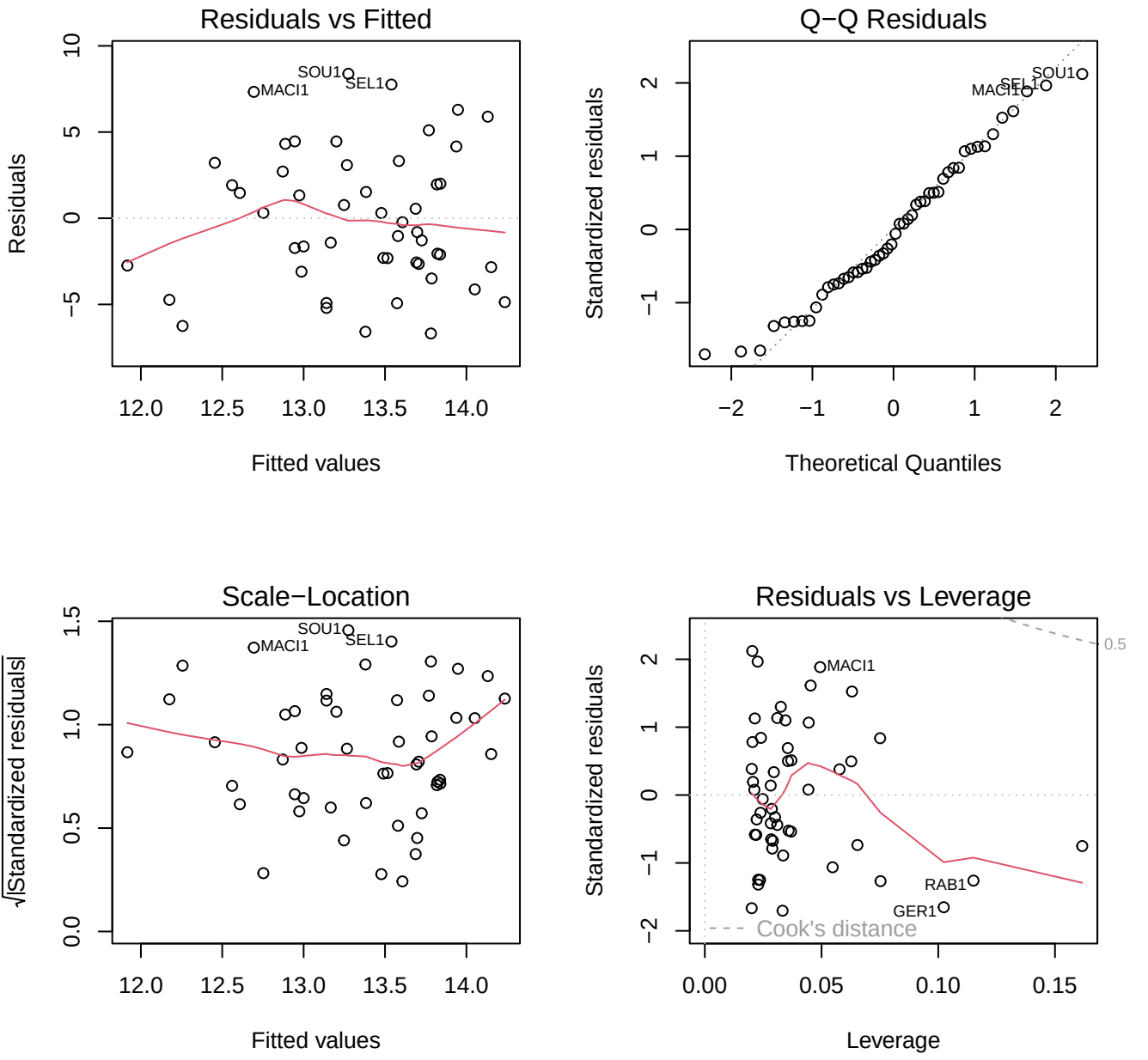

$R^2 = 0.08566915$
p−value: = 0.0391
Bacteria_order_reads
10
15
20
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
cond

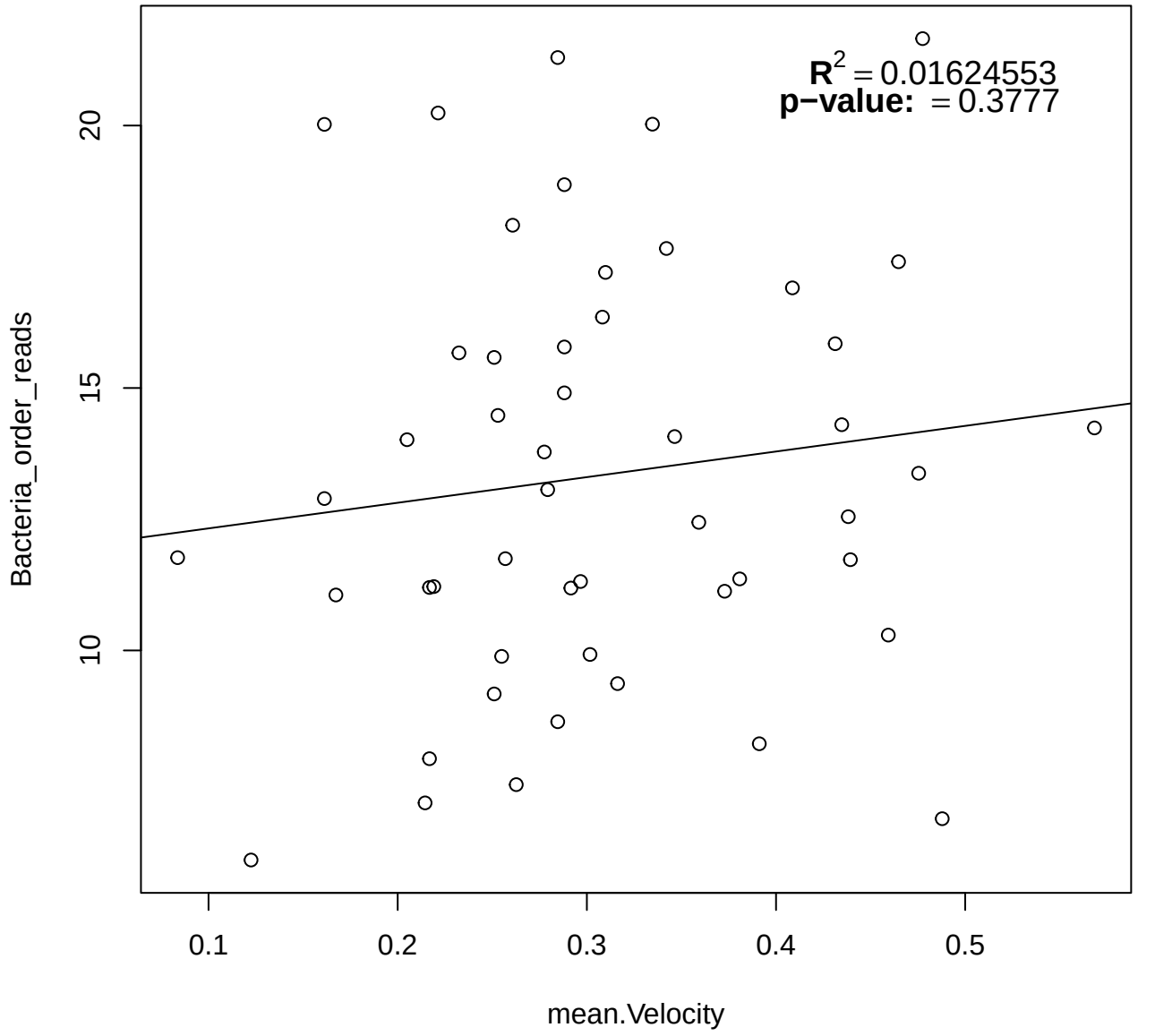

Residuals vs Fitted
Residuals
Fitted values
ERM1
SOU1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
SOU1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
SOU1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
GER1
VEZ1
Cook's distance
0.5
0.5

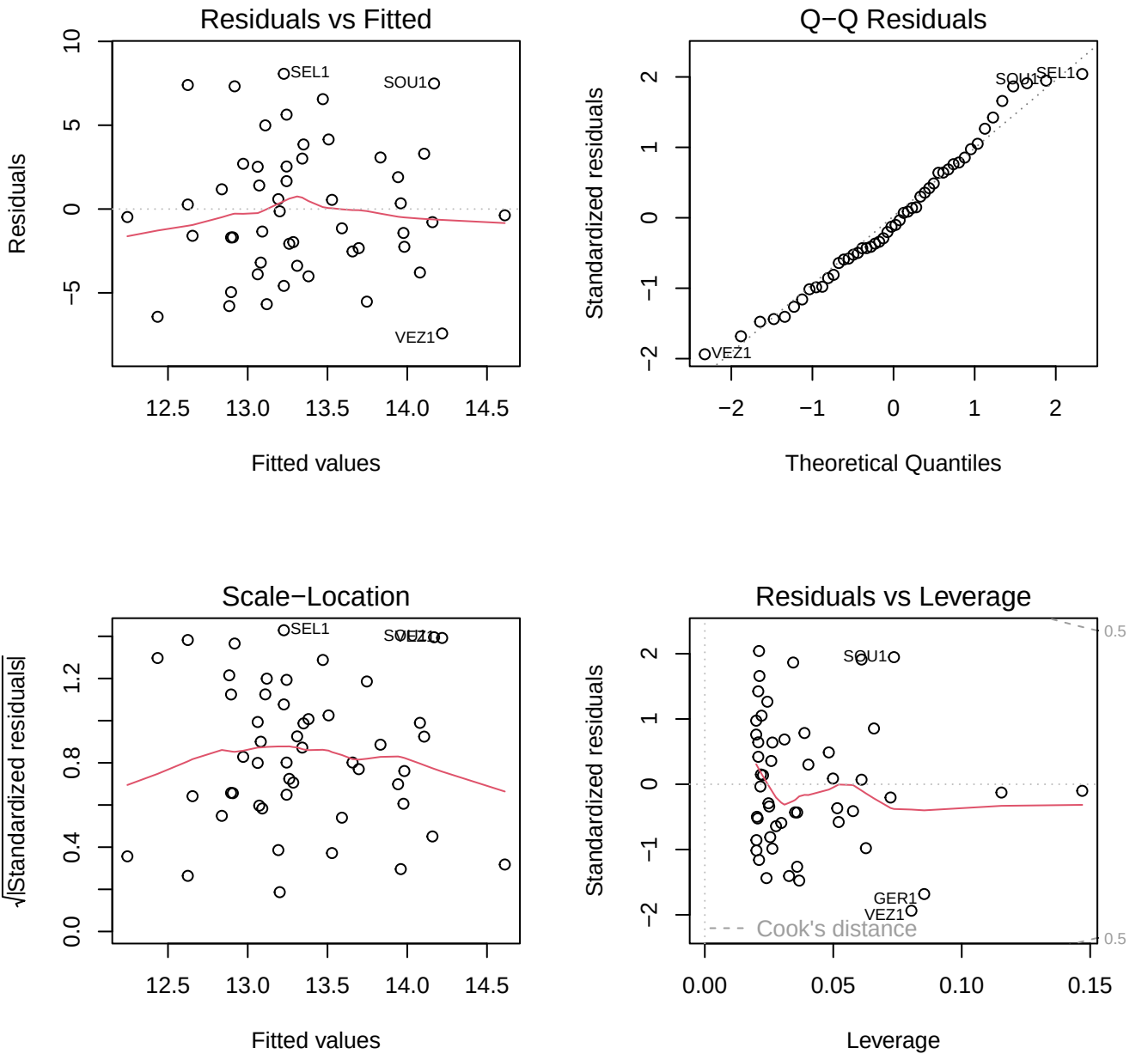

$R^2 = 0.1791242$
p−value: = 0.0022
Bacteria_order_reads
10
15
20
0
1
2
3
4
LUI_500m

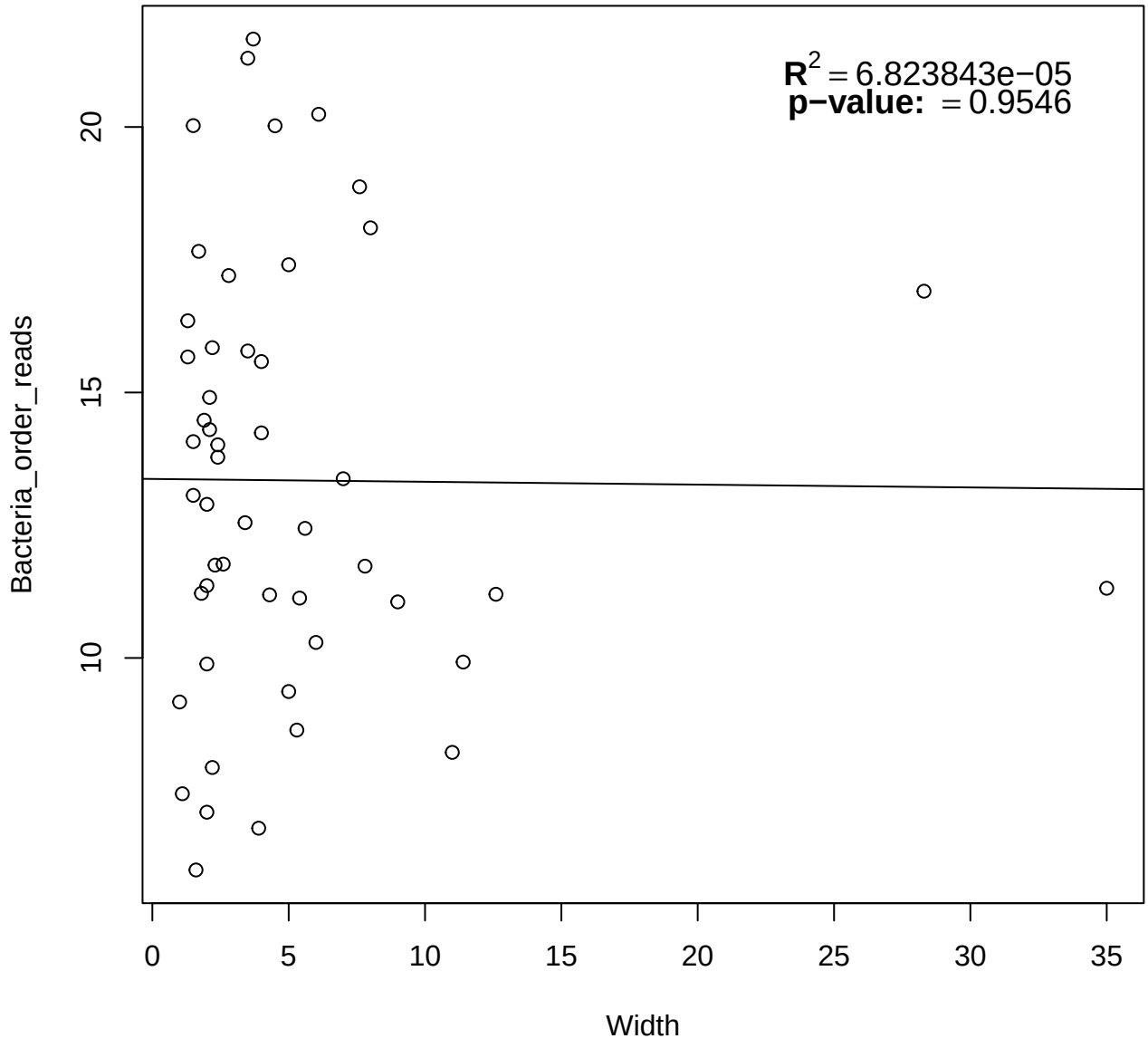

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
SOU1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
SOU1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
SOU1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
HOM1
SEL1
Cook's distance

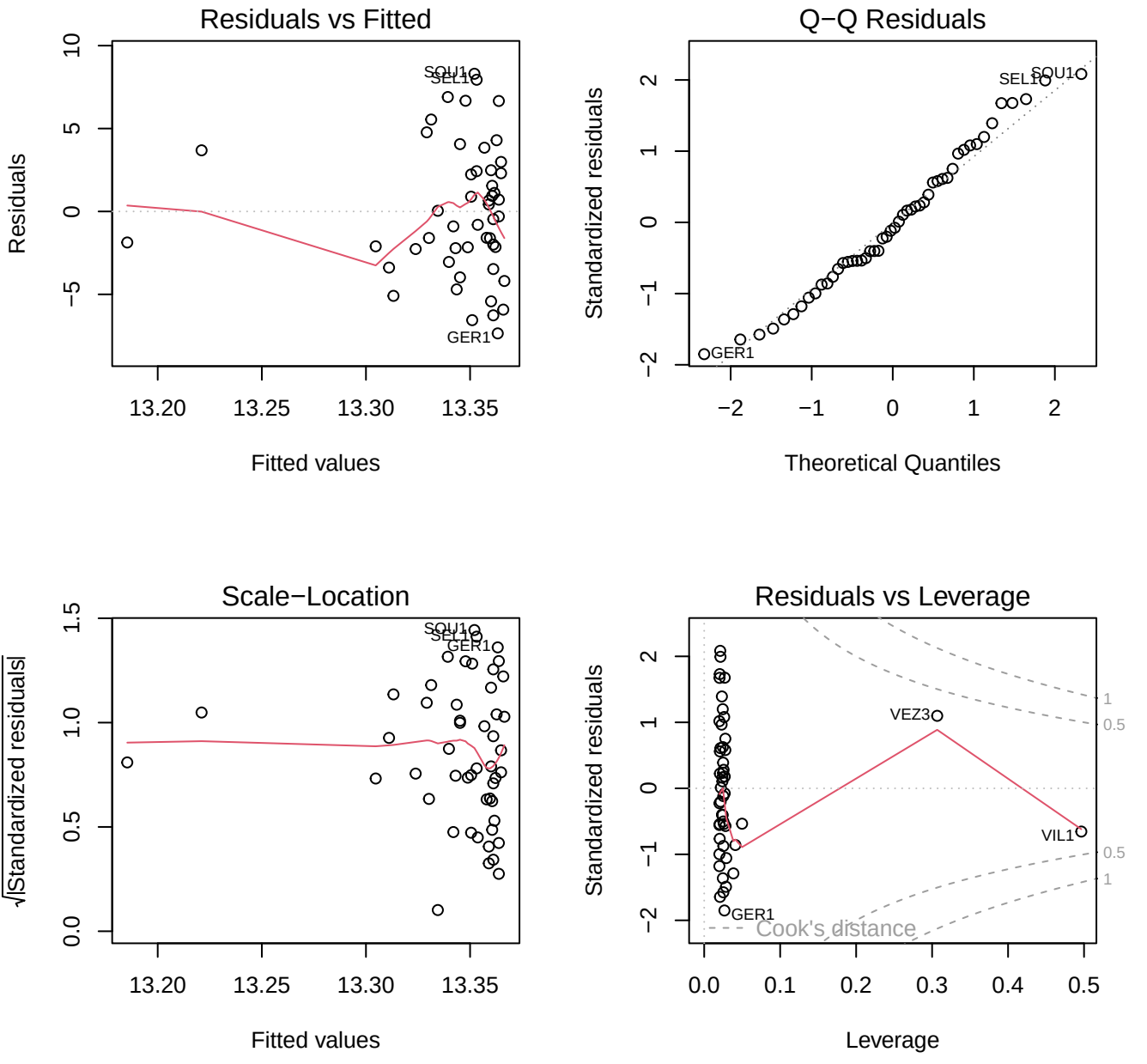

$R^2 = 0.0184613$
p−value: = 0.3468
Bacteria_order_reads
10
15
20
1.0
1.5
2.0
2.5
3.0
3.5
4.0
mean.Depth

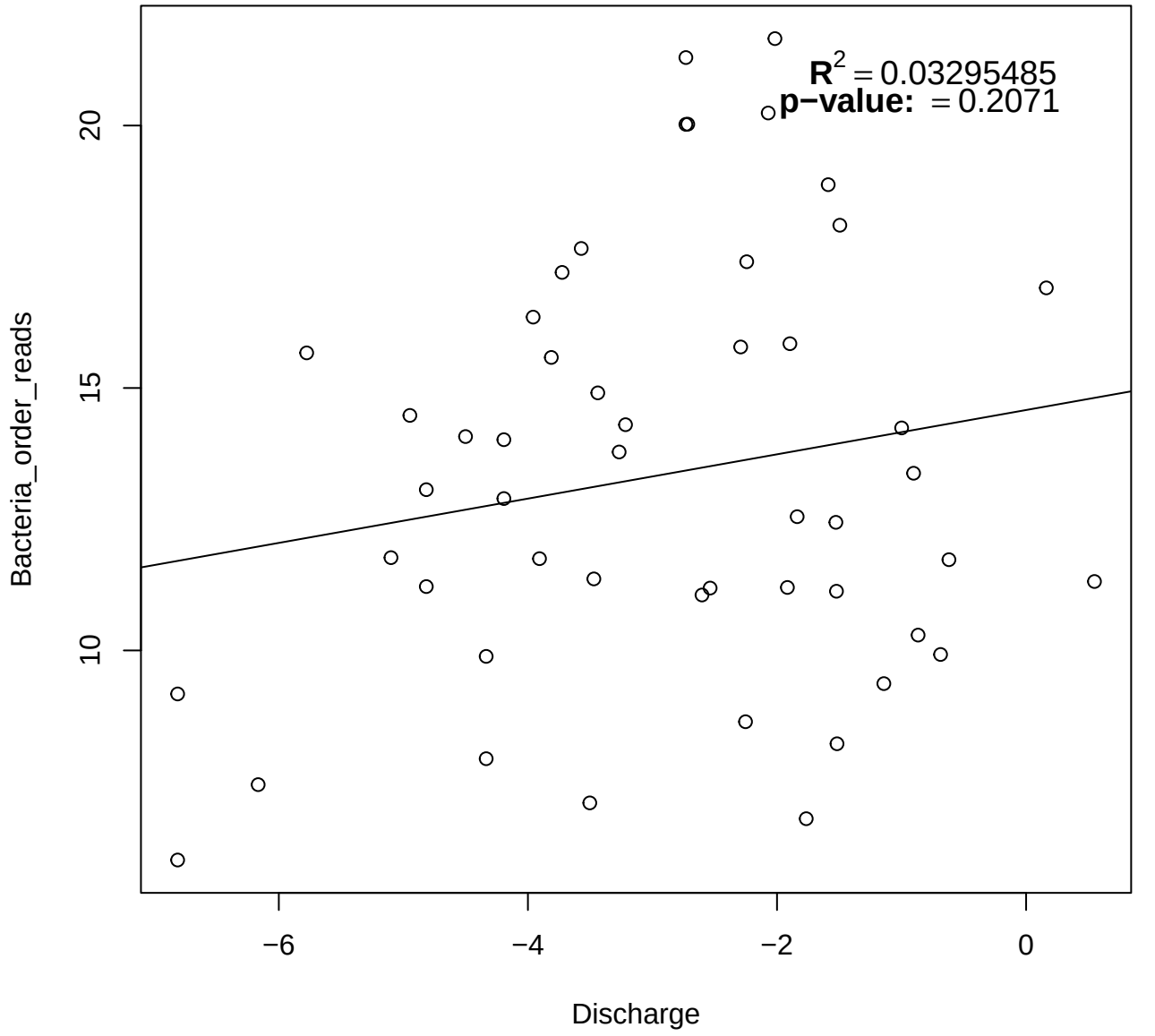

Residuals vs Fitted
Residuals
Fitted values
SOU1
SEL1
MACI1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SOU1
SEL1
MACI1
Scale−Location
√|Standardized residuals|
Fitted values
SOU1
SEL1
MACI1
Residuals vs Leverage
Standardized residuals
Leverage
0.5
MACI1
RAB1
GER1
Cook's distance

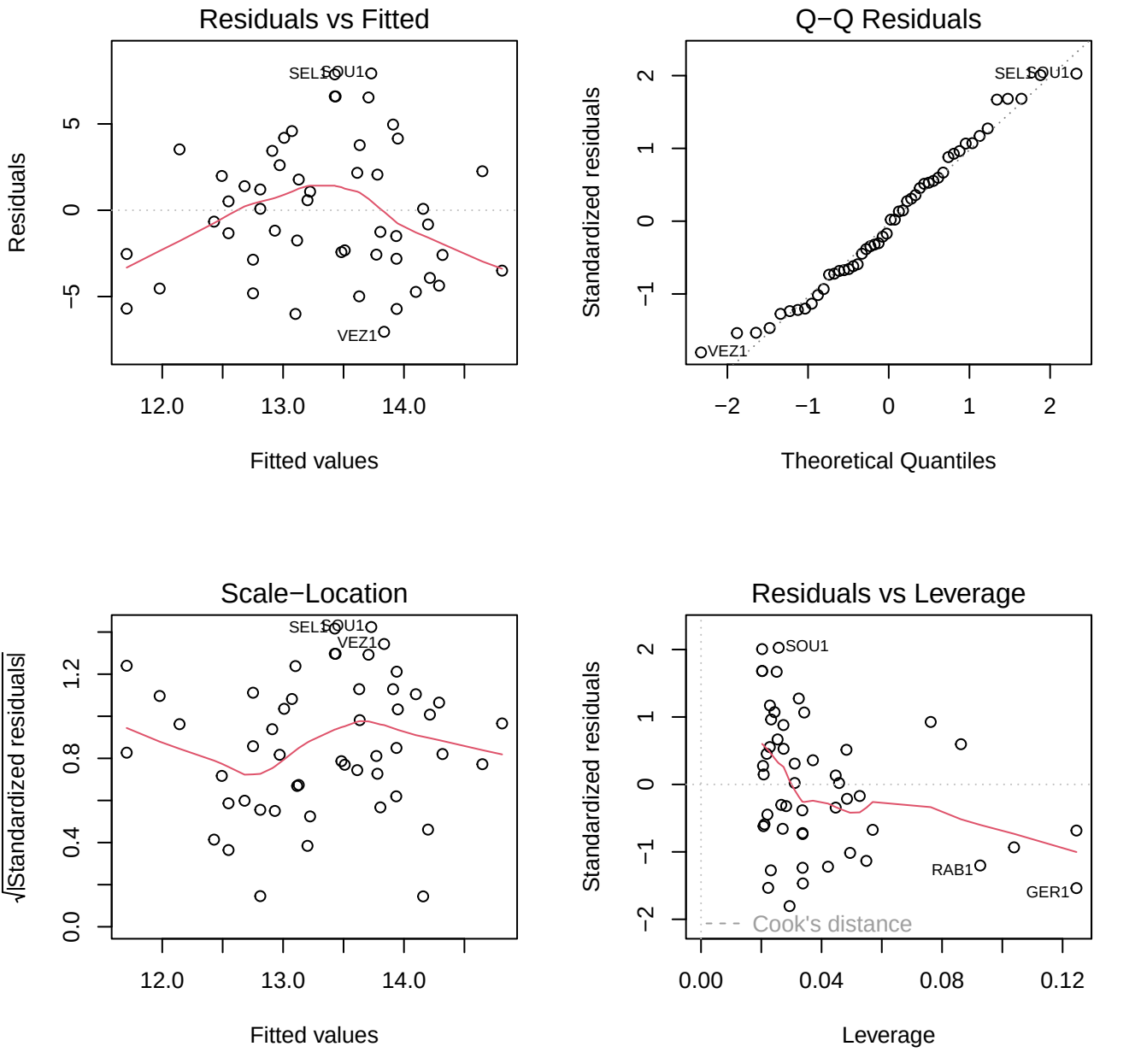

$R^2 = 0.01624553$
p−value: = 0.3777
Bacteria_order_reads
10
15
20
0.1
0.2
0.3
0.4
0.5
mean.Velocity

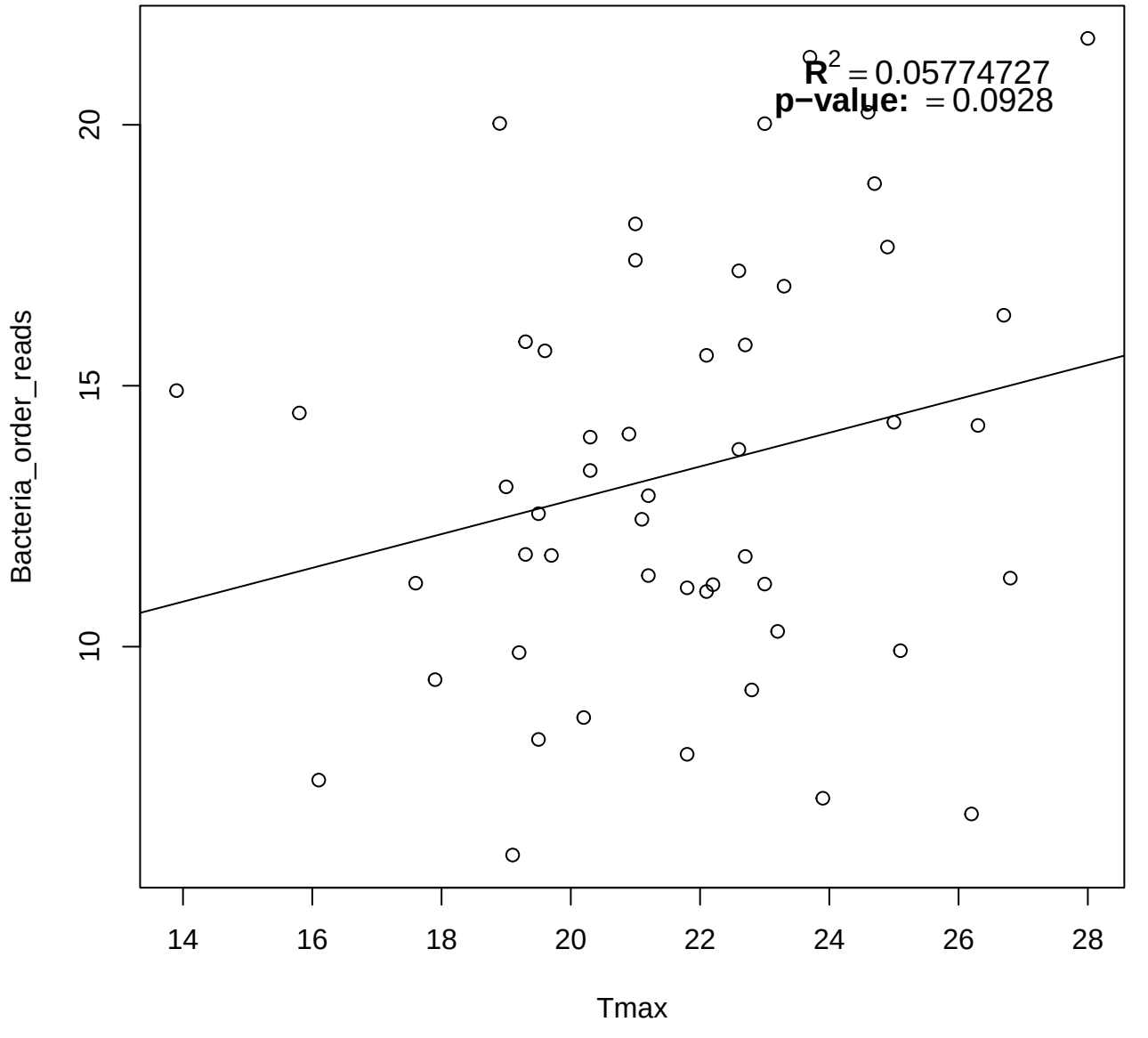

Residuals vs Fitted
Residuals
Fitted values
SEL1
SOU1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SOU1
SEL1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
GER1
VEZ1
Cook's distance

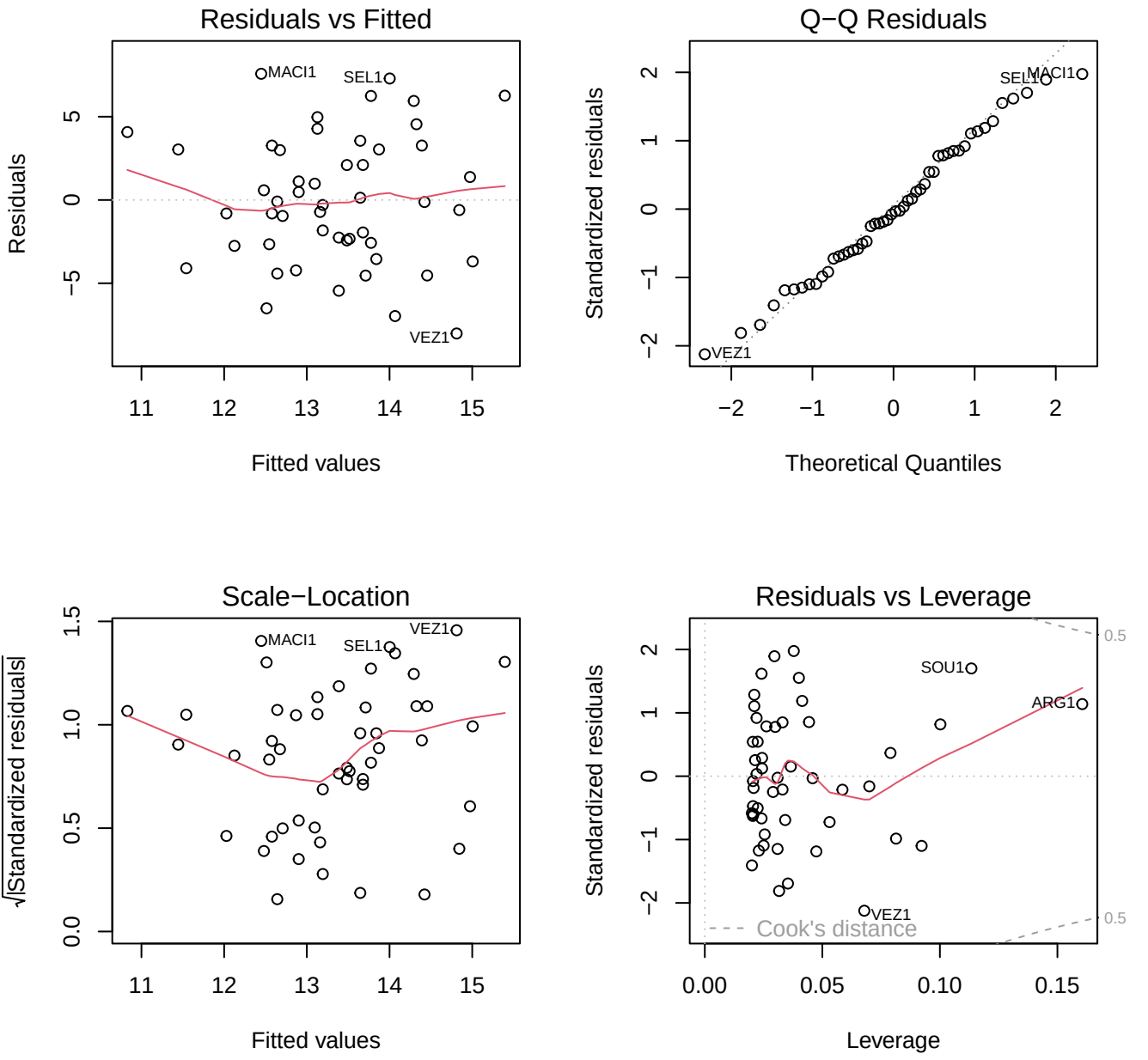

$R^2 = 6.823843e-05$
p−value: = 0.9546
Bacteria_order_reads
Width
0
5
10
15
20
25
30
35
10
15
20

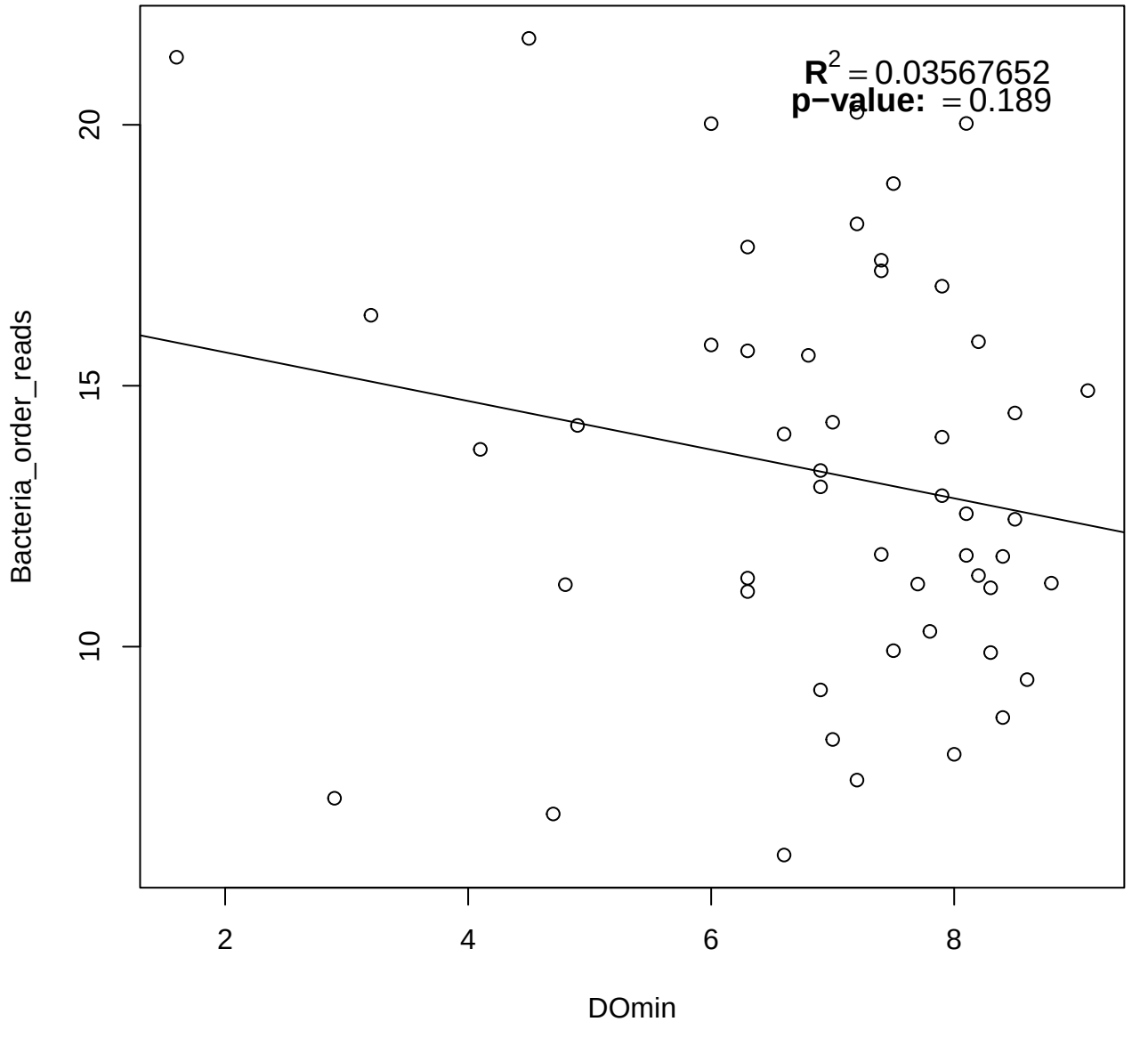

Residuals vs Fitted
Residuals
Fitted values
SQU1
SEL1
GER1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
SQU1
GER1
Scale−Location
√|Standardized residuals|
Fitted values
SQU1
SEL1
GER1
Residuals vs Leverage
Standardized residuals
Leverage
VEZ3
VIL1
GER1
Cook's distance

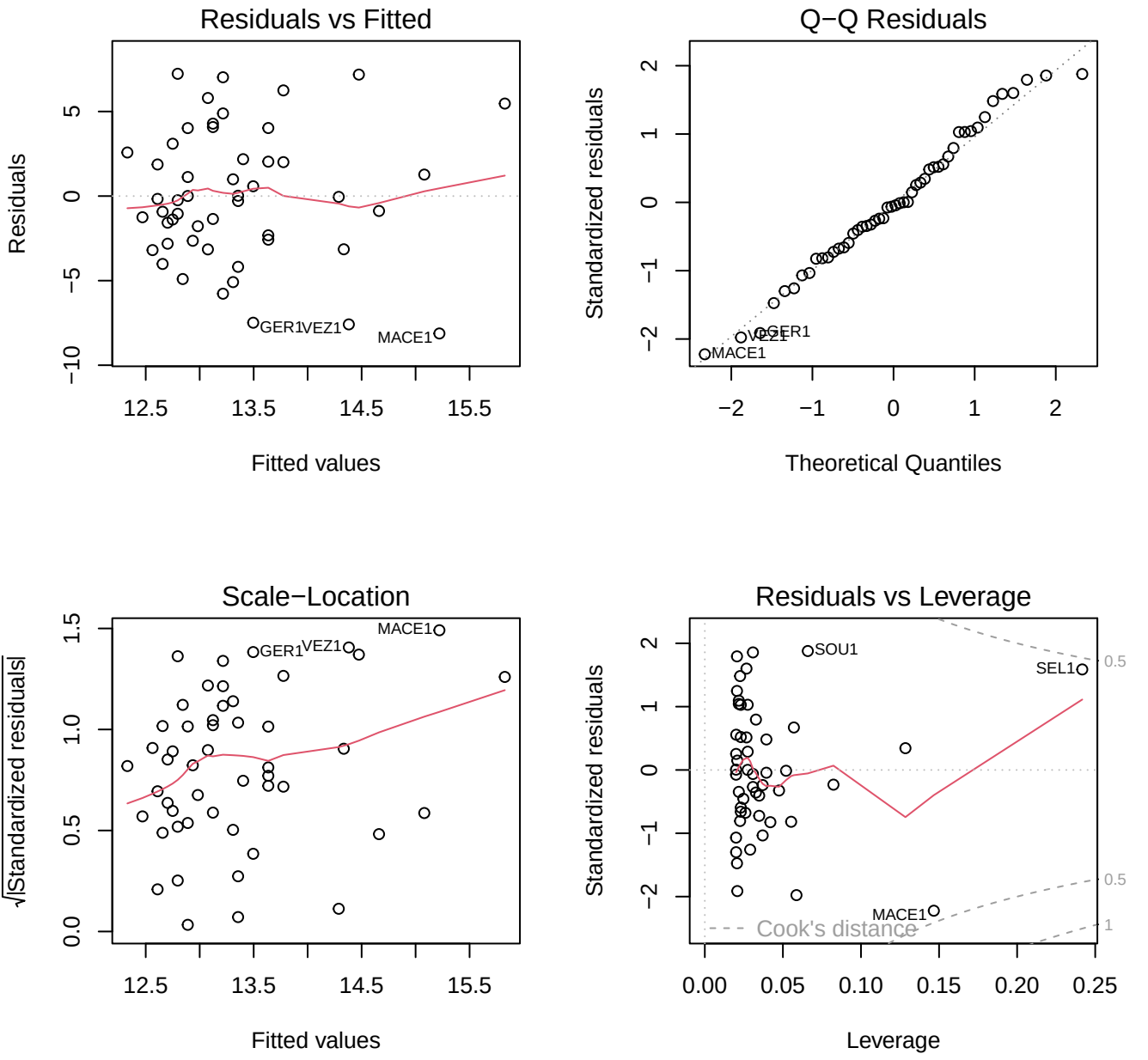

$R^2 = 0.03295485$
p−value: = 0.2071
Bacteria_order_reads
10
15
20
−6
−4
−2
0
Discharge

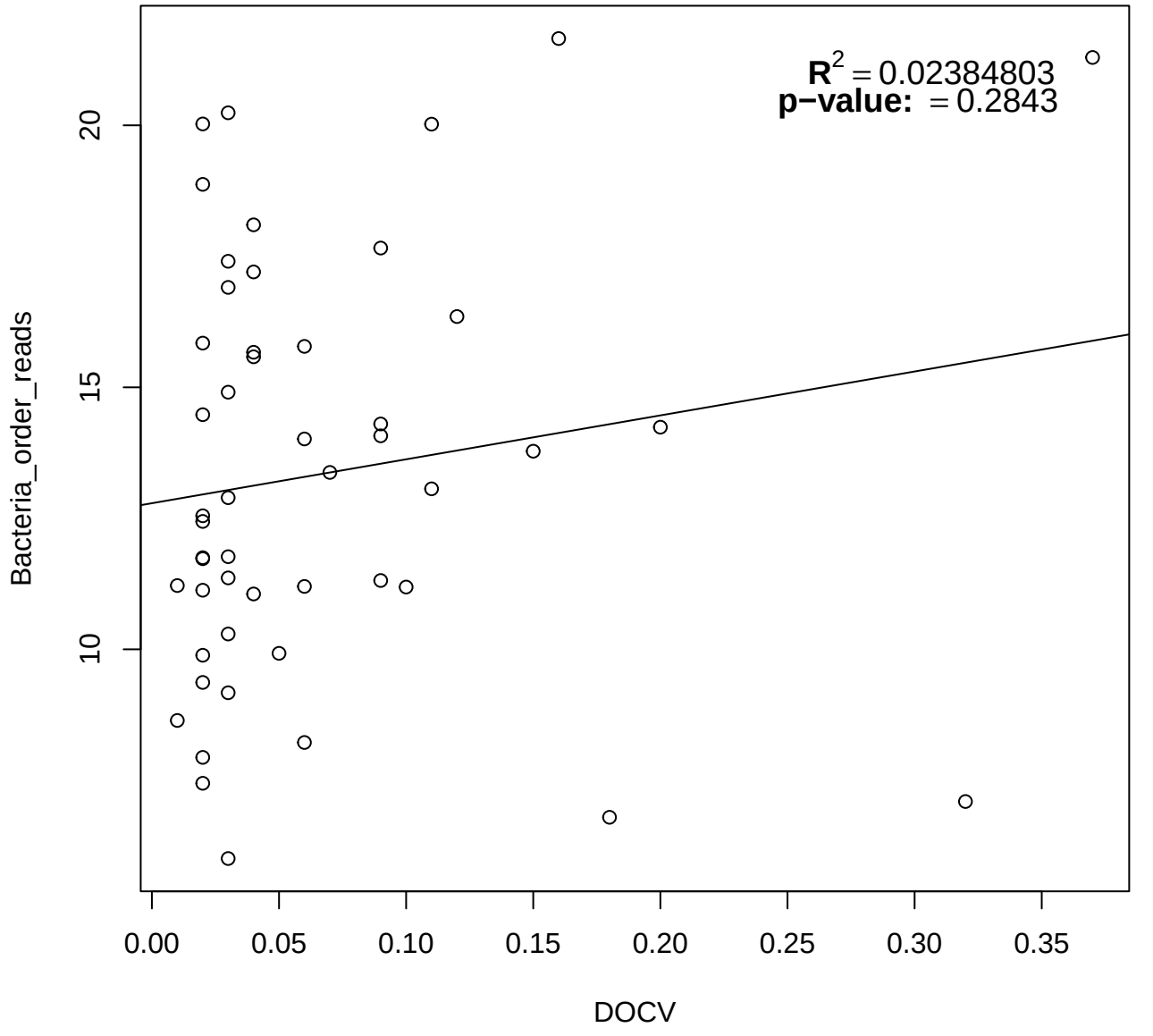

Residuals vs Fitted
Residuals
Fitted values
SEL1
SOU1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SEL1
SOU1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
SEL1
SOU1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
RAB1
GER1
Cook's distance

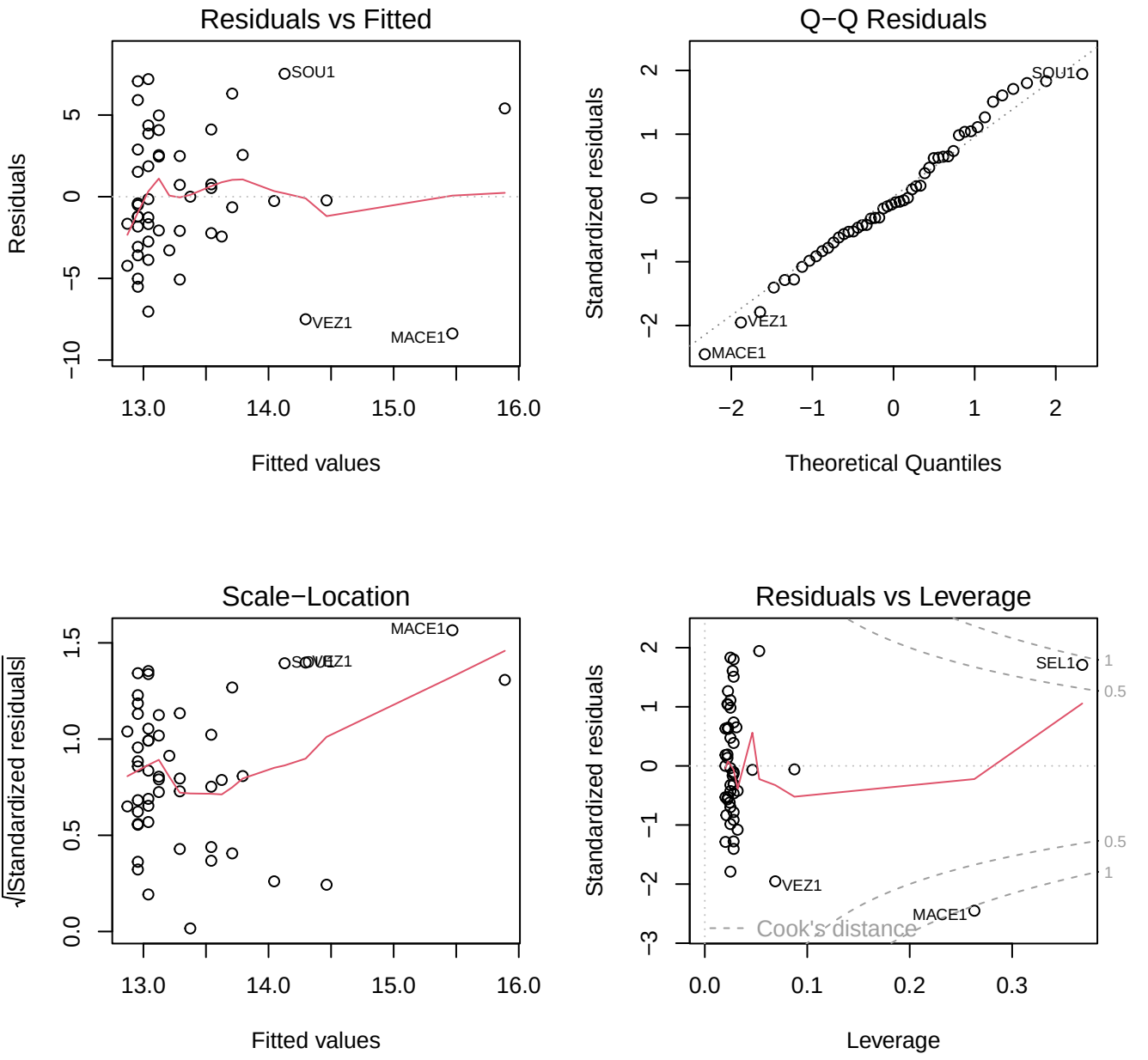

$R^2 = 0.05774727$
p−value: = 0.0928
Bacteria_order_reads
10
15
20
14
16
18
20
22
24
26
28
Tmax

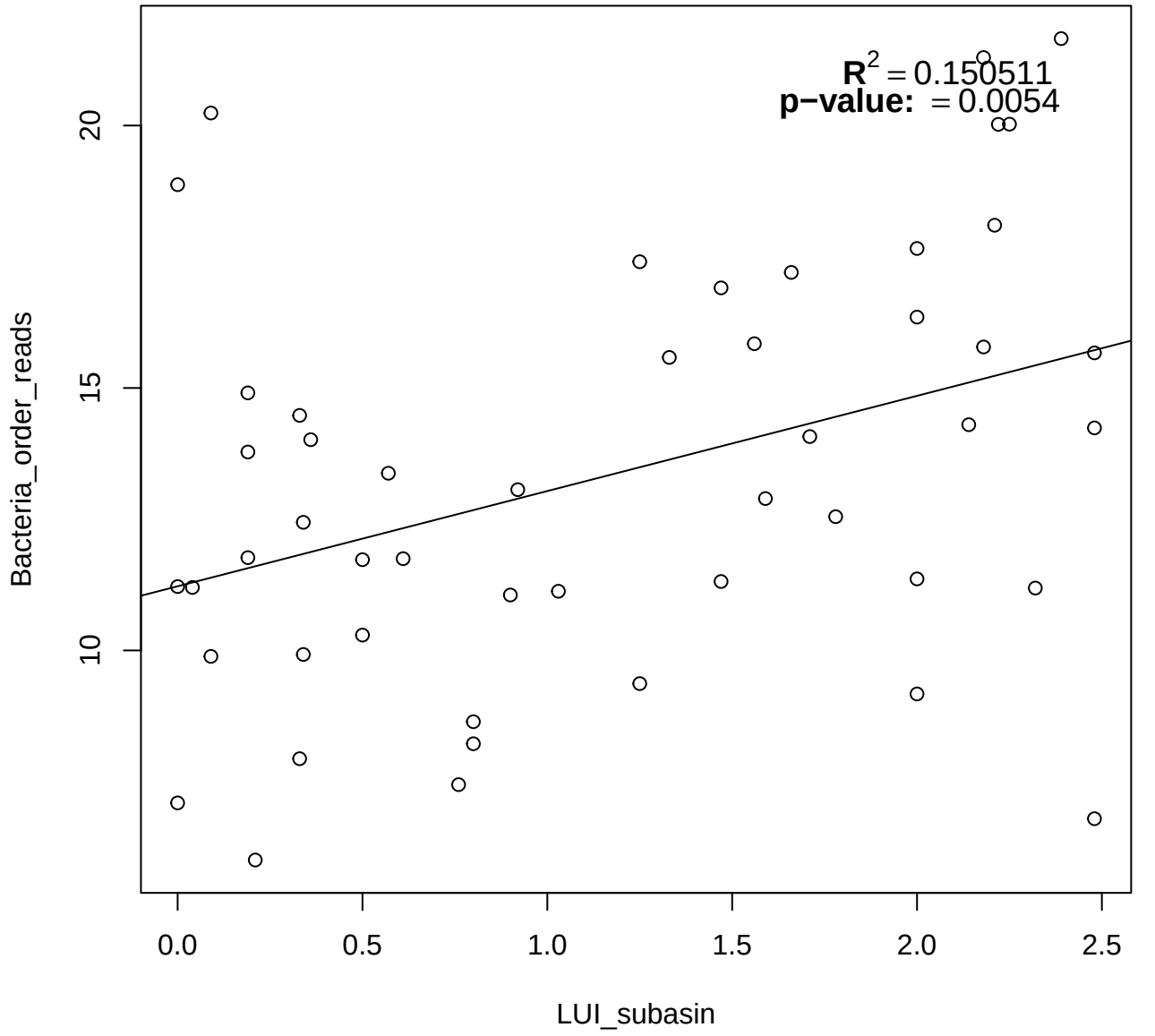

Residuals vs Fitted
Residuals
Fitted values
MACI1
SEL1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
MACI1
SEL1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
MACI1
SEL1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
ARG1
VEZ1
Cook's distance
0.5
0.5

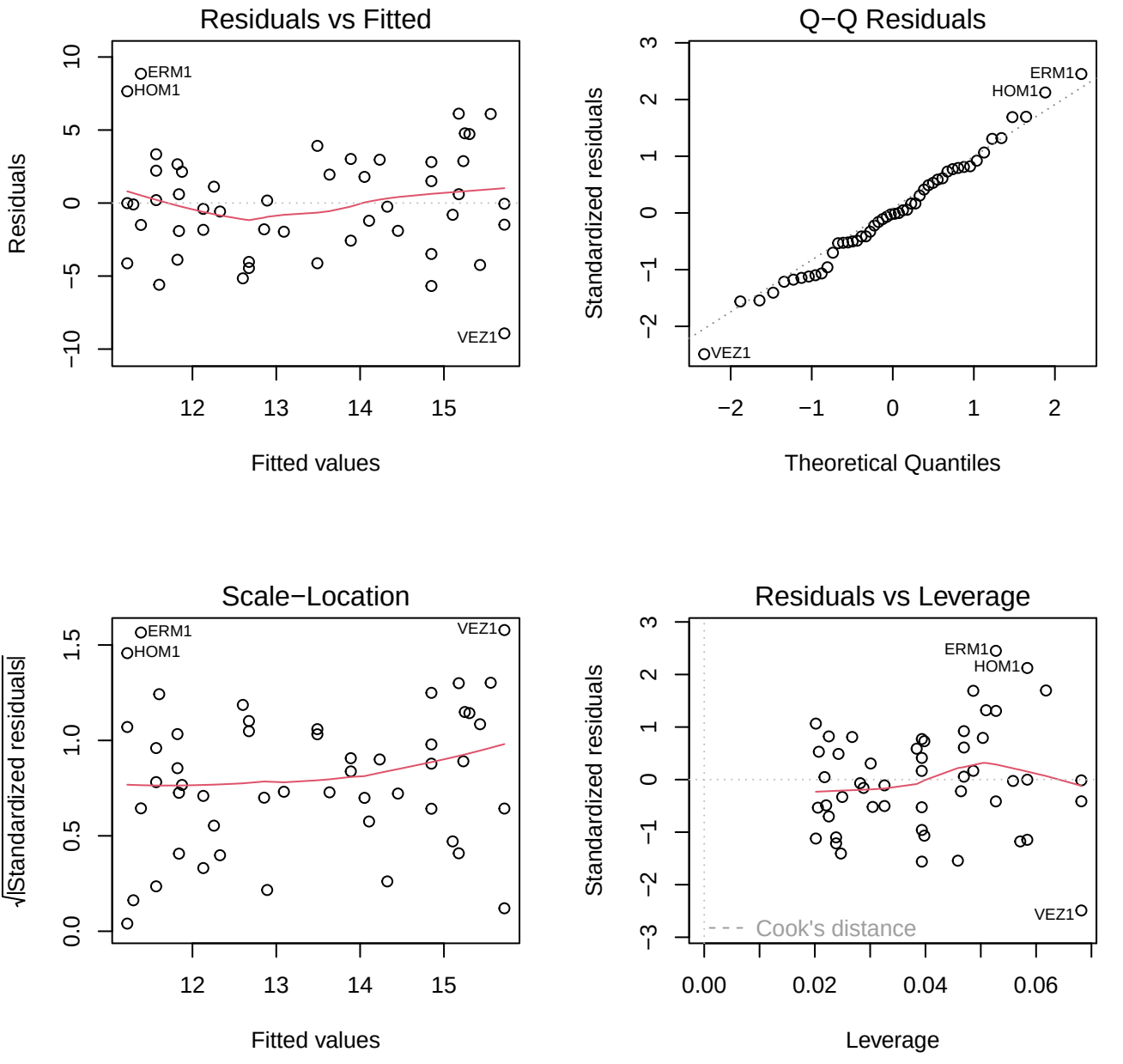

$R^2 = 0.03567652$
p−value: = 0.189
Bacteria_order_reads
DOmin
10
15
20
2
4
6
8

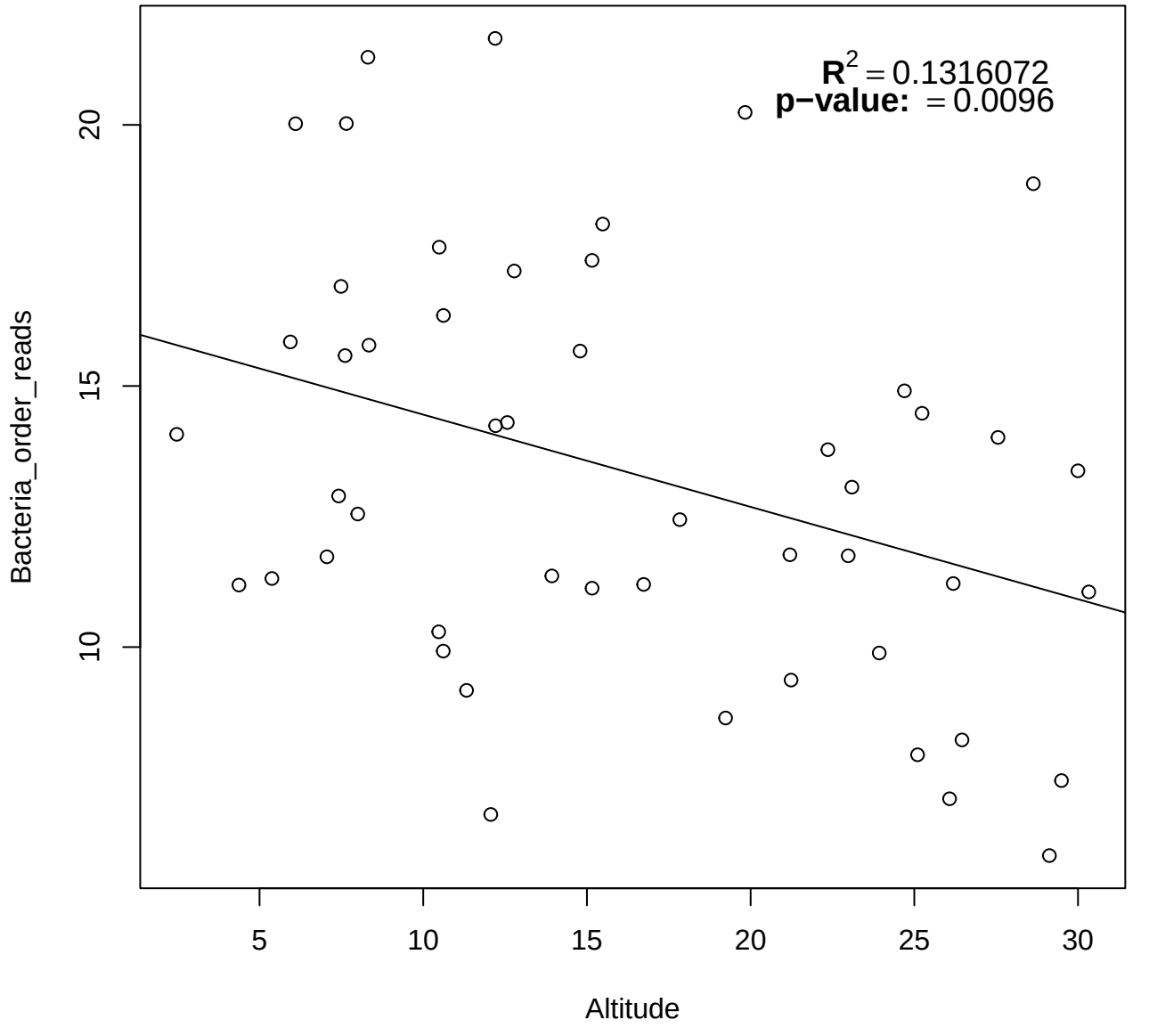

Residuals vs Fitted
Residuals
Fitted values
GER1
VEZ1
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
GER1
VEZ1
MACE1
Scale−Location
√|Standardized residuals|
Fitted values
MACE1
GER1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
SEL1
MACE1
Cook's distance
0.5
0.5
1

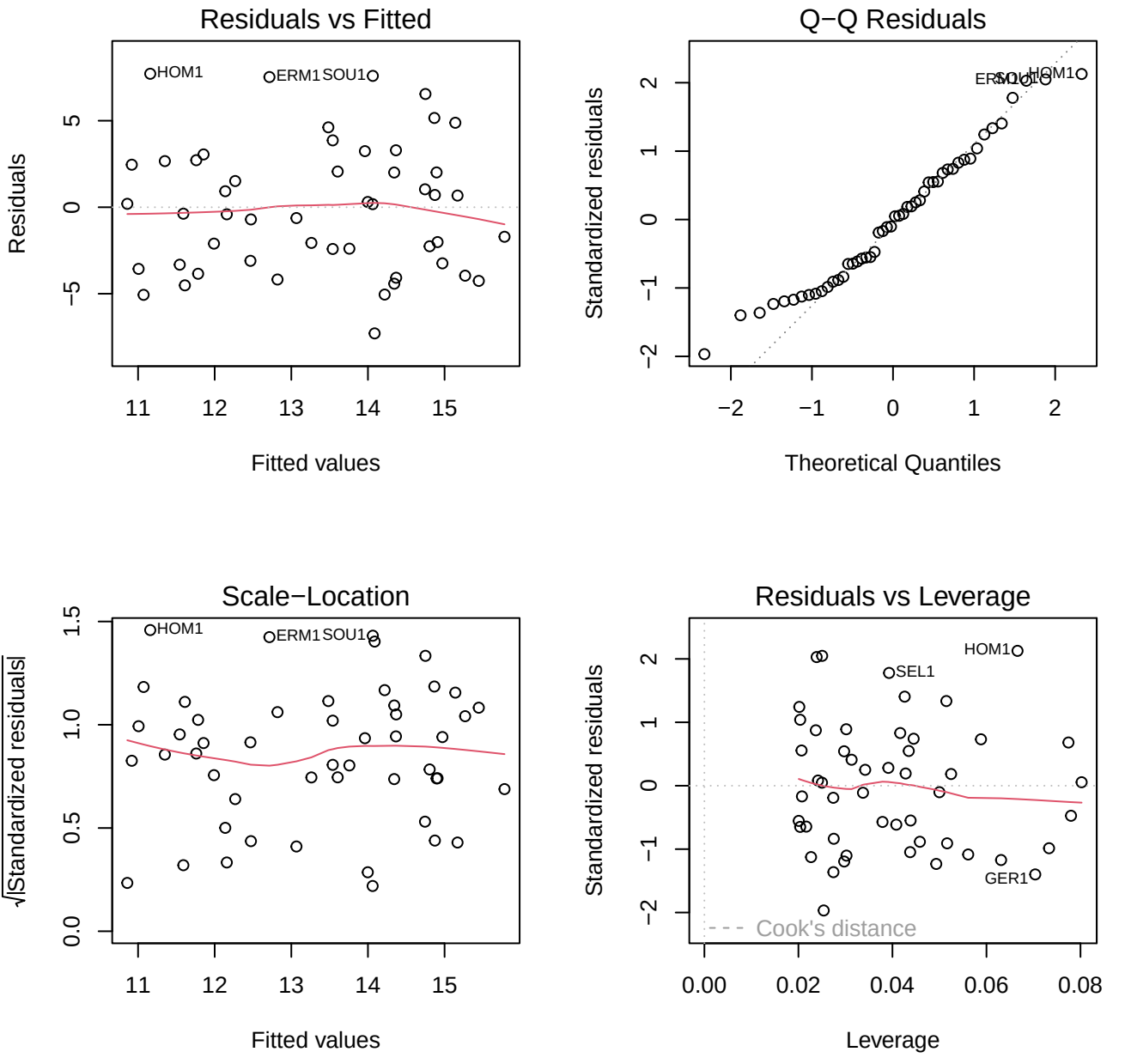

$R^2 = 0.02384803$
p−value: = 0.2843
Bacteria_order_reads
10
15
20
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
DOCV

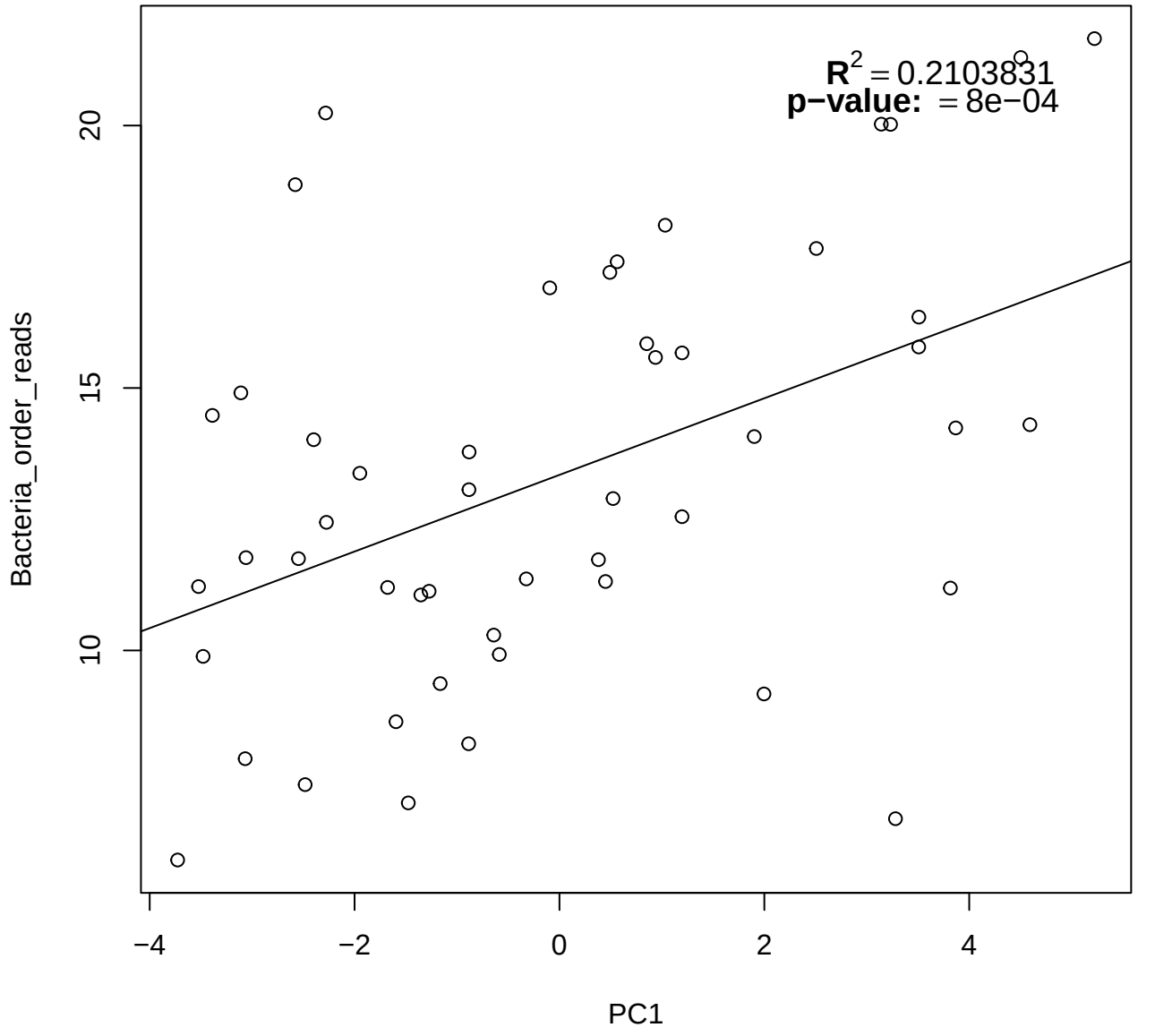

Residuals vs Fitted
Residuals
Fitted values
SOU1
VEZ1
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
SOU1
VEZ1
MACE1
Scale−Location
√|Standardized residuals|
Fitted values
MACE1
SOU1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
VEZ1
MACE1
Cook's distance
1
0.5
0.5
1

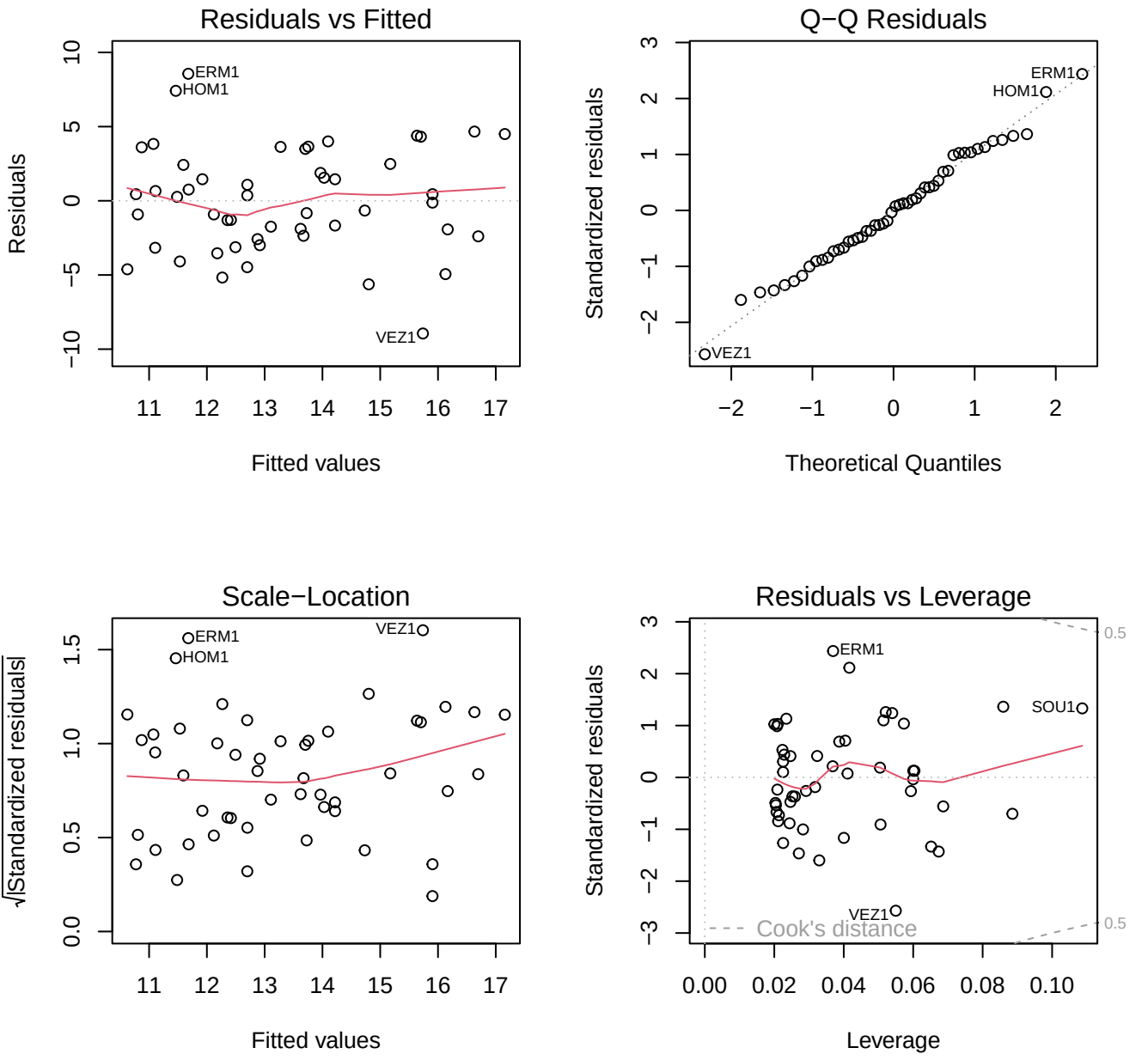

$R^2 = 0.150511$
p−value: = 0.0054
Bacteria_order_reads
10
15
20
0.0
0.5
1.0
1.5
2.0
2.5
LUI_subasin

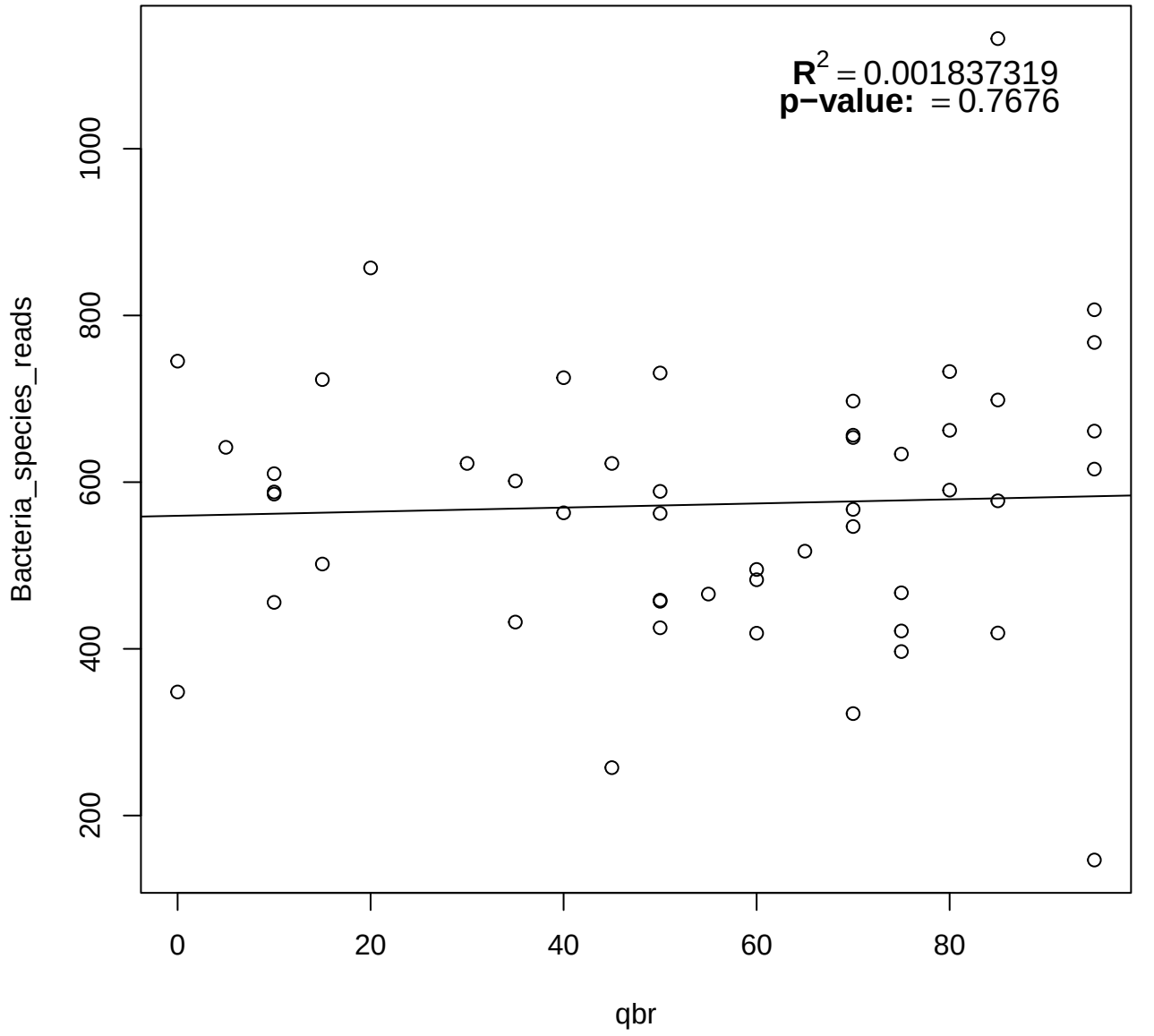

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
HOM1
VEZ1
Cook's distance

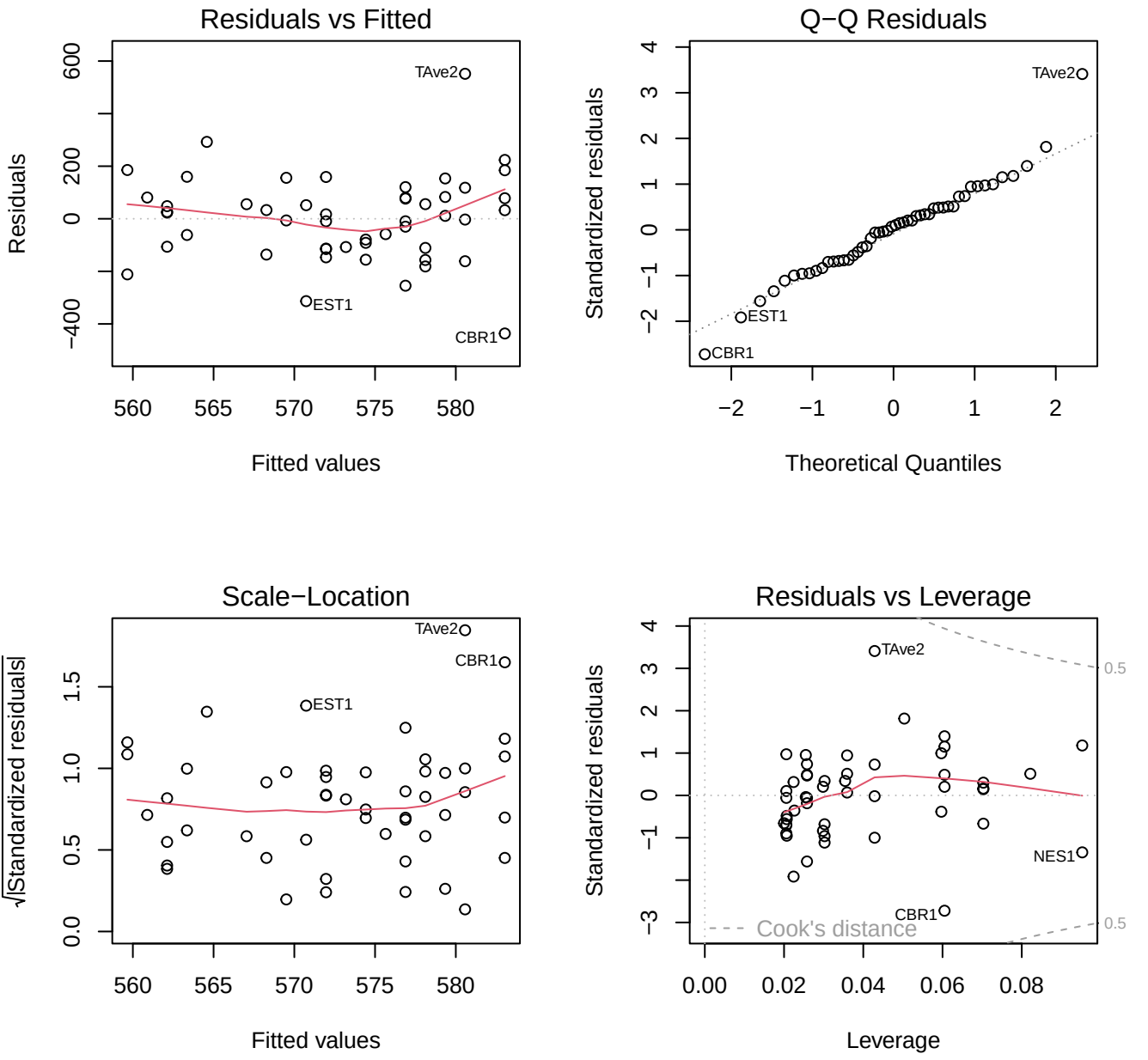

$R^2 = 0.1316072$
p−value: = 0.0096
Bacteria_order_reads
Altitude
10
15
20
5
10
15
20
25
30

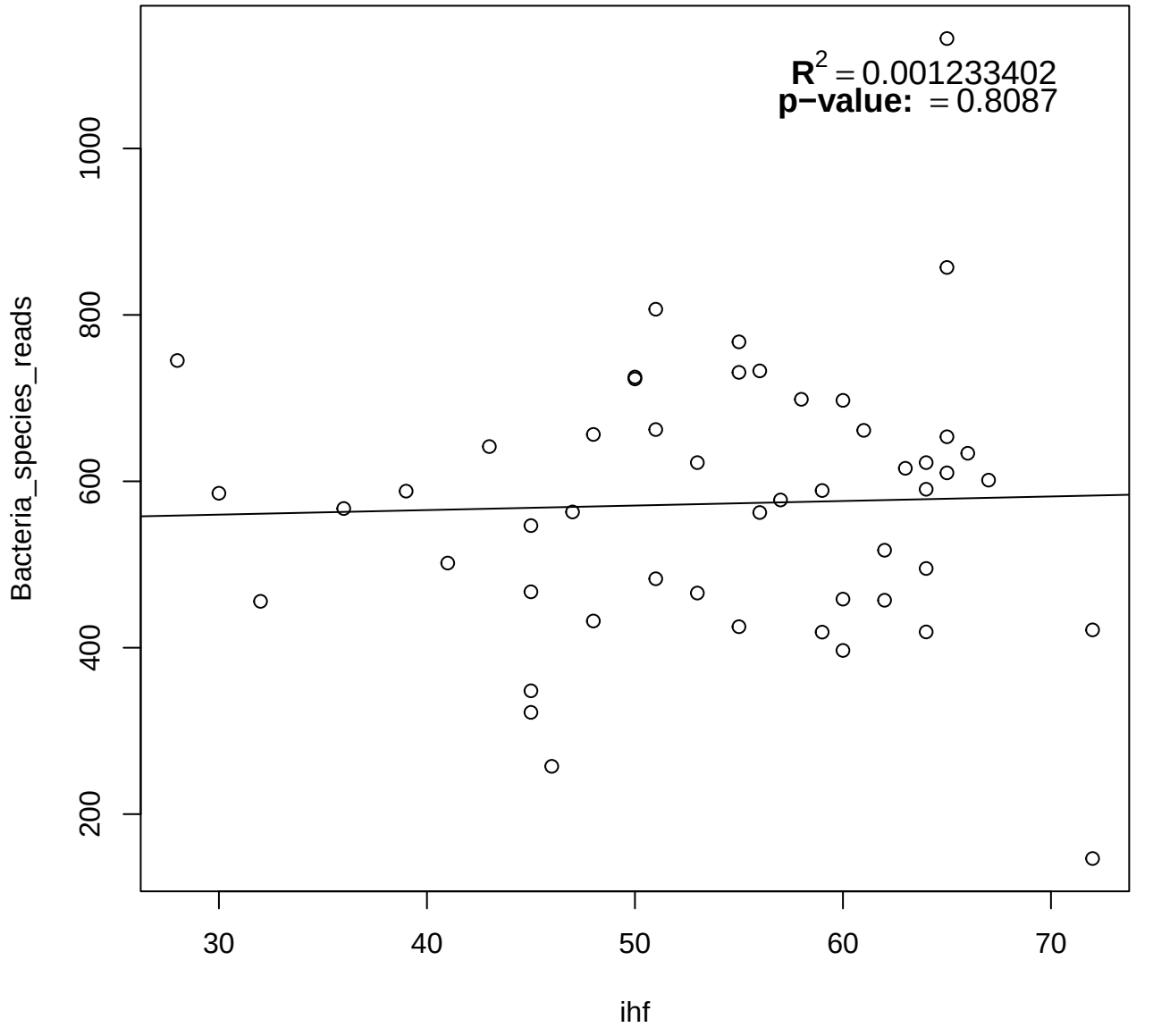

Residuals vs Fitted
Residuals
Fitted values
HOM1
ERM1
SOU1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
SEL1
GER1
Cook's distance

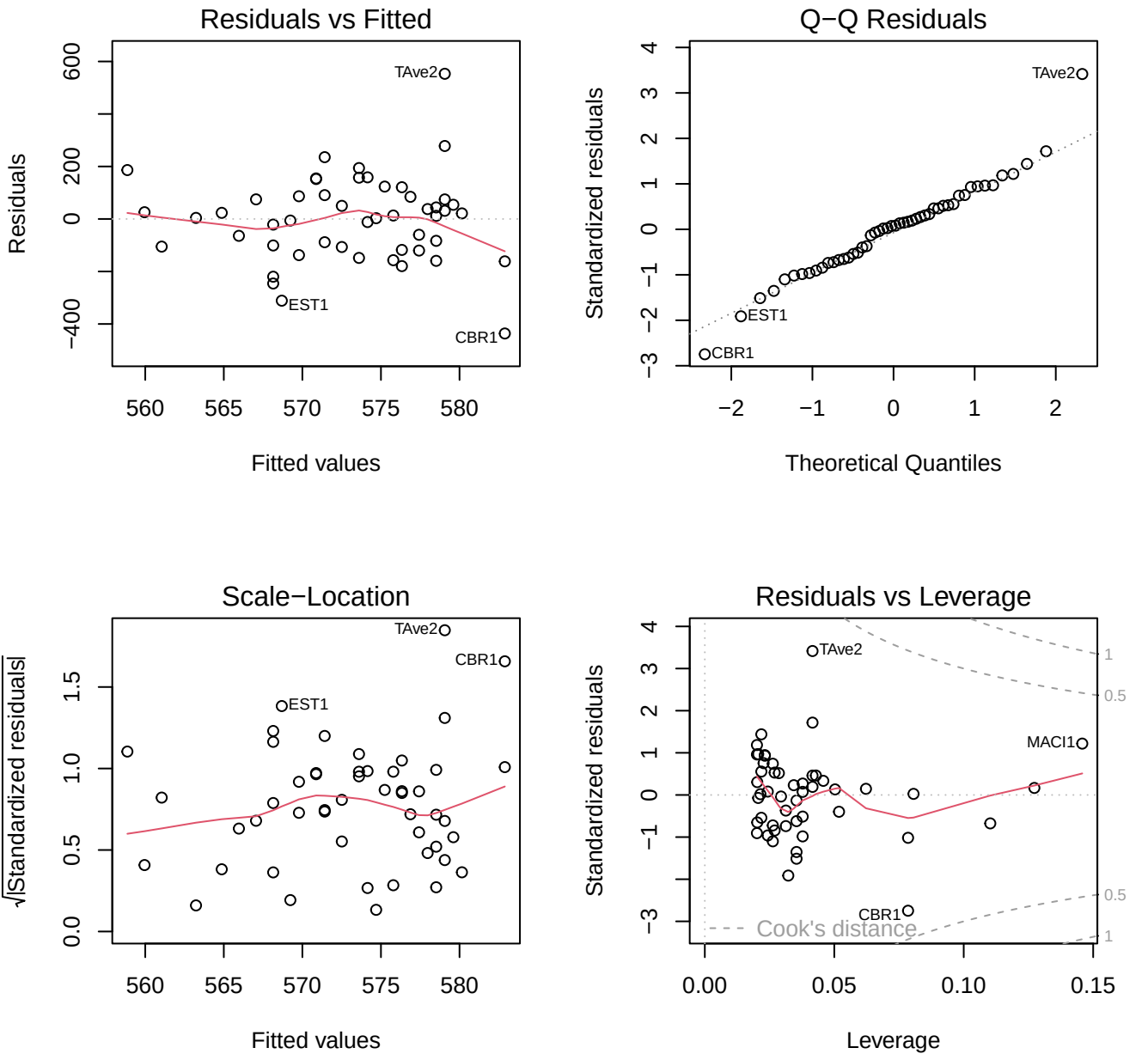

$R^2 = 0.2103831$
p−value: = 8e−04
Bacteria_order_reads
PC1
10
15
20
−4
−2
0
2
4

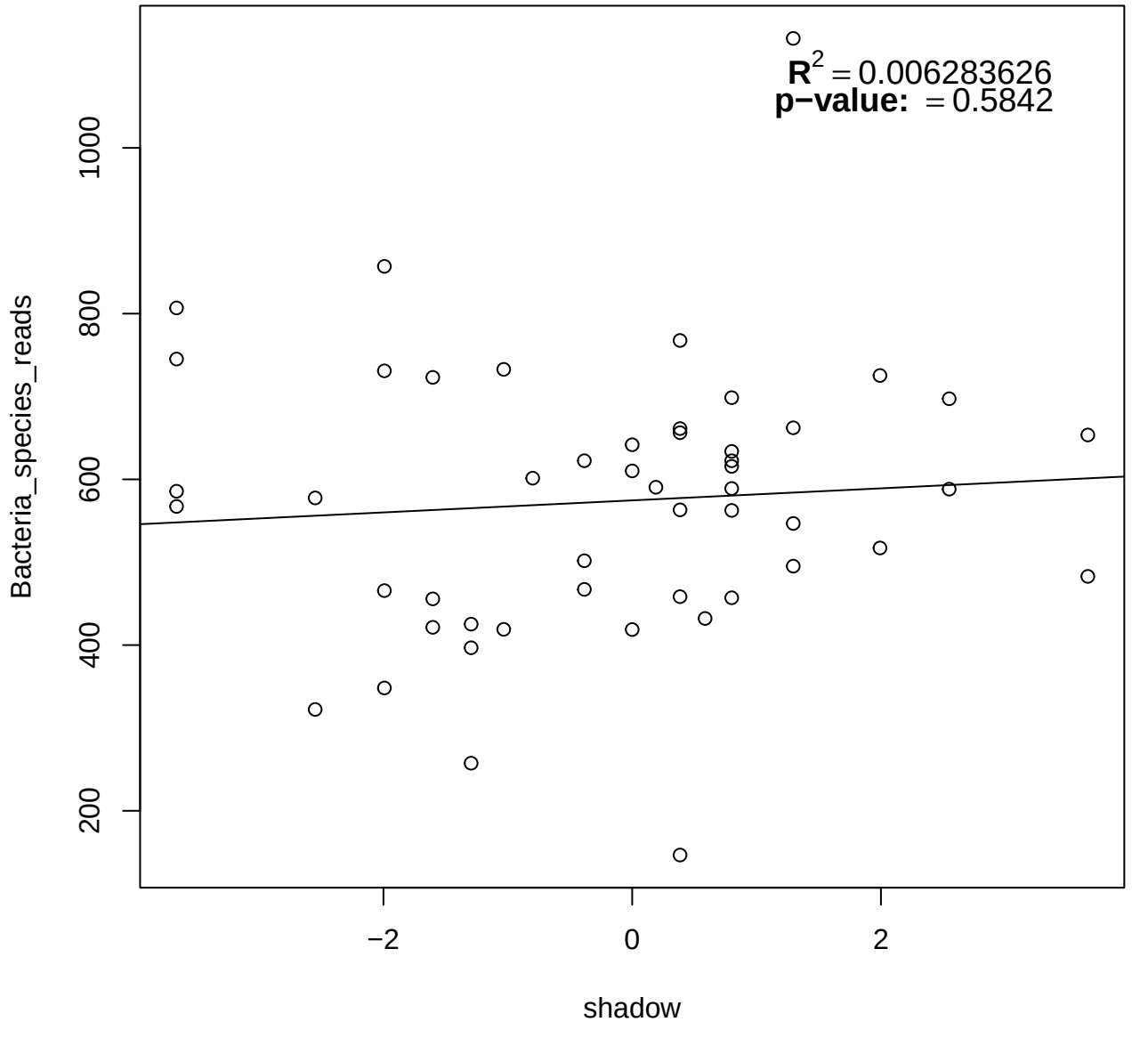

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
SOU1
VEZ1
Cook's distance
0.5
0.5

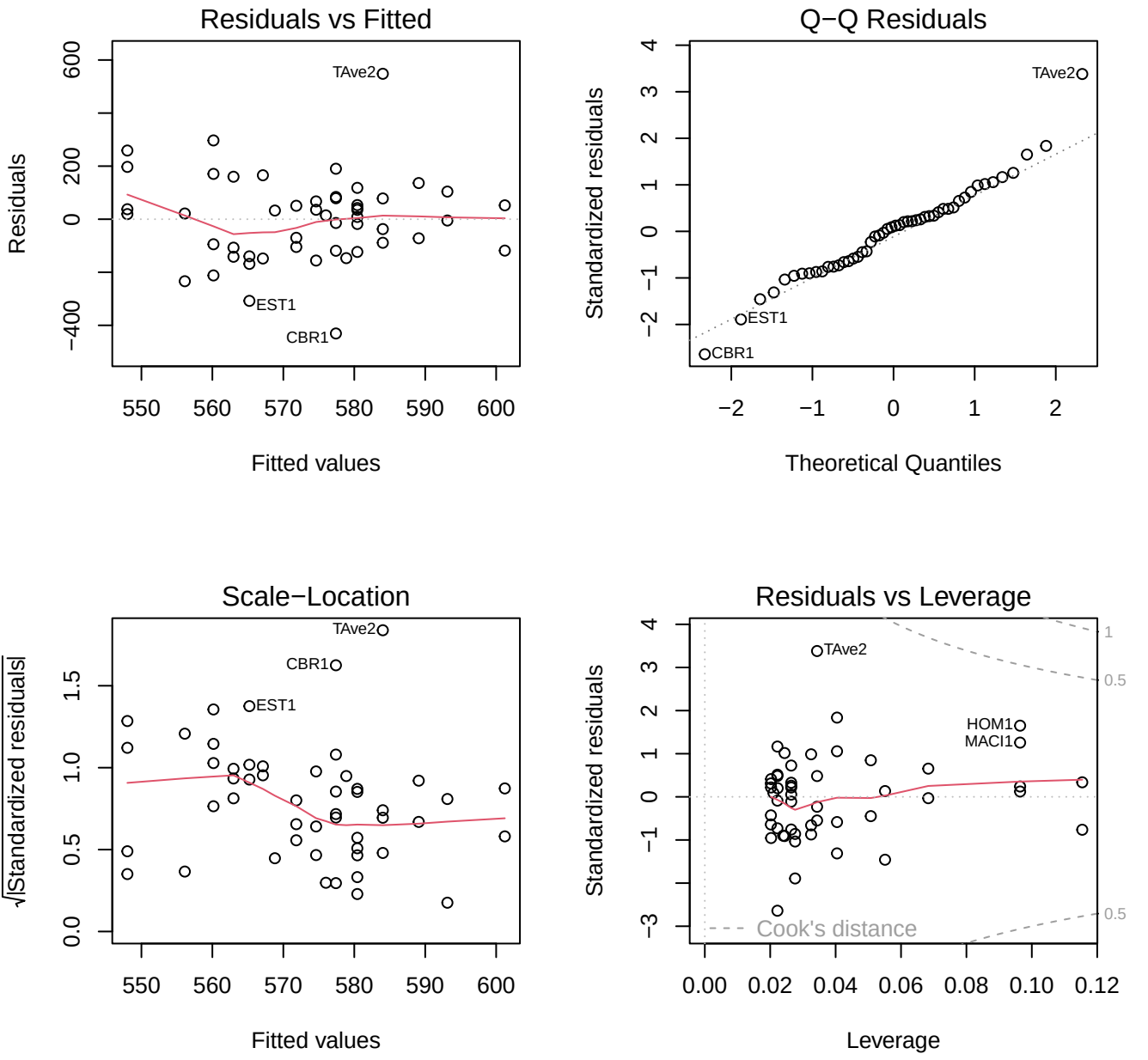

$R^2 = 0.001837319$
p−value: = 0.7676
Bacteria_species_reads
200
400
600
800
1000
0
20
40
60
80
qbr

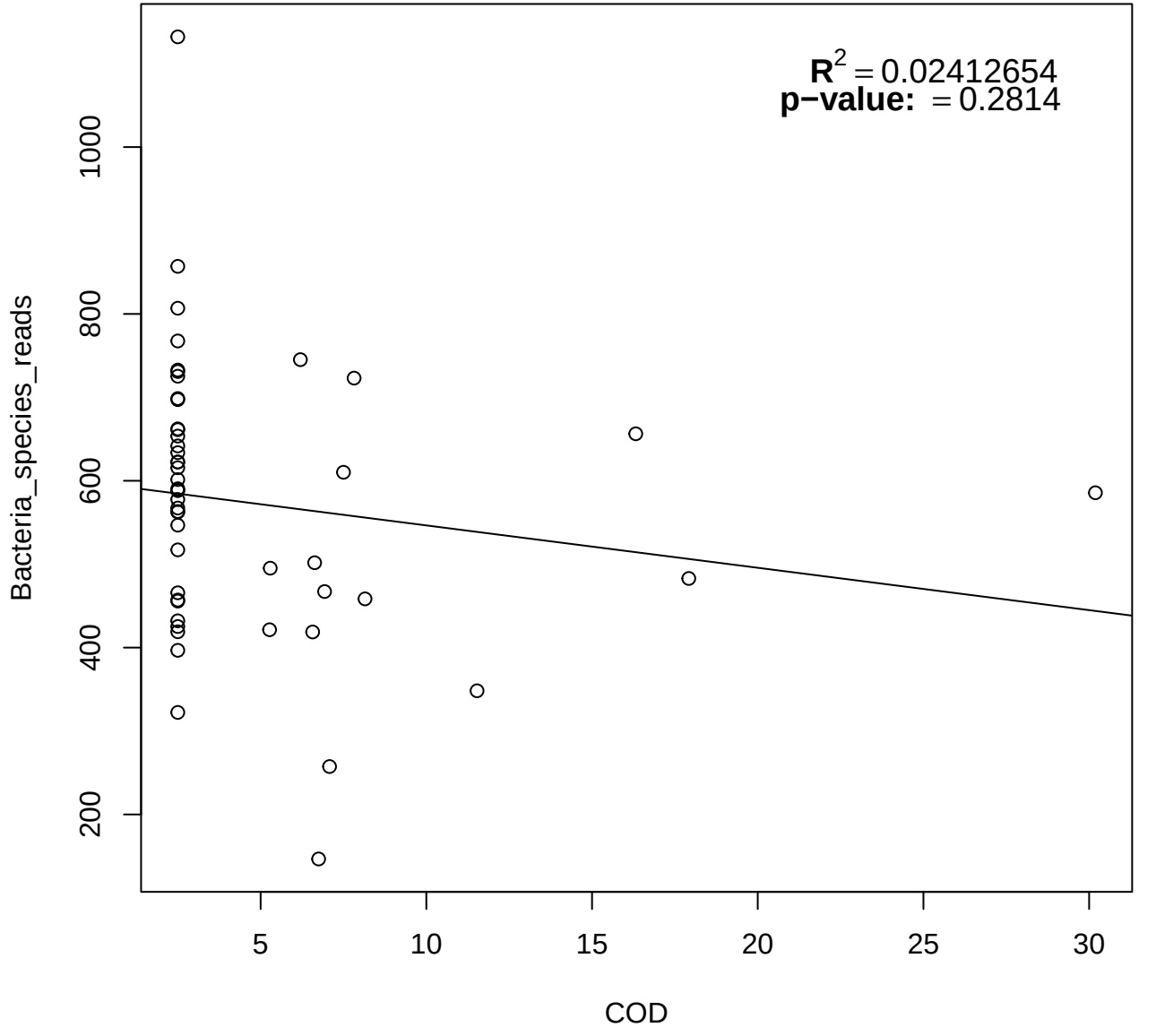

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
NES1
CBR1
Cook's distance
0.5
0.5

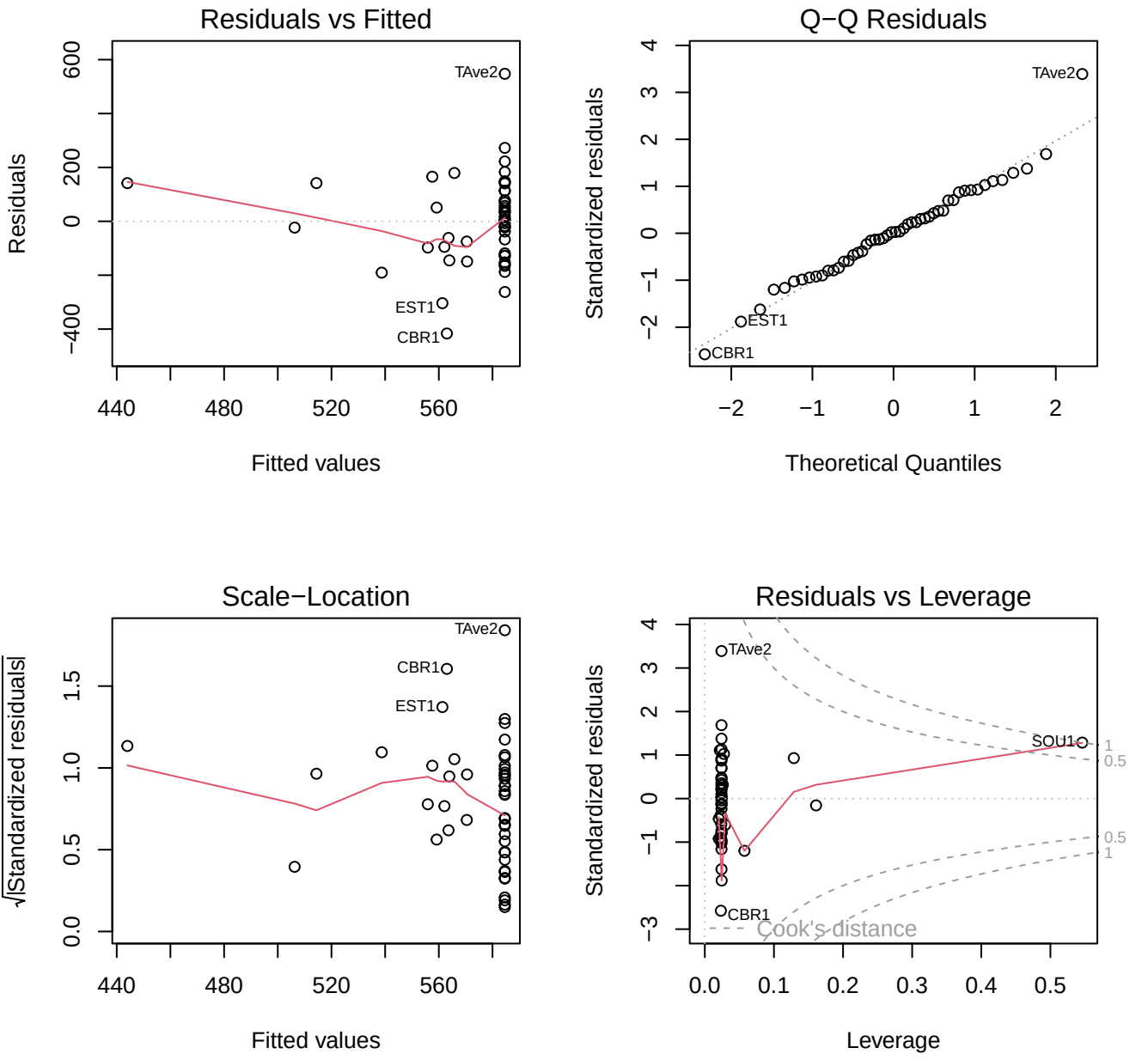

$R^2 = 0.001233402$
p−value: = 0.8087
Bacteria_species_reads
200
400
600
800
1000
30
40
50
60
70
ihf

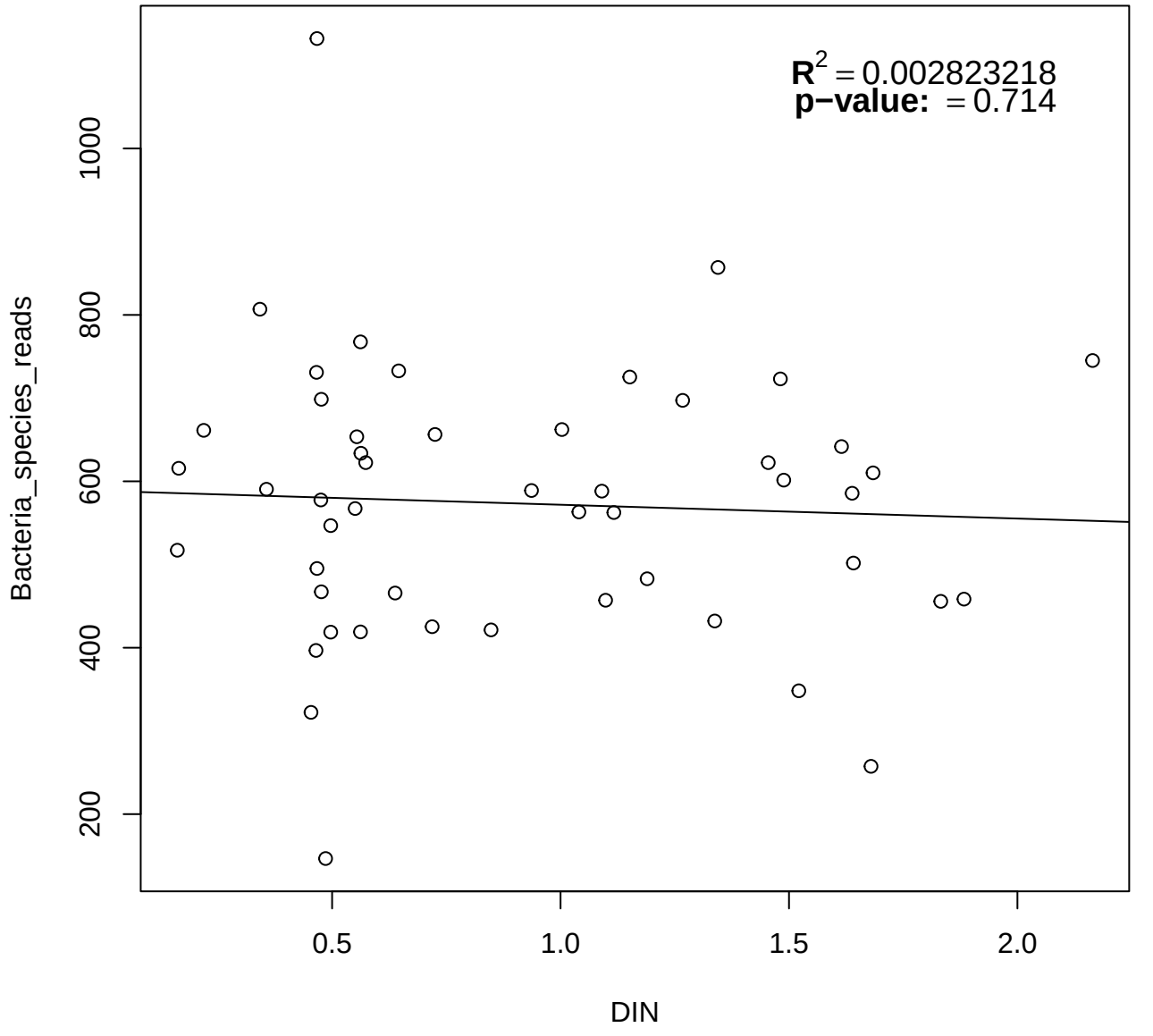

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
MACI1
CBR1
Cook's distance

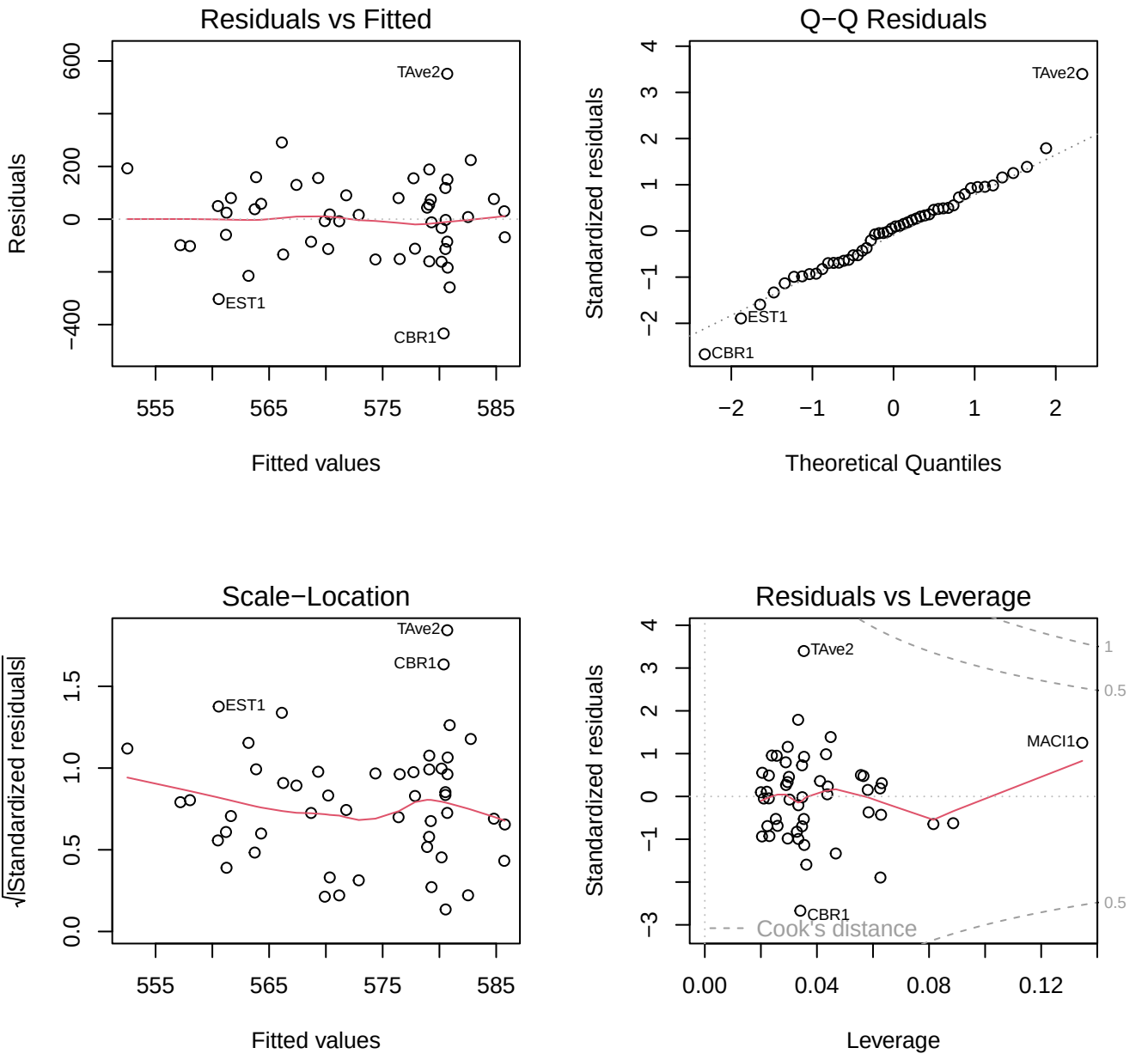

$R^2 = 0.006283626$
p−value: = 0.5842
Bacteria_species_reads
1000
800
600
400
200
−2
0
2
shadow

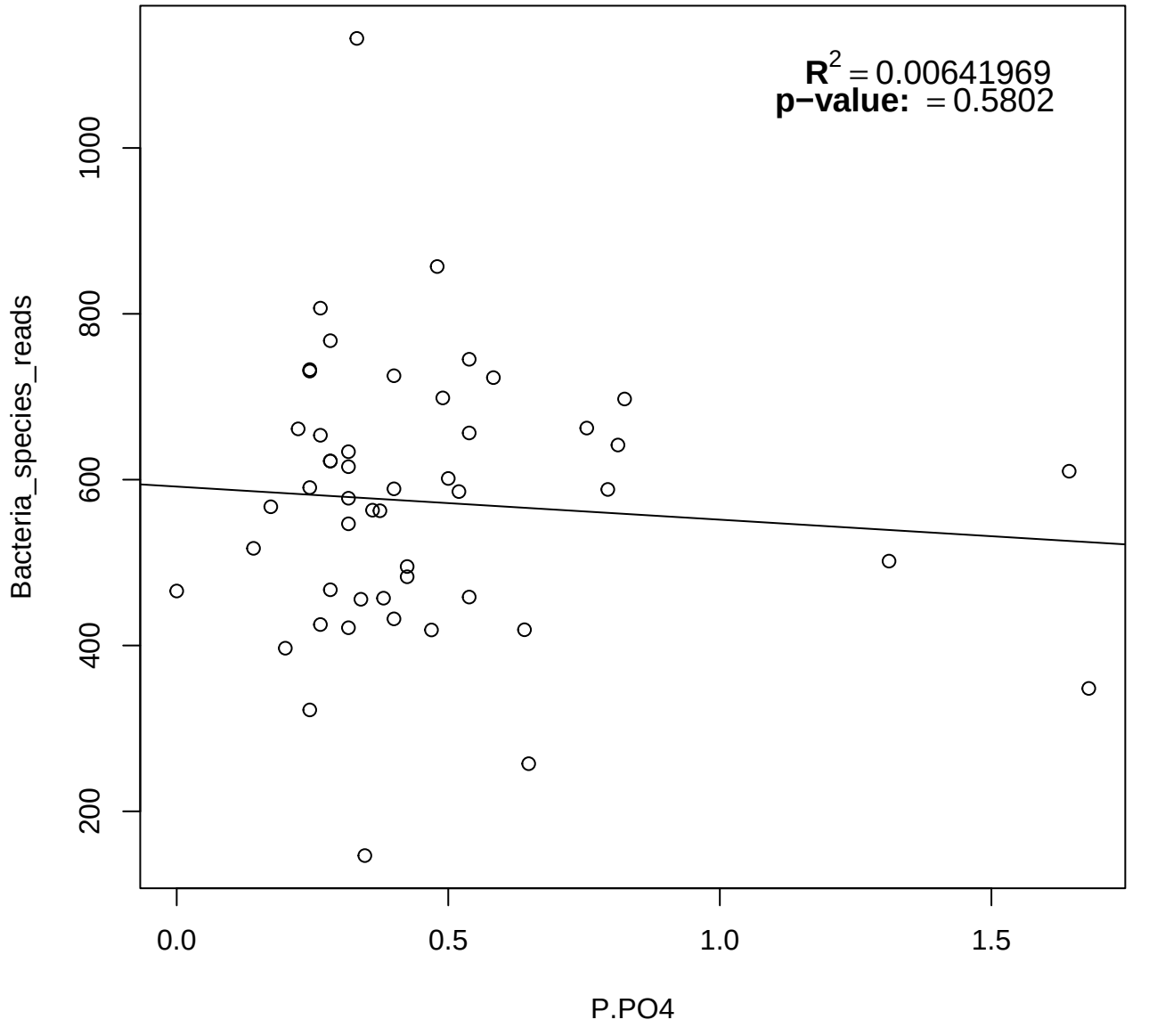

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
HOM1
MACI1
Cook's distance
1
0.5
0.5

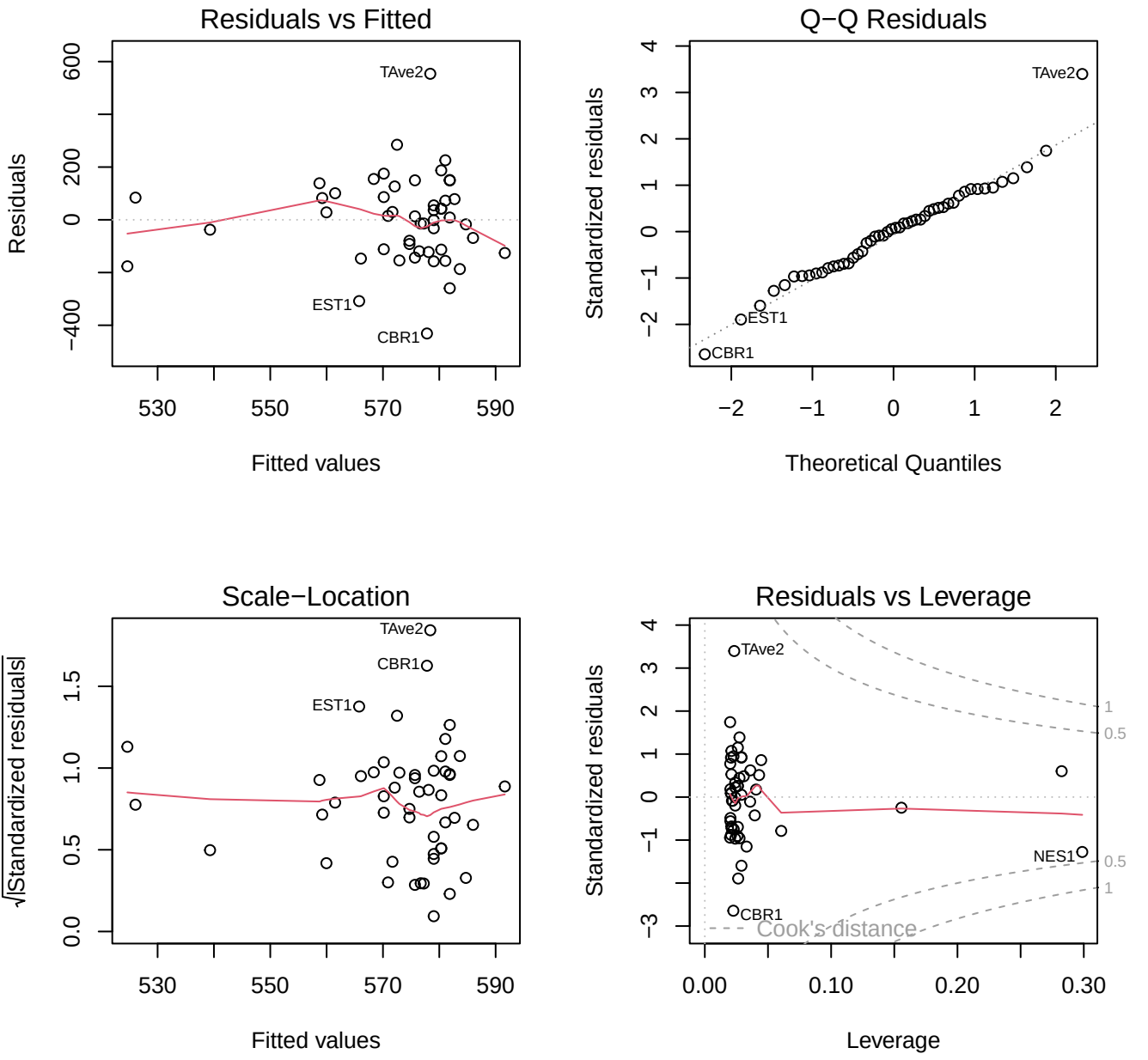

$R^2 = 0.02412654$
p−value: = 0.2814
Bacteria_species_reads
200
400
600
800
1000
5
10
15
20
25
30
COD

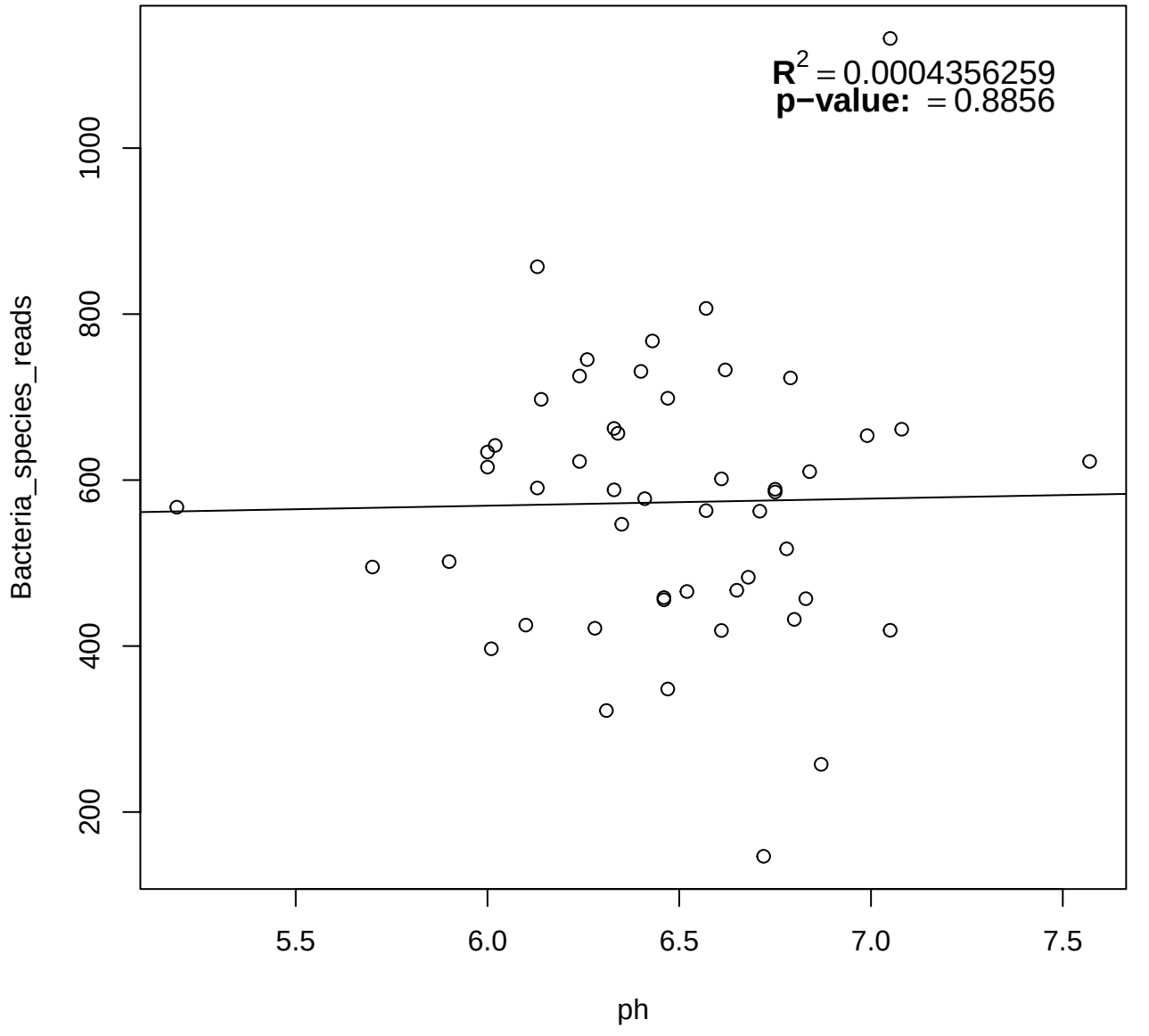

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
SOU1
CBR1
Cook's distance

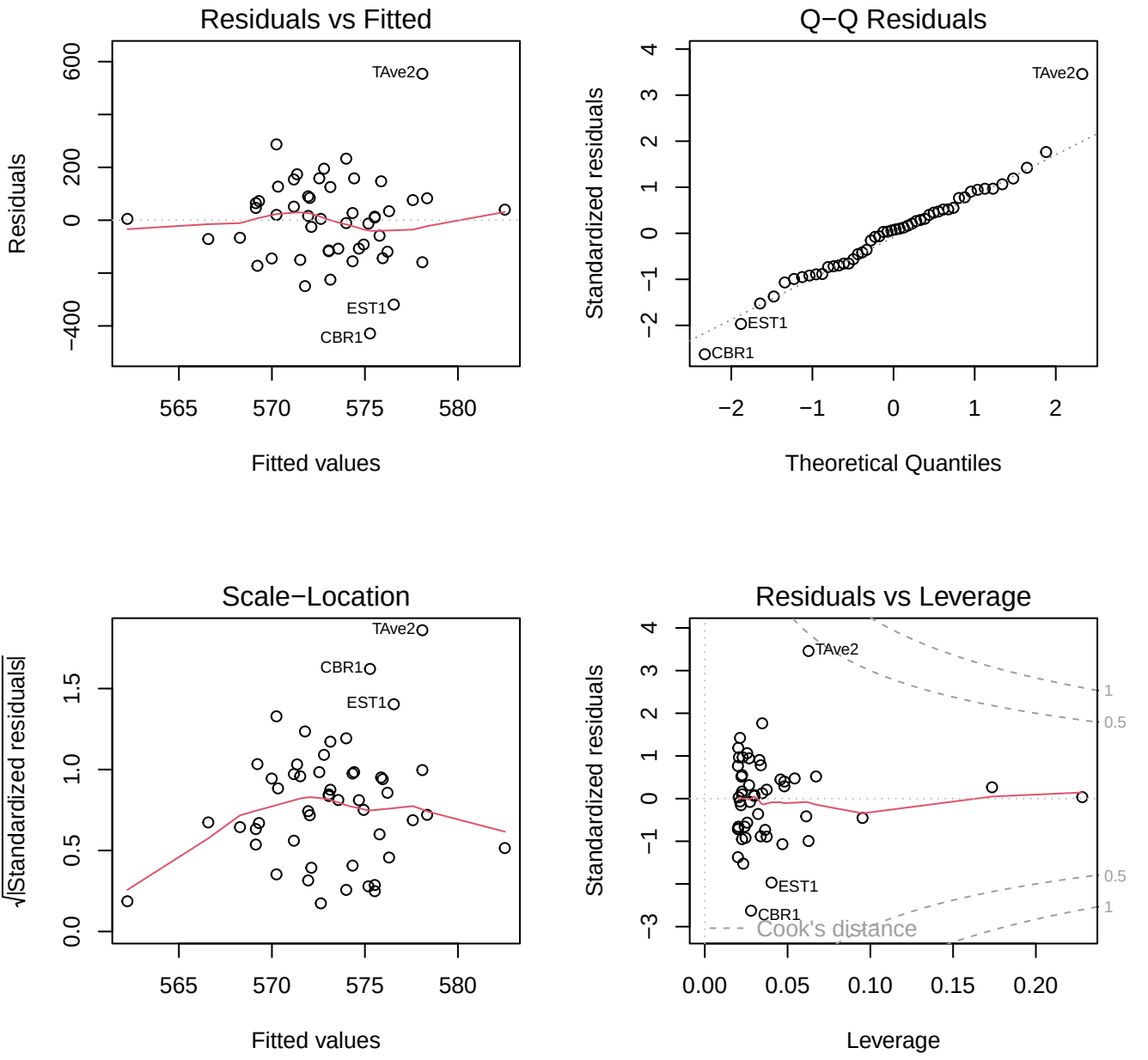

$R^2 = 0.002823218$
p−value: = 0.714
Bacteria_species_reads
200
400
600
800
1000
0.5
1.0
1.5
2.0
DIN

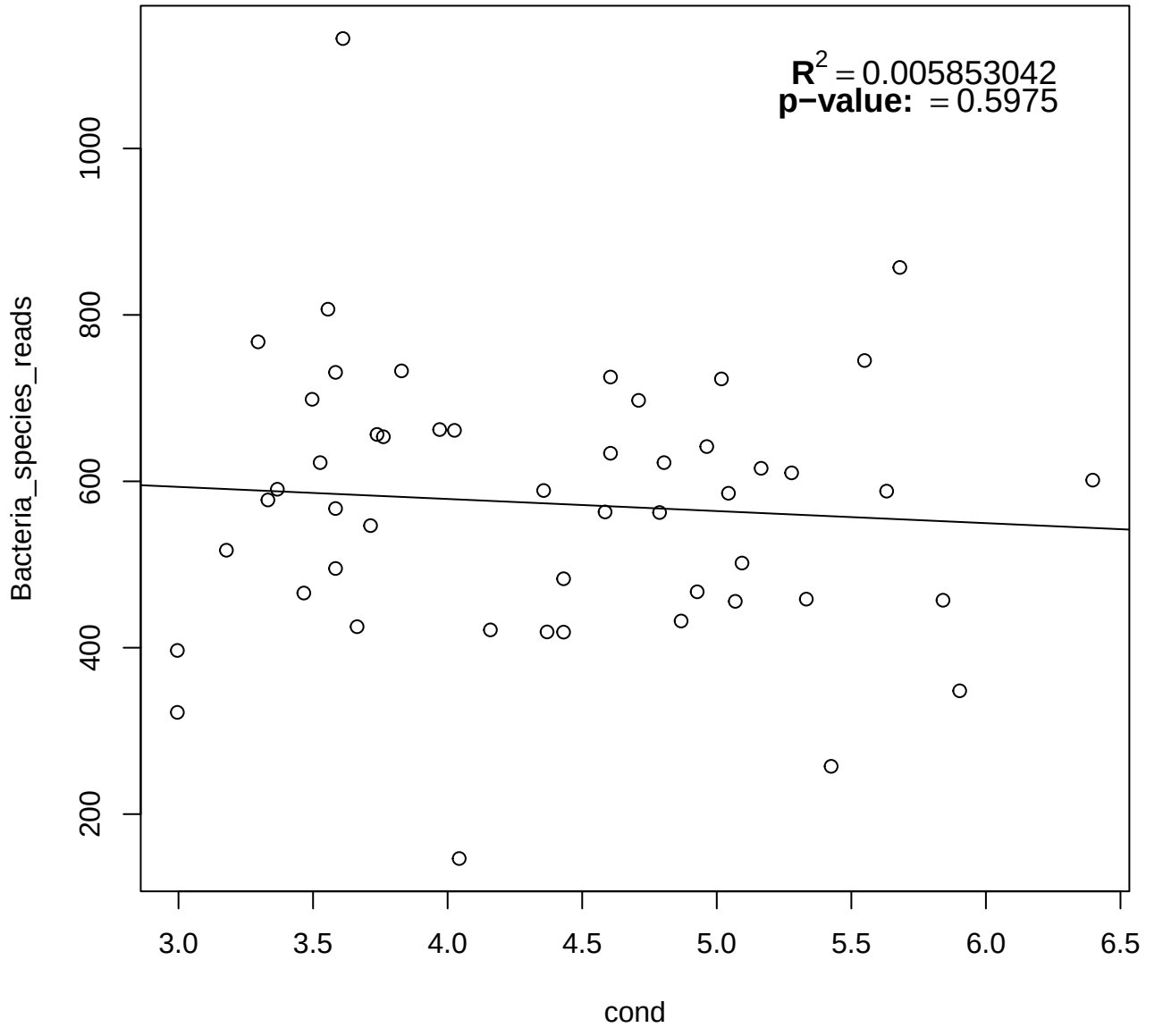

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
MACI1
CBR1
Cook's distance
1
0.5
0.5

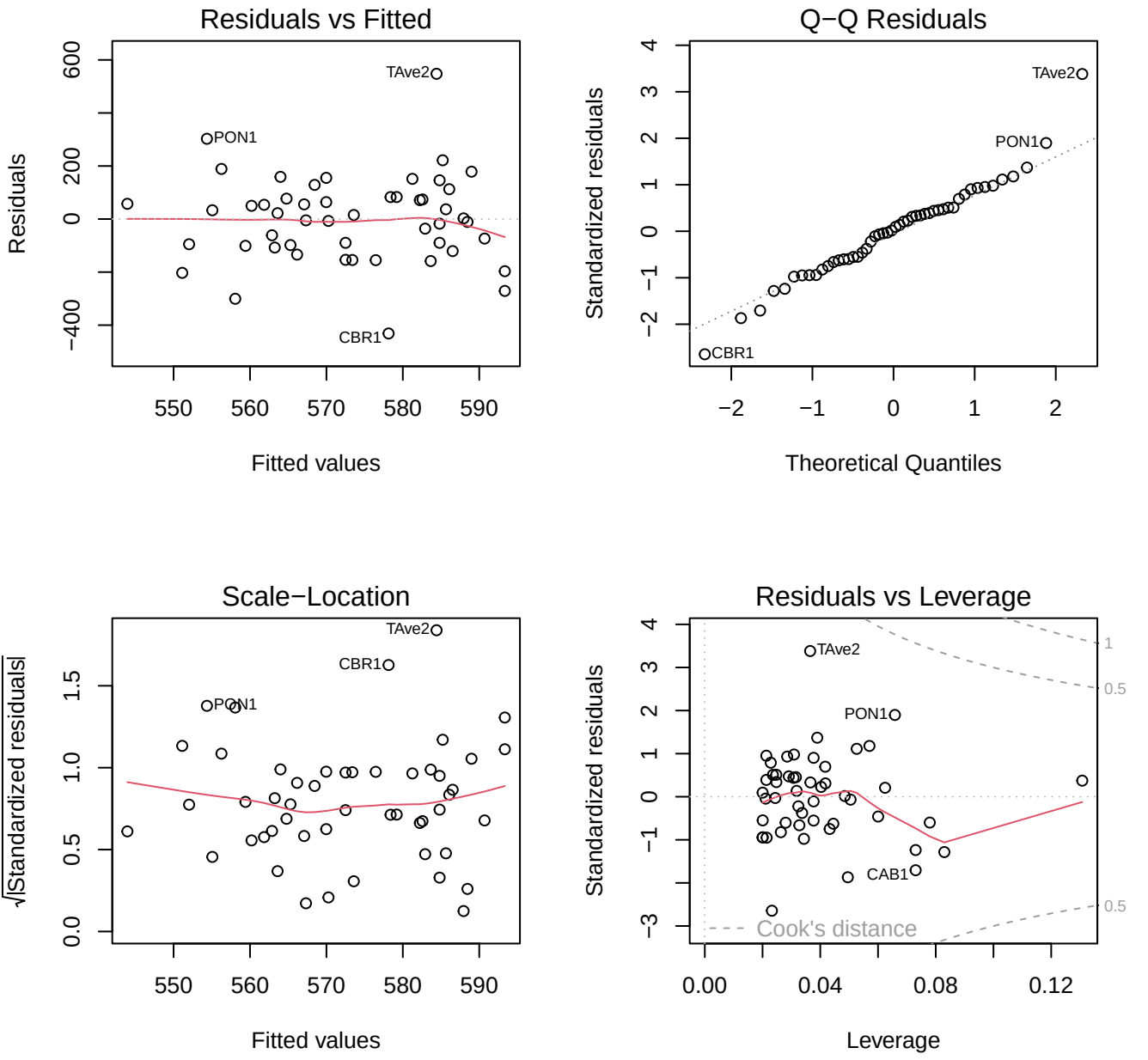

$R^2 = 0.00641969$
p−value: = 0.5802
Bacteria_species_reads
200
400
600
800
1000
0.0
0.5
1.0
1.5
P.PO4

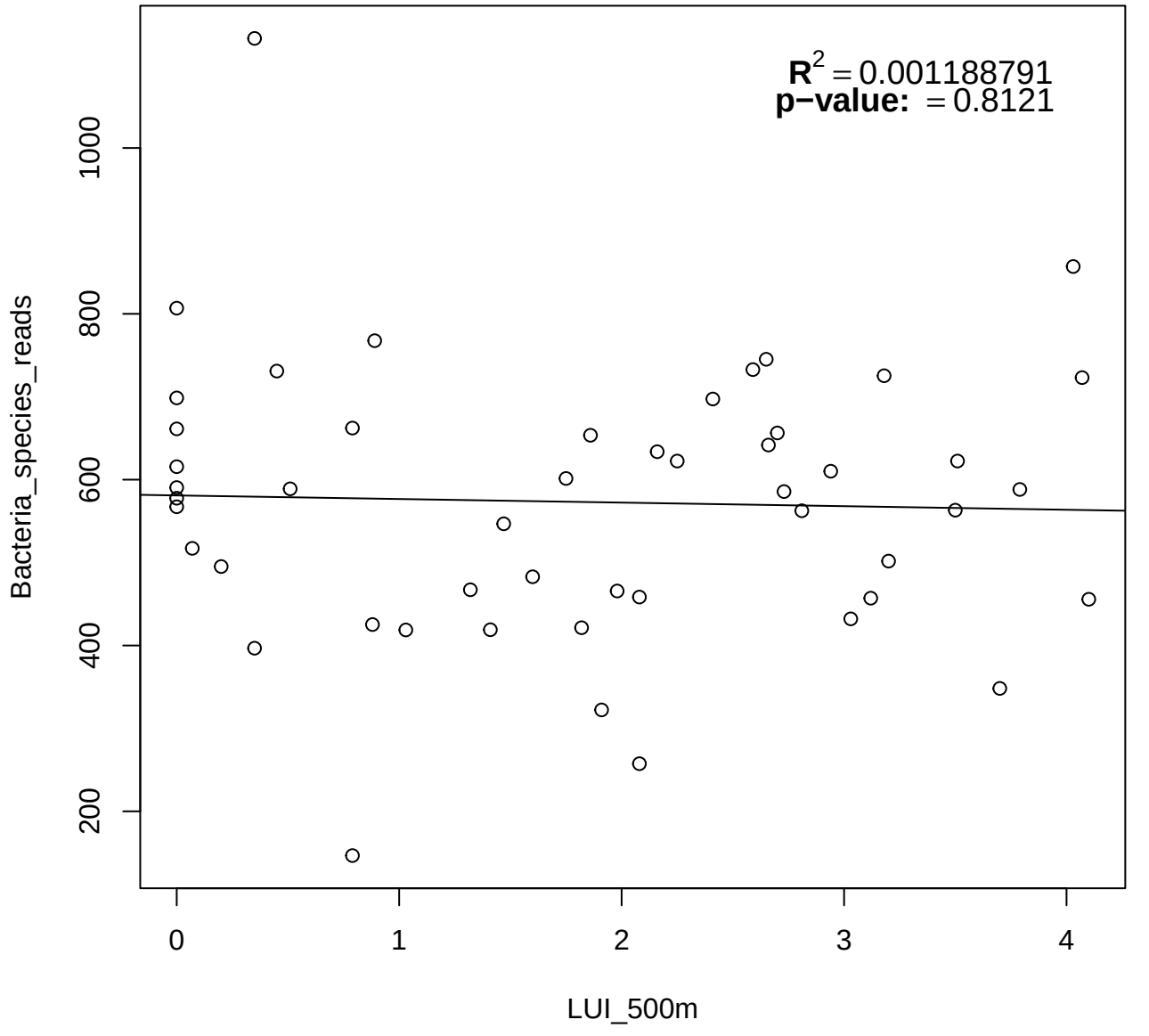

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
NES1
CBR1
Cook's distance

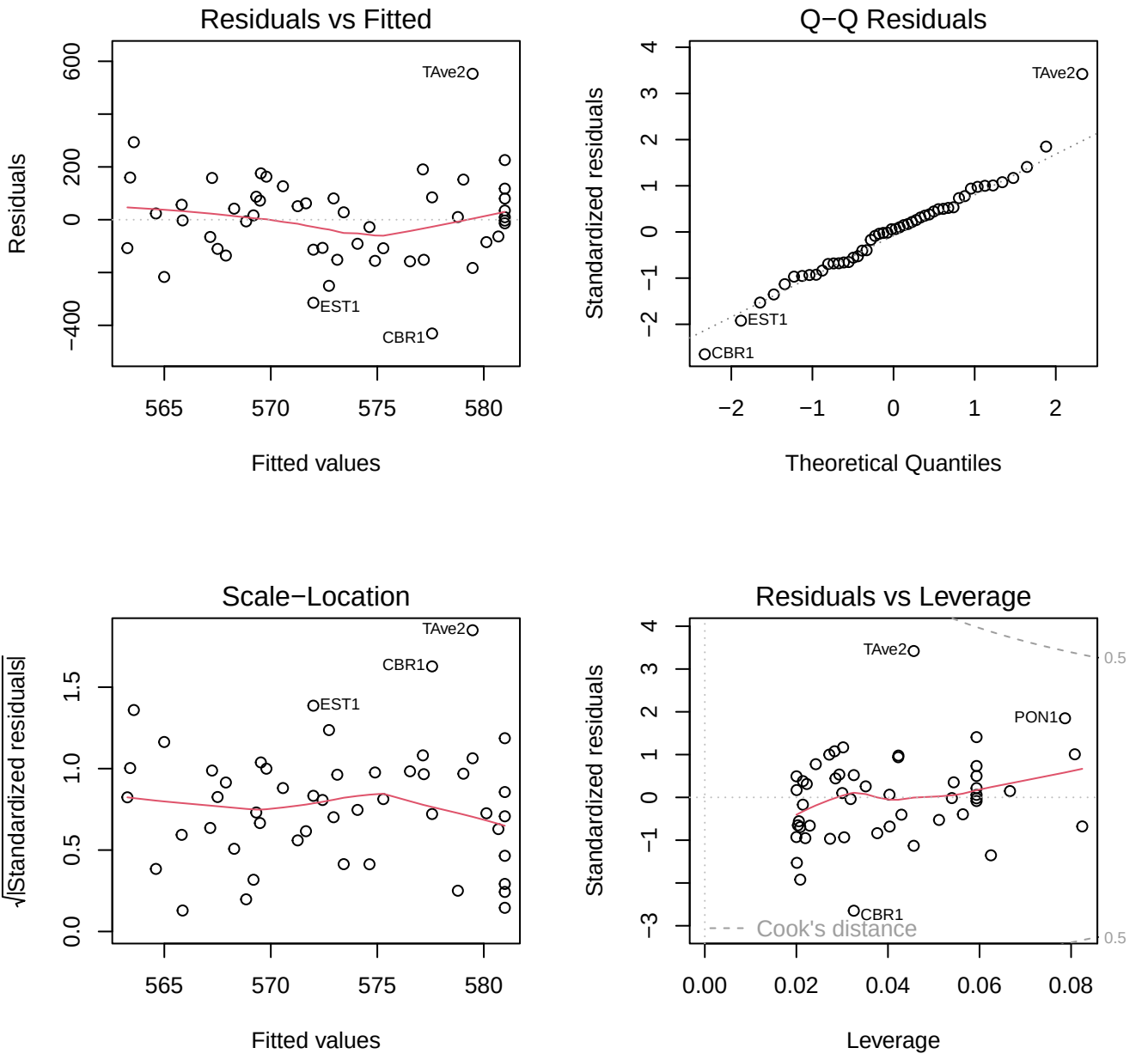

$R^2 = 0.0004356259$
p−value: $= 0.8856$
Bacteria_species_reads
200
400
600
800
1000
5.5
6.0
6.5
7.0
7.5
ph

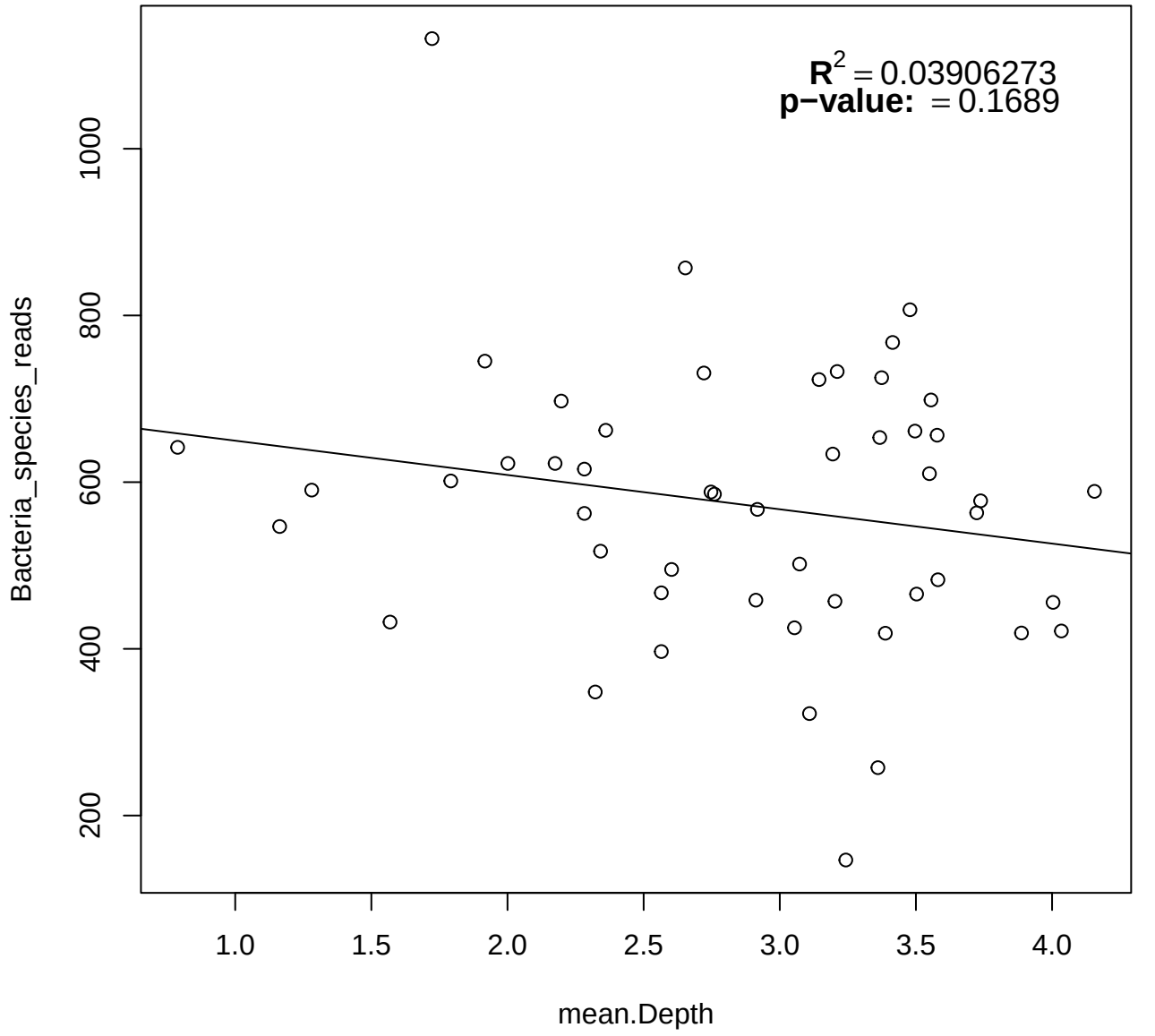

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
EST1
CBR1
Cook's distance
1
0.5
0.5
1

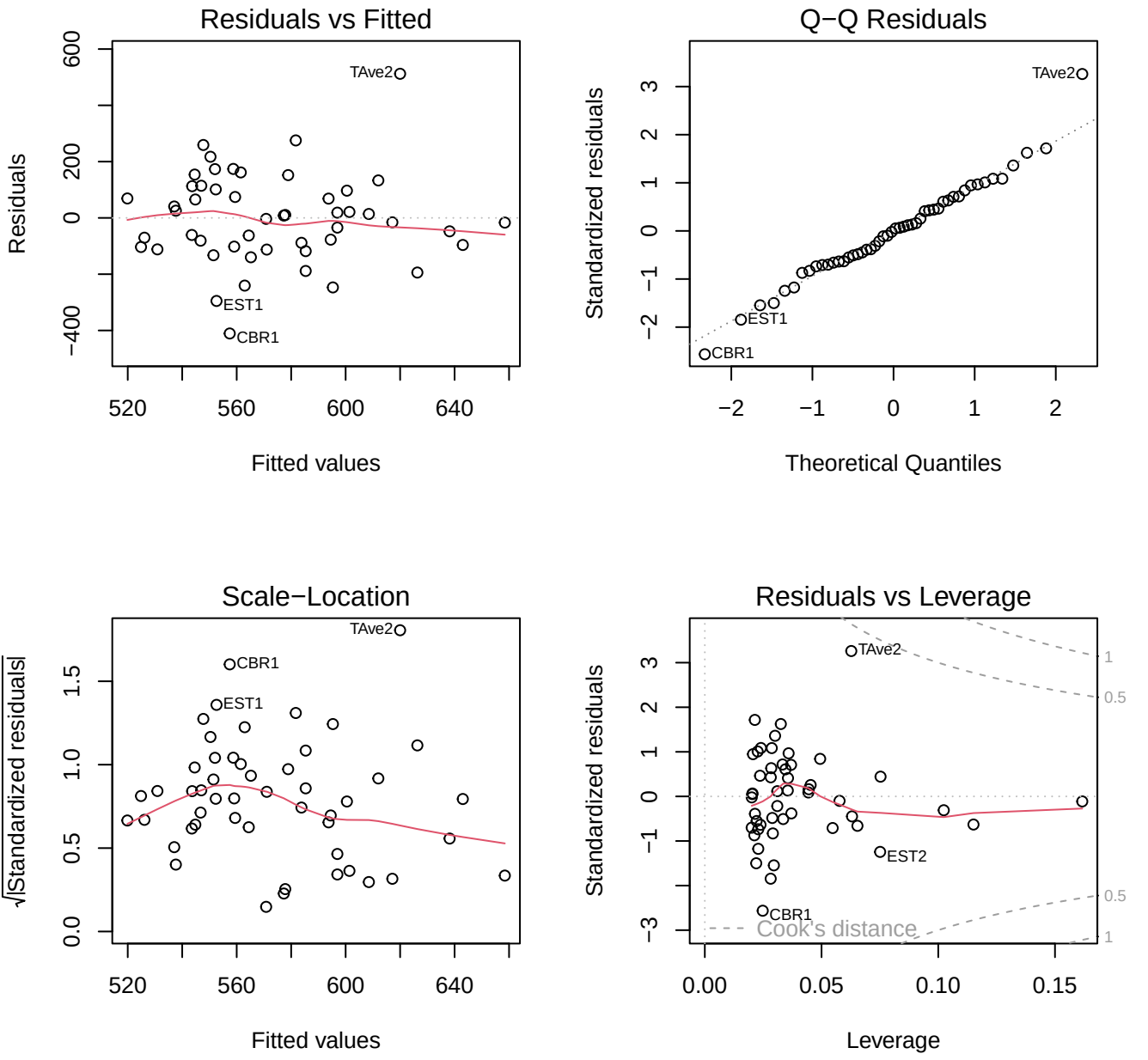

$R^2 = 0.005853042$
p−value: = 0.5975
Bacteria_species_reads
200
400
600
800
1000
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
cond

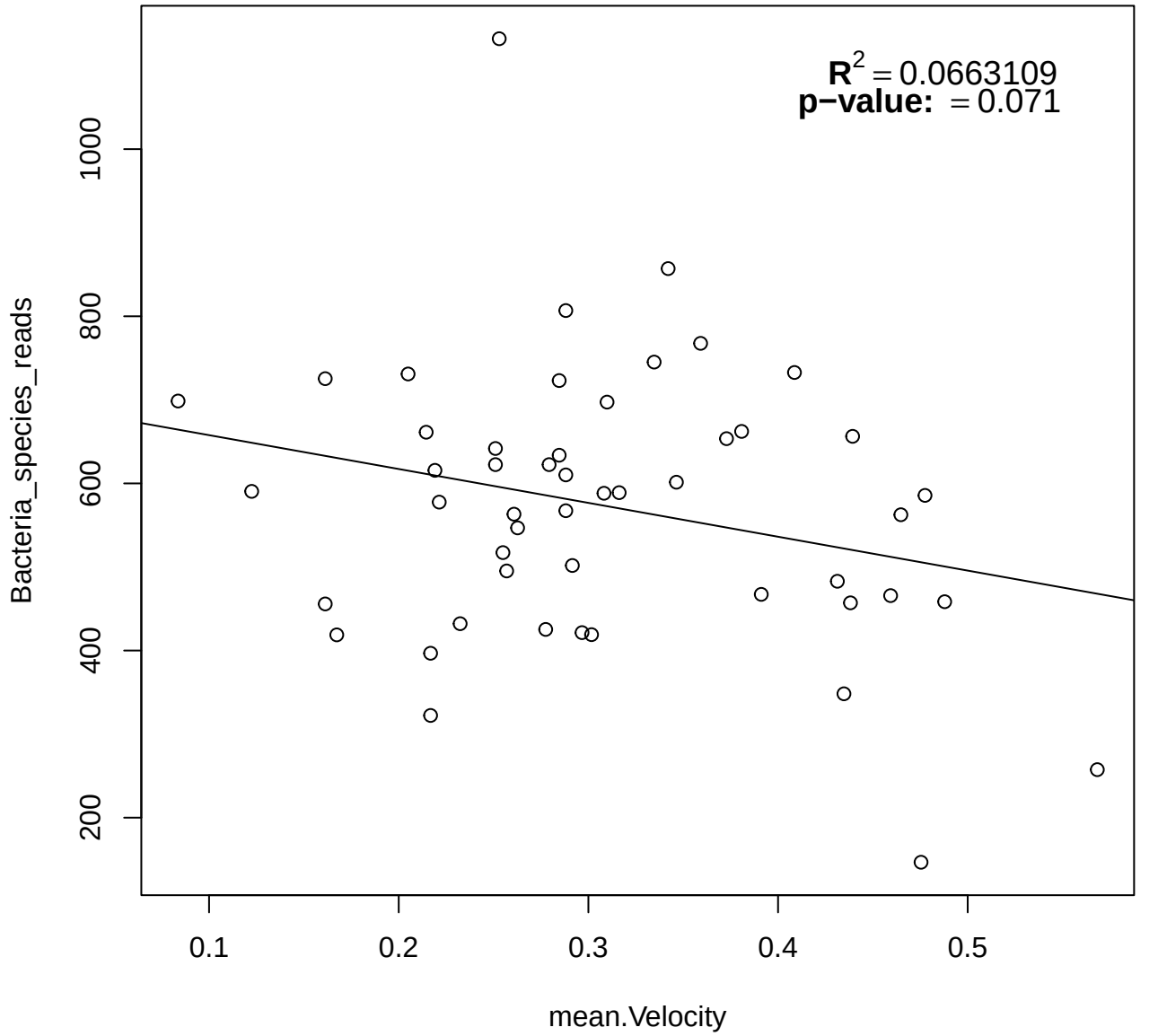

Residuals vs Fitted
Residuals
Fitted values
TAve2
PON1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
PON1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
PON1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
PON1
CAB1
Cook's distance
1
0.5
0.5

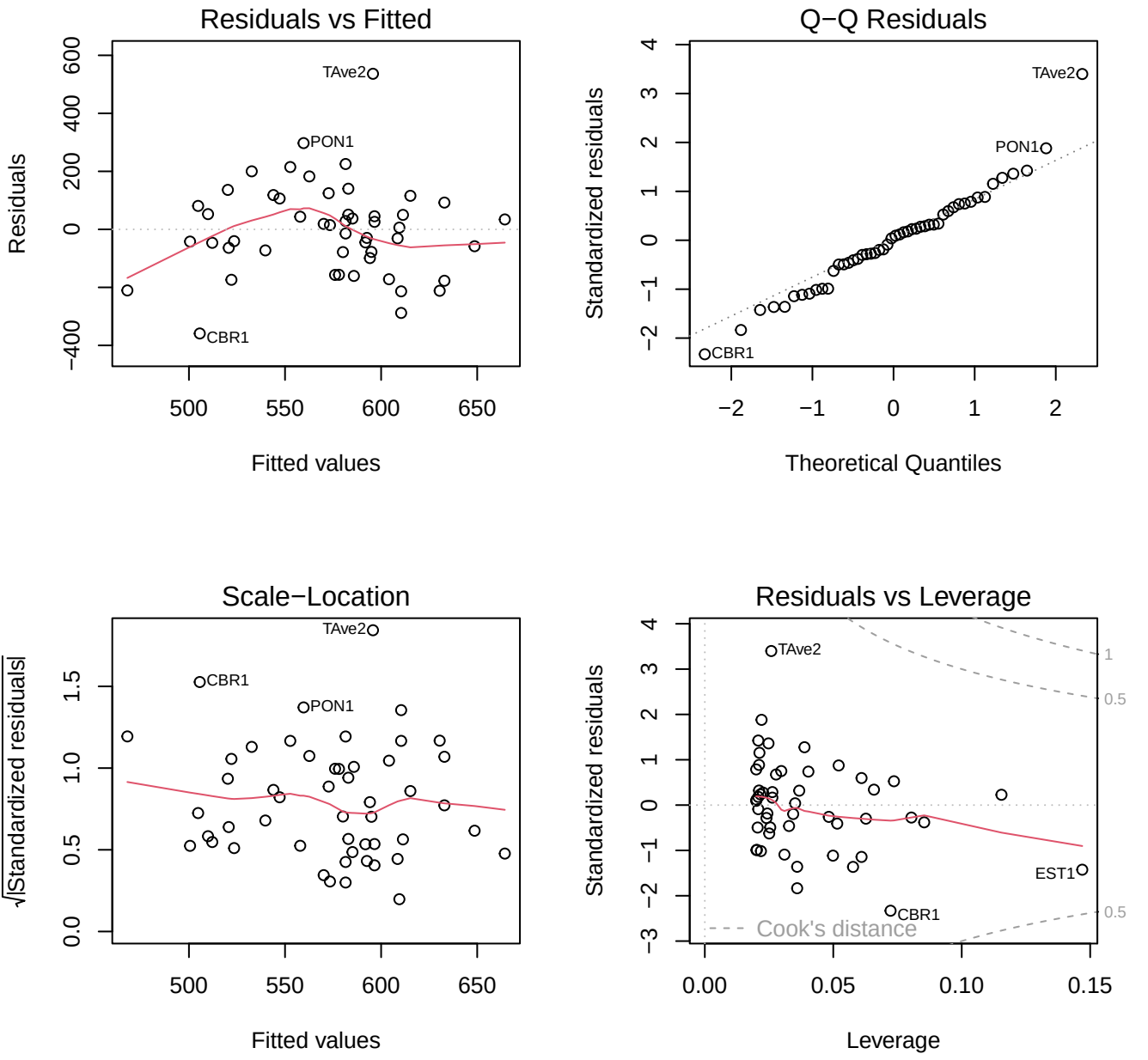

$R^2 = 0.001188791$
p−value: = 0.8121
Bacteria_species_reads
200
400
600
800
1000
0
1
2
3
4
LUI_500m

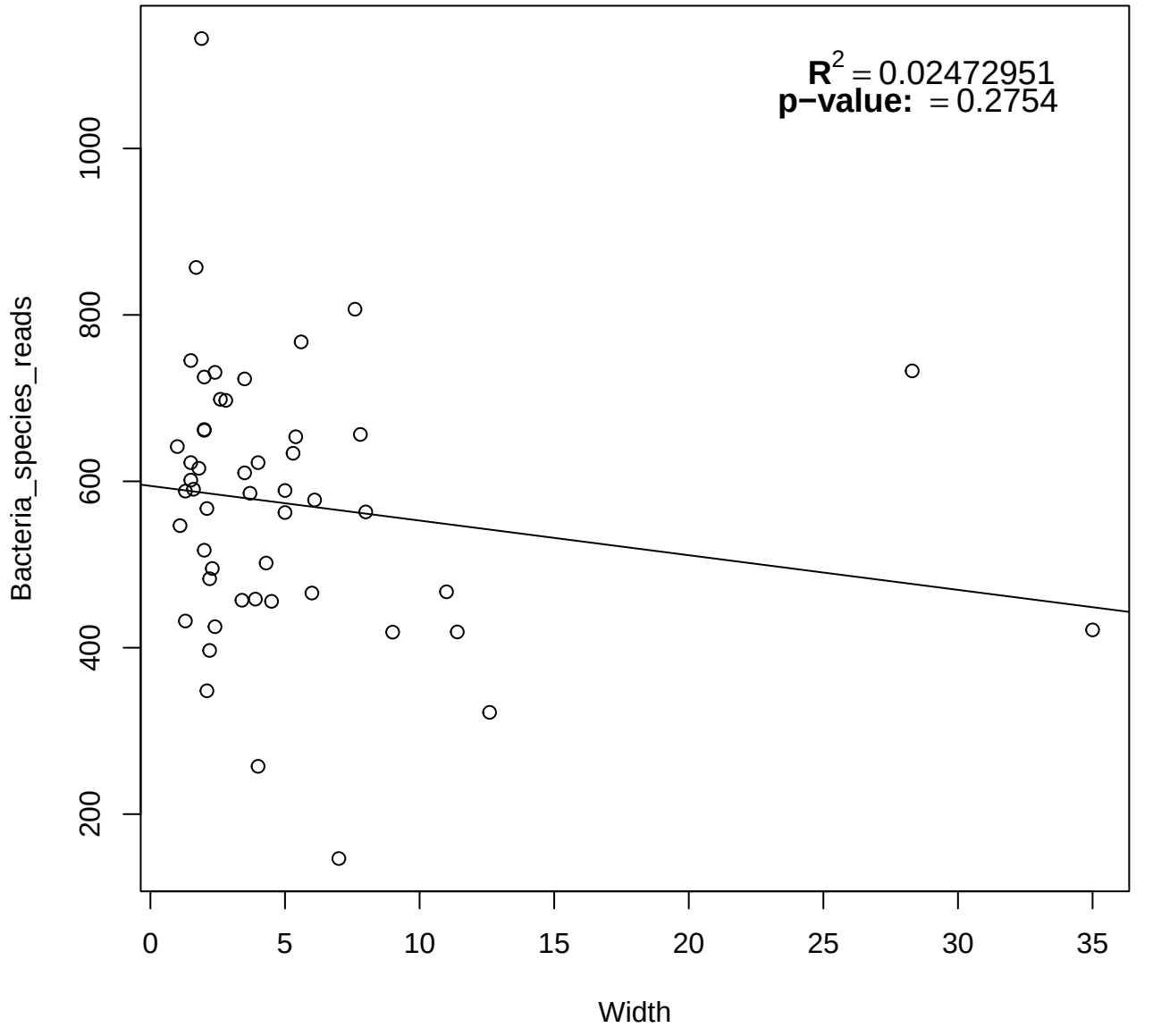

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
PON1
CBR1
Cook's distance
0.5
0.5

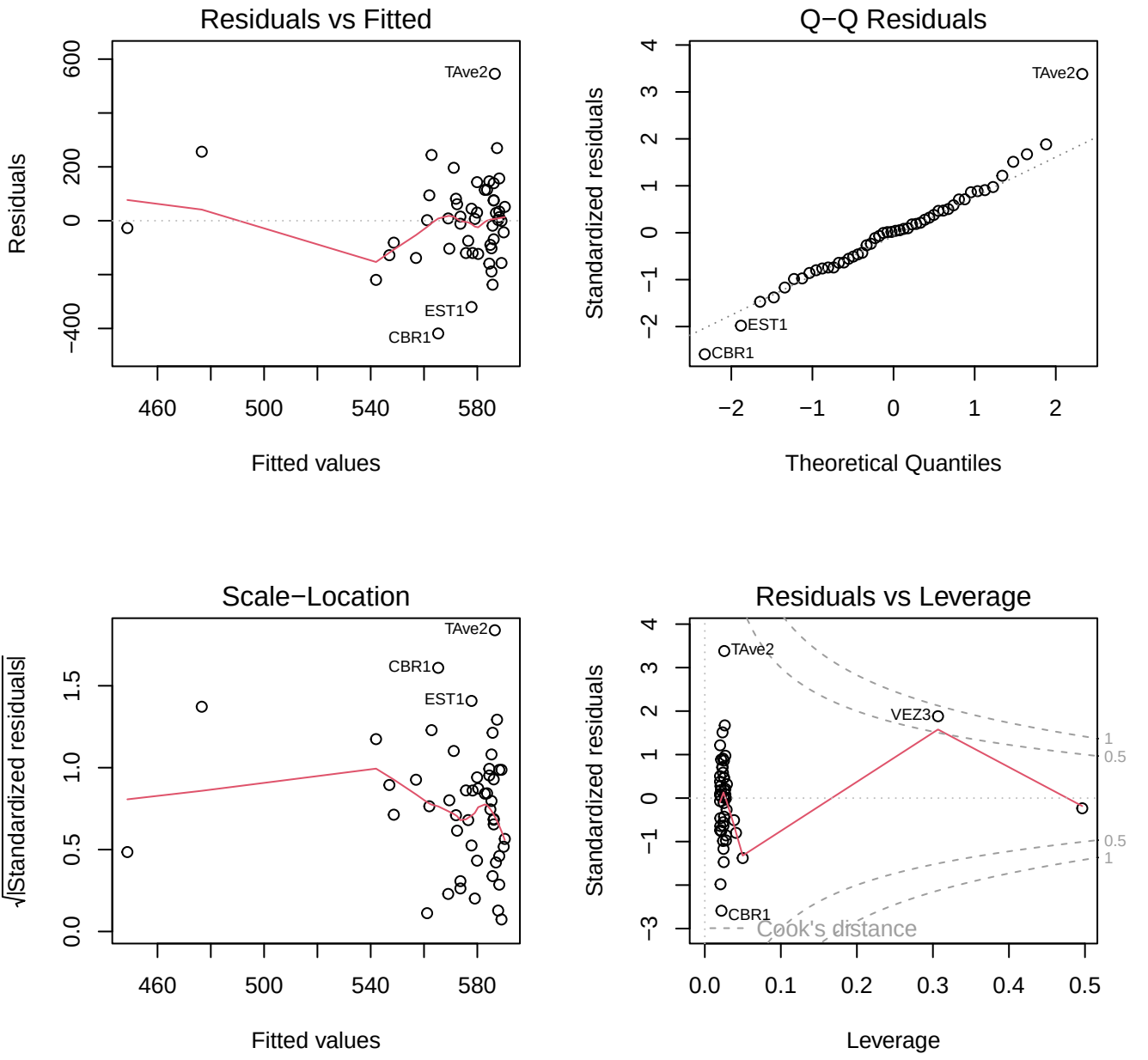

$R^2 = 0.03906273$
p−value: = 0.1689
Bacteria_species_reads
200
400
600
800
1000
1.0
1.5
2.0
2.5
3.0
3.5
4.0
mean.Depth

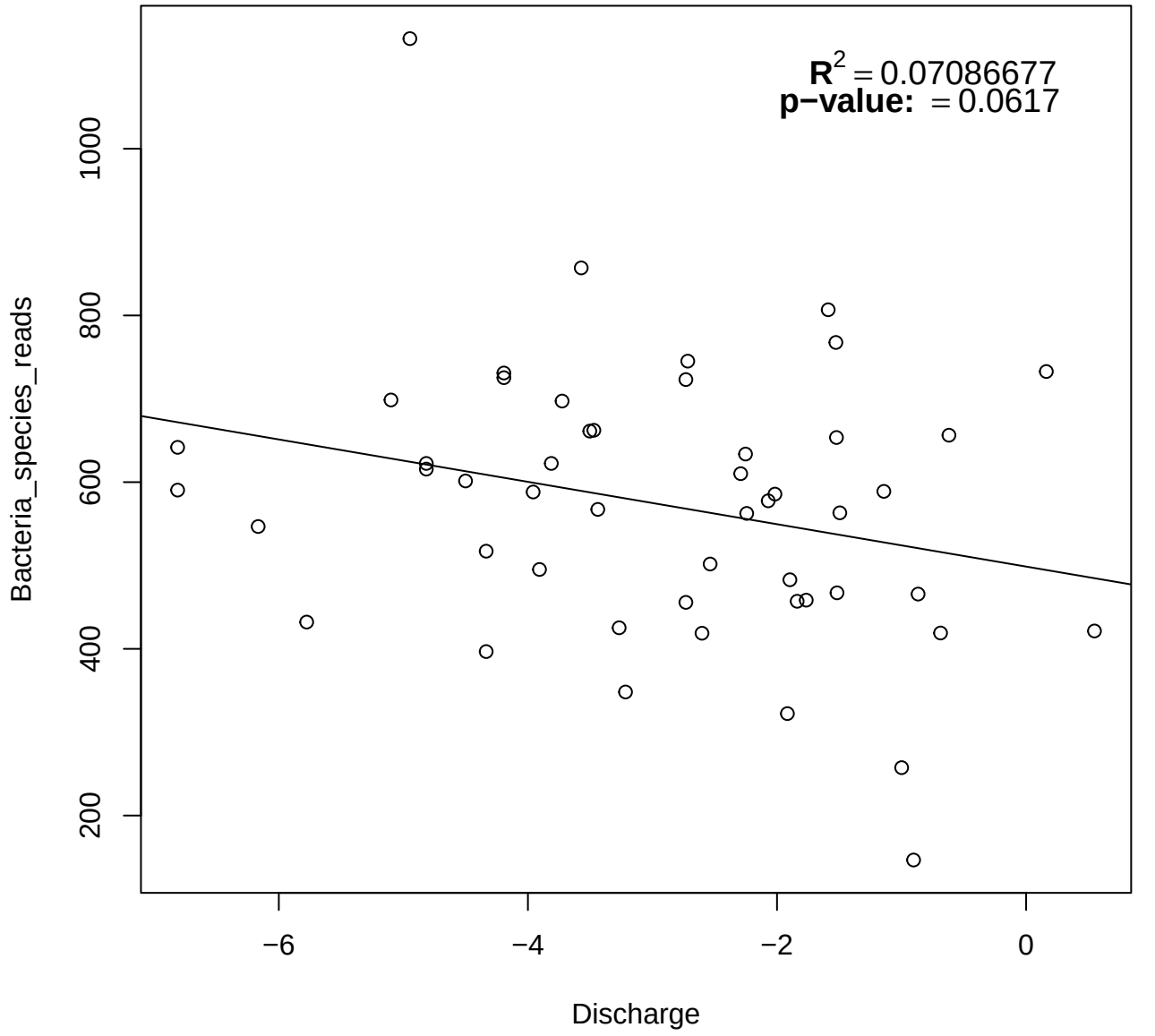

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
EST2
CBR1
Cook's distance

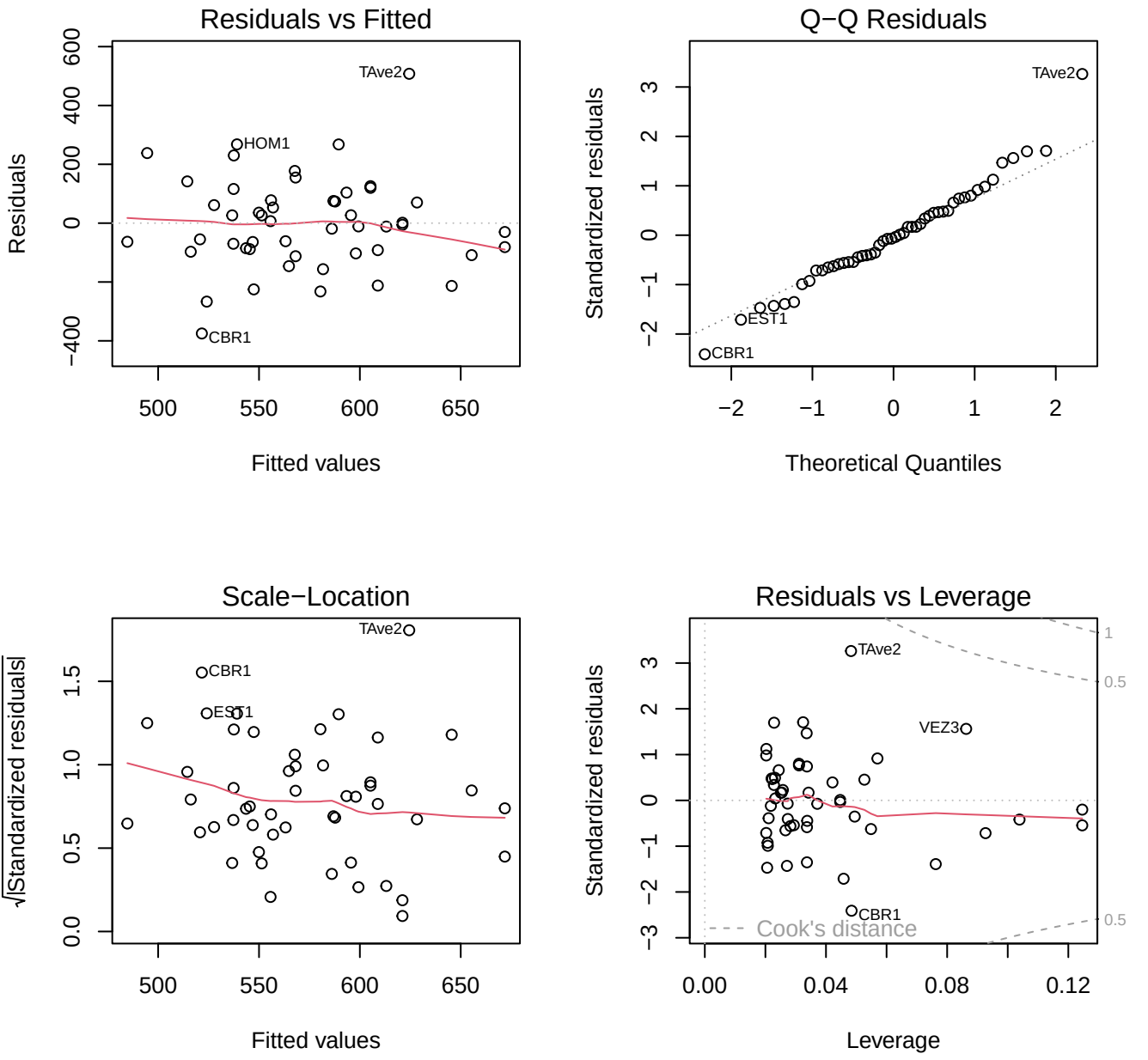

$R^2 = 0.0663109$
p−value: = 0.071
Bacteria_species_reads
200
400
600
800
1000
0.1
0.2
0.3
0.4
0.5
mean.Velocity

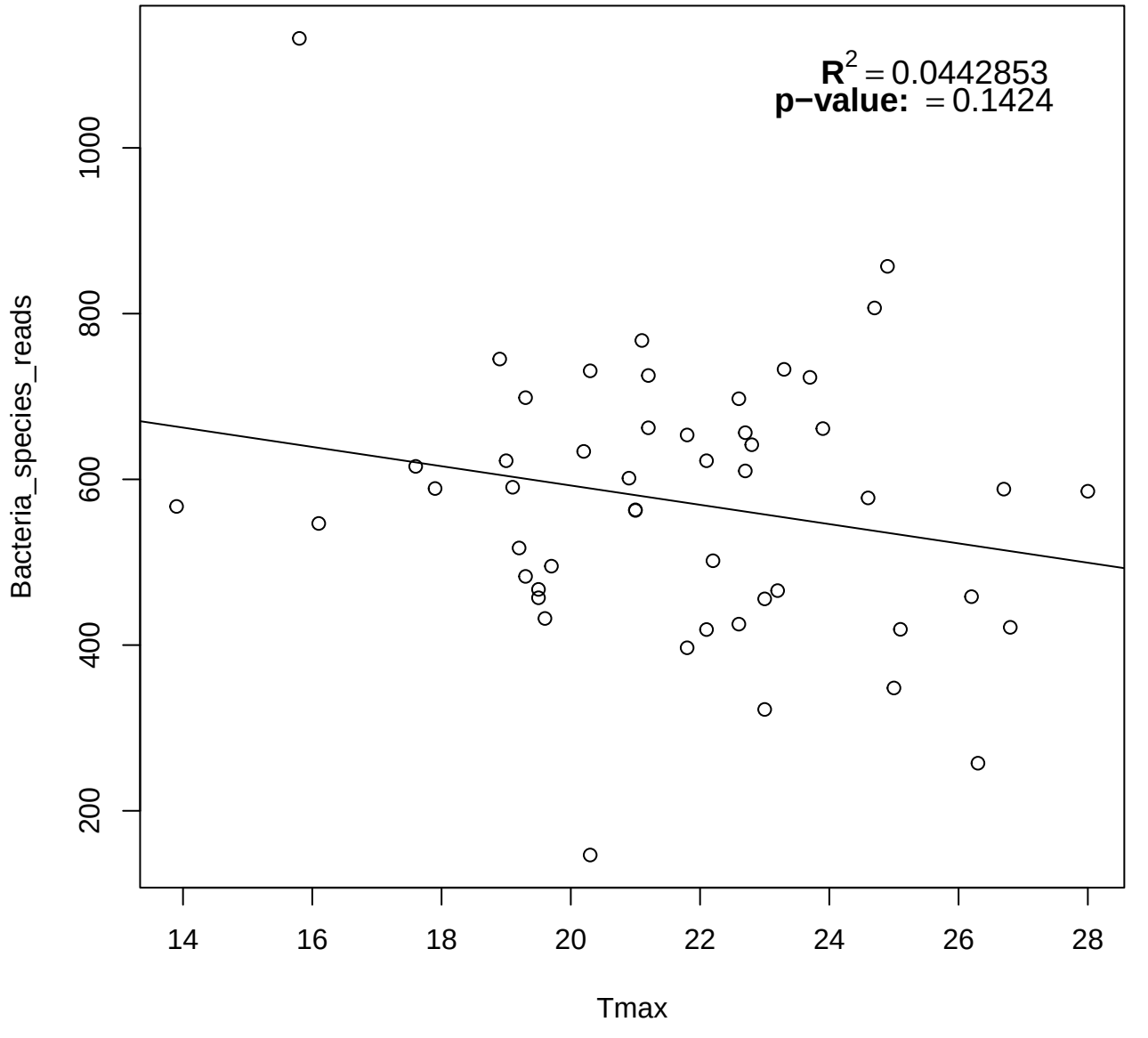

Residuals vs Fitted
Residuals
Fitted values
TAve2
PON1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
PON1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
PON1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
EST1
CBR1
Cook's distance
1
0.5
0.5

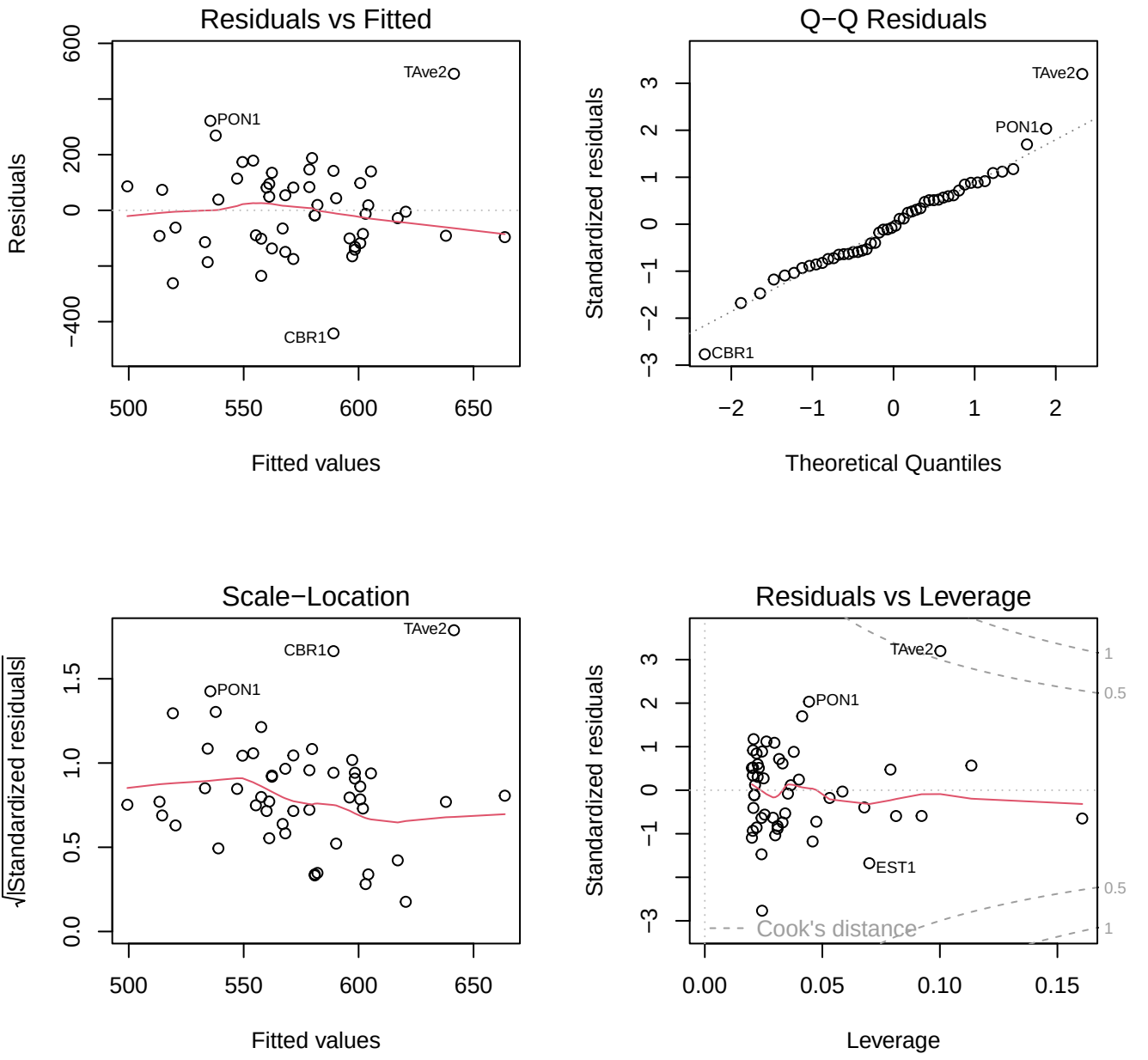

$R^2 = 0.02472951$
p−value: = 0.2754
Bacteria_species_reads
200
400
600
800
1000
0
5
10
15
20
25
30
35
Width

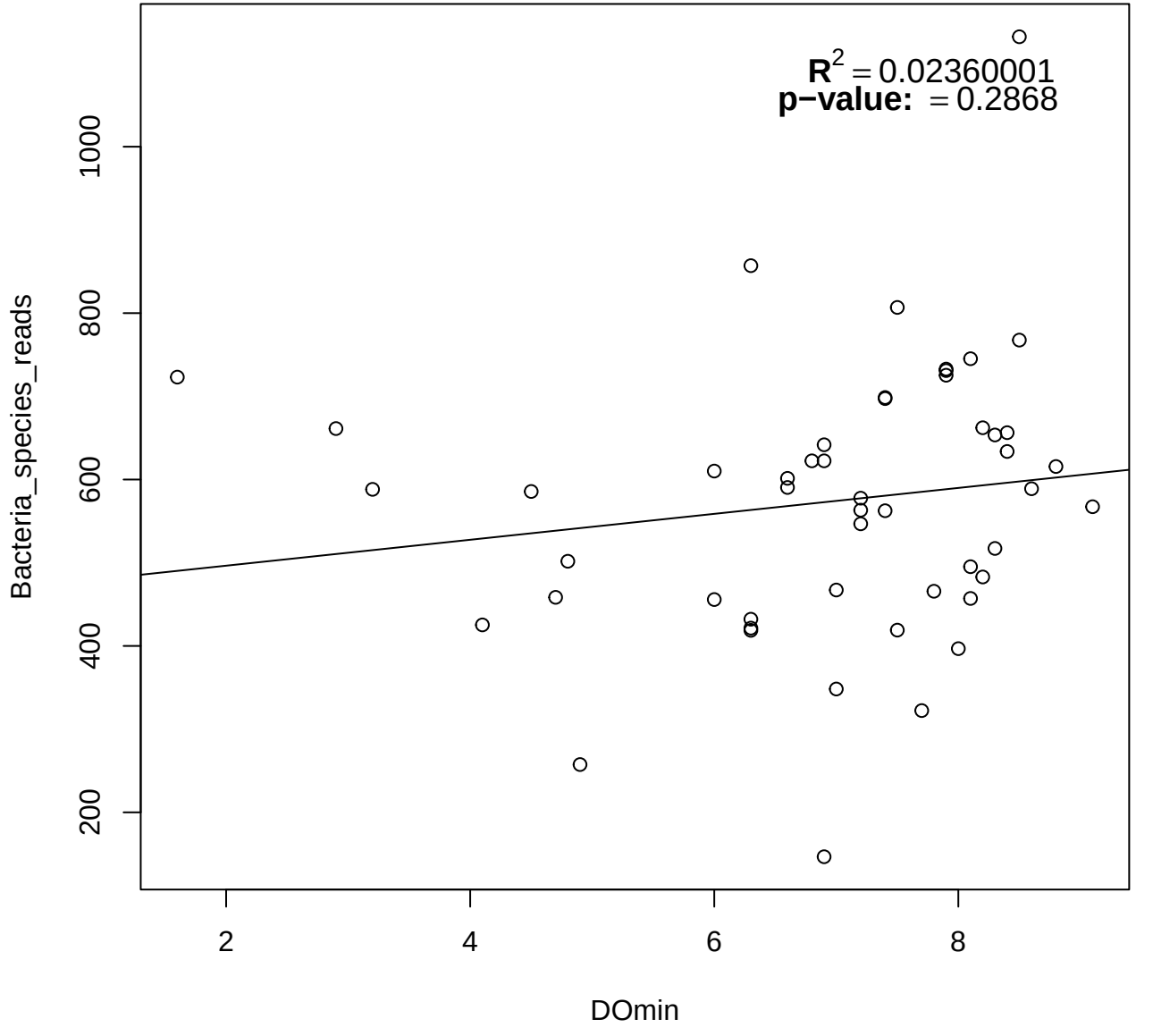

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
VEZ3
CBR1
Cook's distance

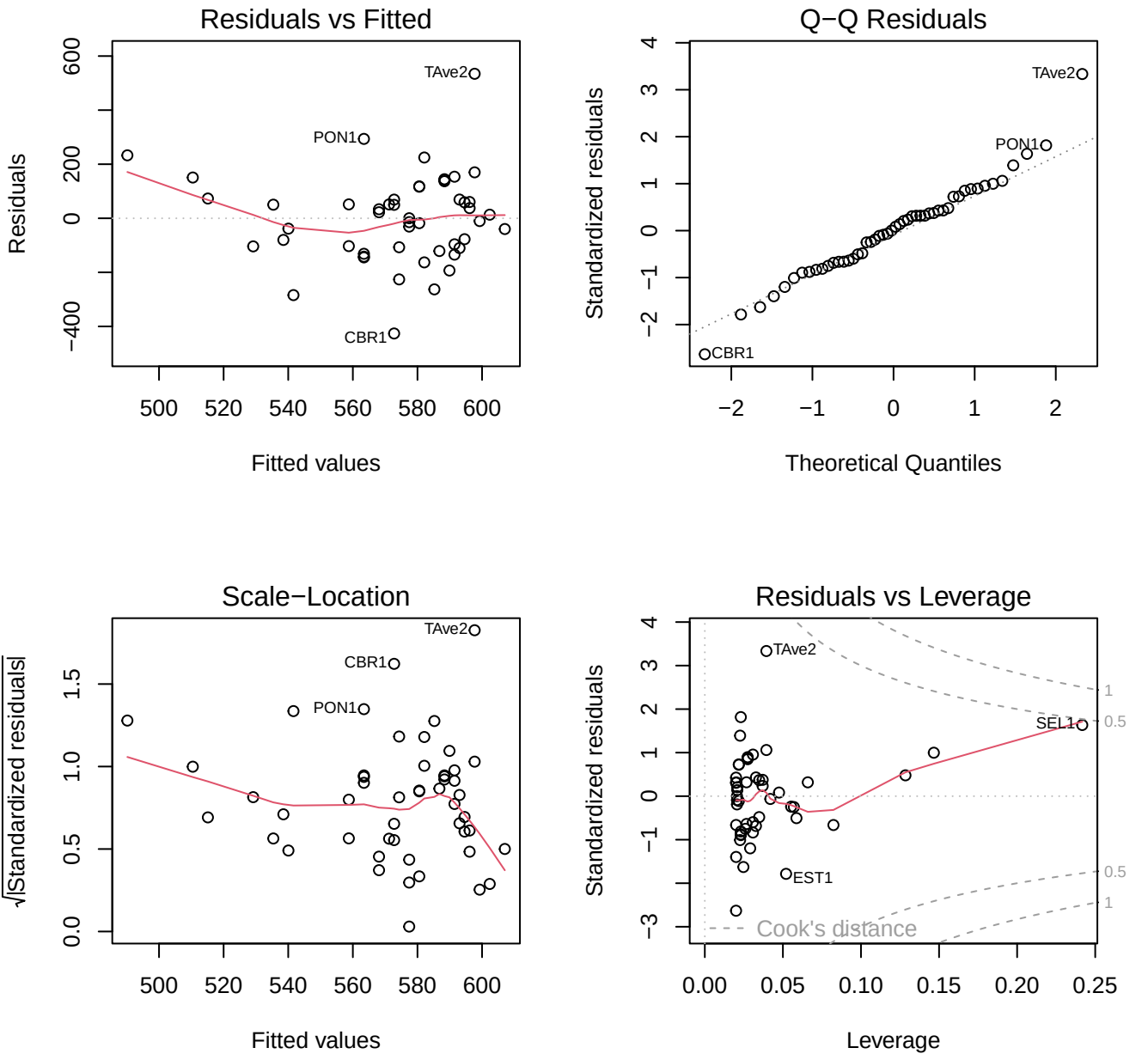

$R^2 = 0.07086677$
p−value: = 0.0617
Bacteria_species_reads
200
400
600
800
1000
−6
−4
−2
0
Discharge

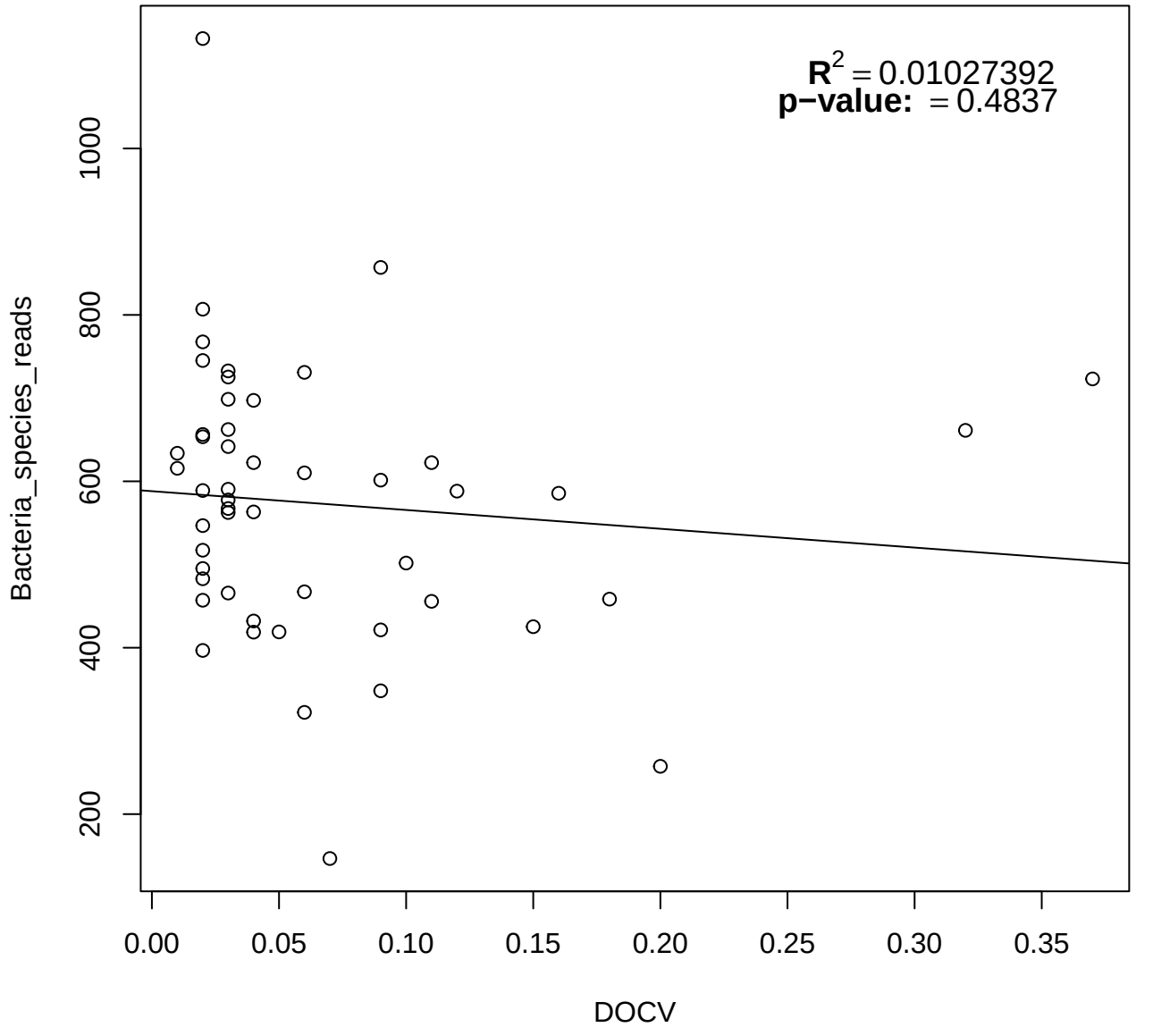

Residuals vs Fitted
Residuals
Fitted values
TAve2
HOM1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
VEZ3
CBR1
Cook's distance

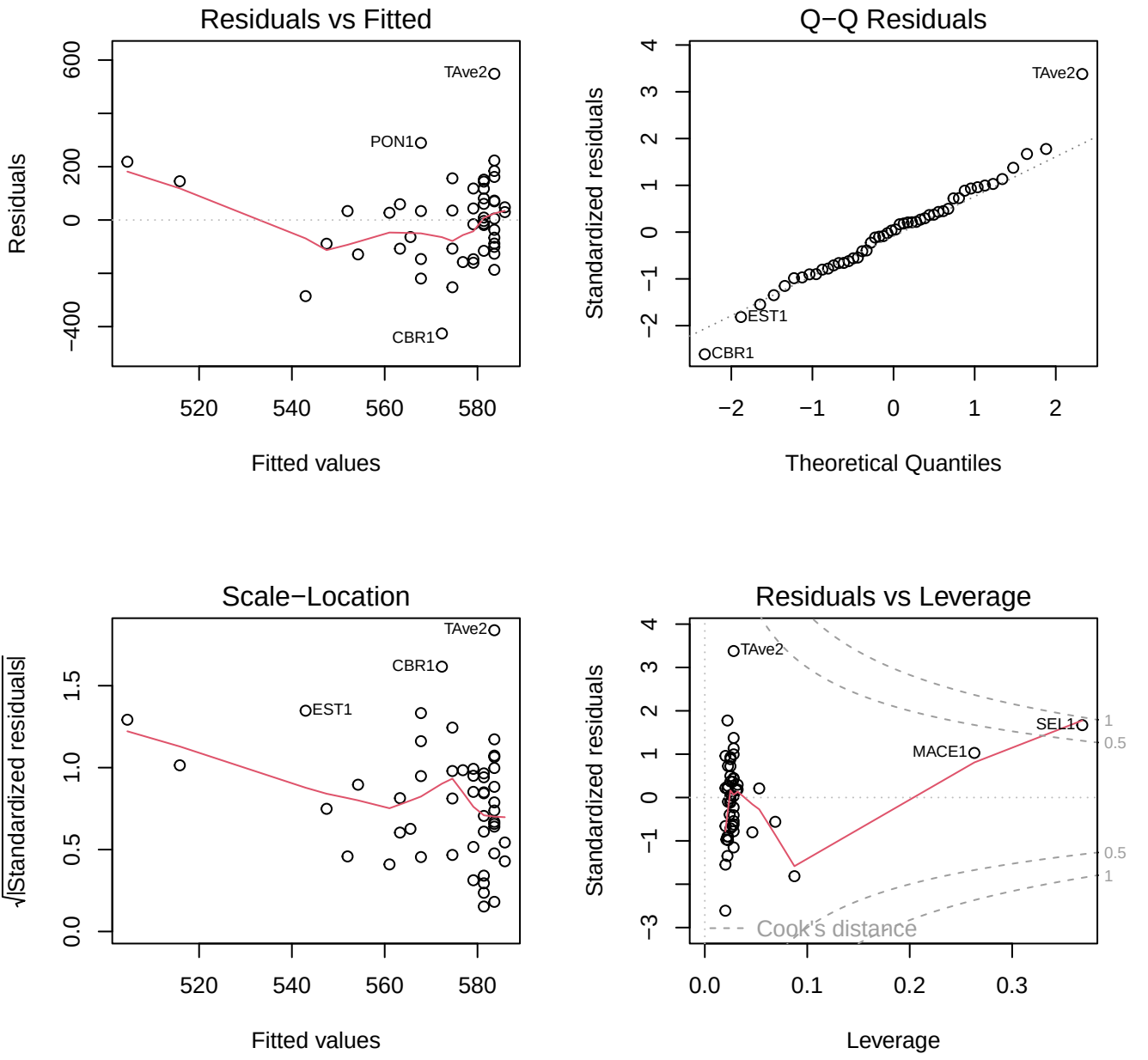

$R^2 = 0.0442853$
p−value: = 0.1424
Bacteria_species_reads
200
400
600
800
1000
14
16
18
20
22
24
26
28
Tmax

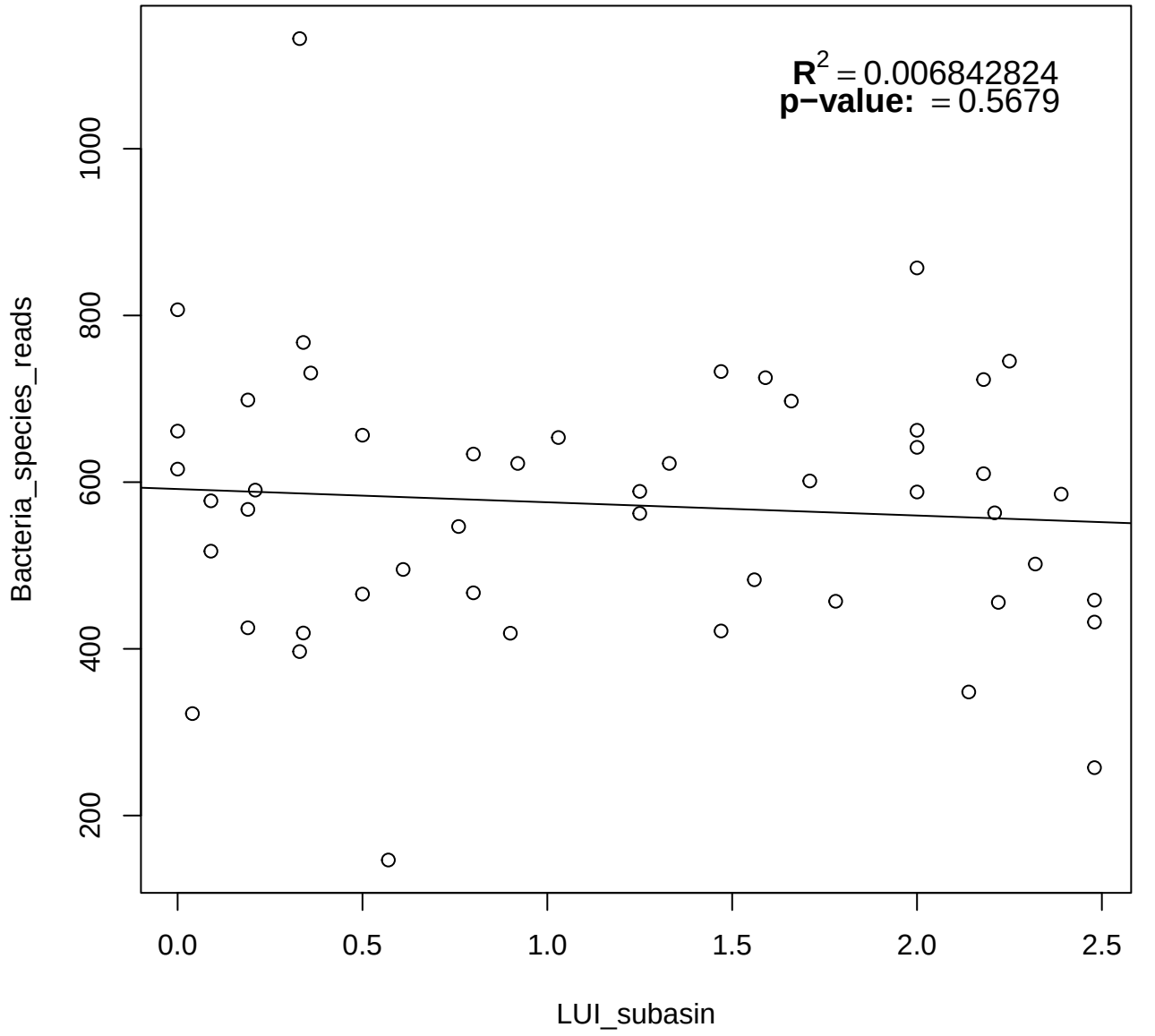

Residuals vs Fitted
Residuals
Fitted values
TAve2
PON1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
PON1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
PON1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
PON1
EST1
Cook's distance
1
0.5
0.5
1

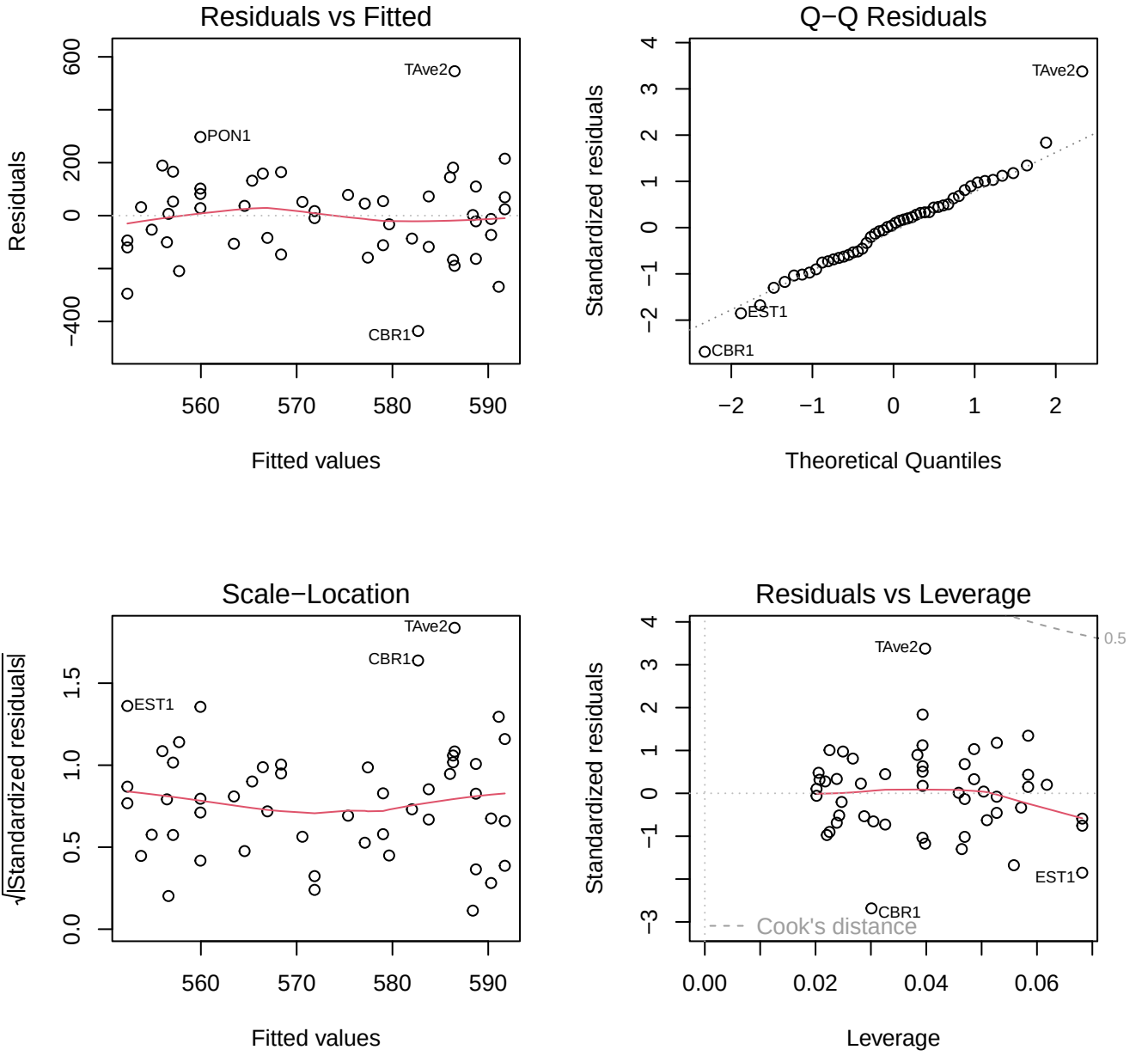

$R^2 = 0.02360001$
p−value: = 0.2868
Bacteria_species_reads
200
400
600
800
1000
2
4
6
8
DOmin

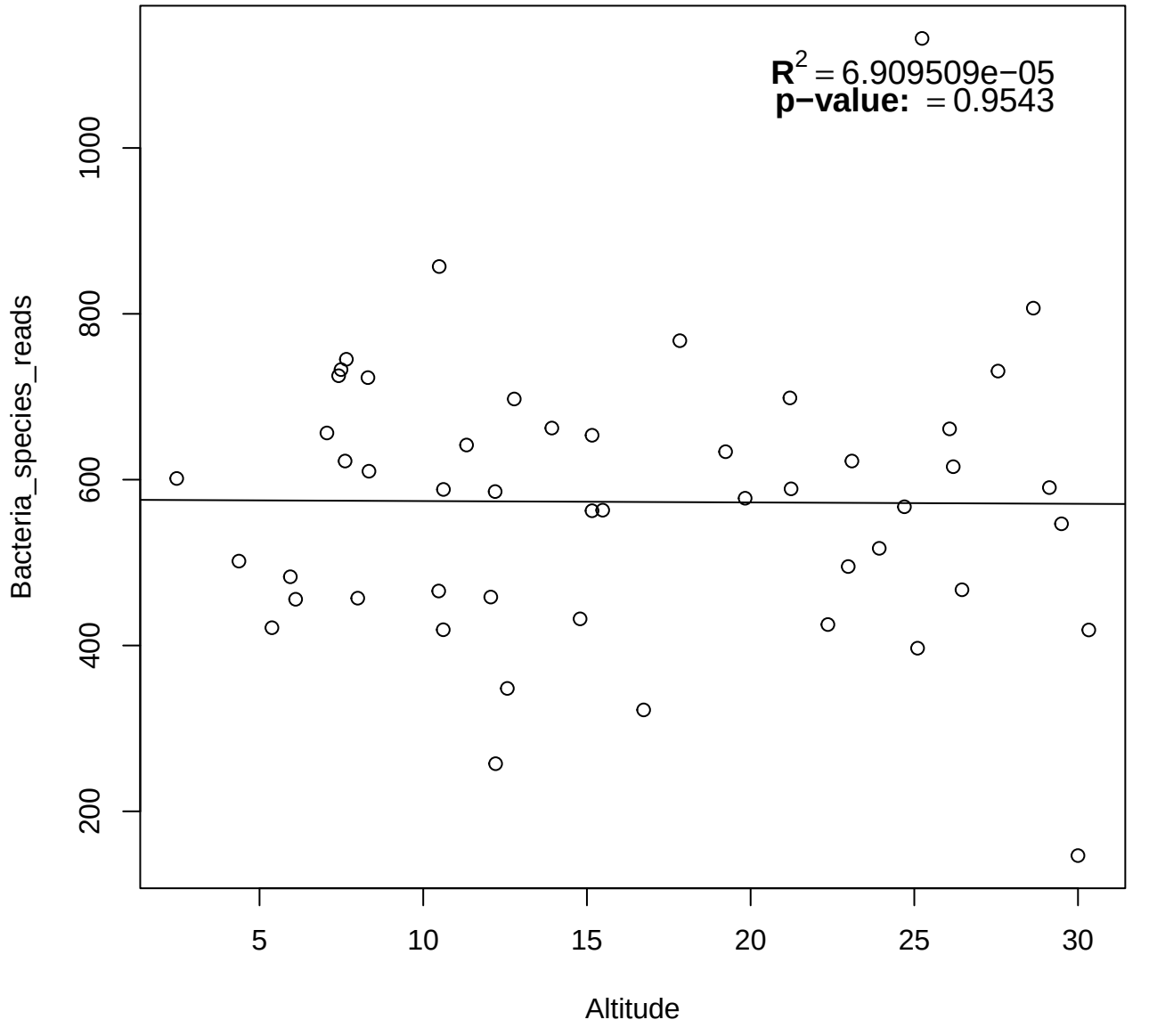

Residuals vs Fitted
Residuals
Fitted values
TAve2
PON1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
PON1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
PON1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
SEL1
EST1
Cook's distance

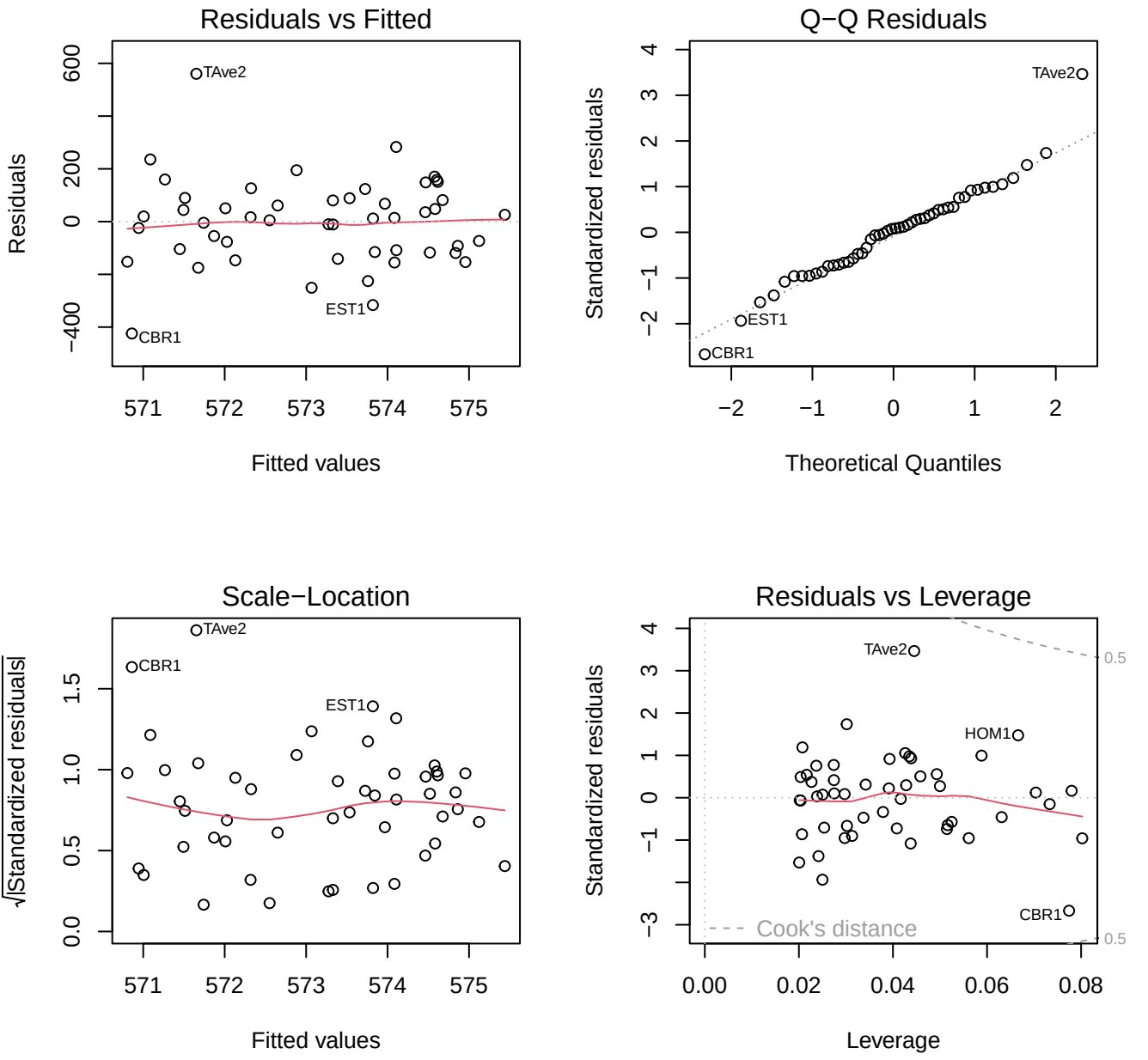

$R^2 = 0.01027392$
p−value: = 0.4837
Bacteria_species_reads
200
400
600
800
1000
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
DOCV

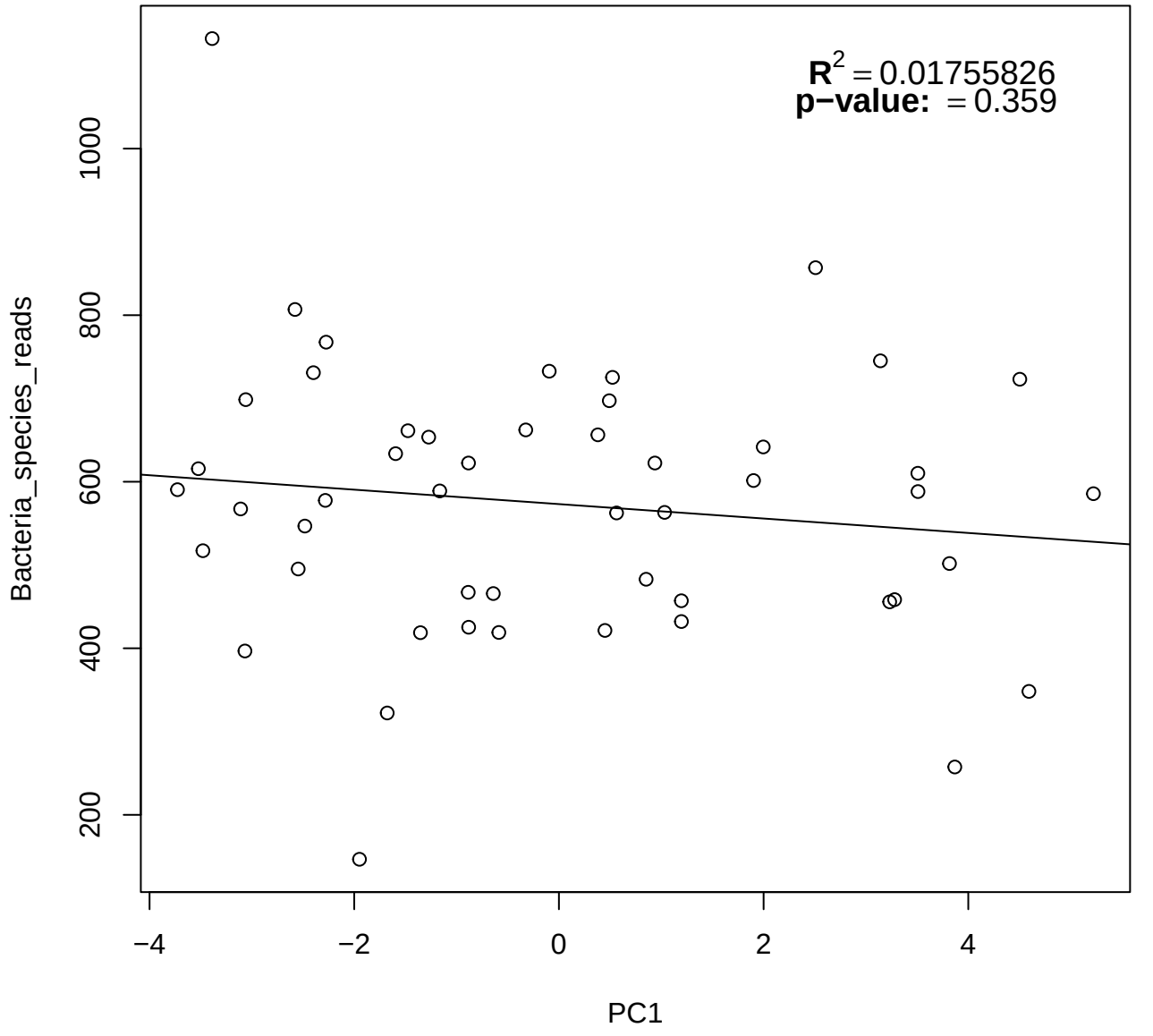

Residuals vs Fitted
Residuals
Fitted values
TAve2
PON1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
SEL1
MACE1
Cook's distance

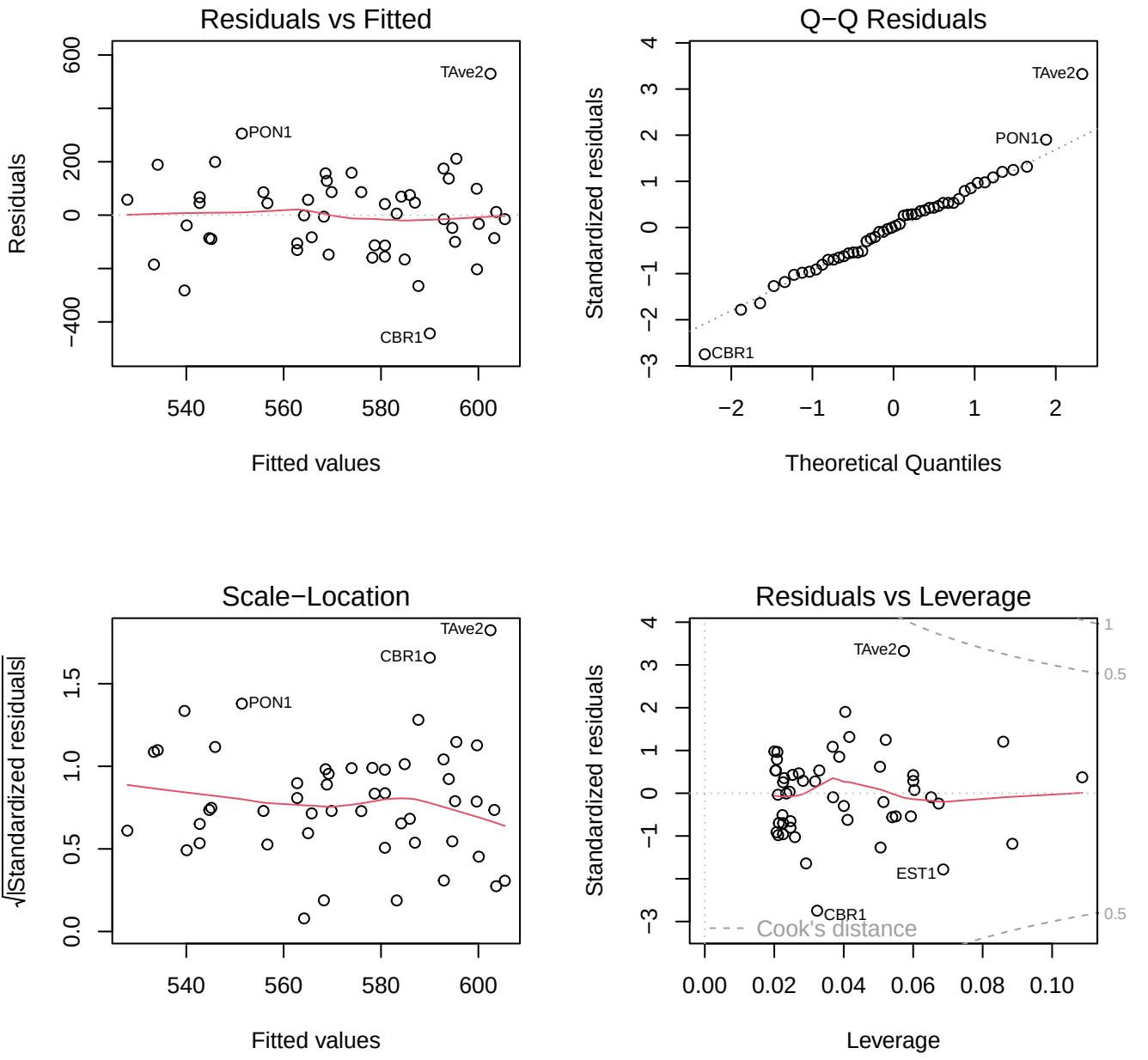

$R^2 = 0.006842824$
p−value: = 0.5679
Bacteria_species_reads
200
400
600
800
1000
0.0
0.5
1.0
1.5
2.0
2.5
LUI_subasin

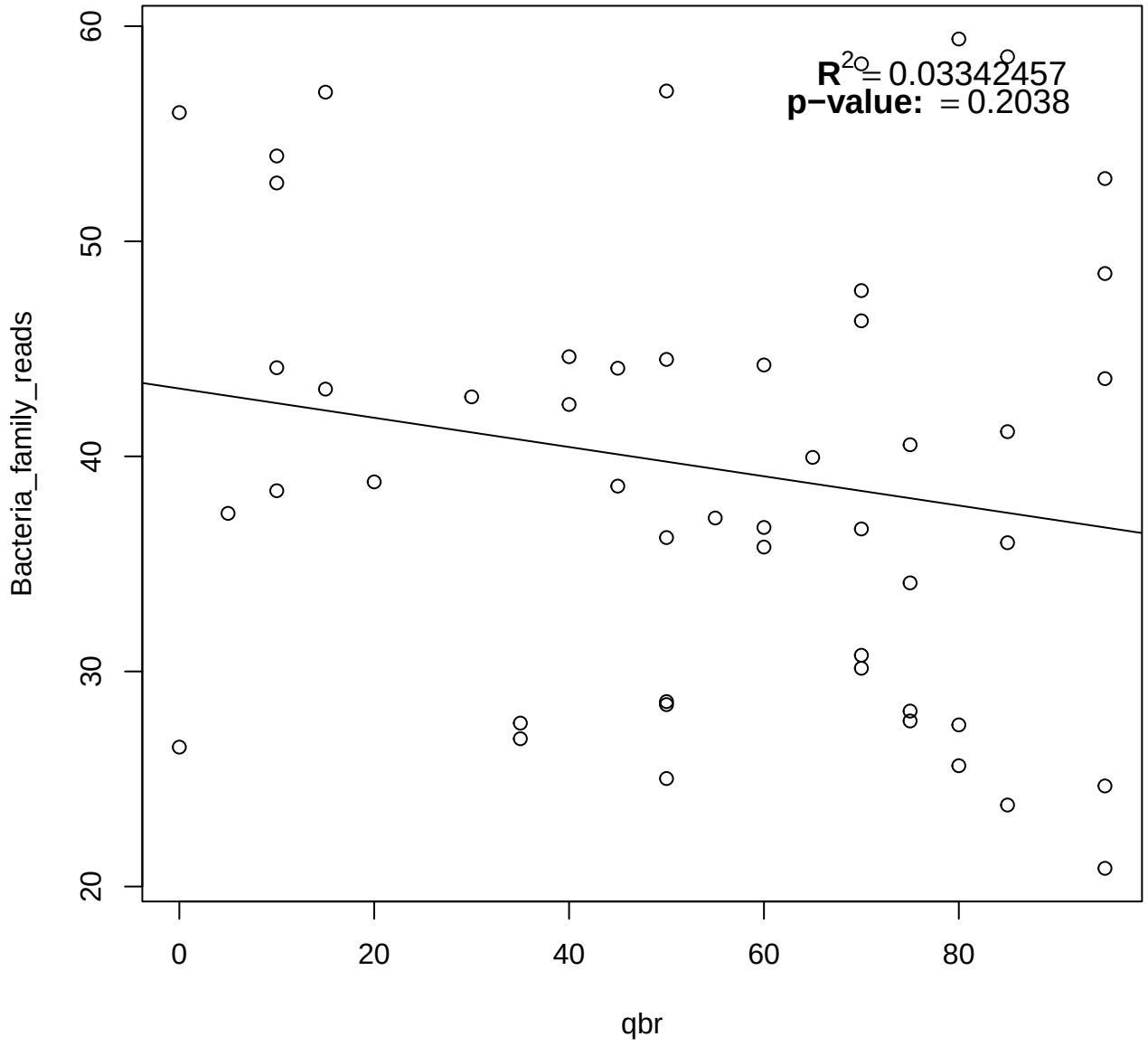

Residuals vs Fitted
Residuals
Fitted values
TAve2
PON1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
EST1
CBR1
Cook's distance
0.5

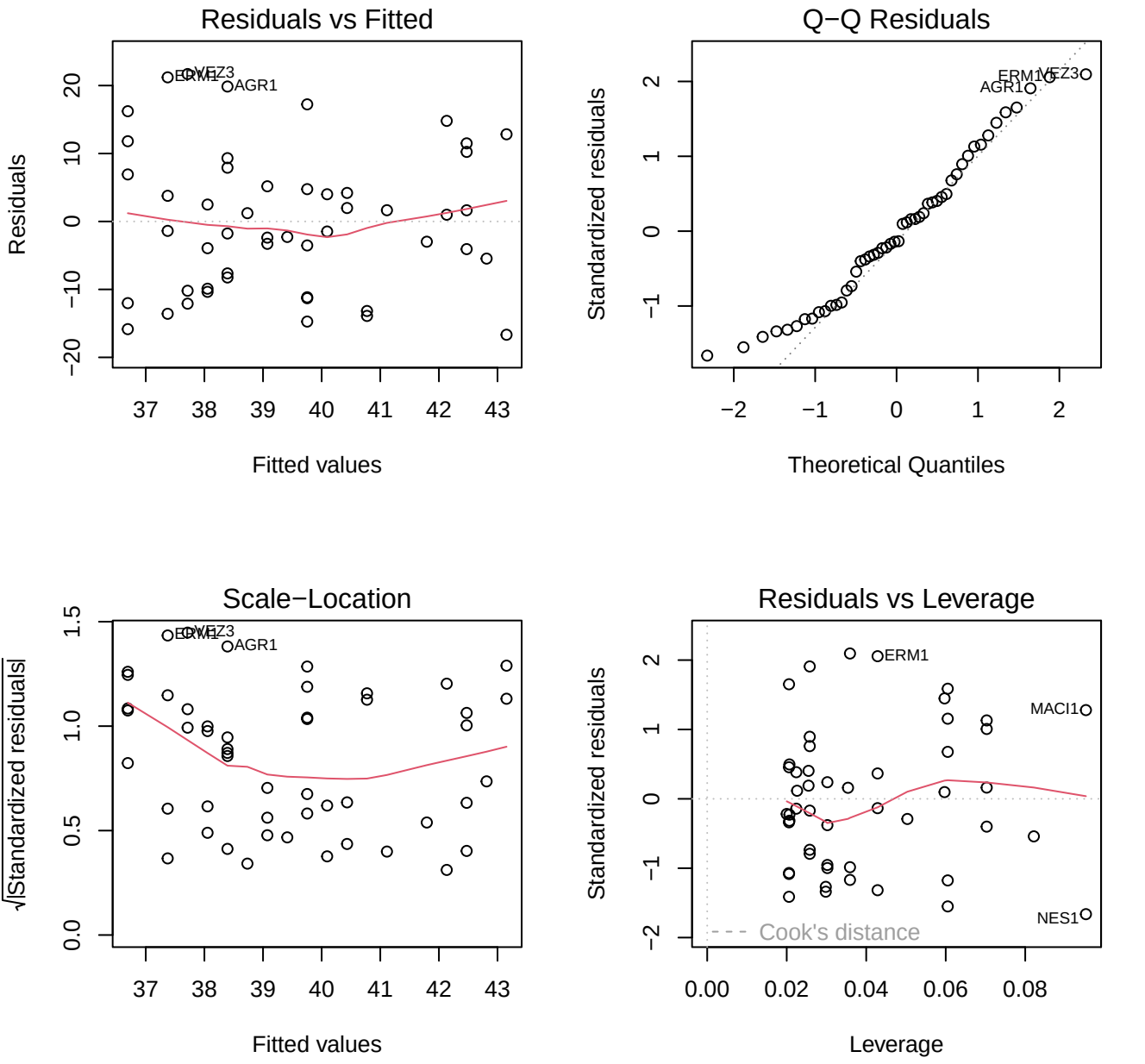

$R^2 = 6.909509e-05$
p−value: = 0.9543
Bacteria_species_reads
200
400
600
800
1000
5
10
15
20
25
30
Altitude

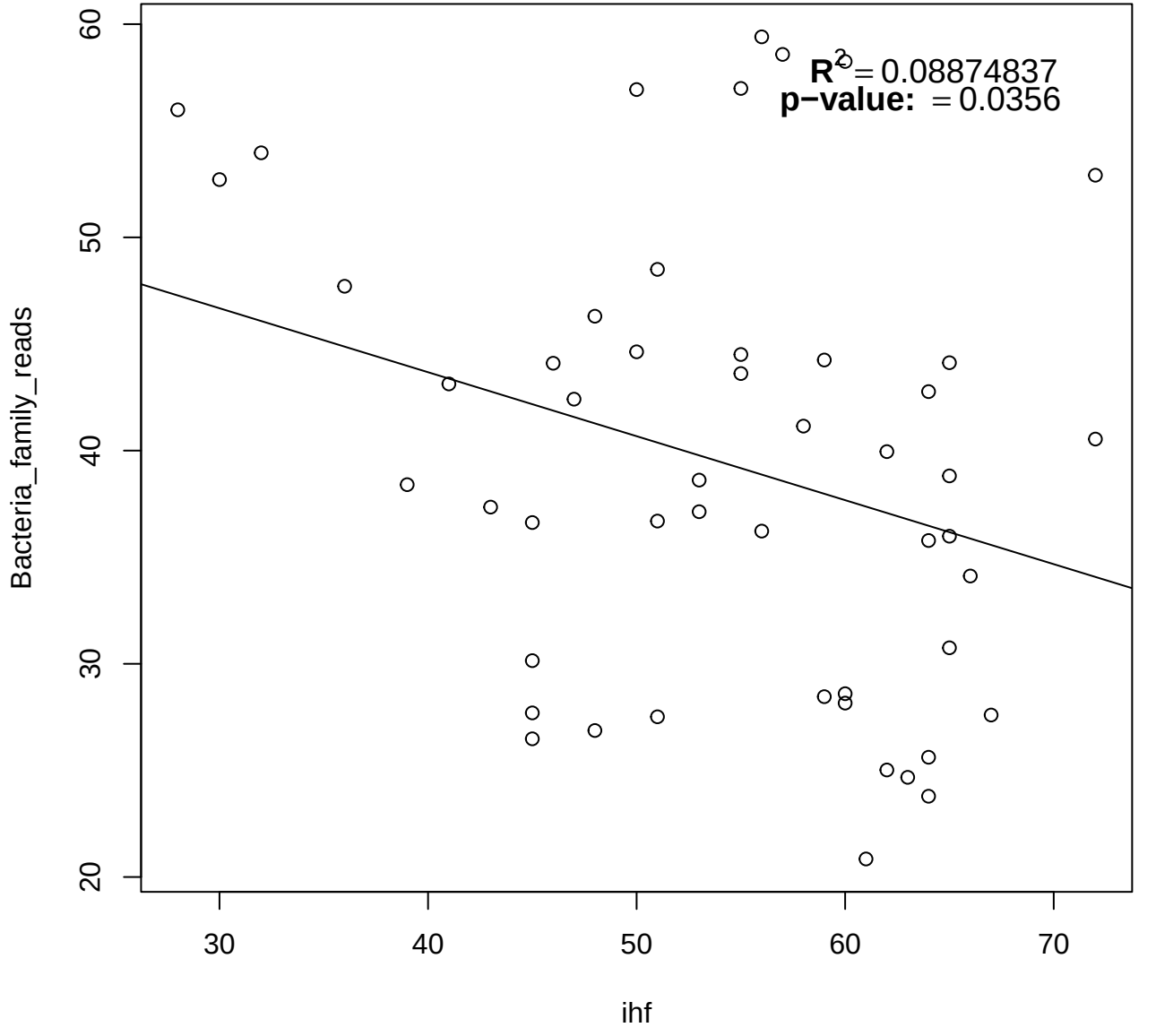

Residuals vs Fitted
Residuals
Fitted values
TAve2
EST1
CBR1
600
200
0
−400
571
572
573
574
575
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
EST1
CBR1
4
3
2
1
0
−1
−2
−2
−1
0
1
2
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
EST1
1.5
1.0
0.5
0.0
571
572
573
574
575
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
HOM1
CBR1
Cook's distance
0.5
0.5
4
3
2
1
0
−1
−3
0.00
0.02
0.04
0.06
0.08

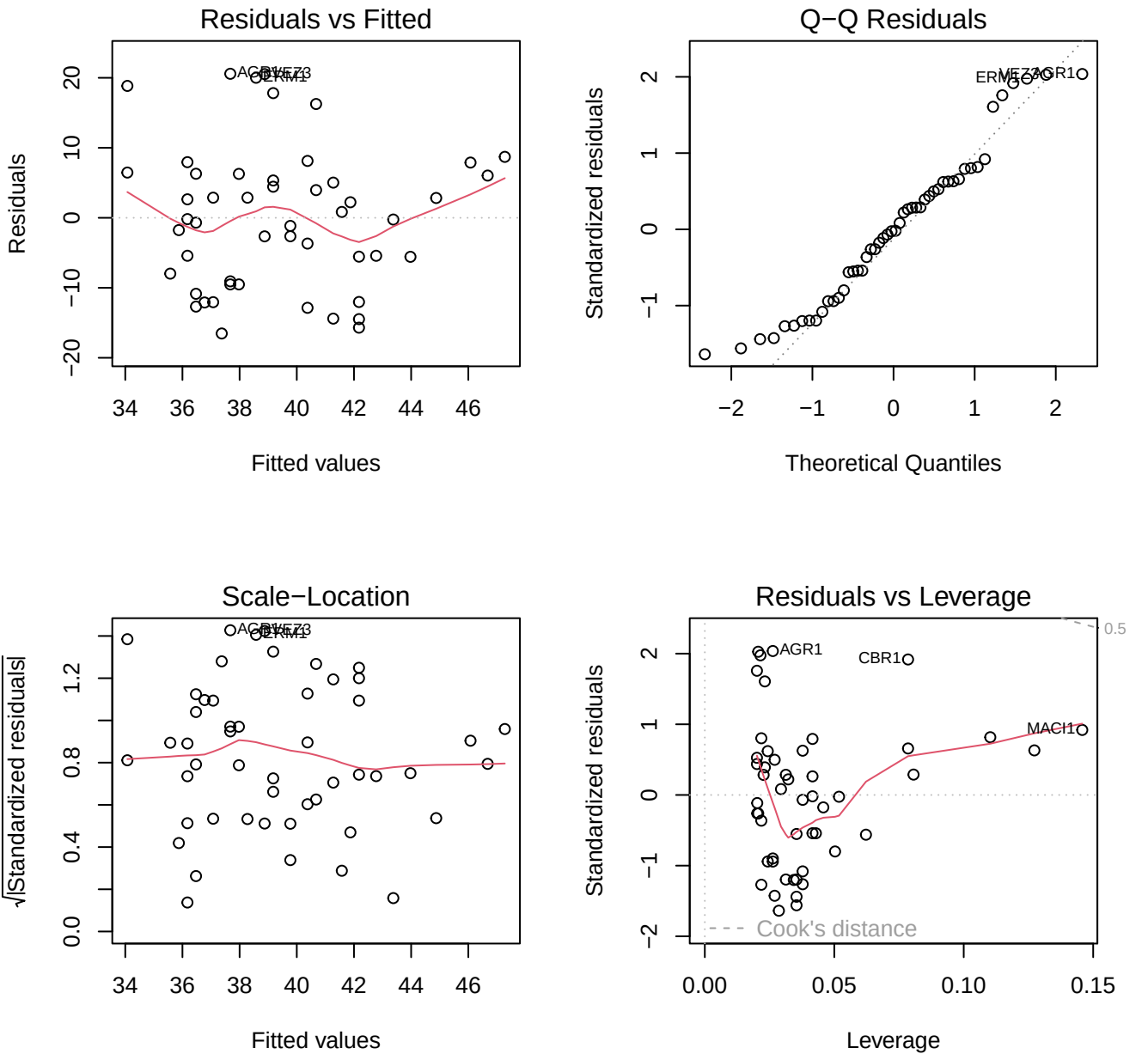

$R^2 = 0.01755826$
p−value: = 0.359
Bacteria_species_reads
200
400
600
800
1000
−4
−2
0
2
4
PC1

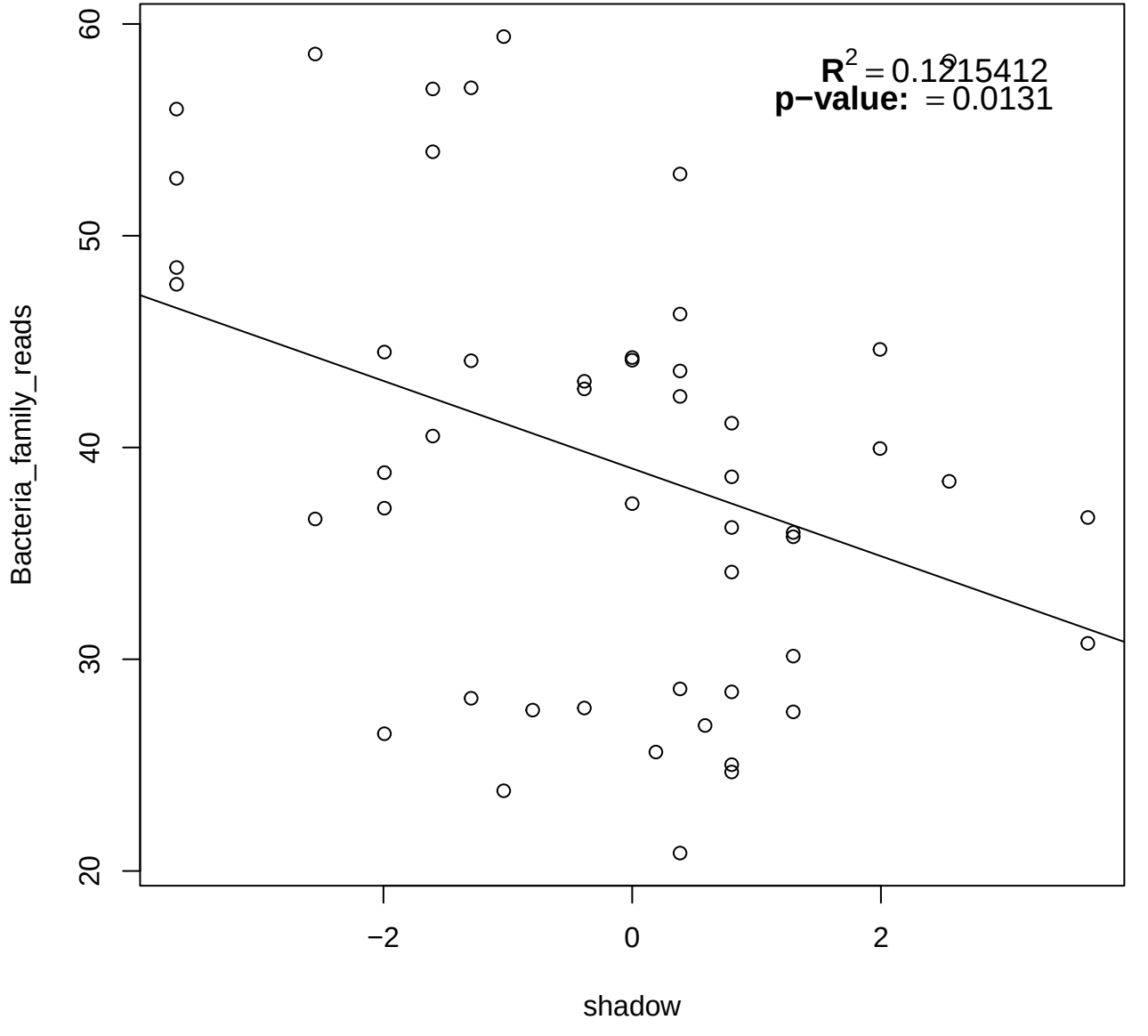

Residuals vs Fitted
Residuals
Fitted values
TAve2
PON1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
TAve2
PON1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
TAve2
CBR1
PON1
Residuals vs Leverage
Standardized residuals
Leverage
TAve2
EST1
CBR1
Cook's distance

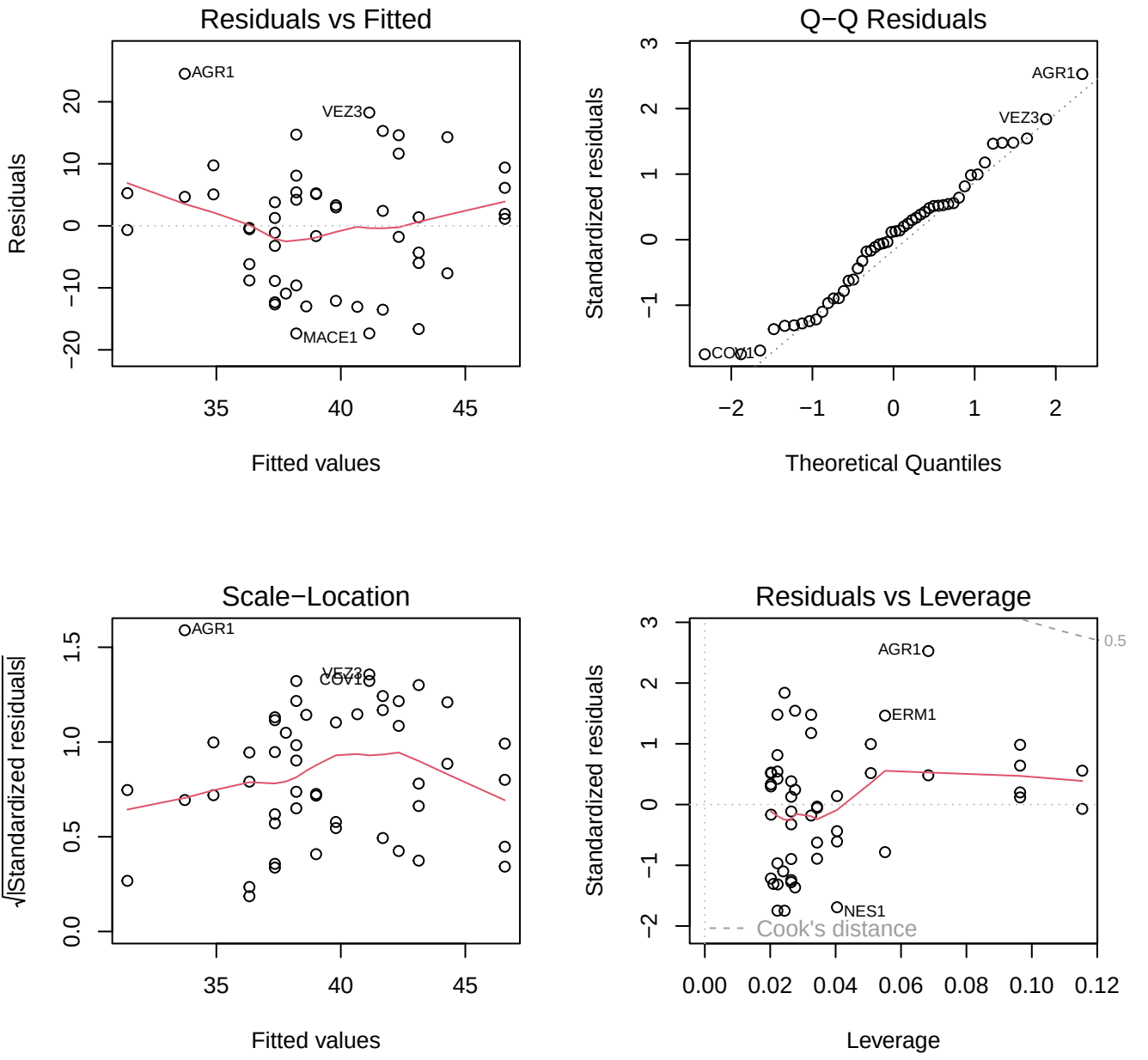

$R^2 = 0.03342457$
p−value: = 0.2038
Bacteria_family_reads
qbr
20
30
40
50
60
0
20
40
60
80

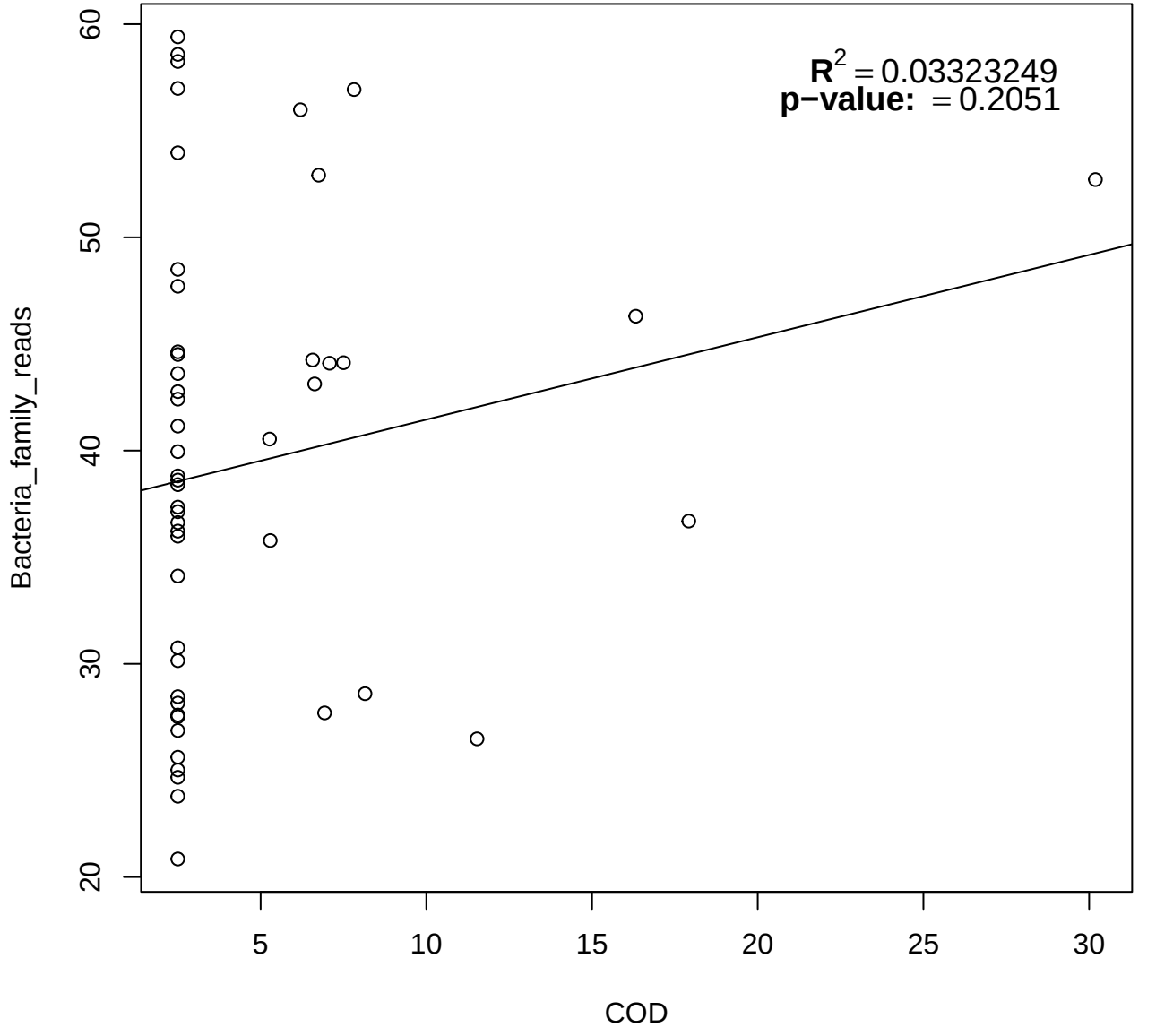

Residuals vs Fitted
Residuals
Fitted values
ERM1
VEZ3
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
VEZ3
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
VEZ3
AGR1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
MACI1
NES1
Cook's distance

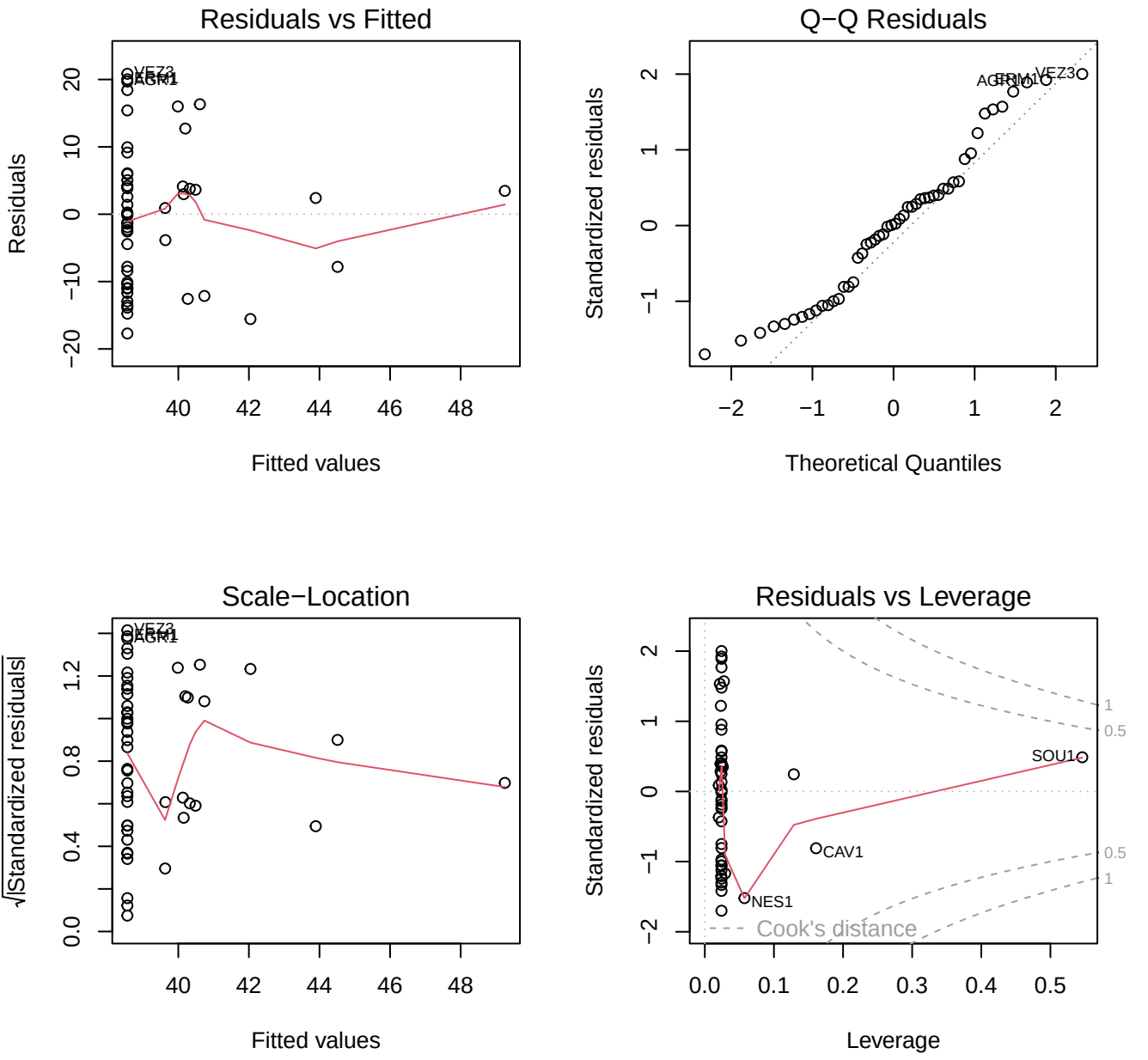

$R^2 = 0.08874837$
p−value: = 0.0356
Bacteria_family_reads
ihf
20
30
40
50
60
30
40
50
60
70

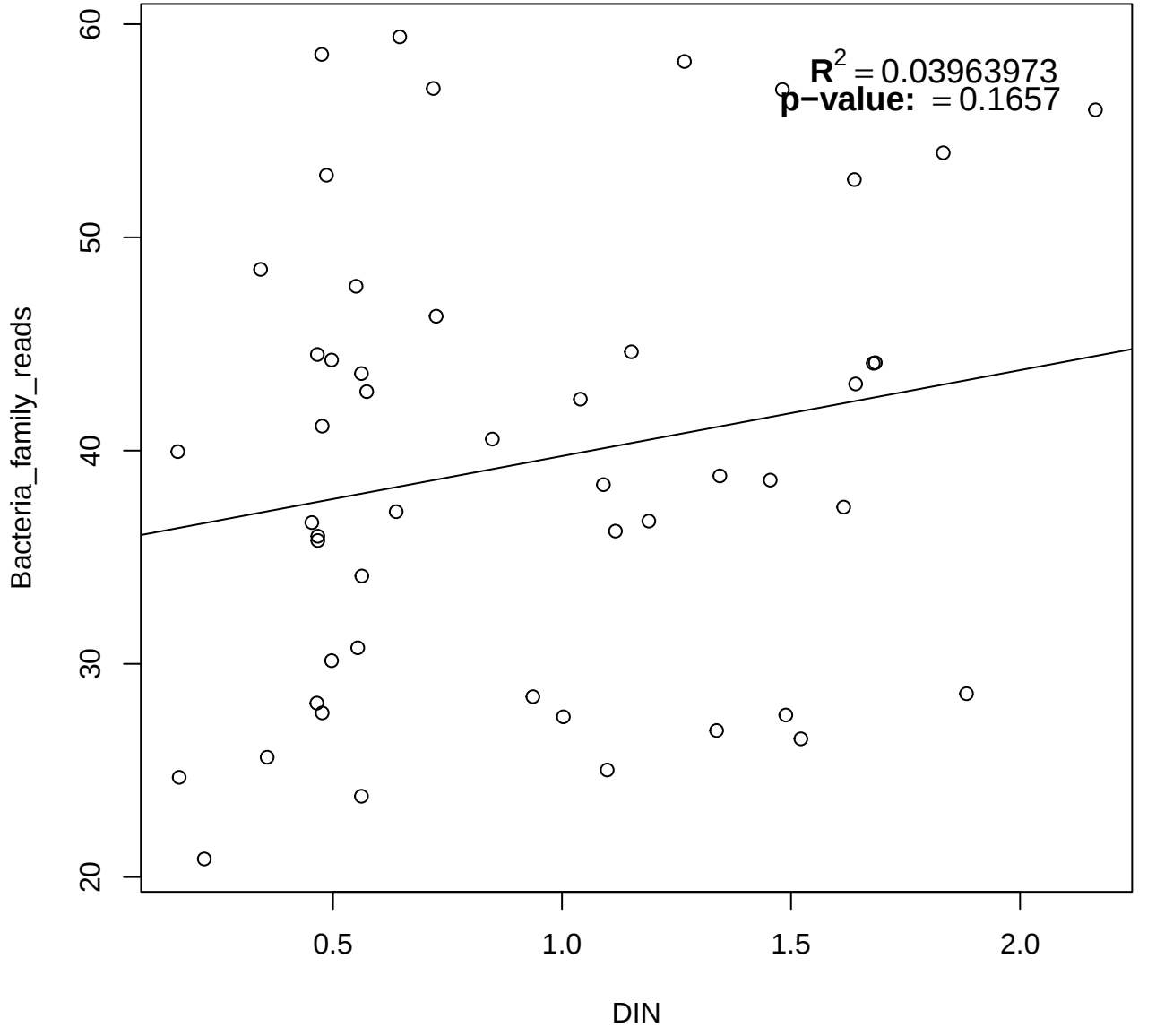

Residuals vs Fitted
Residuals
Fitted values
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
VEZ3
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
AGR1
CBR1
MACI1
Cook's distance
0.5

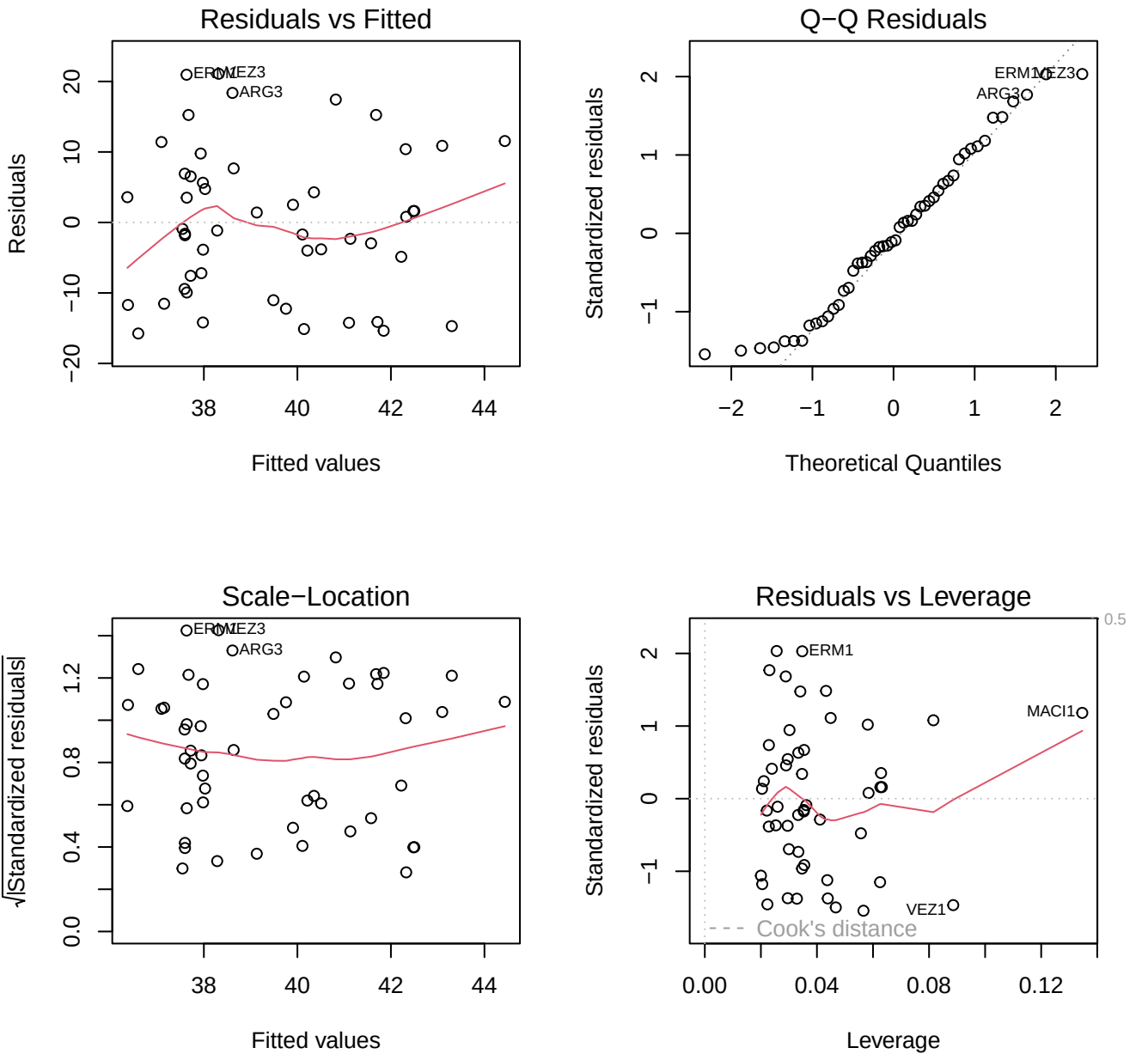

$R^2 = 0.1215412$
p−value: = 0.0131
Bacteria_family_reads
shadow
60
50
40
30
20
−2
0
2

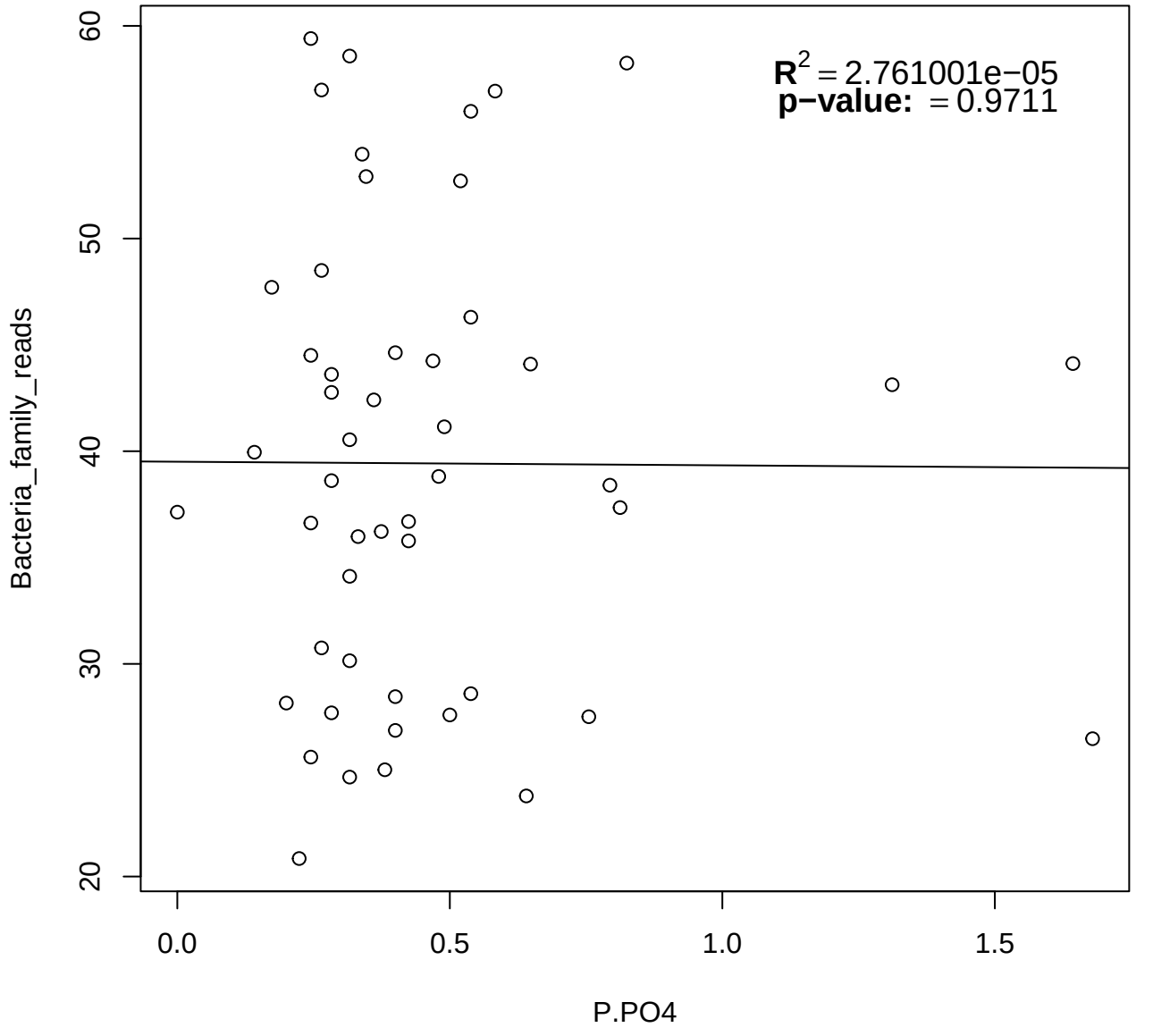

Residuals vs Fitted
Residuals
Fitted values
AGR1
VEZ3
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
AGR1
VEZ3
COV1
Scale−Location
√|Standardized residuals|
Fitted values
AGR1
VEZ3
COV1
Residuals vs Leverage
Standardized residuals
Leverage
AGR1
ERM1
NES1
0.5
Cook's distance

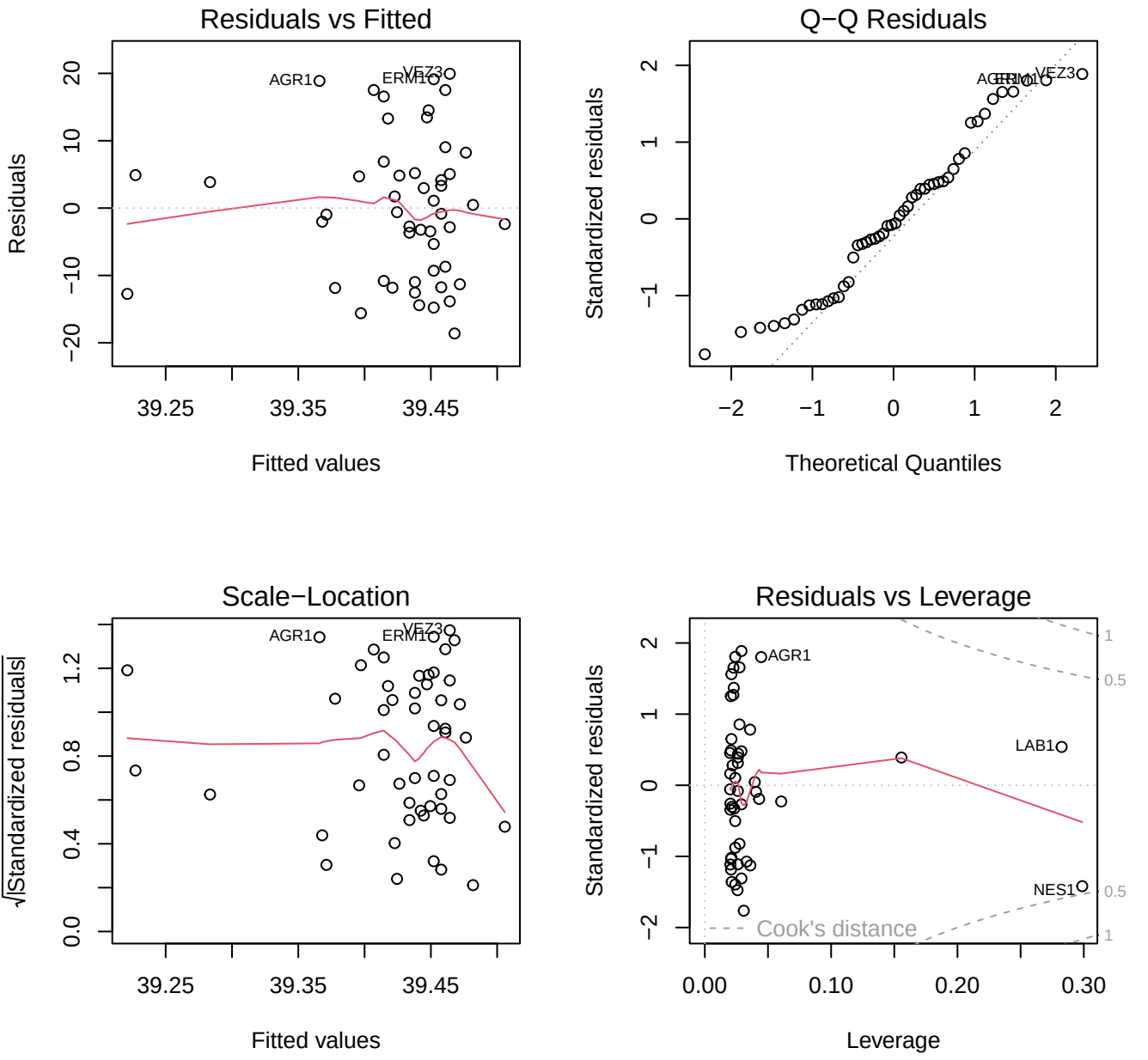

$R^2 = 0.03323249$
p−value: = 0.2051
Bacteria_family_reads
COD
20
30
40
50
60
5
10
15
20
25
30

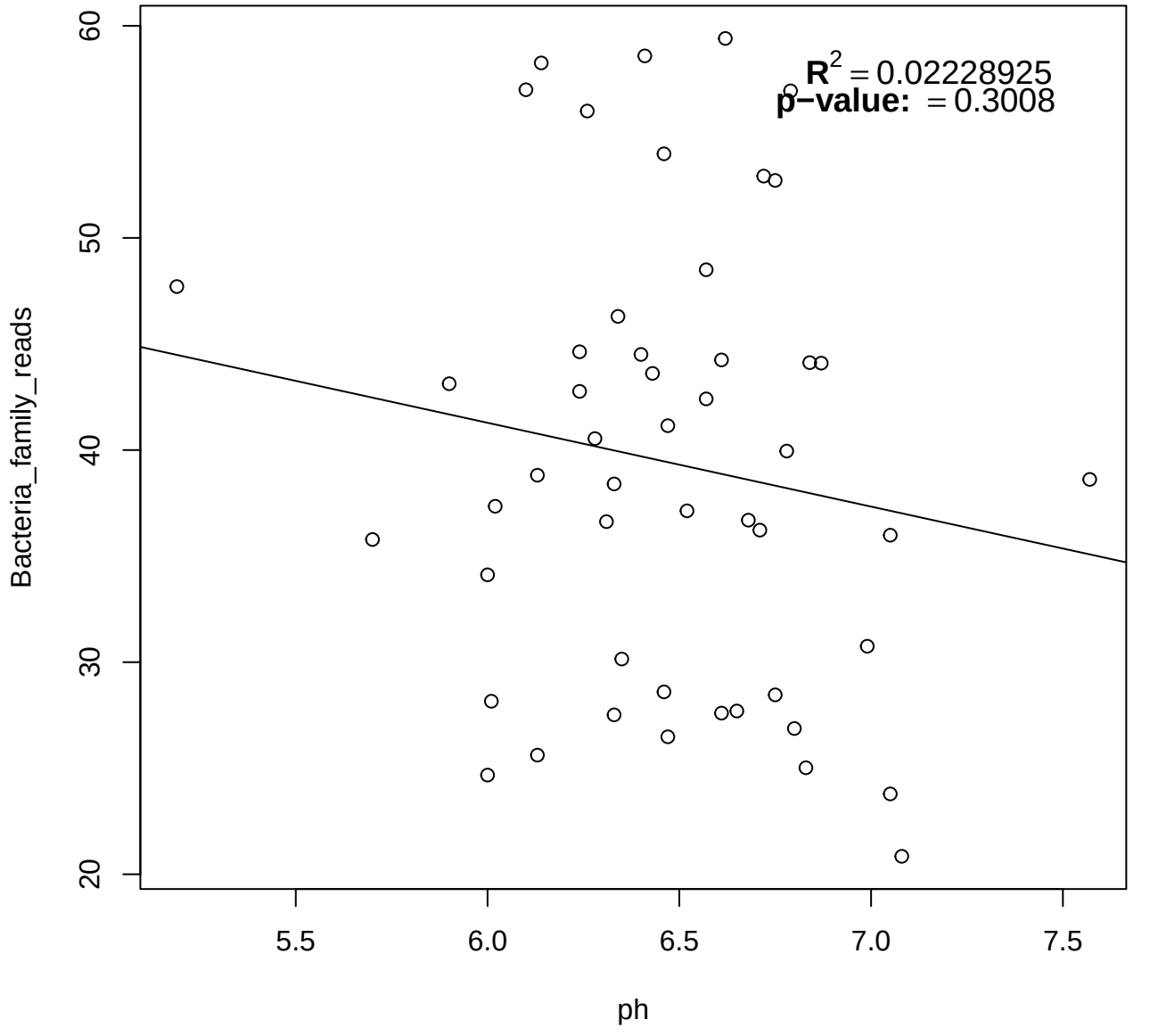

Residuals vs Fitted
Residuals
Fitted values
VEZ3
AGRI1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
AGRI1
VEZ3
Scale−Location
√|Standardized residuals|
Fitted values
VEZ3
AGRI1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
CAV1
NES1
Cook's distance

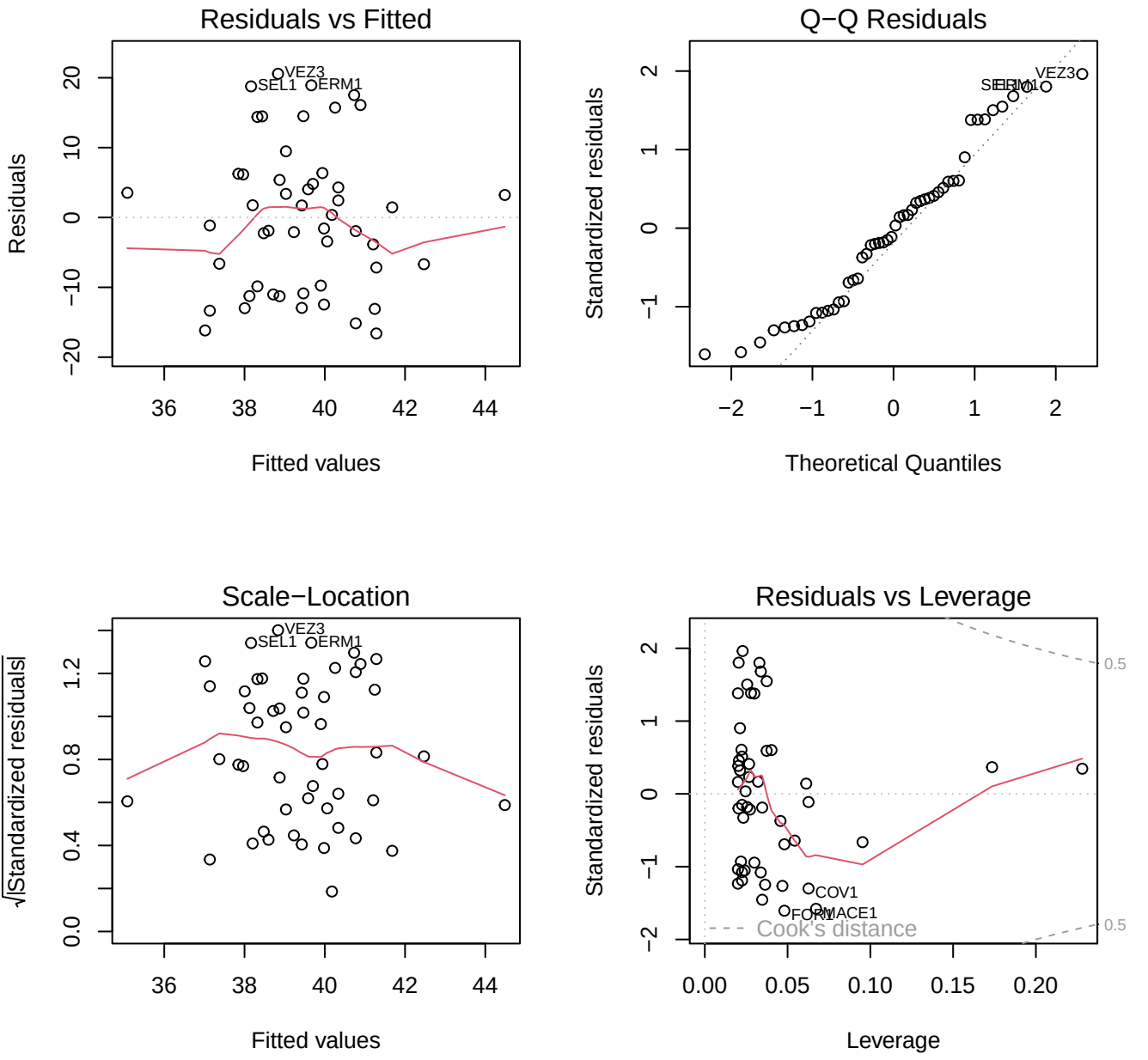

$R^2 = 0.03963973$
p−value: = 0.1657
Bacteria_family_reads
DIN
20
30
40
50
60
0.5
1.0
1.5
2.0

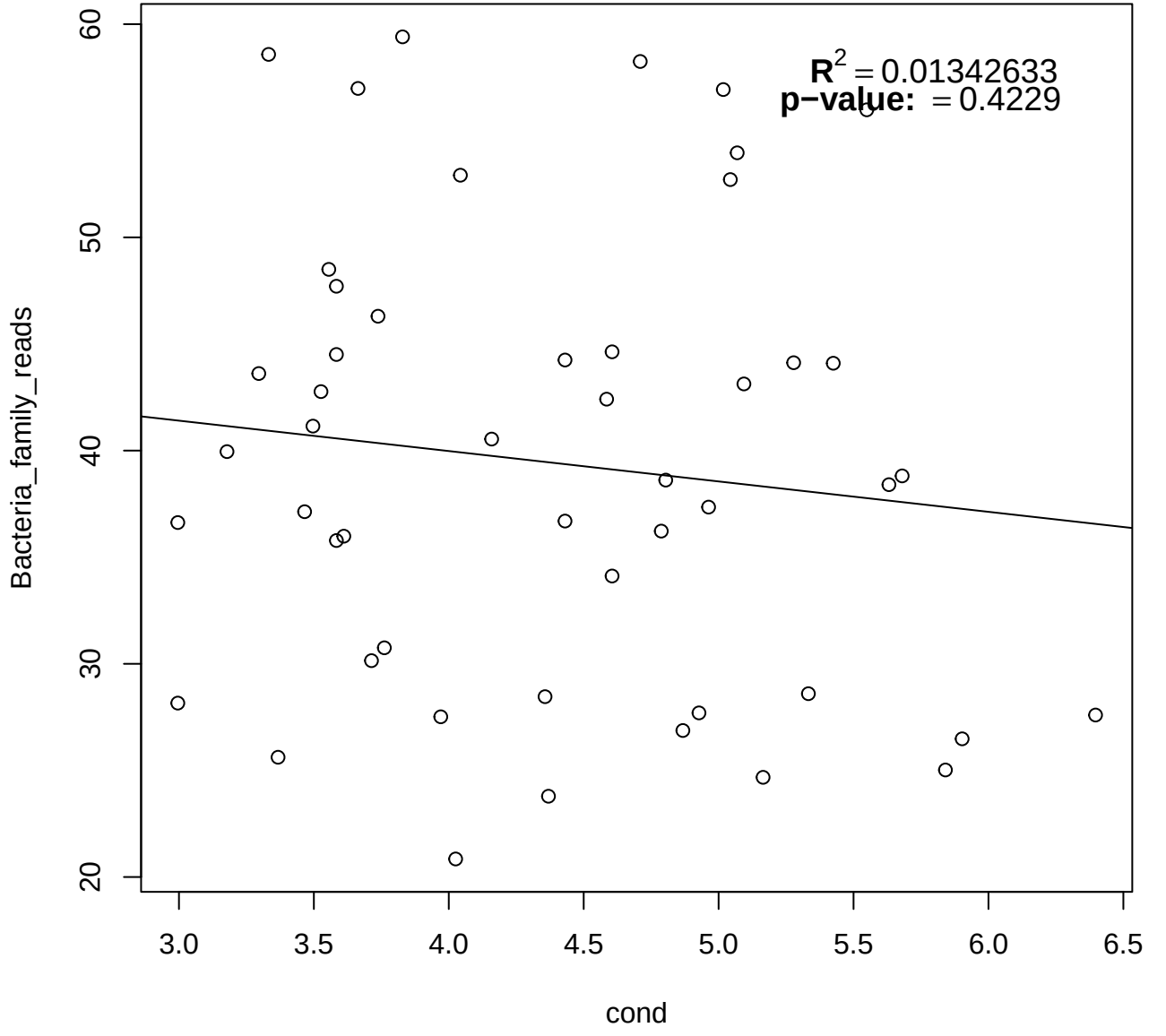

Residuals vs Fitted
Residuals
Fitted values
ERM1
VEZ3
ARG3
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
VEZ3
ARG3
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
VEZ3
ARG3
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
MACI1
VEZ1
Cook's distance
0.5

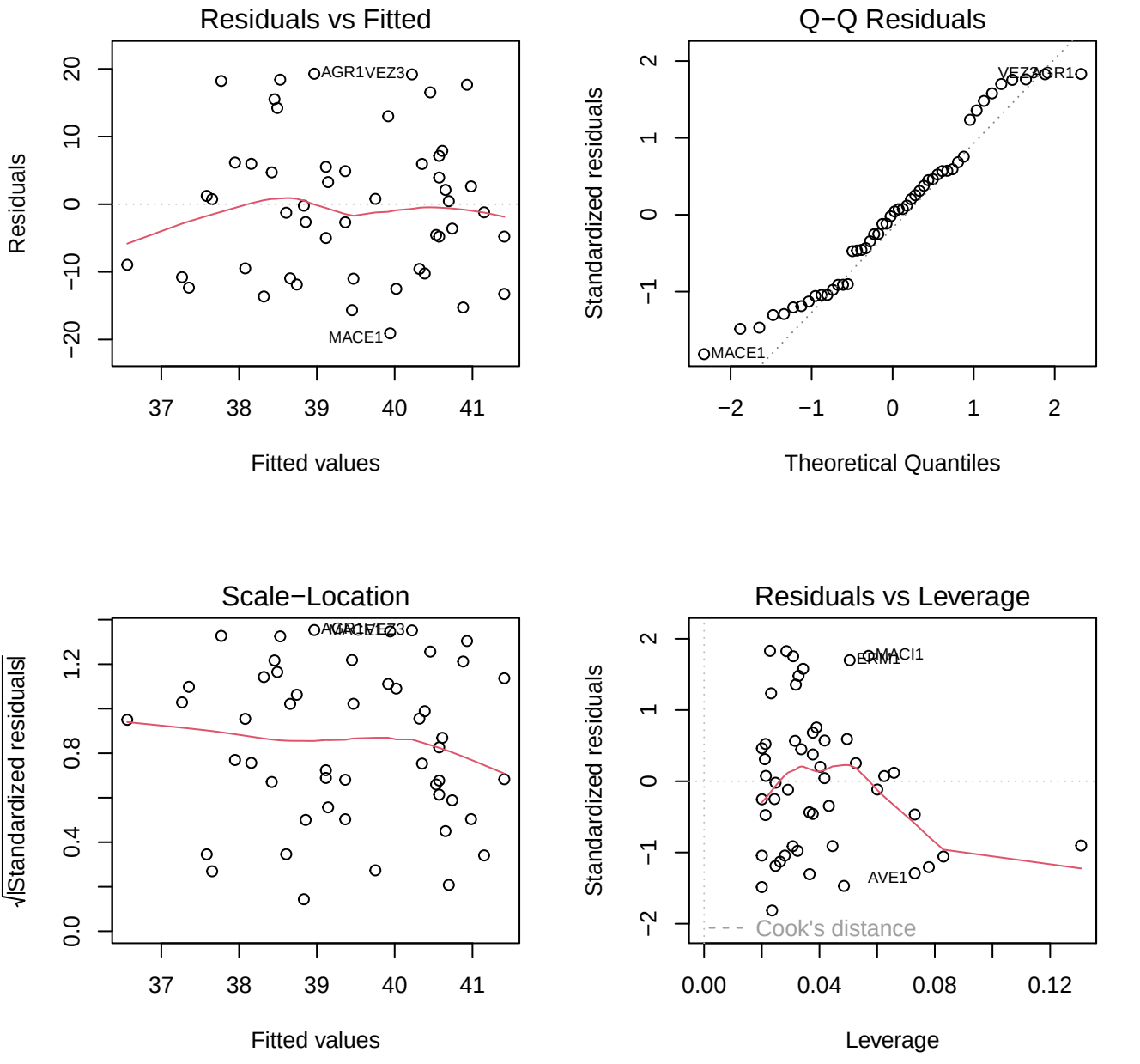

$R^2 = 2.761001e-05$
p−value: = 0.9711
Bacteria_family_reads
P.PO4
20
30
40
50
60
0.0
0.5
1.0
1.5

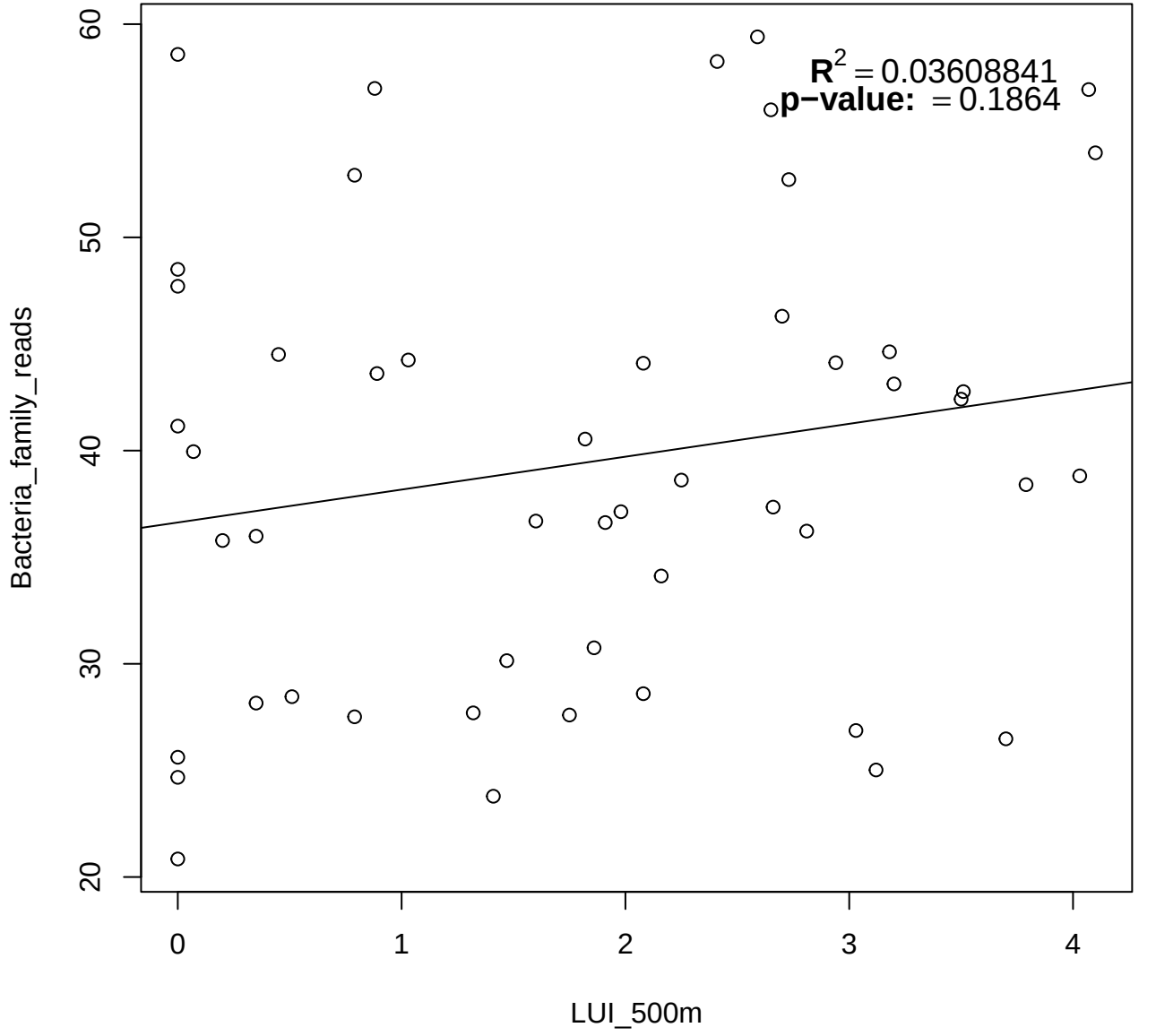

Residuals vs Fitted
Residuals
Fitted values
AGR1
ERM1
VEZ3
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
AGR1
LAB1
NES1
Cook's distance

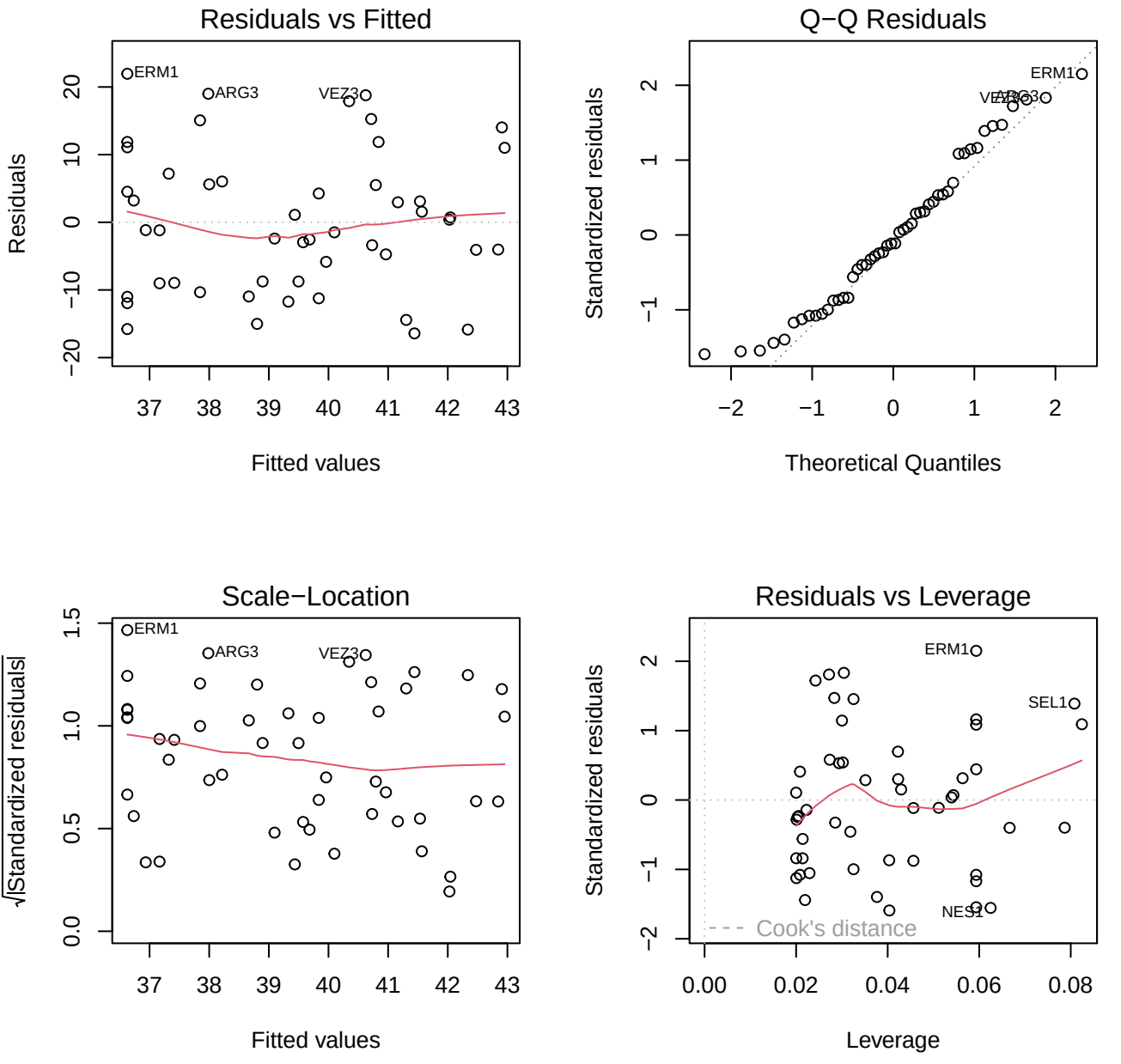

$R^2 = 0.02228925$
p−value: = 0.3008
Bacteria_family_reads
ph
20
30
40
50
60
5.5
6.0
6.5
7.0
7.5

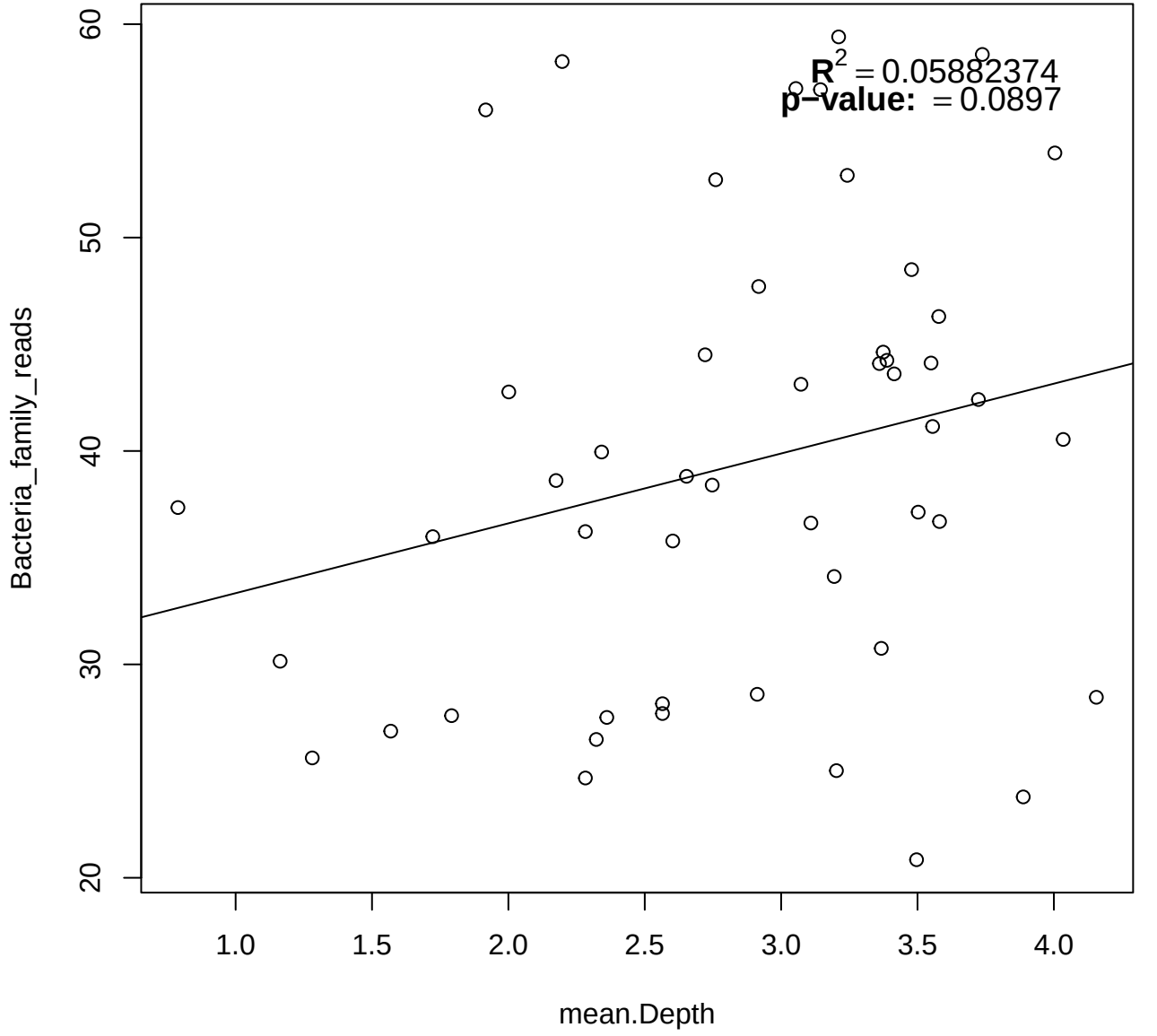

Residuals vs Fitted
Residuals
Fitted values
VEZ3
SEL1
ERM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
Cook's distance
COV1
FORM
ACE1
0.5

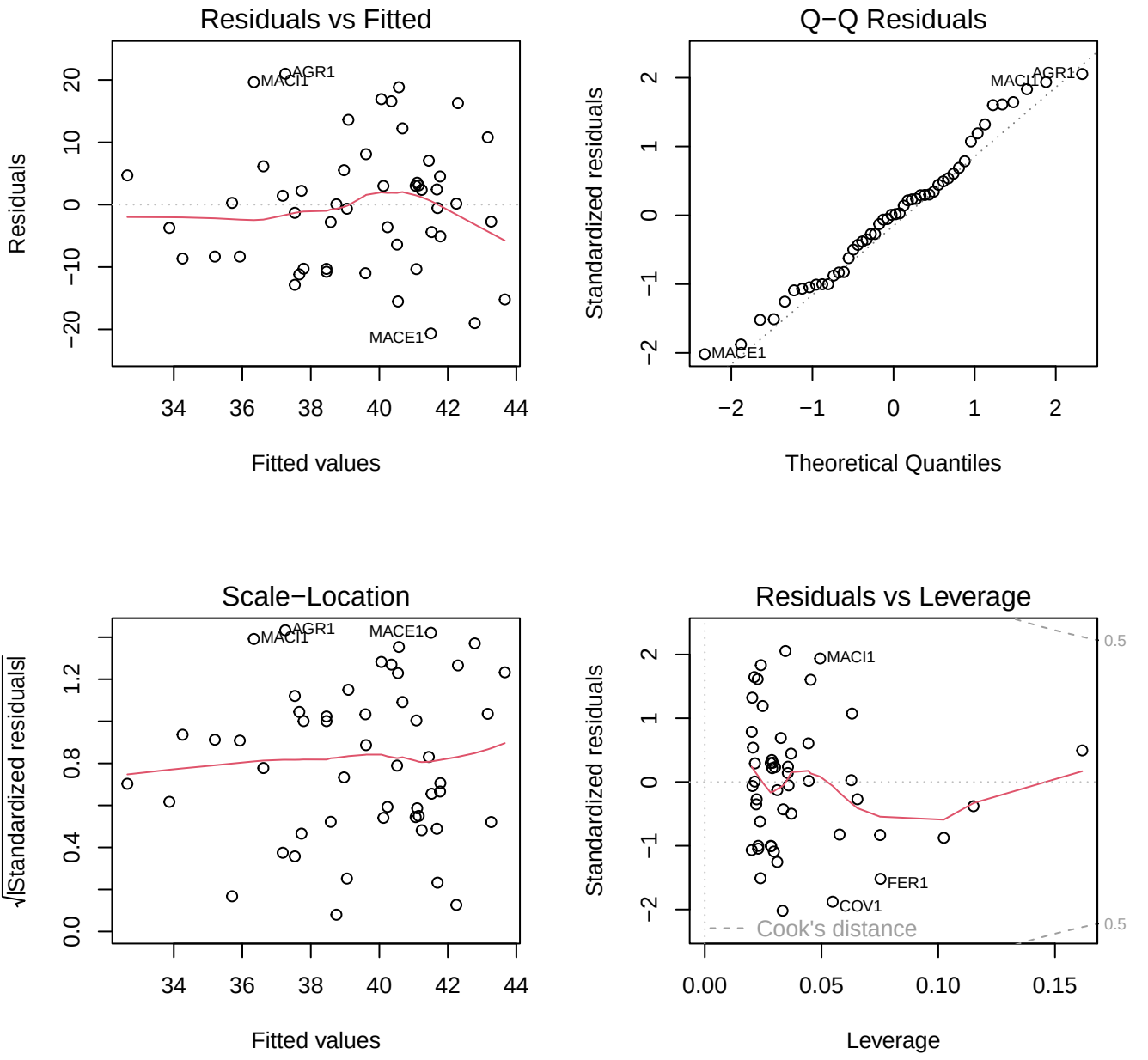

$R^2 = 0.01342633$
p−value: = 0.4229
Bacteria_family_reads
cond
20
30
40
50
60
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5

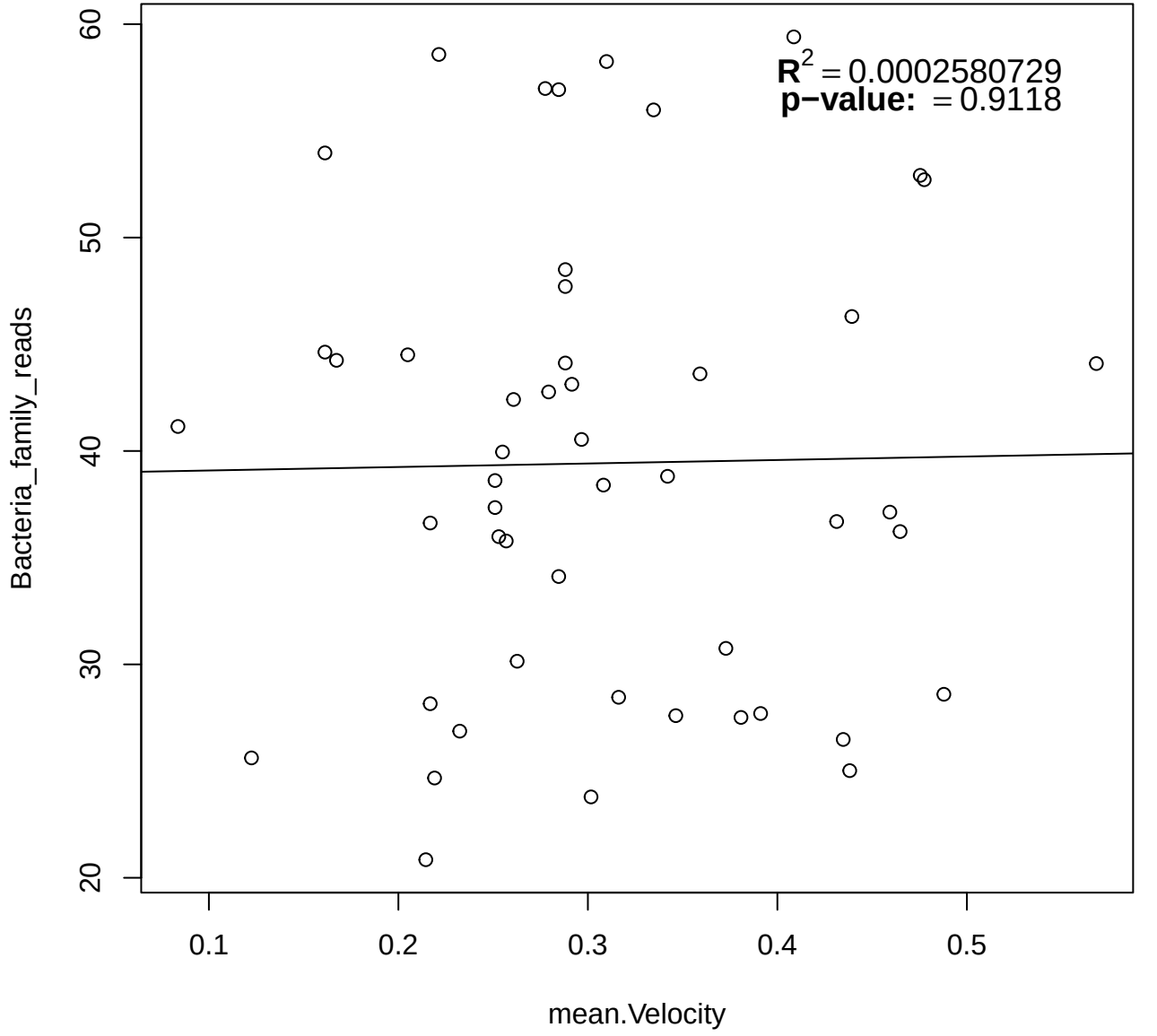

Residuals vs Fitted
Residuals
Fitted values
AGR1
VEZ3
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
VEZ3
AGR1
MACE1
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
MACI1
EXM1
AVE1
Cook's distance

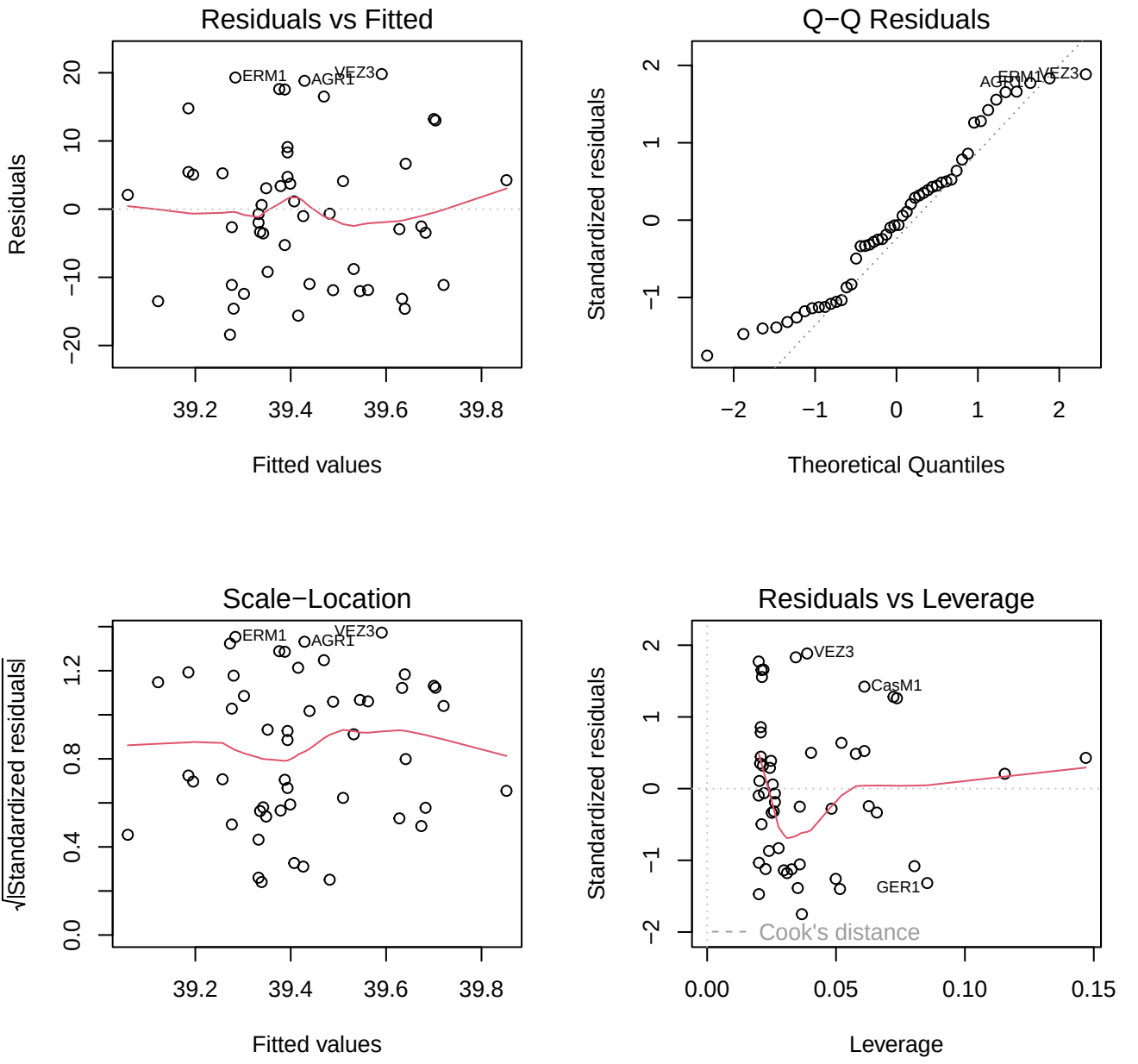

$R^2 = 0.03608841$
p−value: = 0.1864
Bacteria_family_reads
LUI_500m
20
30
40
50
60
0
1
2
3
4

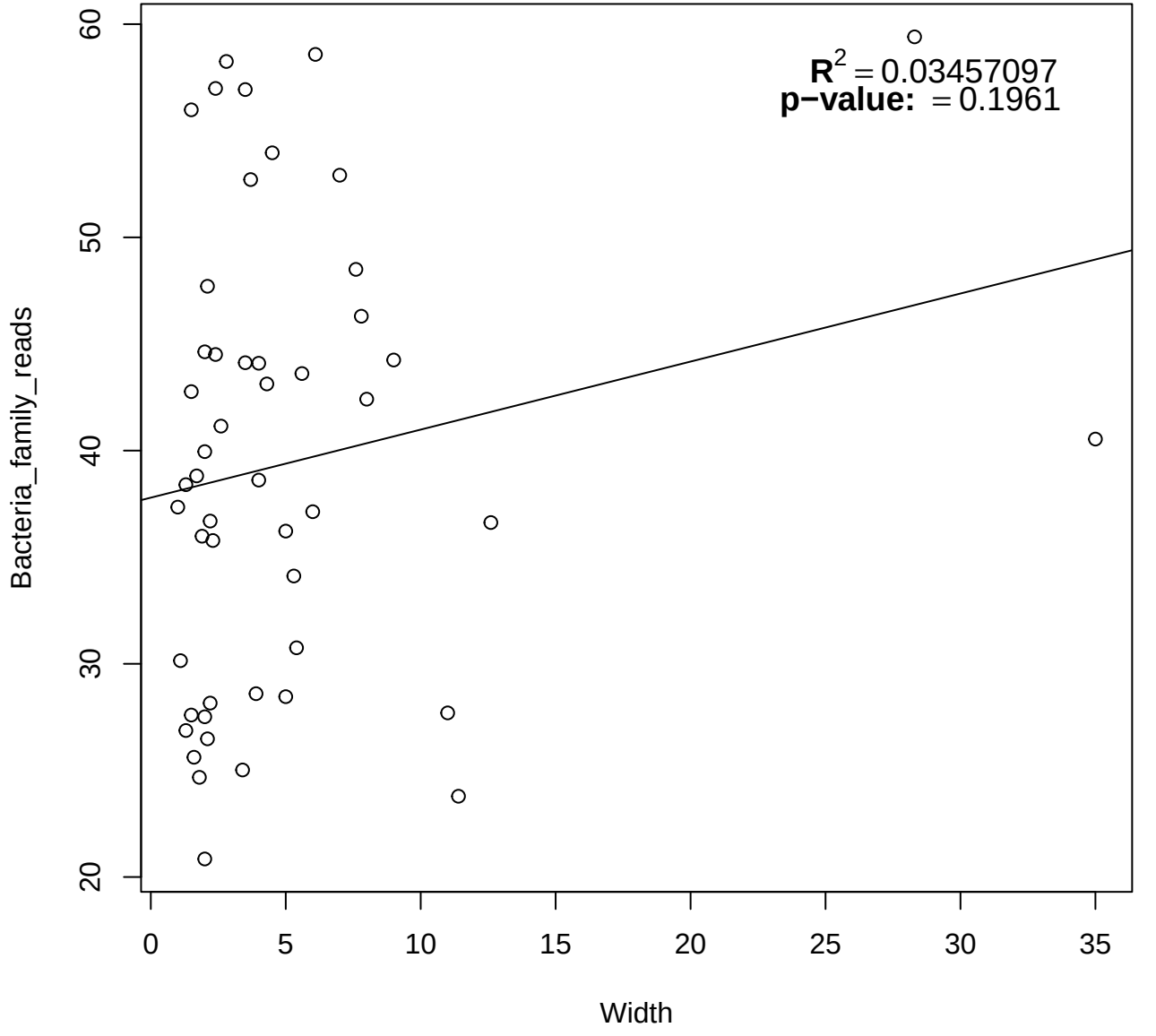

Residuals vs Fitted
Residuals
Fitted values
ERM1
ARG3
VEZ3
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
ARG3
VEZ3
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
SEL1
NES1
Cook's distance

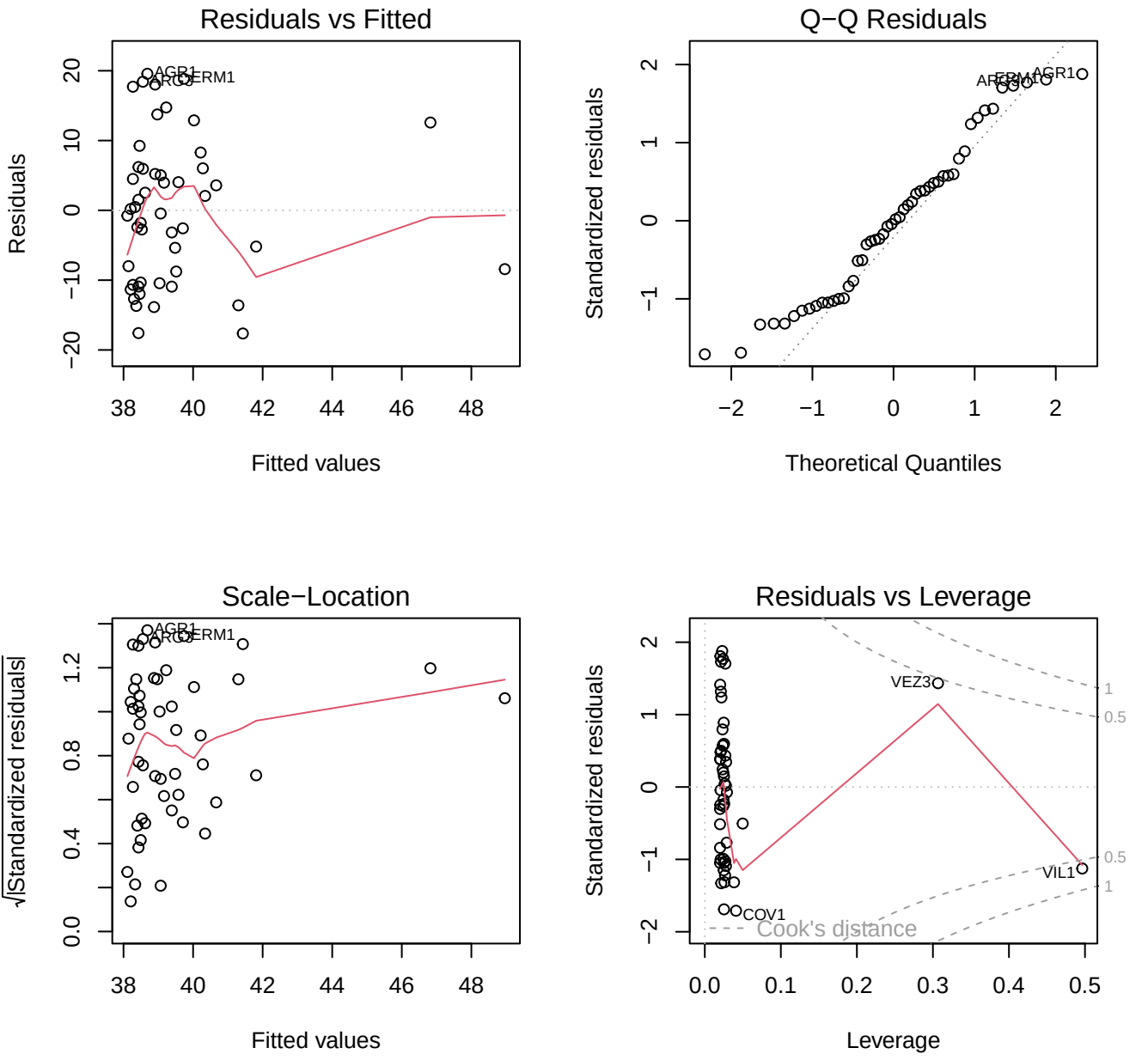

$R^2 = 0.05882374$
p−value: = 0.0897
Bacteria_family_reads
mean.Depth
20
30
40
50
60
1.0
1.5
2.0
2.5
3.0
3.5
4.0

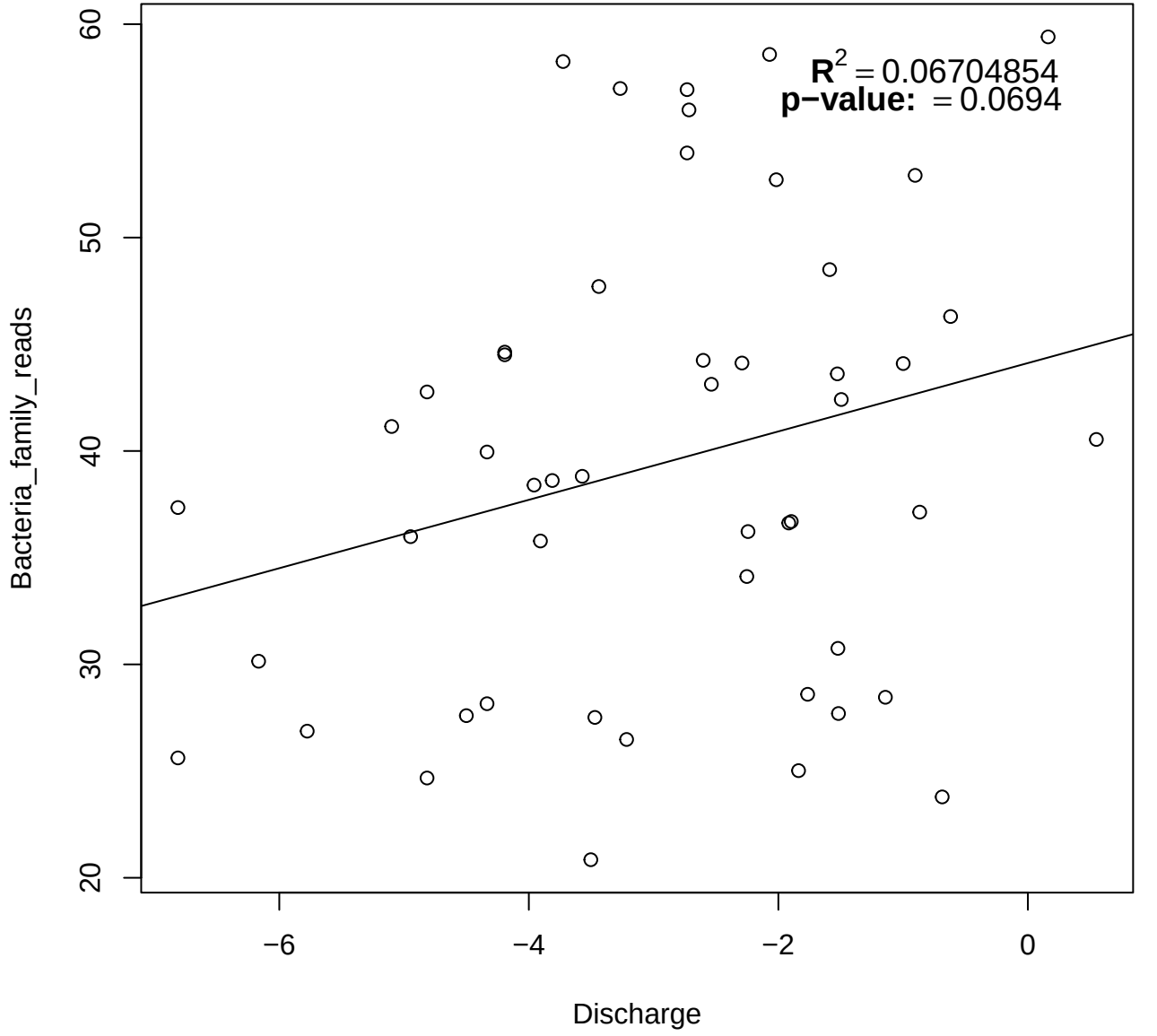

Residuals vs Fitted
Residuals
Fitted values
AGR1
MACI1
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
AGR1
MACI1
MACE1
Scale−Location
√|Standardized residuals|
Fitted values
AGR1
MACI1
MACE1
Residuals vs Leverage
Standardized residuals
Leverage
MACI1
FER1
COV1
Cook's distance
0.5
0.5

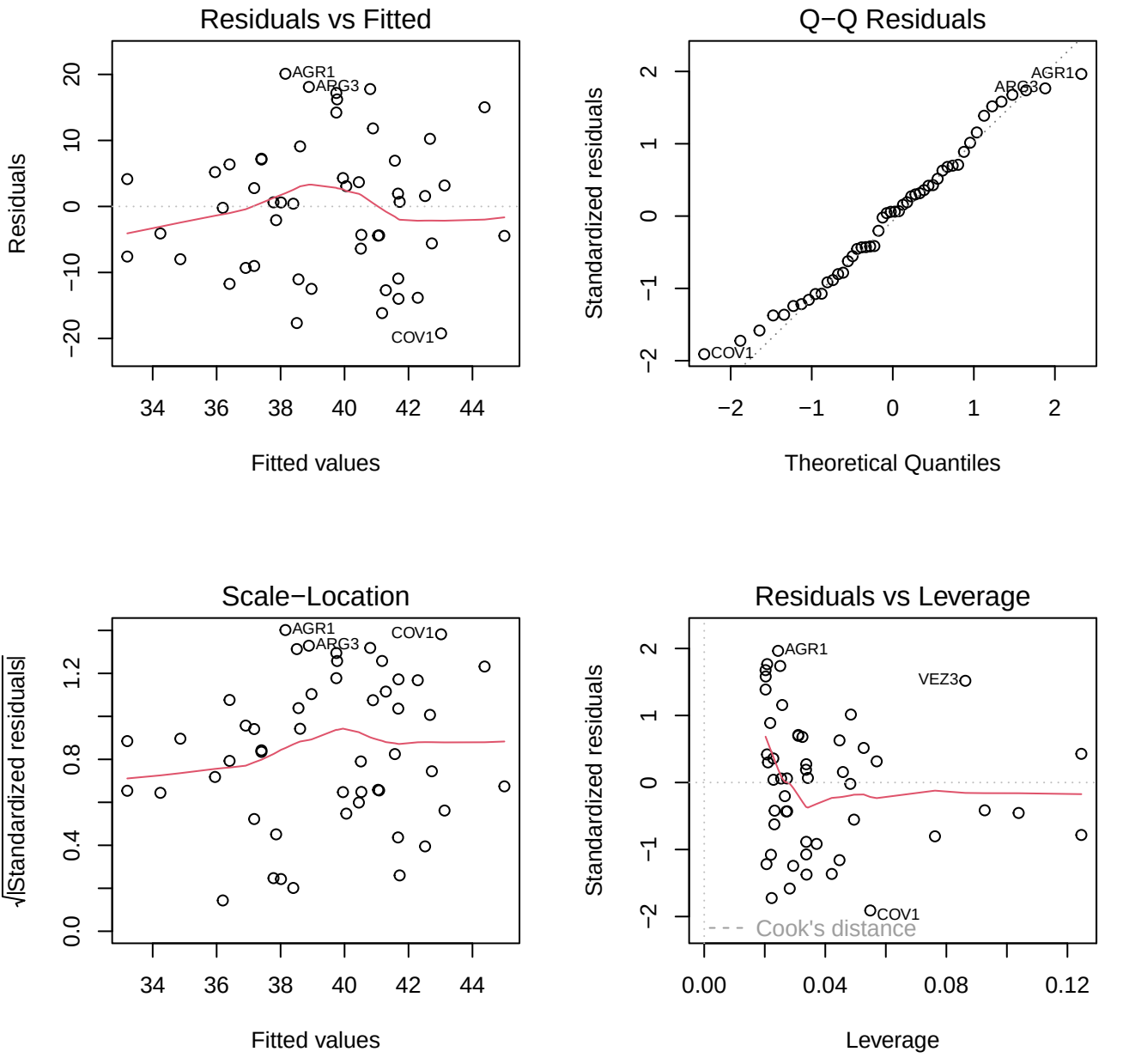

$R^2 = 0.0002580729$
p−value: = 0.9118
Bacteria_family_reads
mean.Velocity
20
30
40
50
60
0.1
0.2
0.3
0.4
0.5

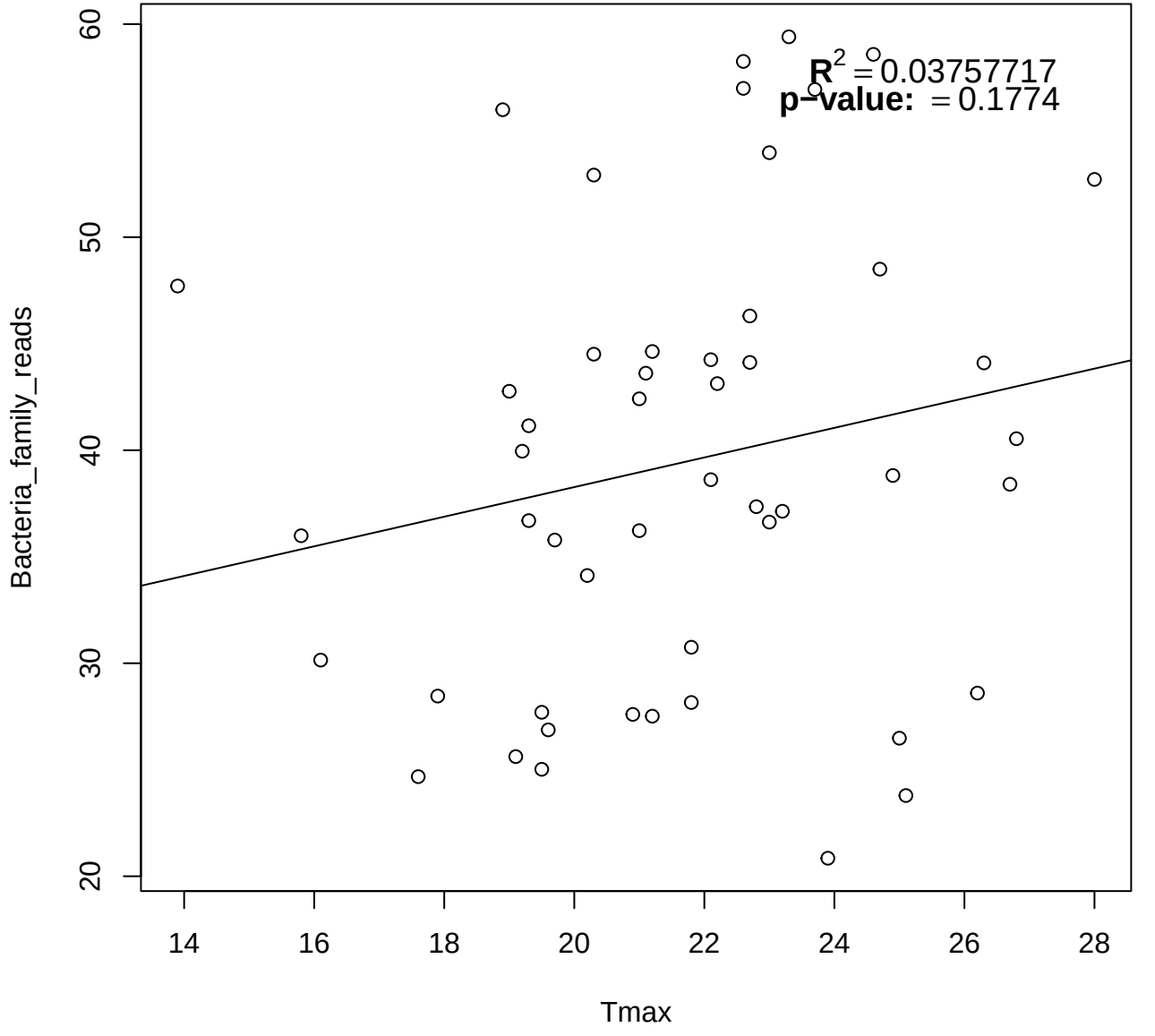

Residuals vs Fitted
Residuals
Fitted values
ERM1
AGR1
VEZ3
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
VEZ3
CasM1
GER1
Cook's distance

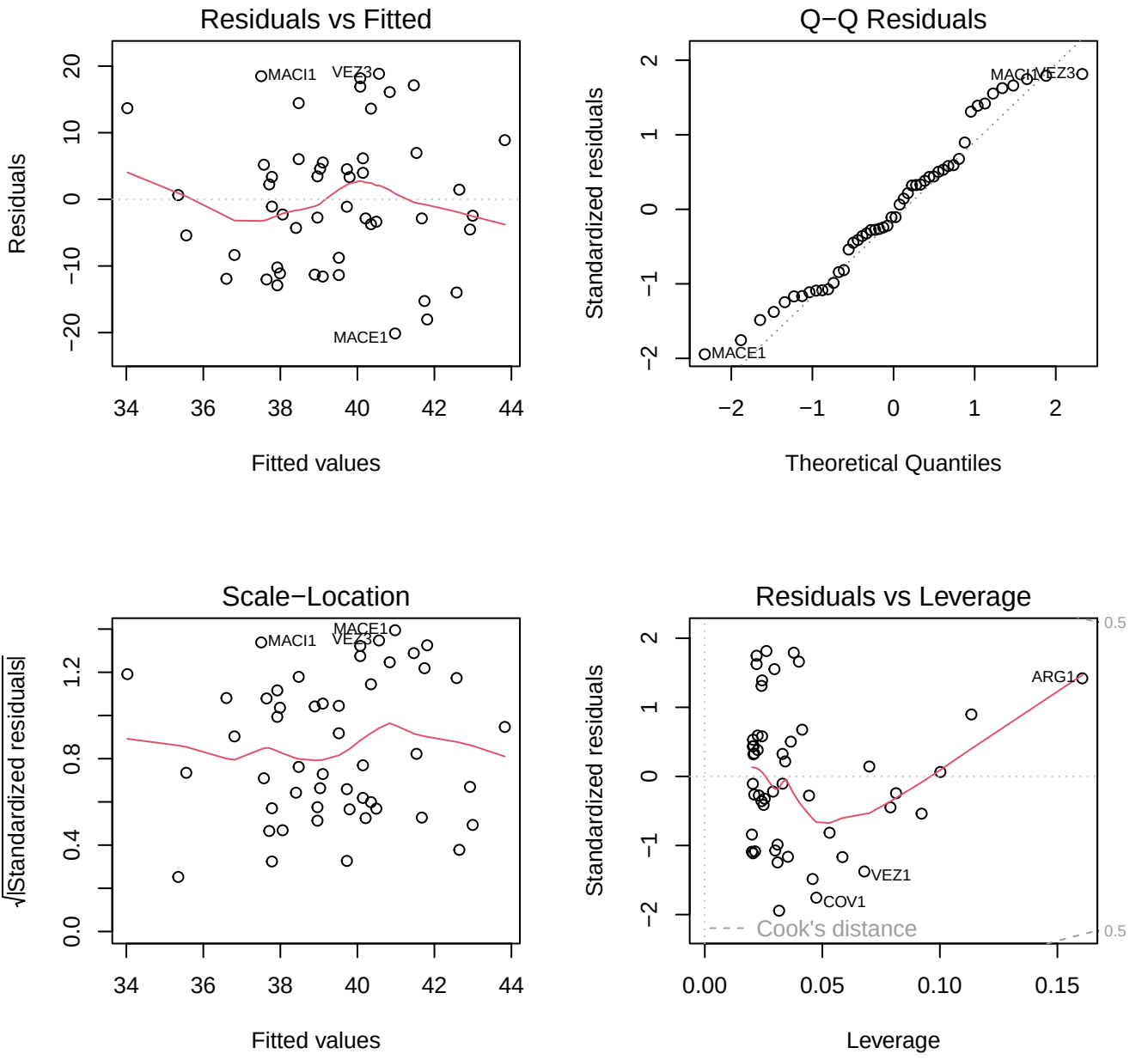

$R^2 = 0.03457097$
p−value: = 0.1961
Bacteria_family_reads
Width
20
30
40
50
60
0
5
10
15
20
25
30
35

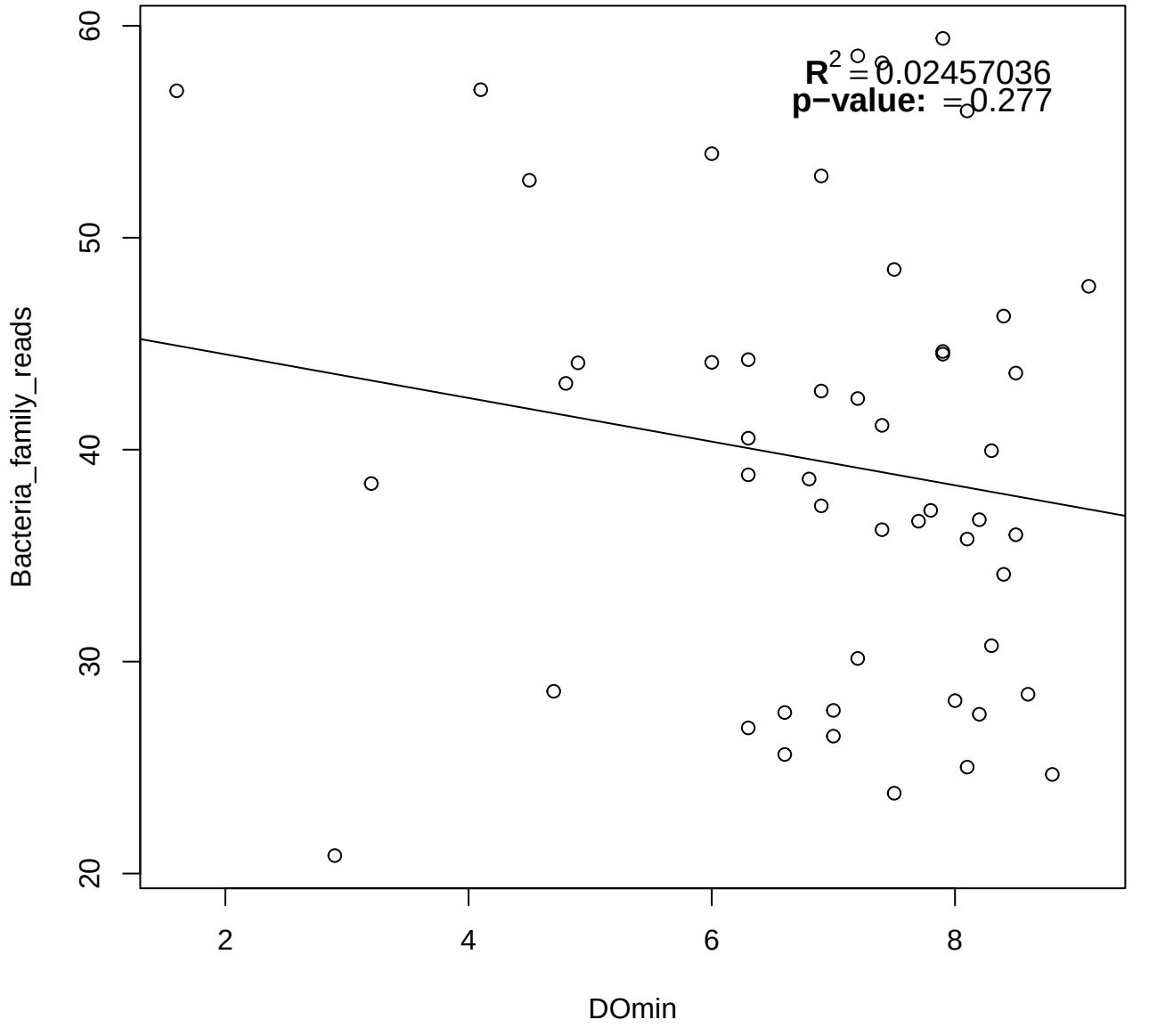

Residuals vs Fitted
Residuals
Fitted values
AGR1
ARG
ERM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
VEZ3
VIL1
COV1
Cook's distance

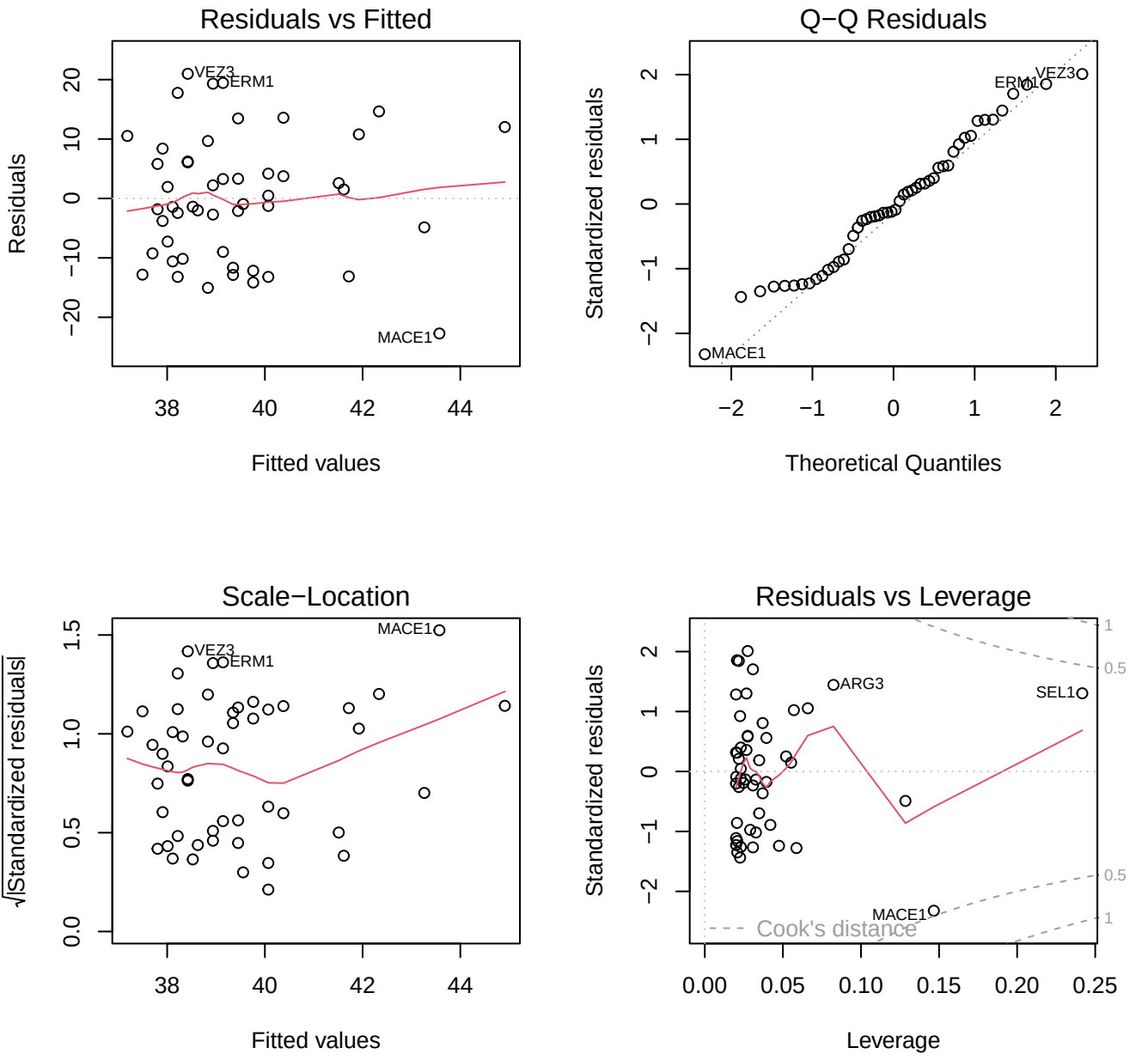

$R^2 = 0.06704854$
p−value: = 0.0694
Bacteria_family_reads
Discharge
60
50
40
30
20
−6
−4
−2
0

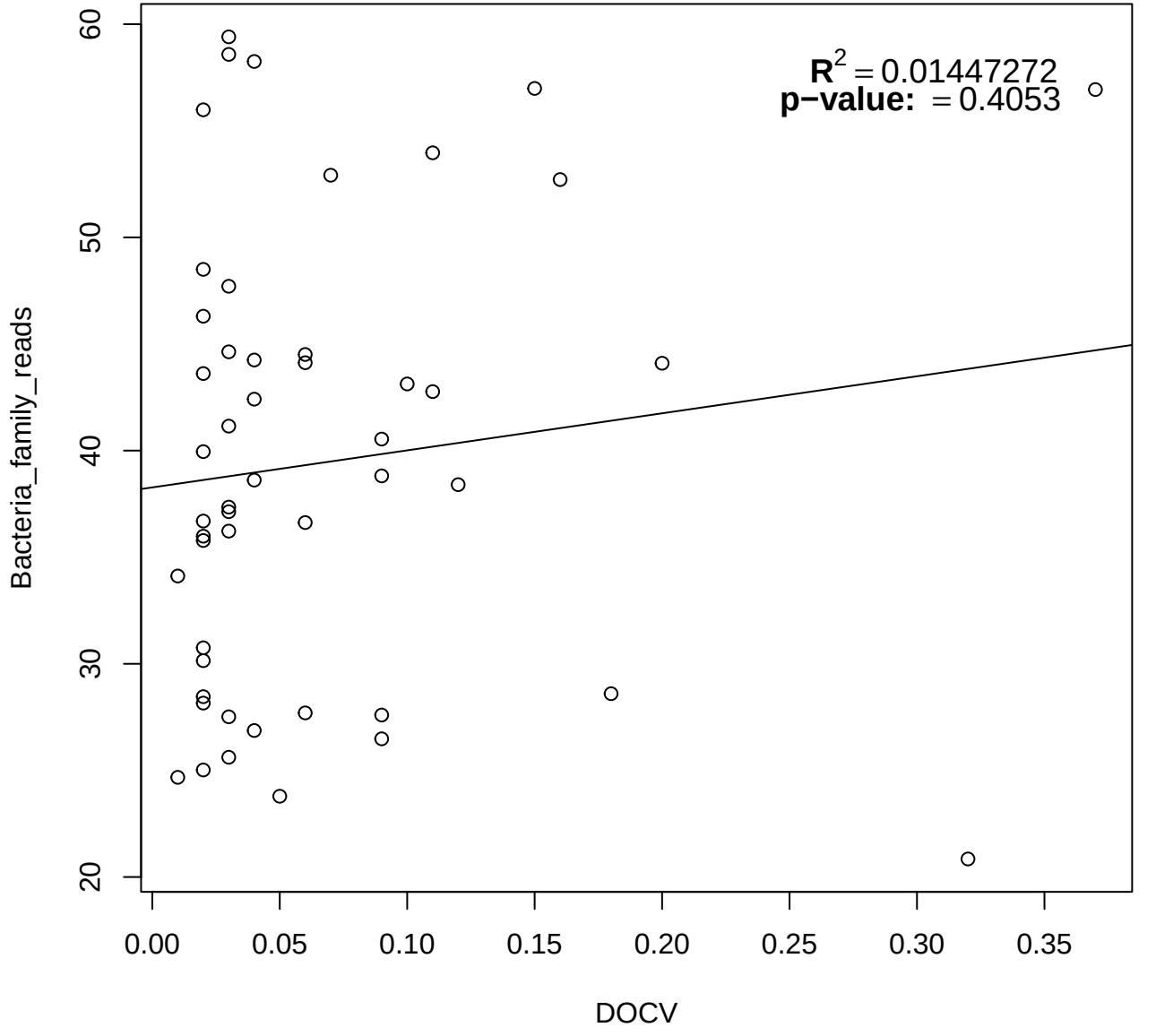

Residuals vs Fitted
Residuals
Fitted values
AGR1
ARG3
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
AGR1
ARG3
COV1
Scale−Location
√|Standardized residuals|
Fitted values
AGR1
ARG3
COV1
Residuals vs Leverage
Standardized residuals
Leverage
AGR1
VEZ3
COV1
Cook's distance

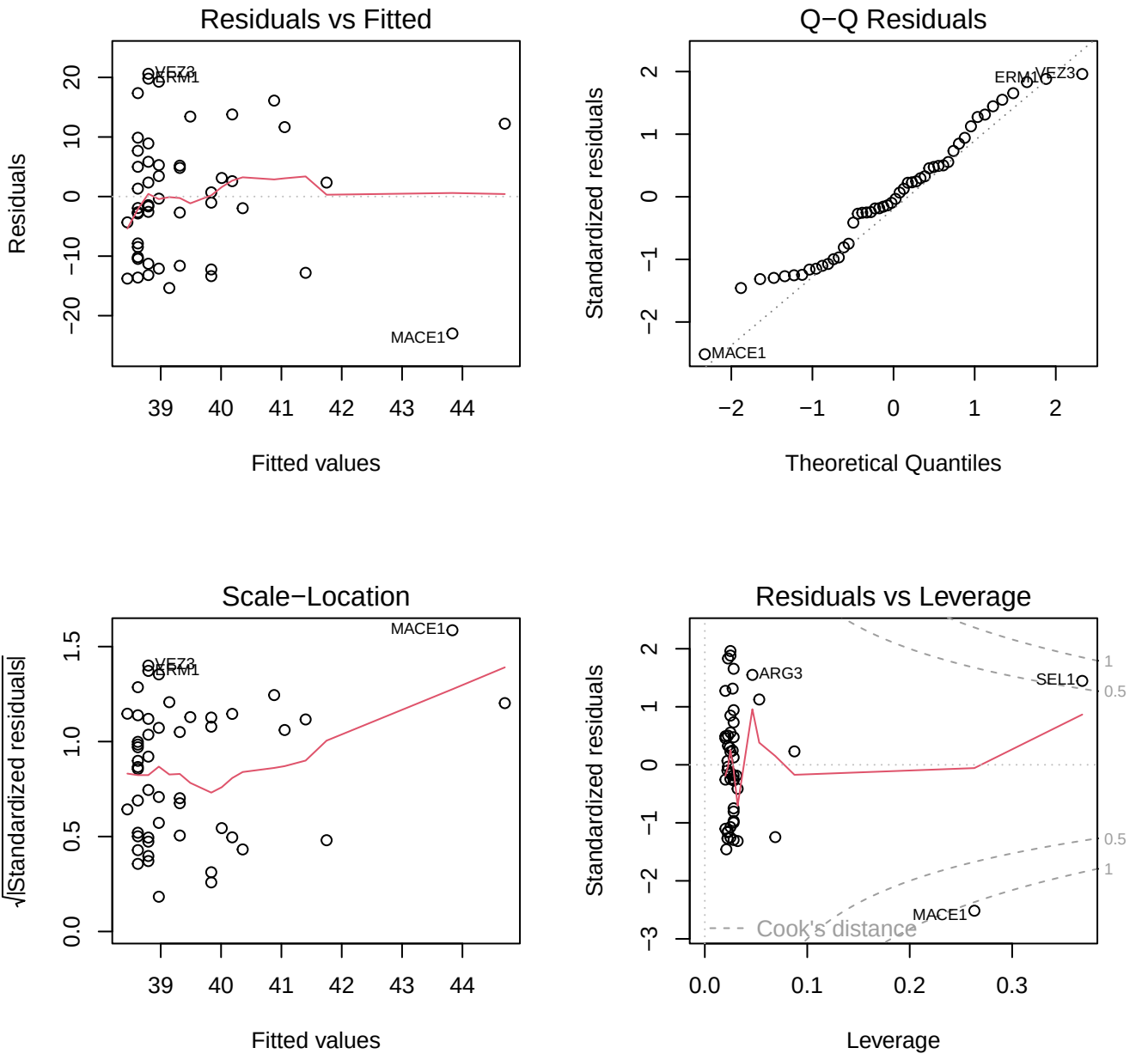

$R^2 = 0.03757717$
p−value: = 0.1774
Bacteria_family_reads
Tmax
20
30
40
50
60
14
16
18
20
22
24
26
28

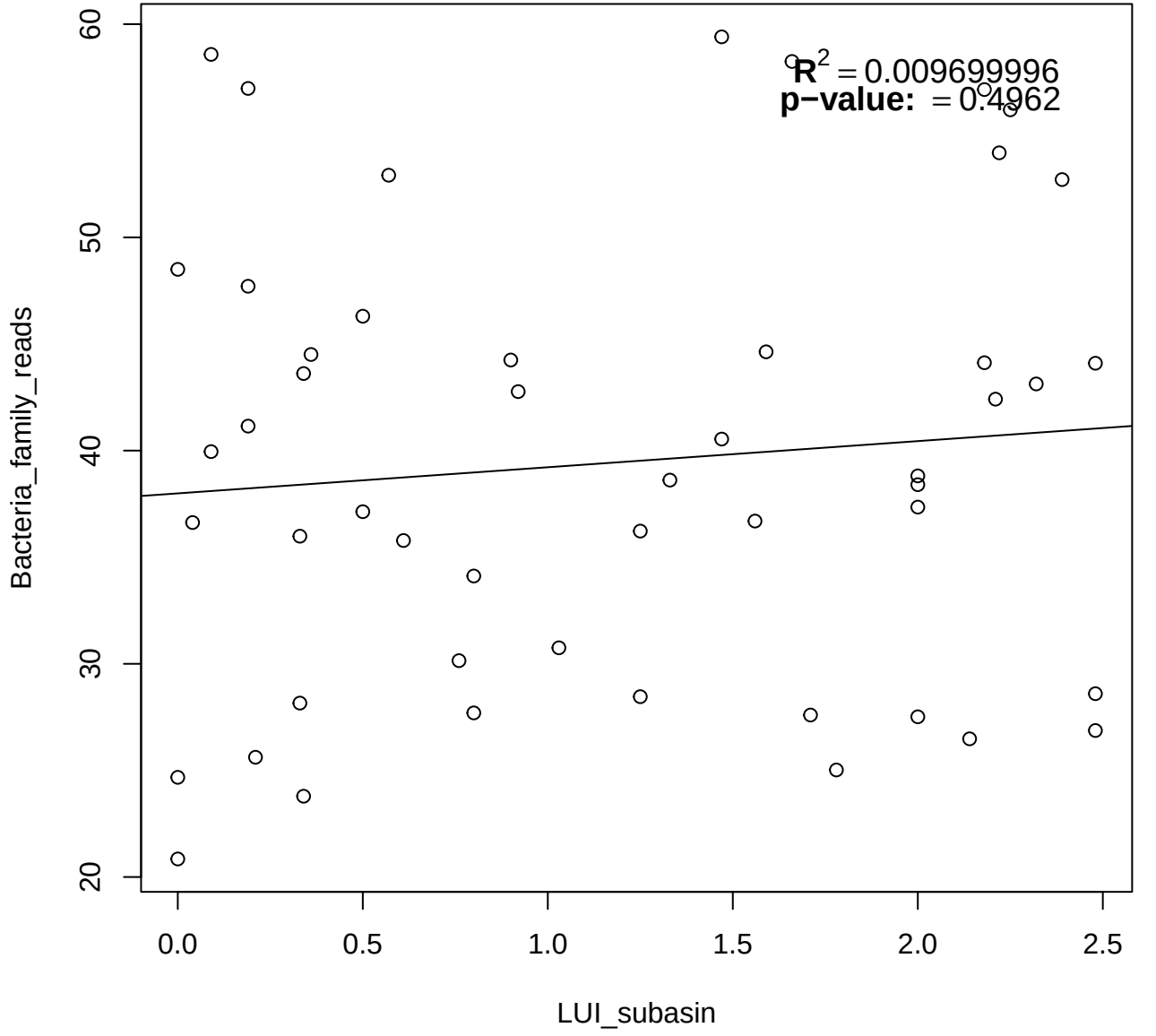

Residuals vs Fitted
Residuals
Fitted values
MACI1
VEZ3
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
MACI1
VEZ3
MACE1
Scale−Location
√|Standardized residuals|
Fitted values
MACE1
MACI1
VEZ3
Residuals vs Leverage
Standardized residuals
Leverage
ARG1
VEZ1
COV1
Cook's distance
0.5
0.5

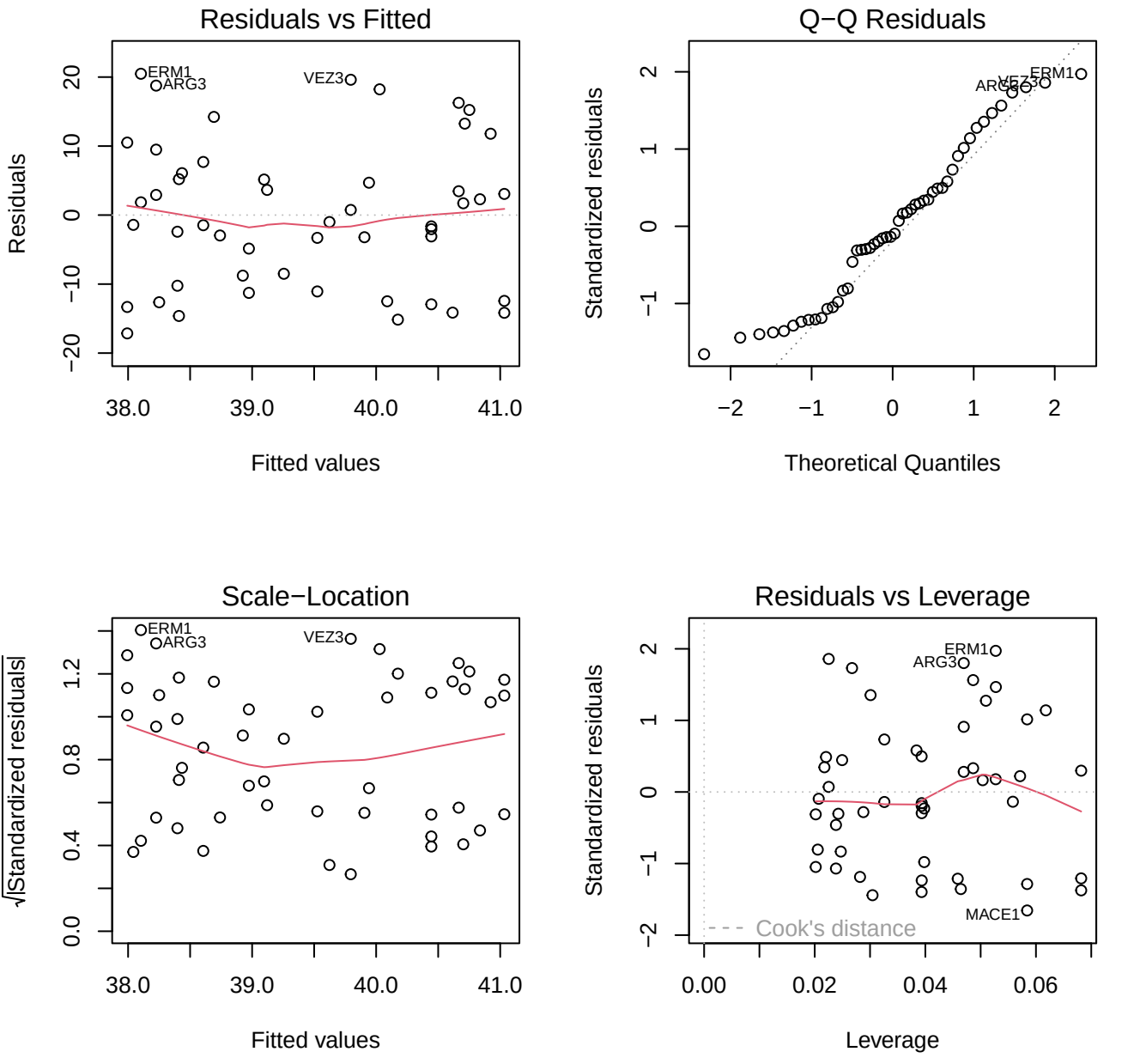

$R^2 = 0.02457036$
p−value: = 0.277
Bacteria_family_reads
DOmin
20
30
40
50
60
2
4
6
8

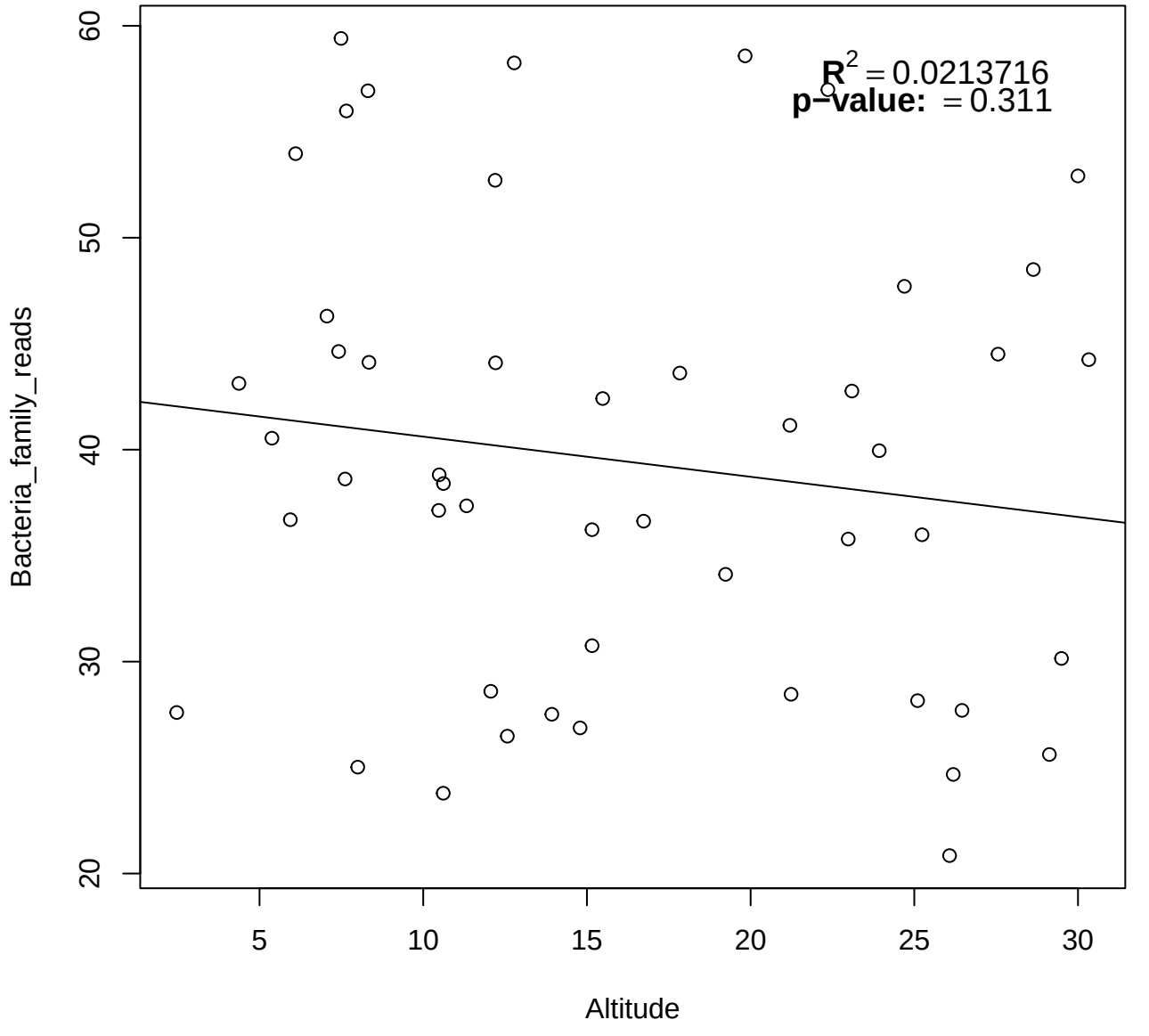

Residuals vs Fitted
Residuals
Fitted values
VEZ3
ERM1
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
VEZ3
MACE1
Scale−Location
√|Standardized residuals|
Fitted values
MACE1
VEZ3
ERM1
Residuals vs Leverage
Standardized residuals
Leverage
ARG3
SEL1
MACE1
Cook's distance

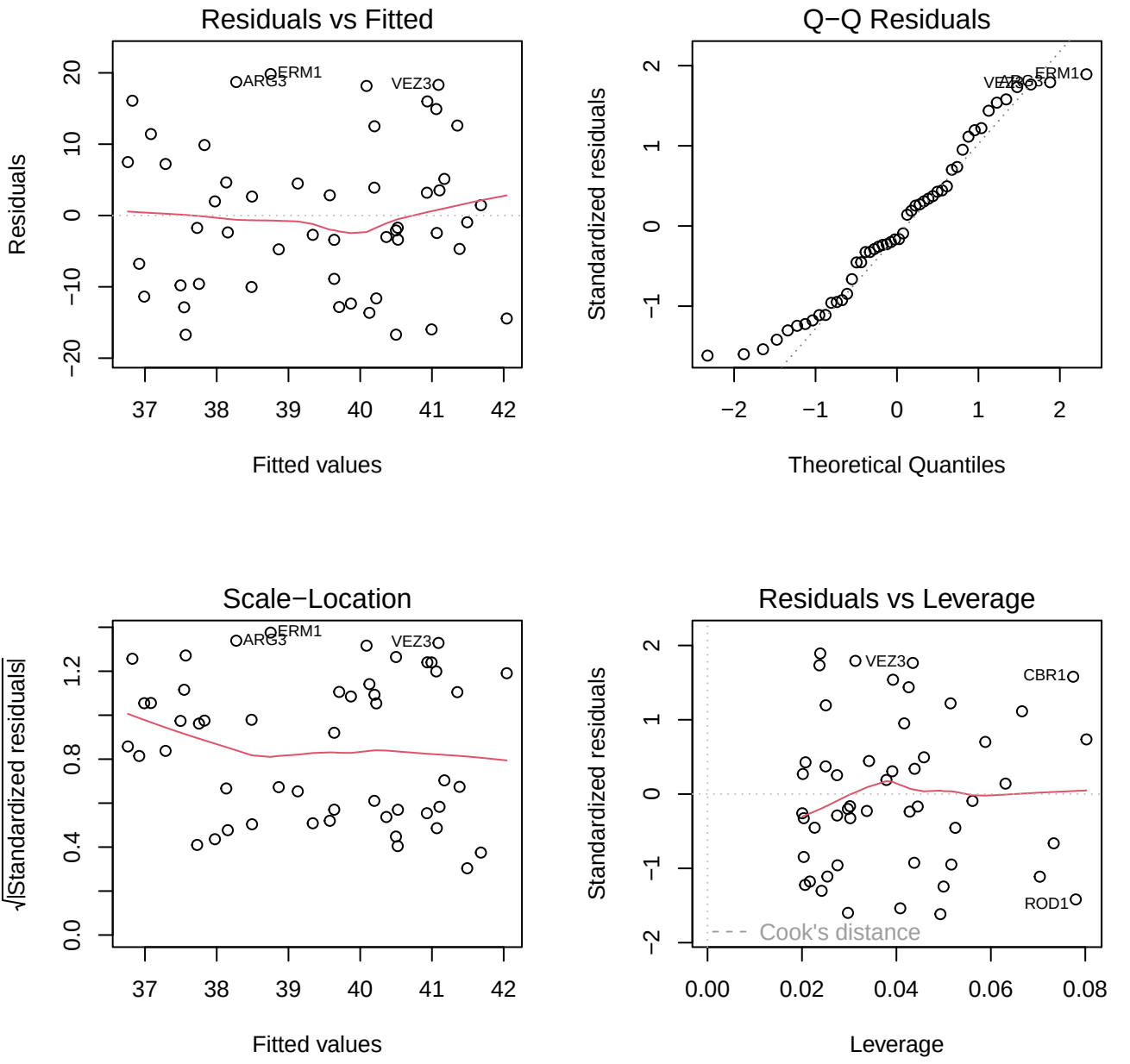

$R^2 = 0.01447272$
p−value: = 0.4053
Bacteria_family_reads
DOCV
20
30
40
50
60
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35

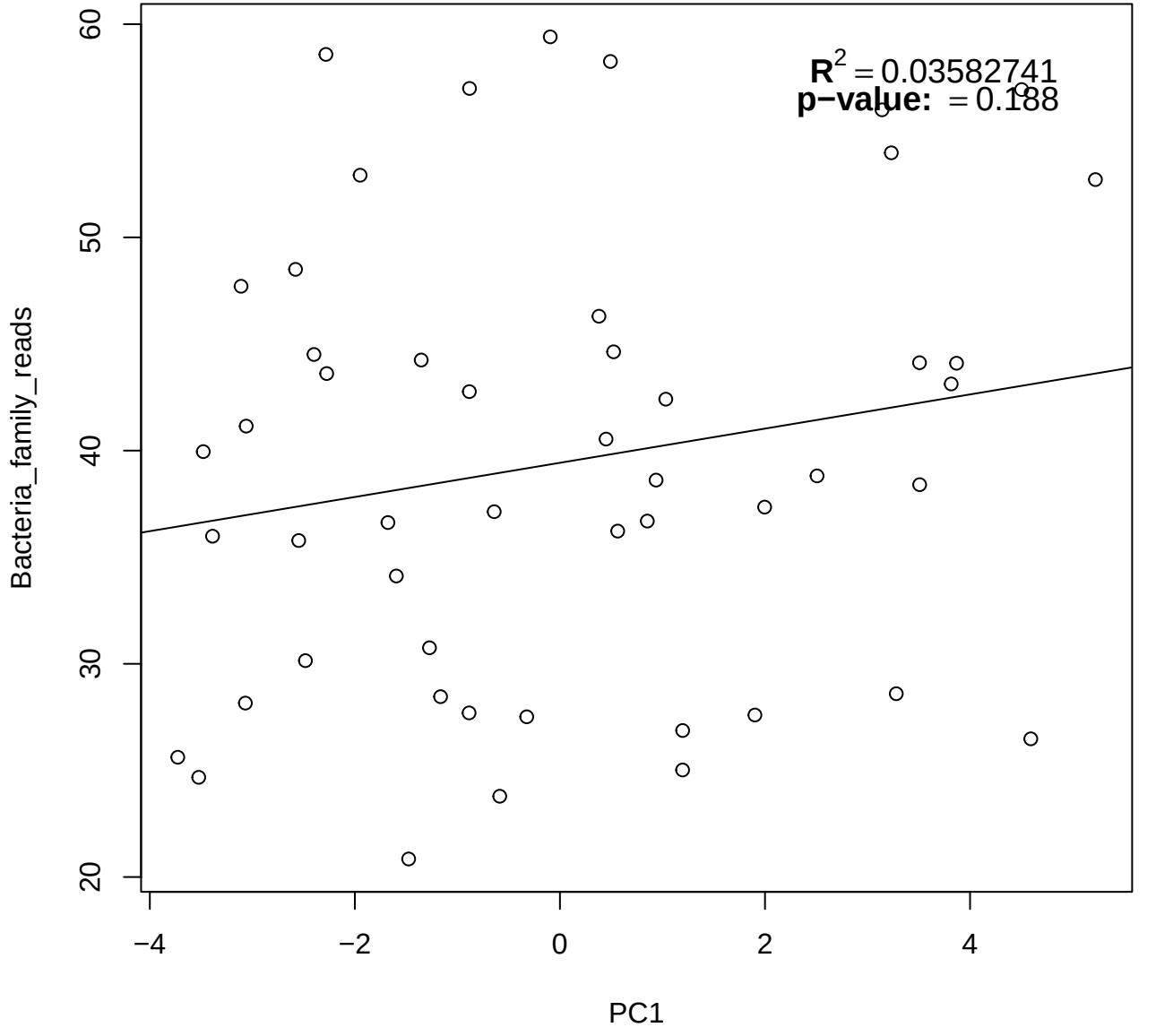

Residuals vs Fitted
Residuals
Fitted values
VEZ3
ERM1
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
VEZ3
MACE1
Scale−Location
√|Standardized residuals|
Fitted values
MACE1
VEZ3
ERM1
Residuals vs Leverage
Standardized residuals
Leverage
ARG3
SEL1
MACE1
Cook's distance

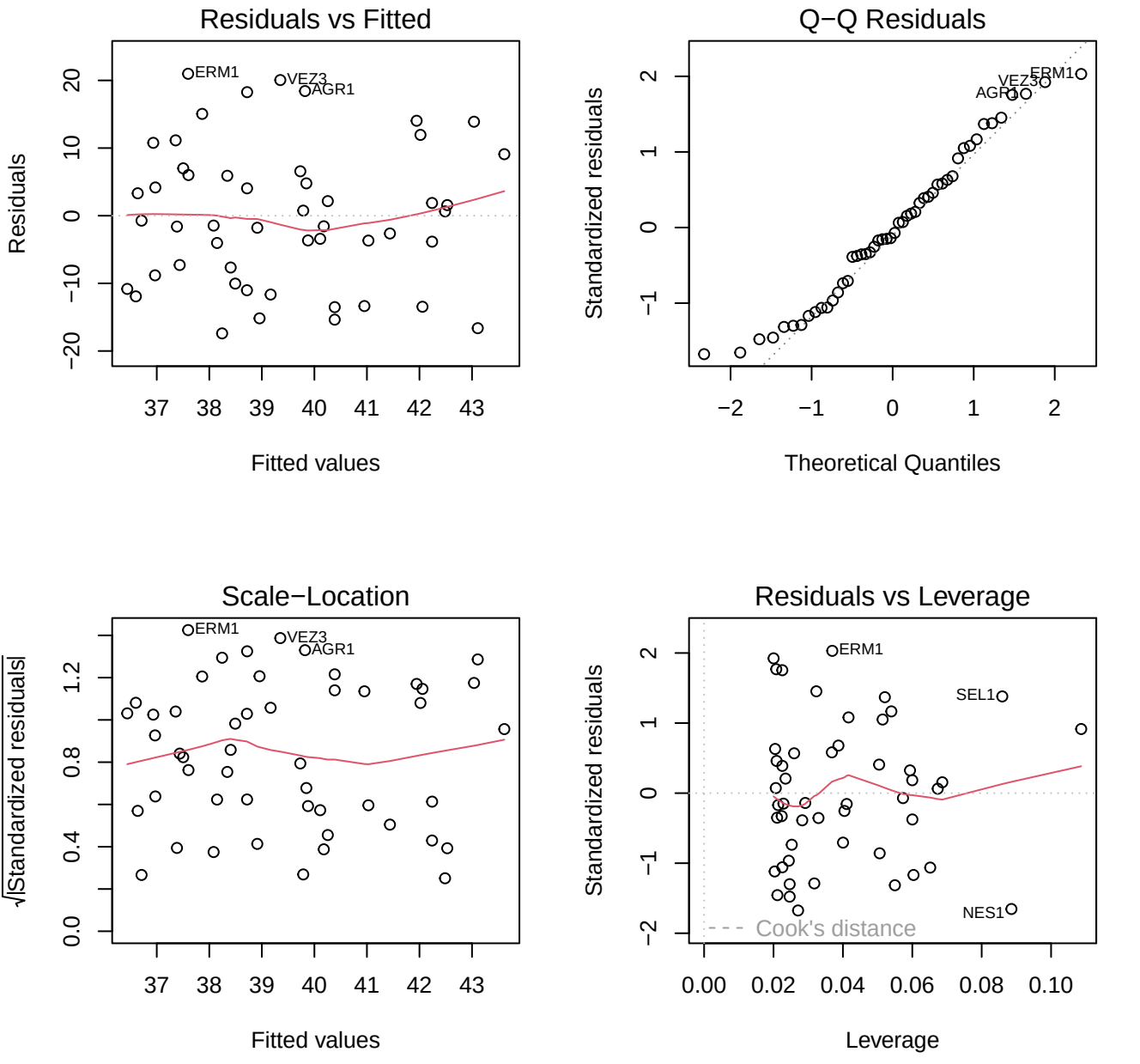

$R^2 = 0.009699996$
p−value: = 0.4962
Bacteria_family_reads
LUI_subasin
20
30
40
50
60
0.0
0.5
1.0
1.5
2.0
2.5

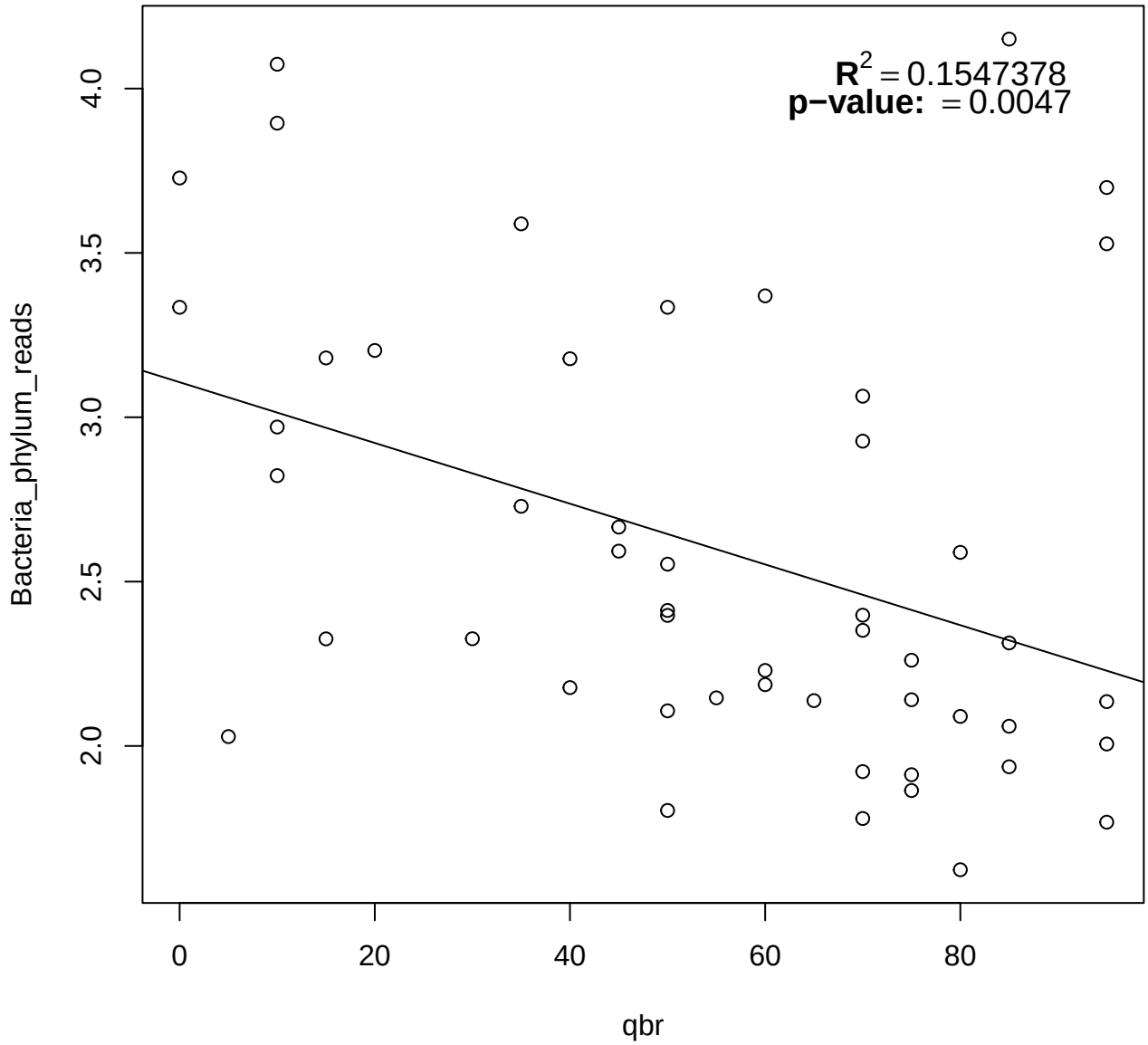

Residuals vs Fitted
Residuals
Fitted values
ERM1
ARG3
VEZ3
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
ARG3
VEZ3
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
ARG3
VEZ3
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
ARG3
MACE1
Cook's distance

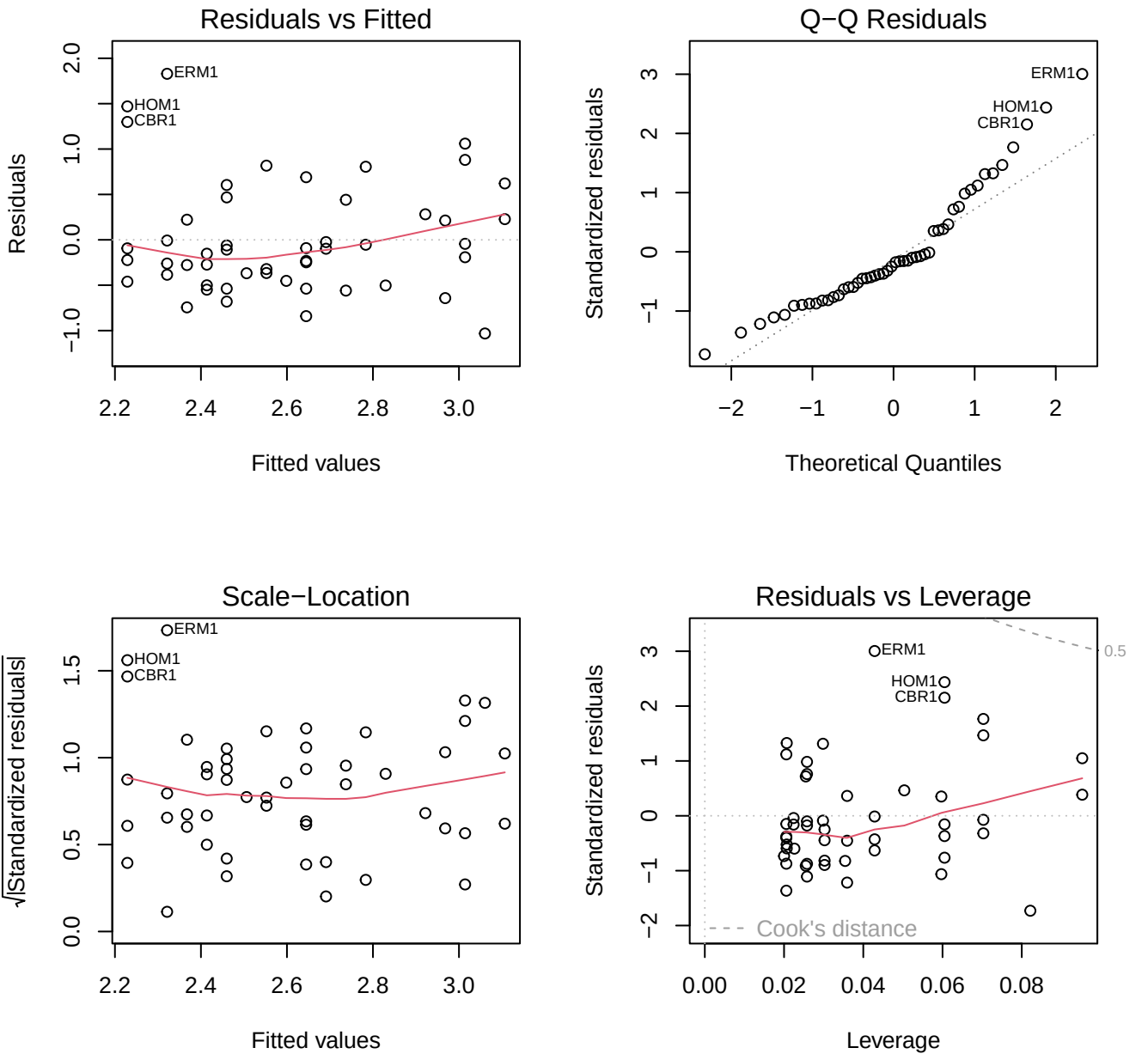

$R^2 = 0.0213716$
p−value: = 0.311
Bacteria_family_reads
Altitude
20
30
40
50
60
5
10
15
20
25
30

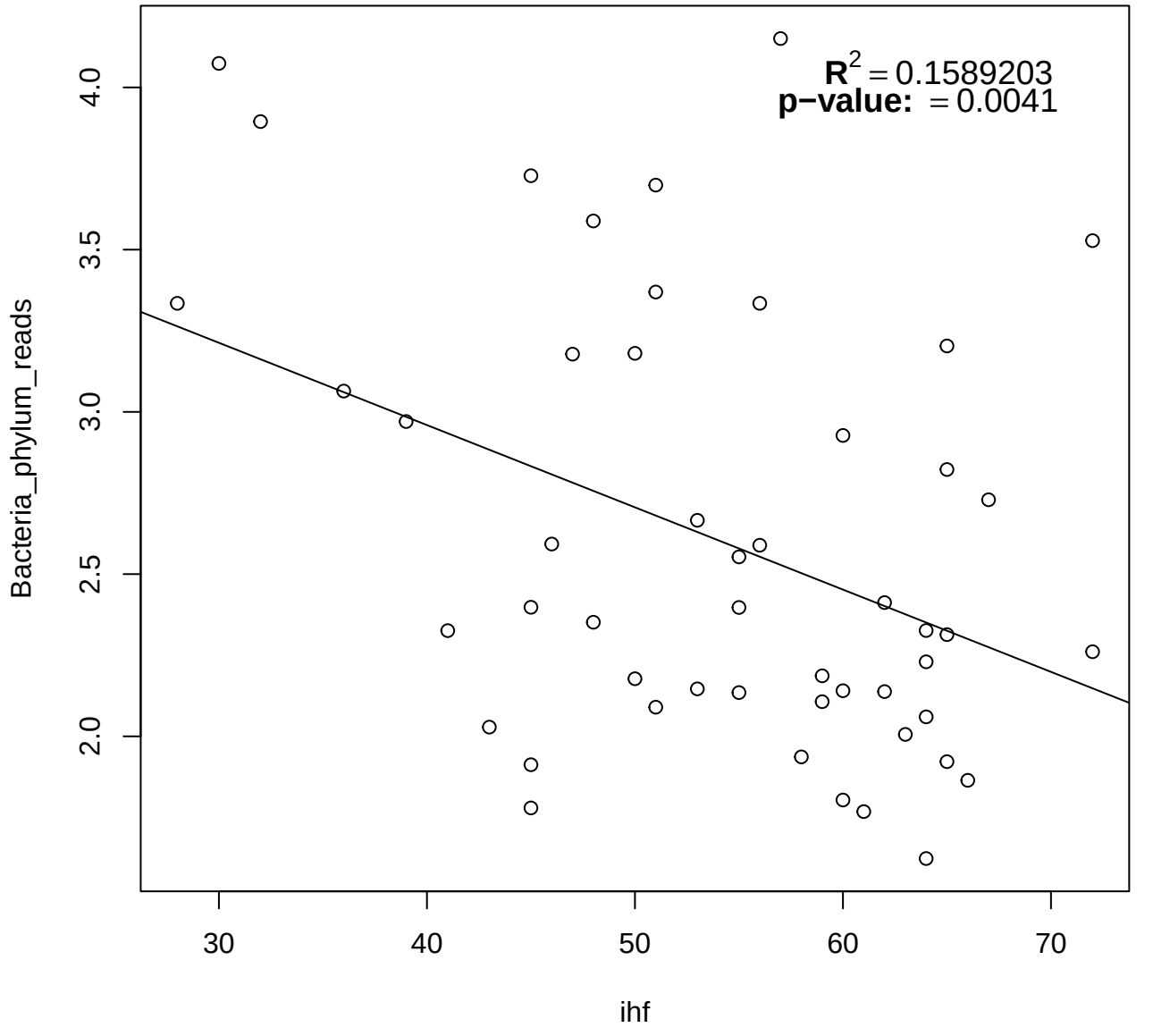

Residuals vs Fitted
Residuals
Fitted values
ARG3
ERM1
VEZ3
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
Scale−Location
√|Standardized residuals|
Fitted values
ARG3
ERM1
VEZ3
Residuals vs Leverage
Standardized residuals
Leverage
VEZ3
CBR1
ROD1
Cook's distance

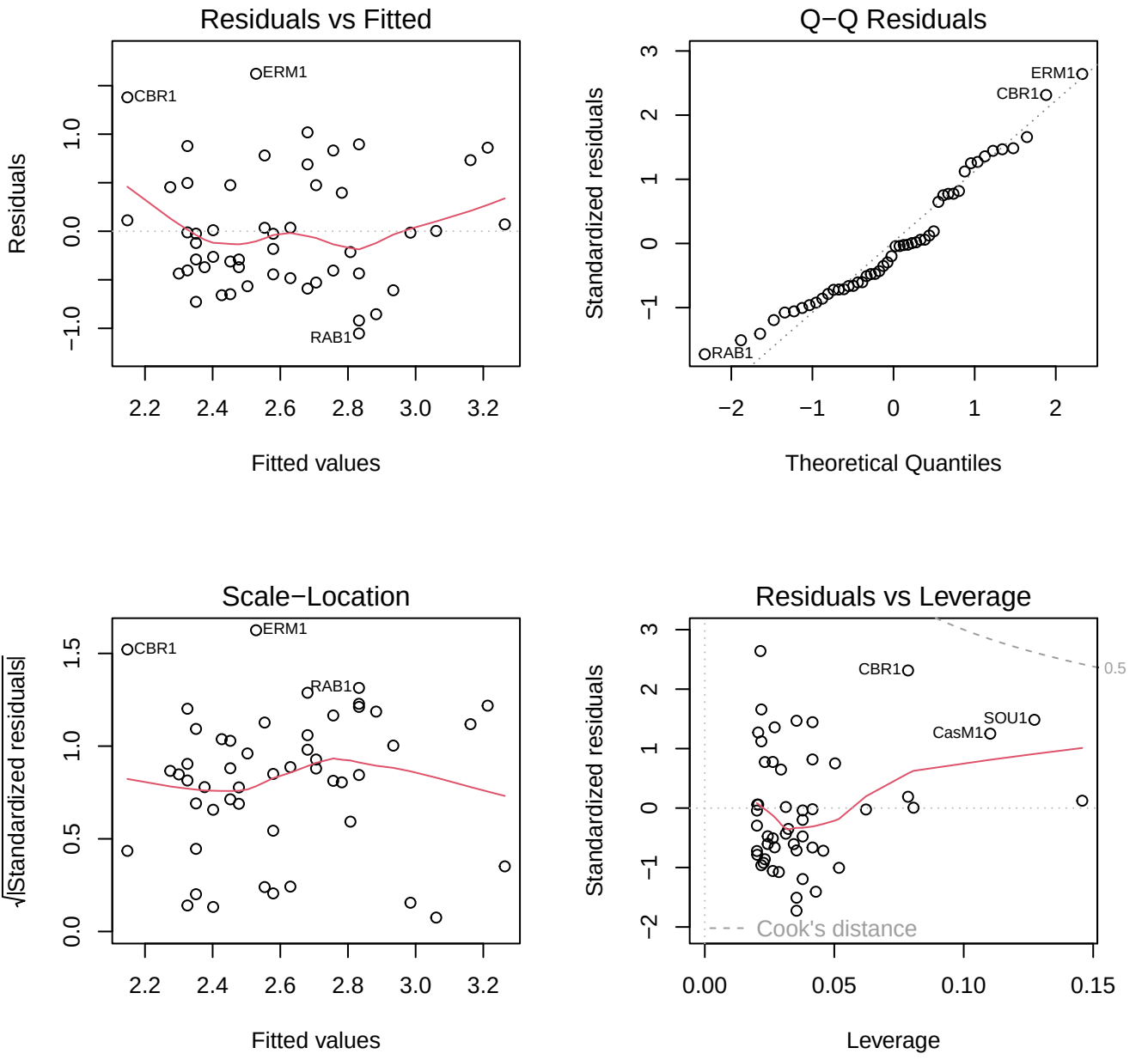

$R^2 = 0.03582741$
p−value: = 0.188
Bacteria_family_reads
PC1
20
30
40
50
60
−4
−2
0
2
4

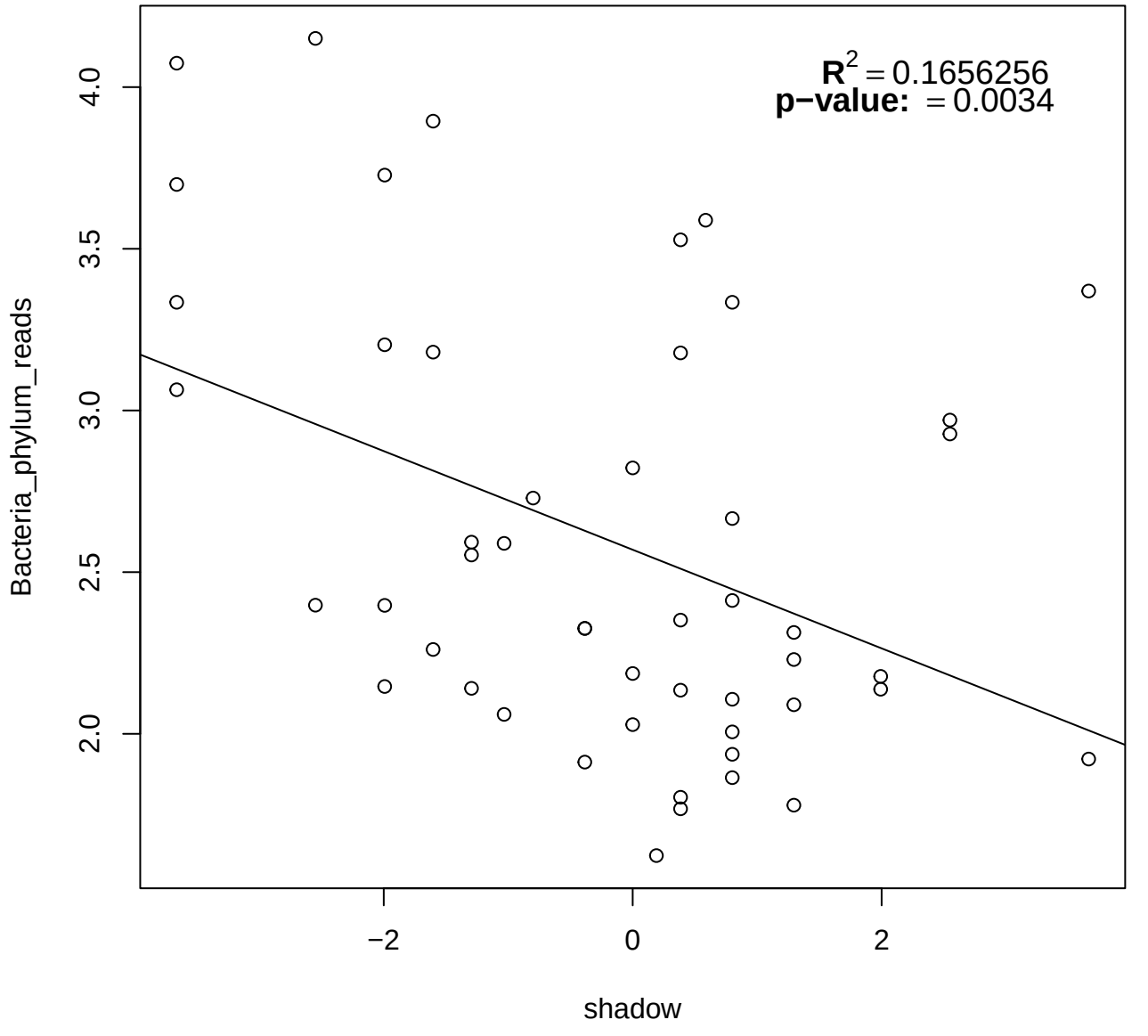

Residuals vs Fitted
Residuals
Fitted values
ERM1
VEZ3
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
VEZ3
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
VEZ3
AGR1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
SEL1
NES1
Cook's distance

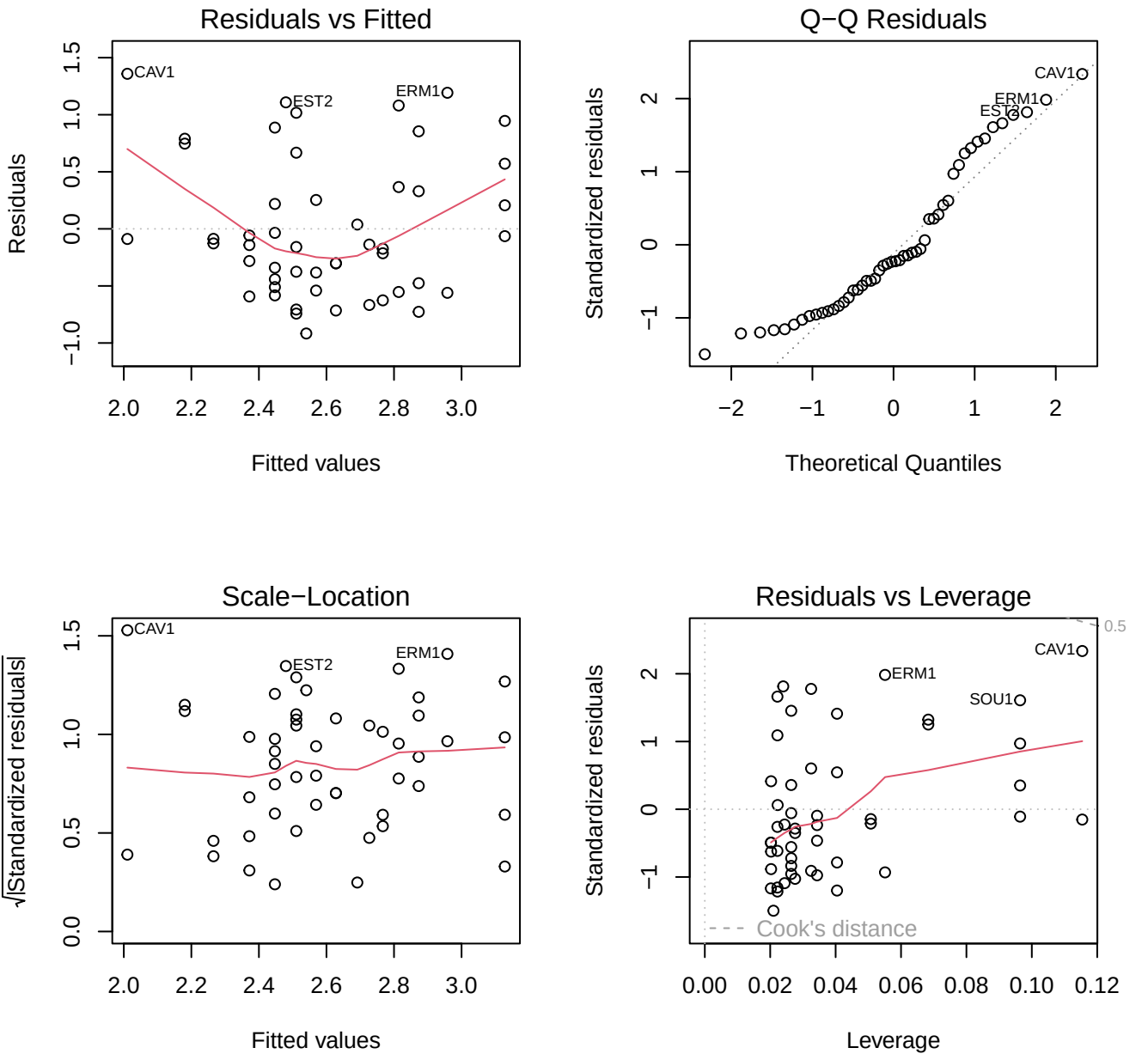

$R^2 = 0.1547378$
p−value: = 0.0047
Bacteria_phylum_reads
2.0
2.5
3.0
3.5
4.0
0
20
40
60
80
qbr

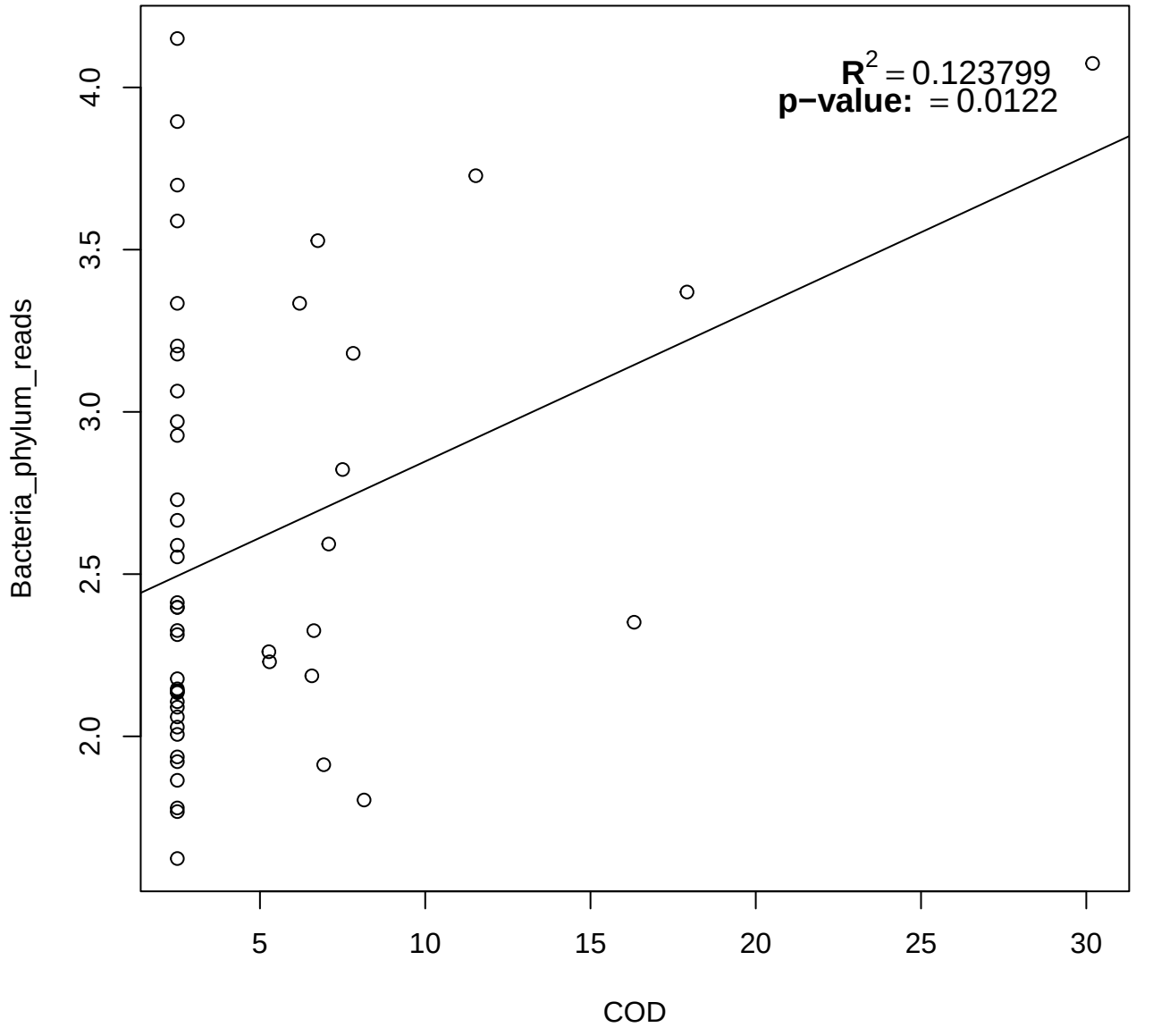

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
CBR1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
HOM1
CBR1
0.5
Cook's distance

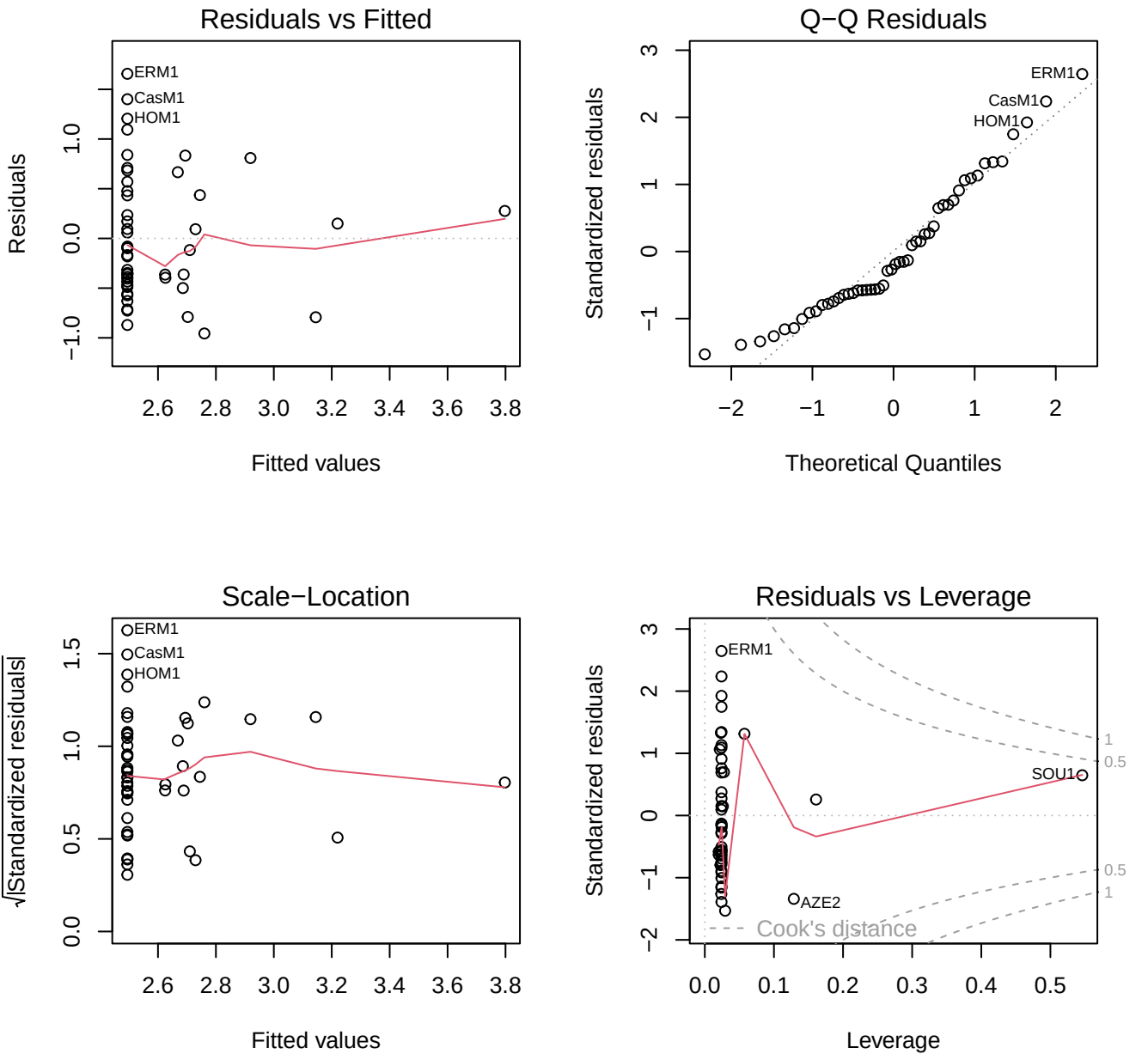

$R^2 = 0.1589203$
p−value: = 0.0041
Bacteria_phylum_reads
ihf
2.0
2.5
3.0
3.5
4.0
30
40
50
60
70

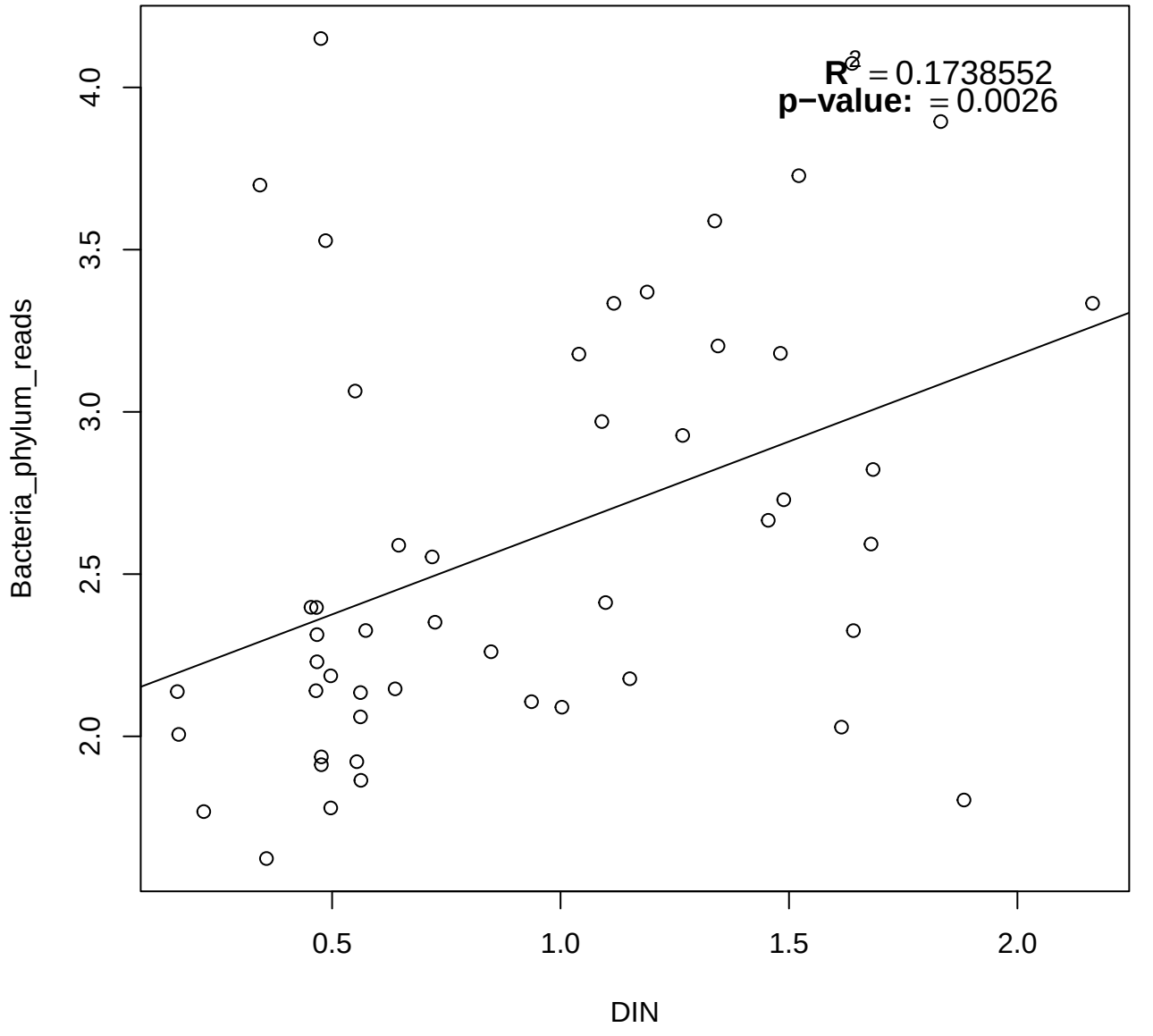

Residuals vs Fitted
Residuals
Fitted values
CBR1
ERM1
RAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
CBR1
RAB1
Scale−Location
√|Standardized residuals|
Fitted values
CBR1
ERM1
RAB1
Residuals vs Leverage
Standardized residuals
Leverage
CBR1
SOU1
CasM1
0.5
Cook's distance

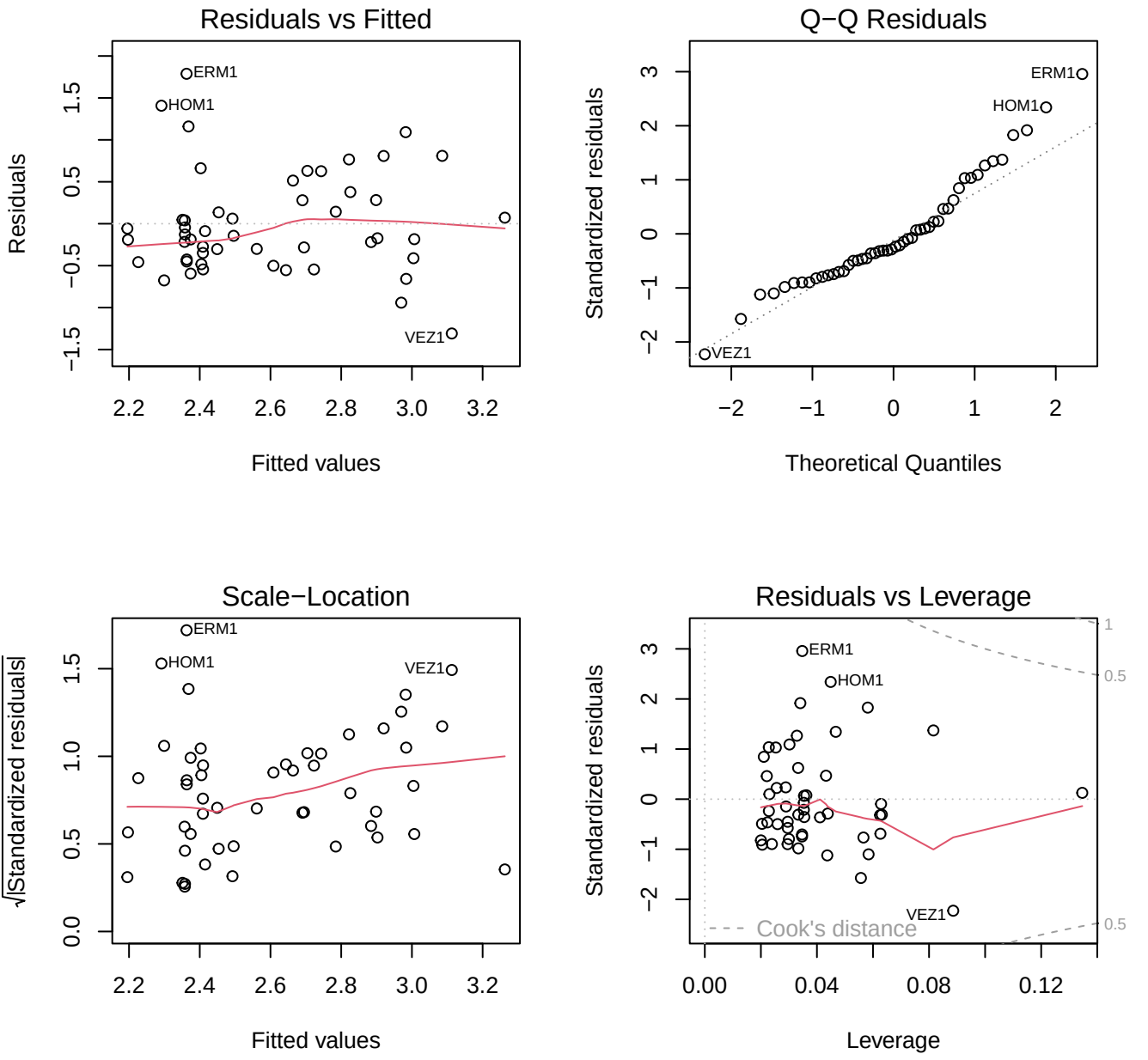

$R^2 = 0.1656256$
p−value: = 0.0034
Bacteria_phylum_reads
4.0
3.5
3.0
2.5
2.0
−2
0
2
shadow

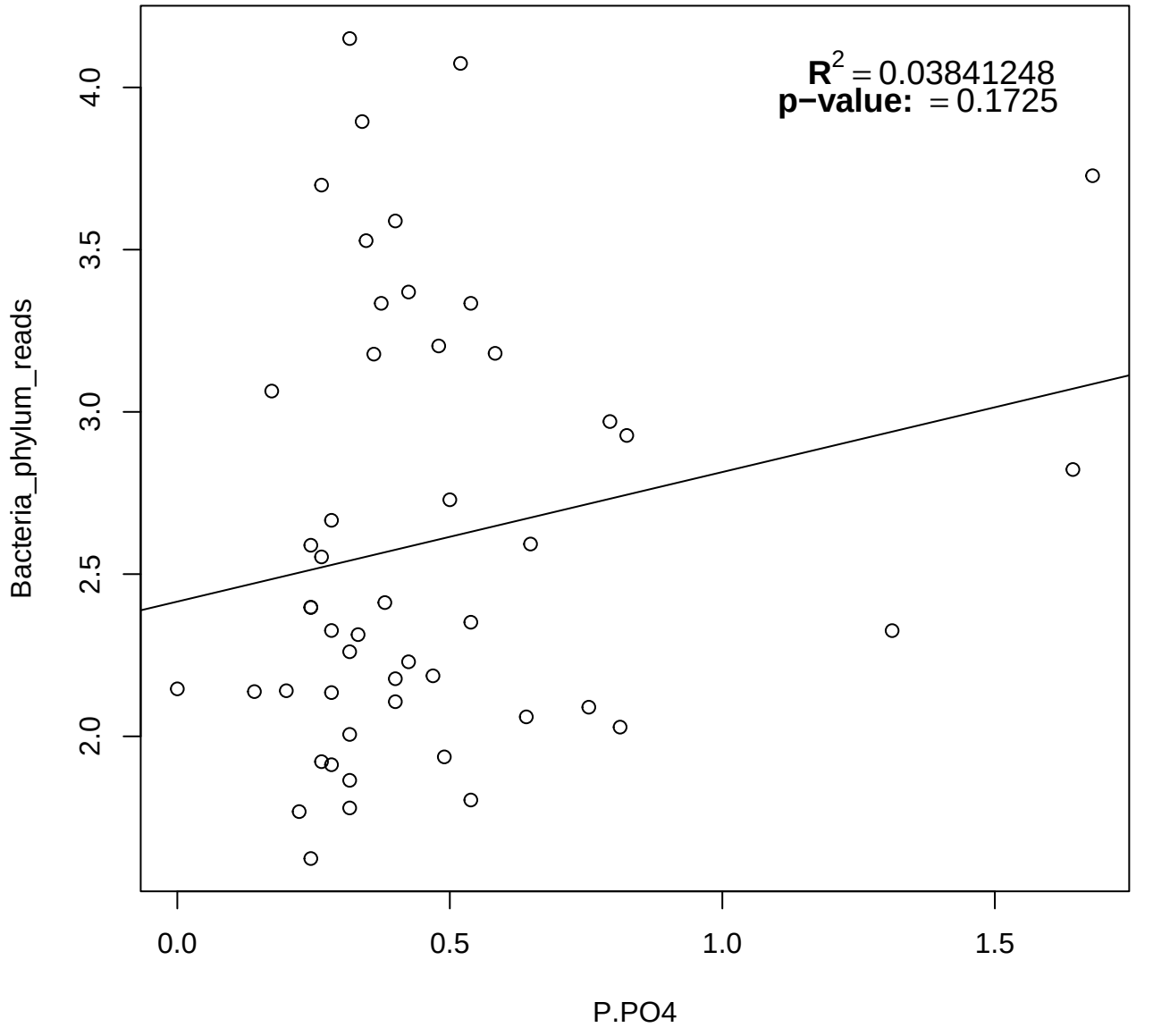

Residuals vs Fitted
Residuals
Fitted values
CAV1
EST2
ERM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
CAV1
ERM1
EST2
Scale−Location
√|Standardized residuals|
Fitted values
CAV1
EST2
ERM1
Residuals vs Leverage
Standardized residuals
Leverage
CAV1
ERM1
SOU1
Cook's distance

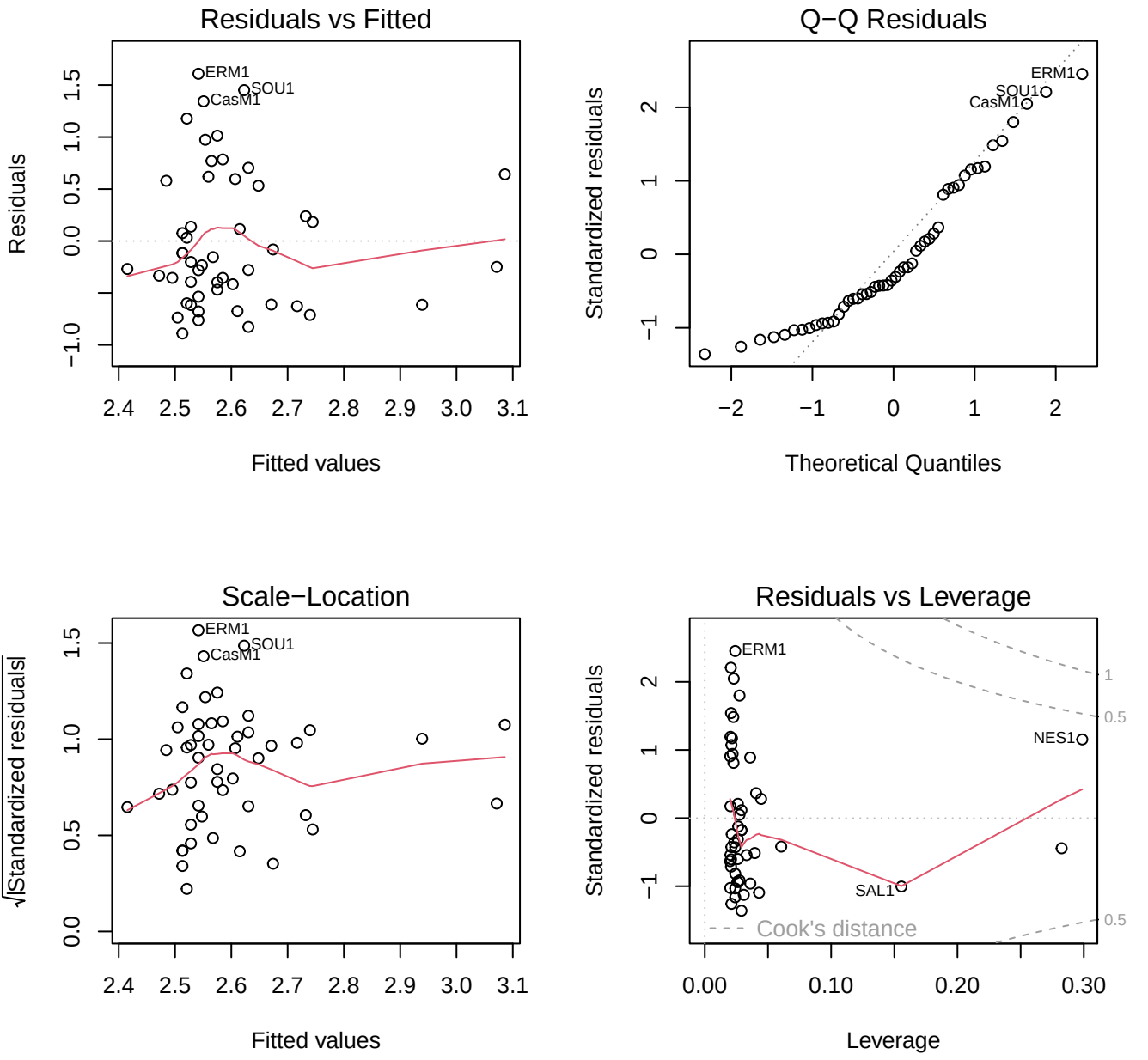

$R^2 = 0.123799$
p−value: = 0.0122
Bacteria_phylum_reads
2.0
2.5
3.0
3.5
4.0
5
10
15
20
25
30
COD

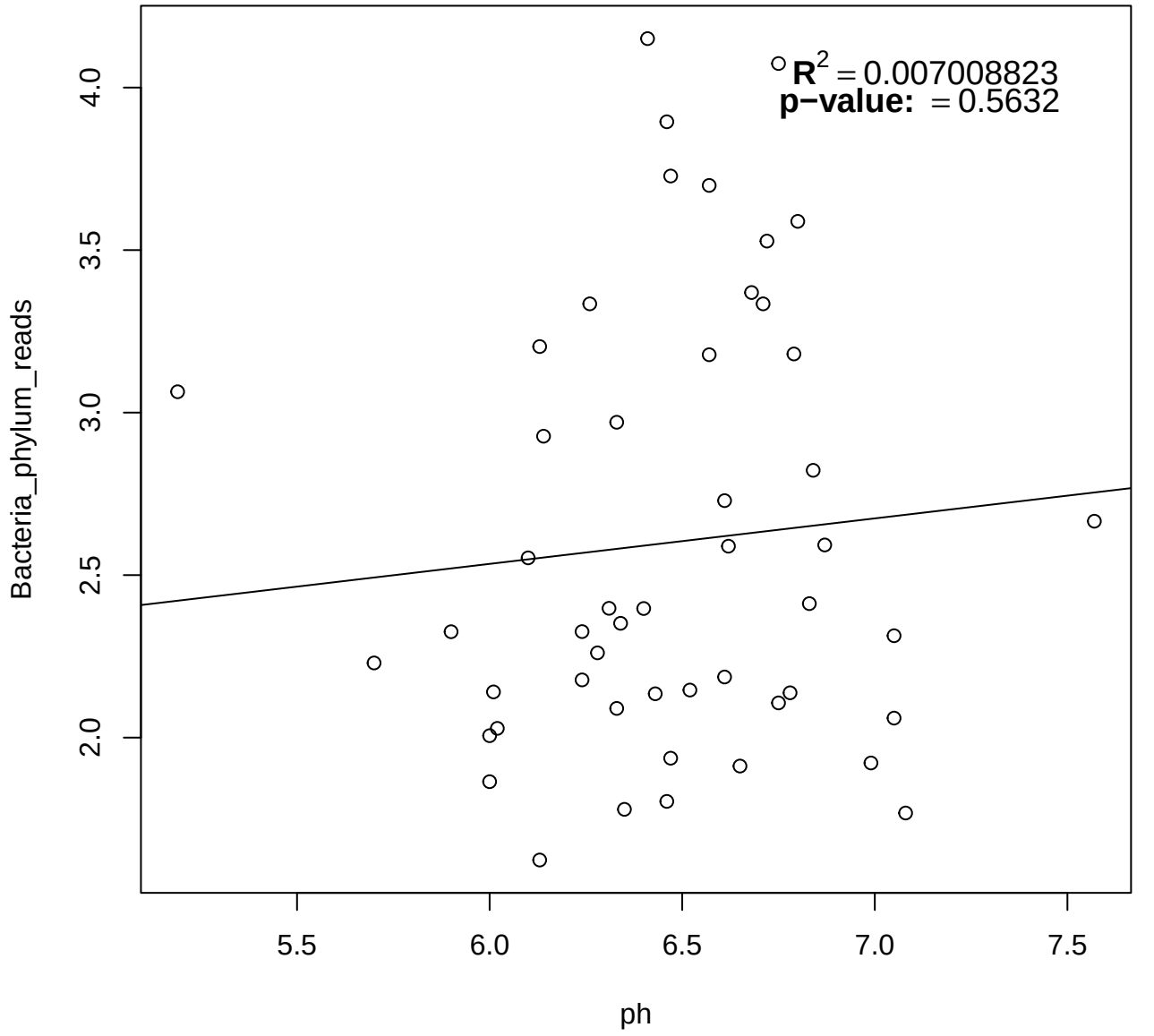

Residuals vs Fitted
Residuals
Fitted values
ERM1
CasM1
HOM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
CasM1
HOM1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
CasM1
HOM1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
SOU1
AZE2
Cook's distance

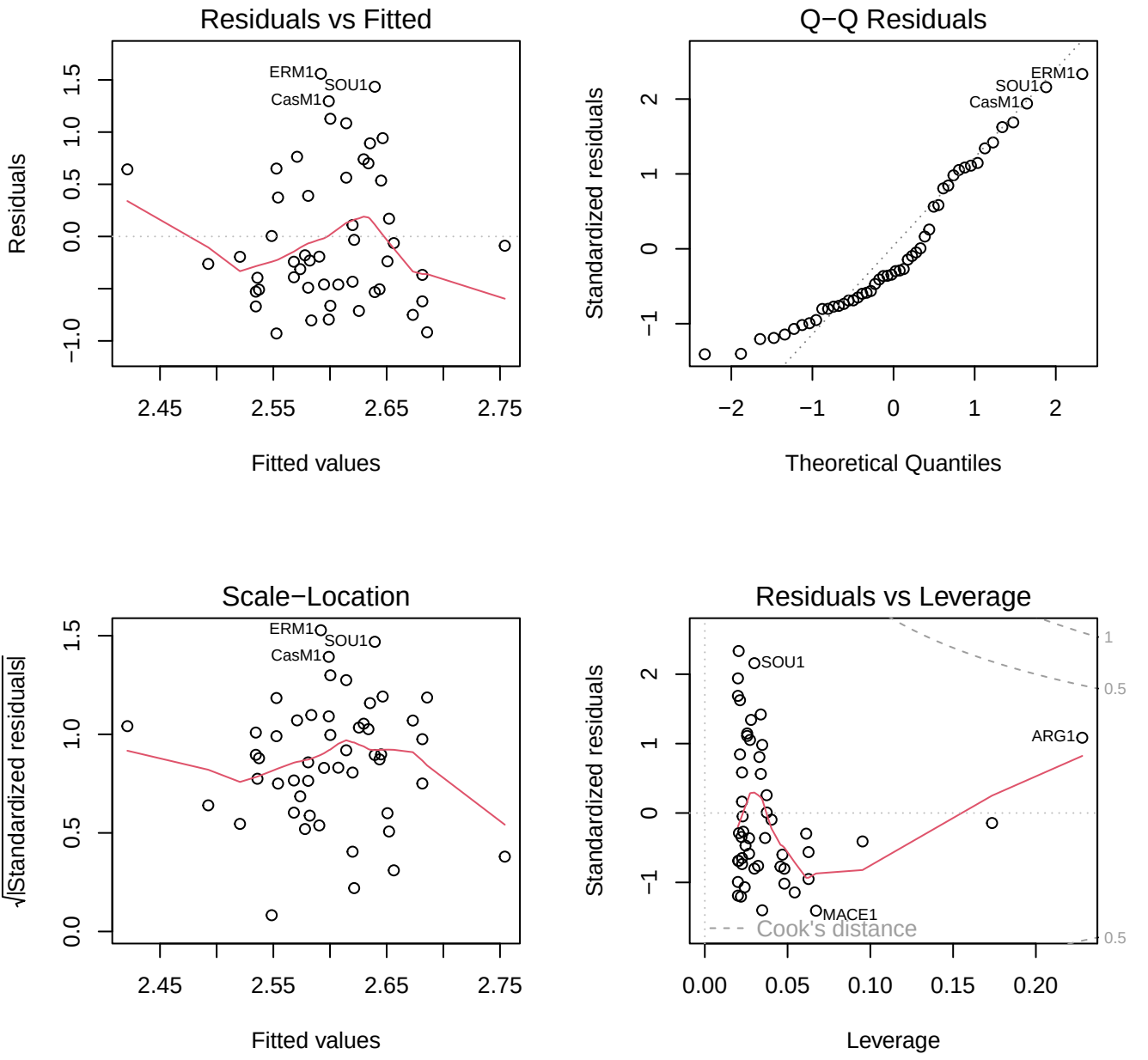

$R^2 = 0.1738552$
p−value: = 0.0026
Bacteria_phylum_reads
DIN
2.0
2.5
3.0
3.5
4.0
0.5
1.0
1.5
2.0

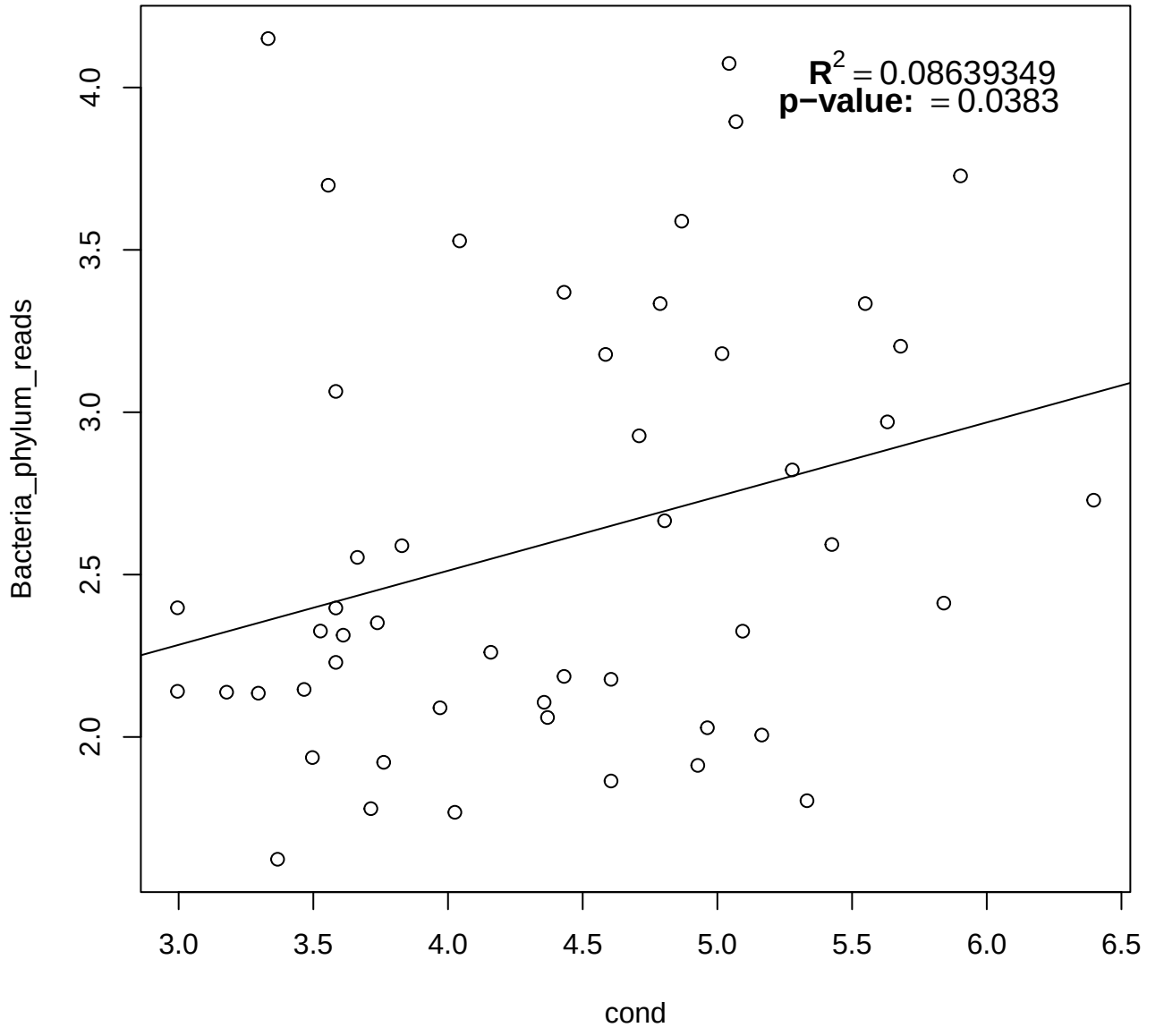

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
HOM1
VEZ1
Cook's distance

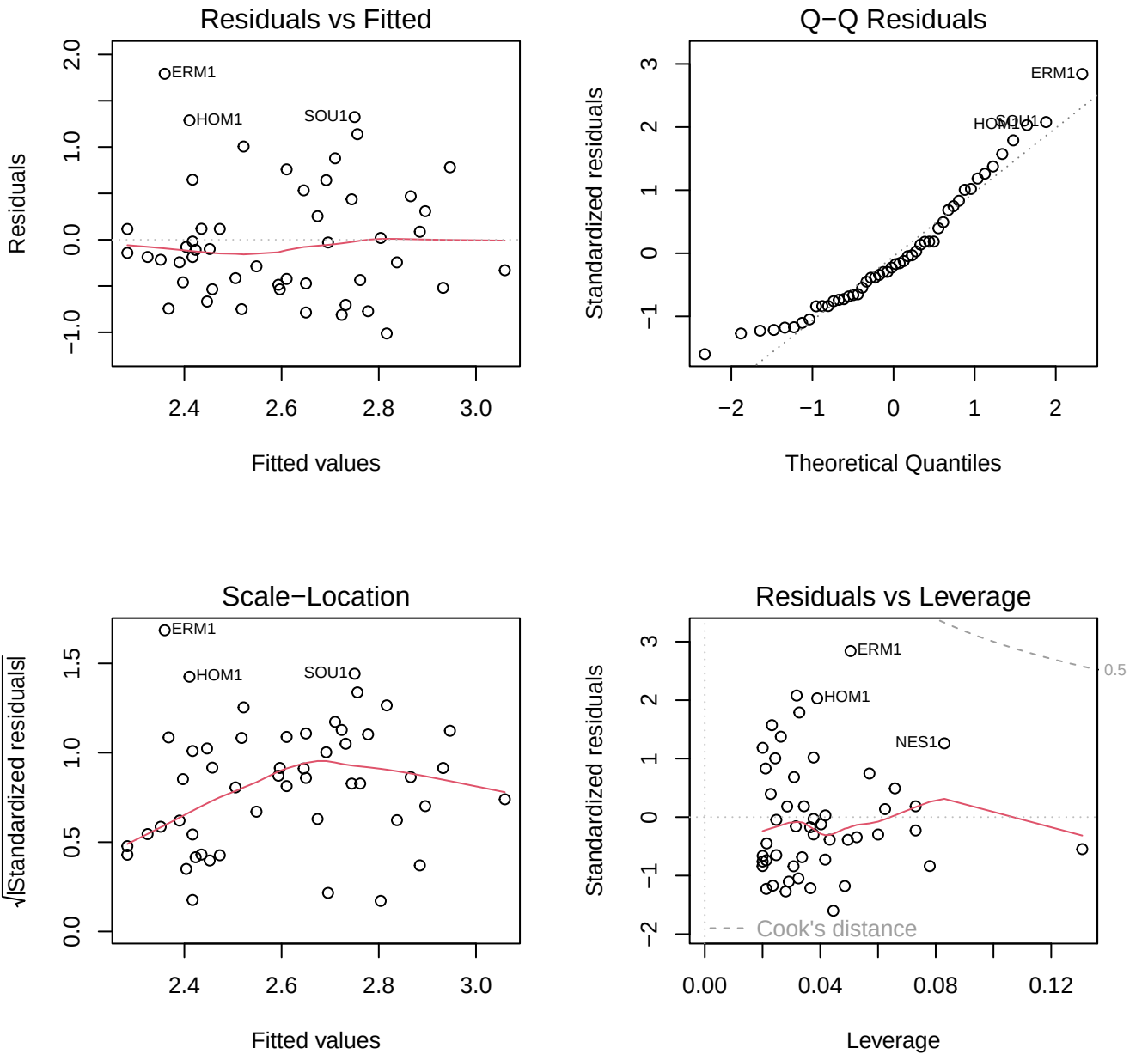

$R^2 = 0.03841248$
p−value: = 0.1725
Bacteria_phylum_reads
2.0
2.5
3.0
3.5
4.0
0.0
0.5
1.0
1.5
P.PO4

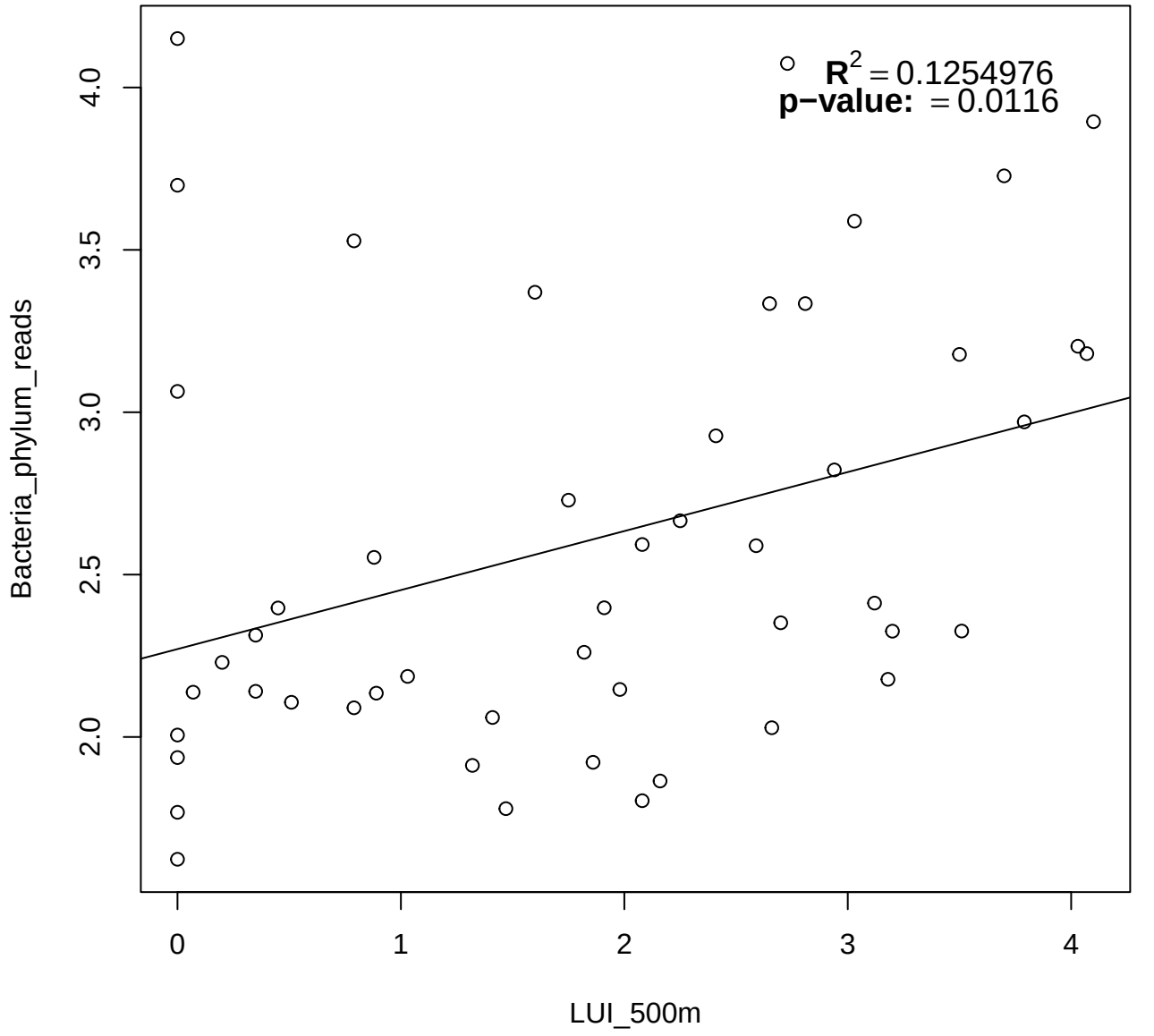

Residuals vs Fitted
Residuals
Fitted values
ERM1
SOU1
CasM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
SOU1
CasM1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
SOU1
CasM1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
NES1
SAL1
Cook's distance
1
0.5
0.5

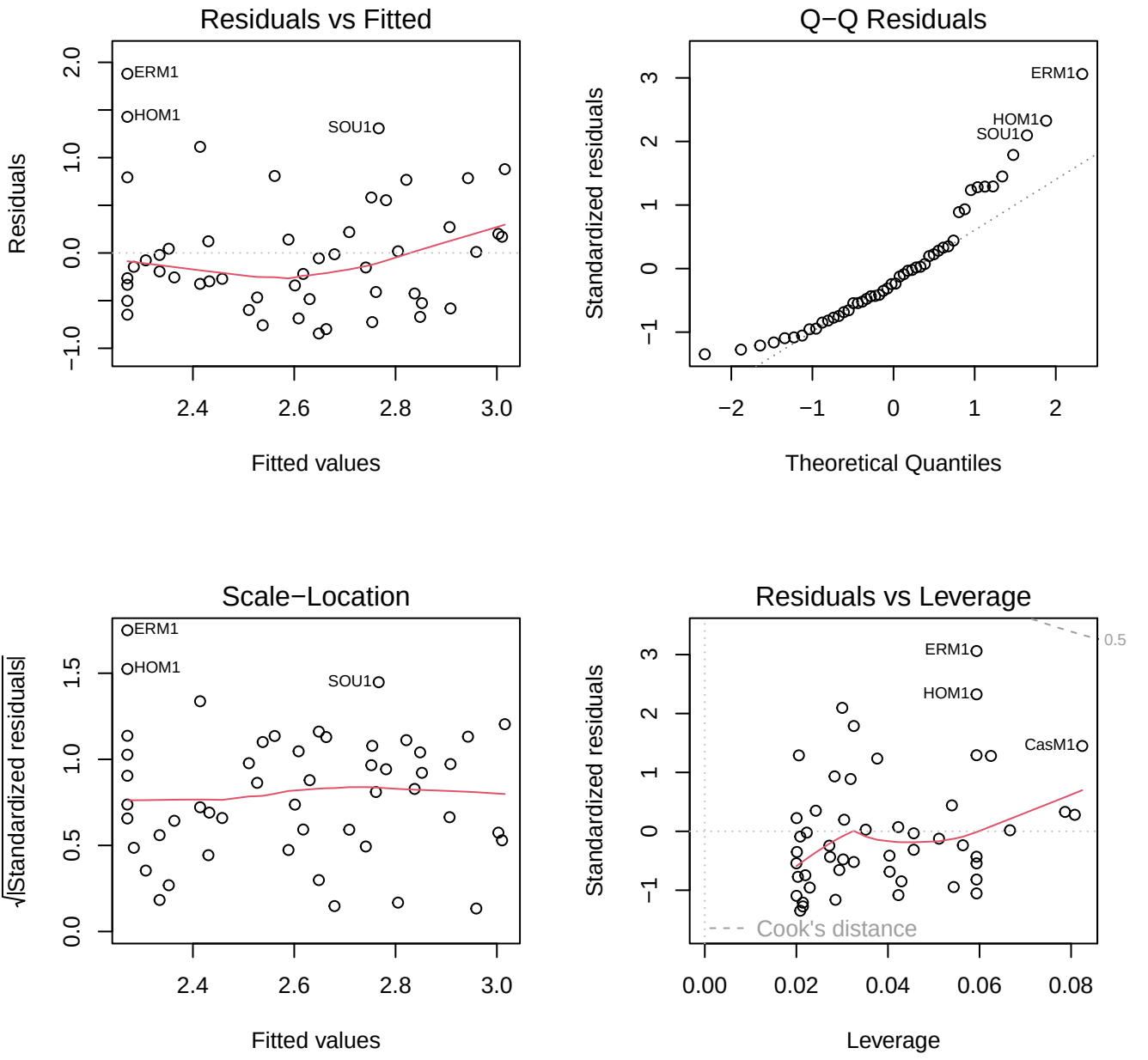

$R^2 = 0.007008823$
p−value: = 0.5632
Bacteria_phylum_reads
ph
2.0
2.5
3.0
3.5
4.0
5.5
6.0
6.5
7.0
7.5

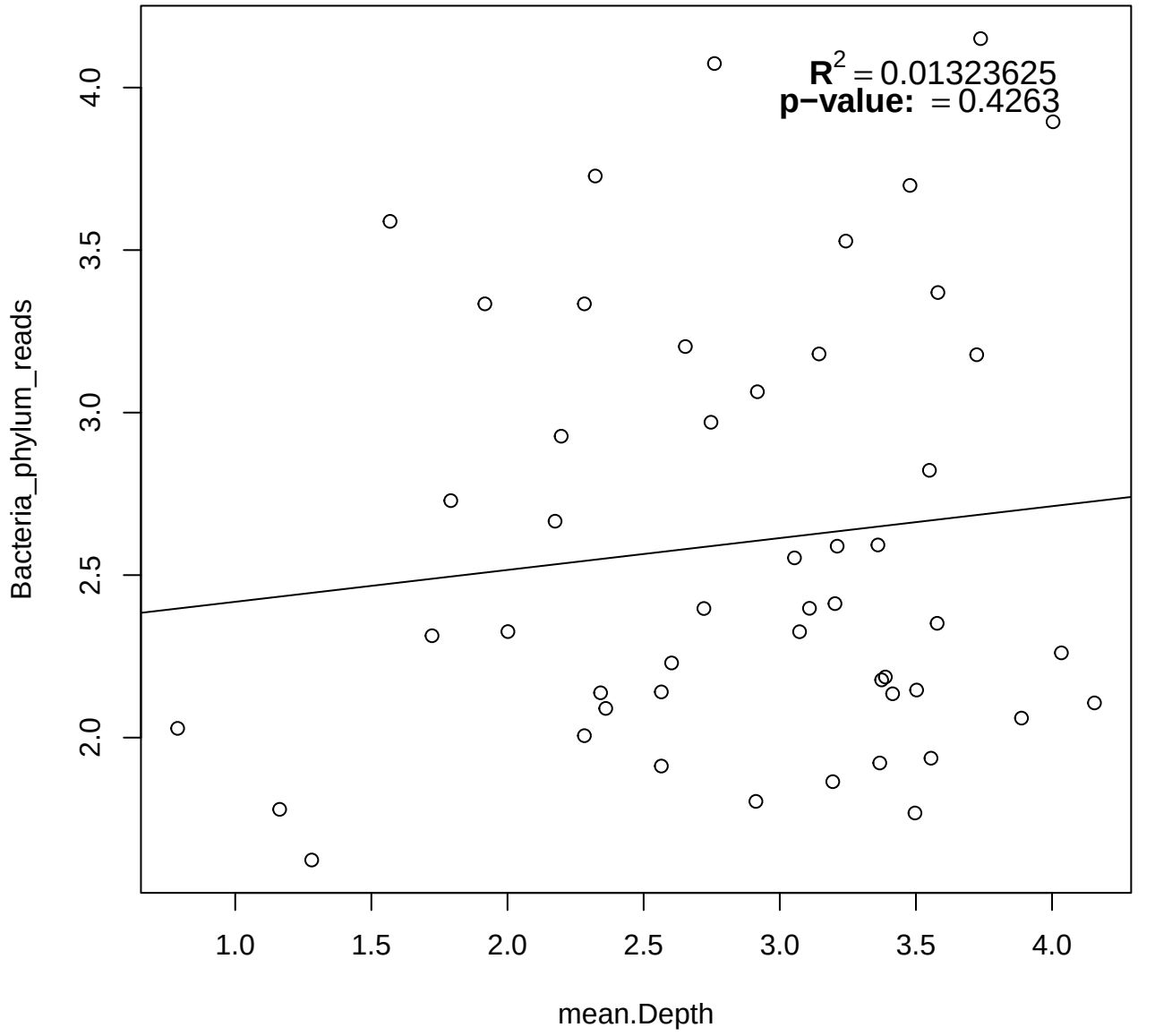

Residuals vs Fitted
Residuals
Fitted values
ERM1
SOU1
CasM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
SOU1
CasM1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
SOU1
CasM1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
ARG1
MACE1
Cook's distance

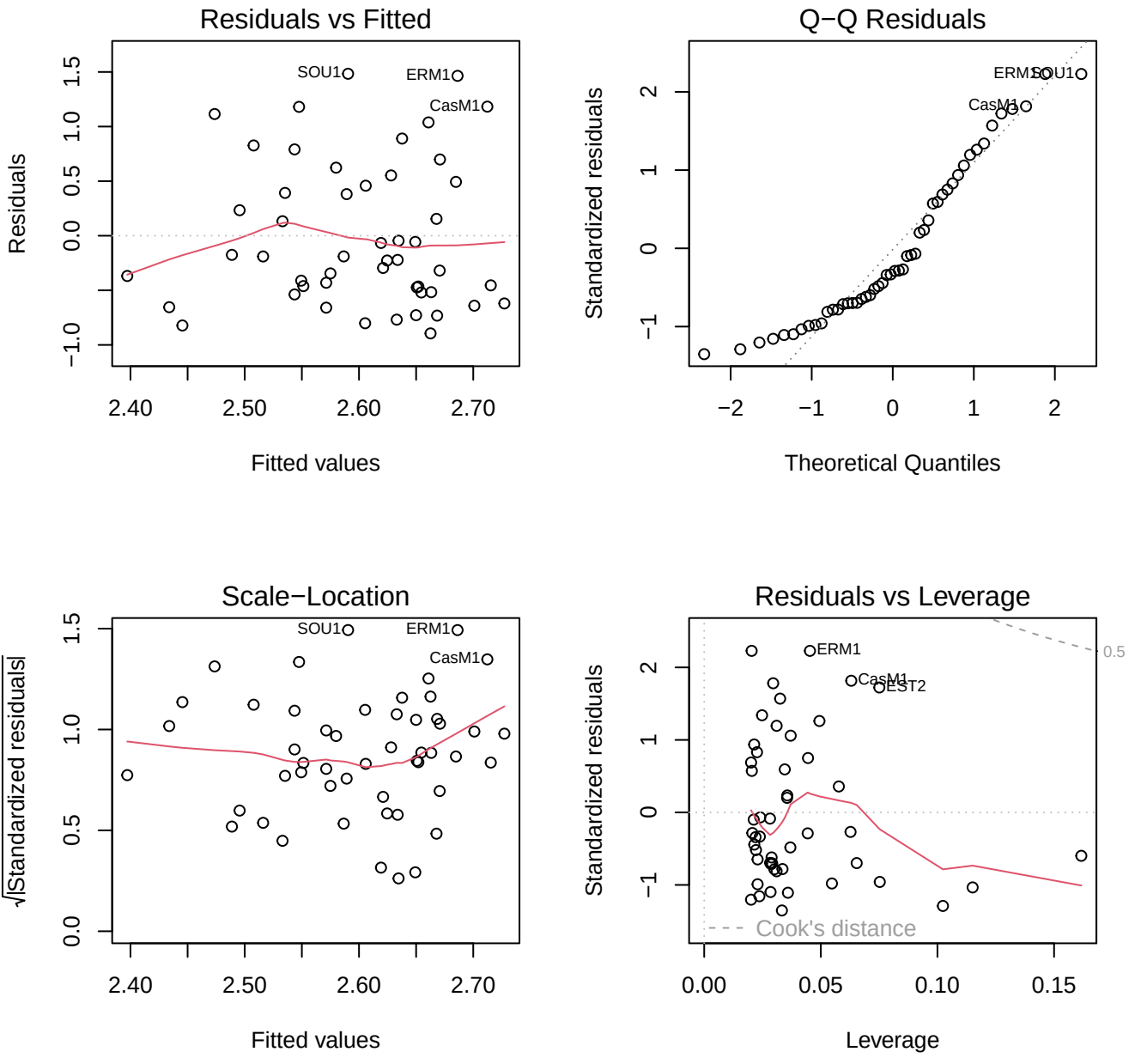

$R^2 = 0.08639349$
p−value: = 0.0383
Bacteria_phylum_reads
cond
2.0
2.5
3.0
3.5
4.0
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5

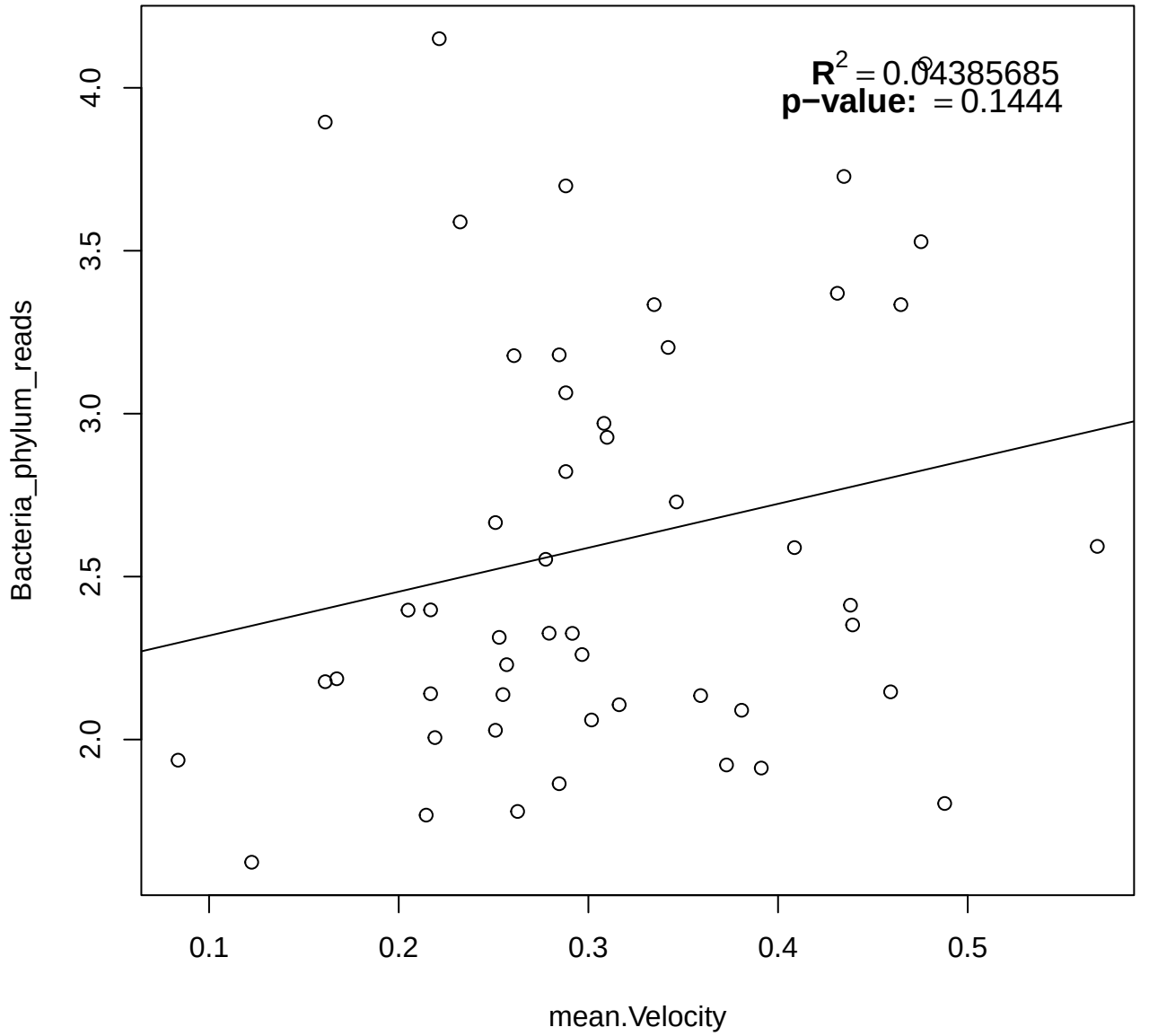

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
SOU1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
SOU1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
SOU1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
HOM1
NES1
0.5
Cook's distance

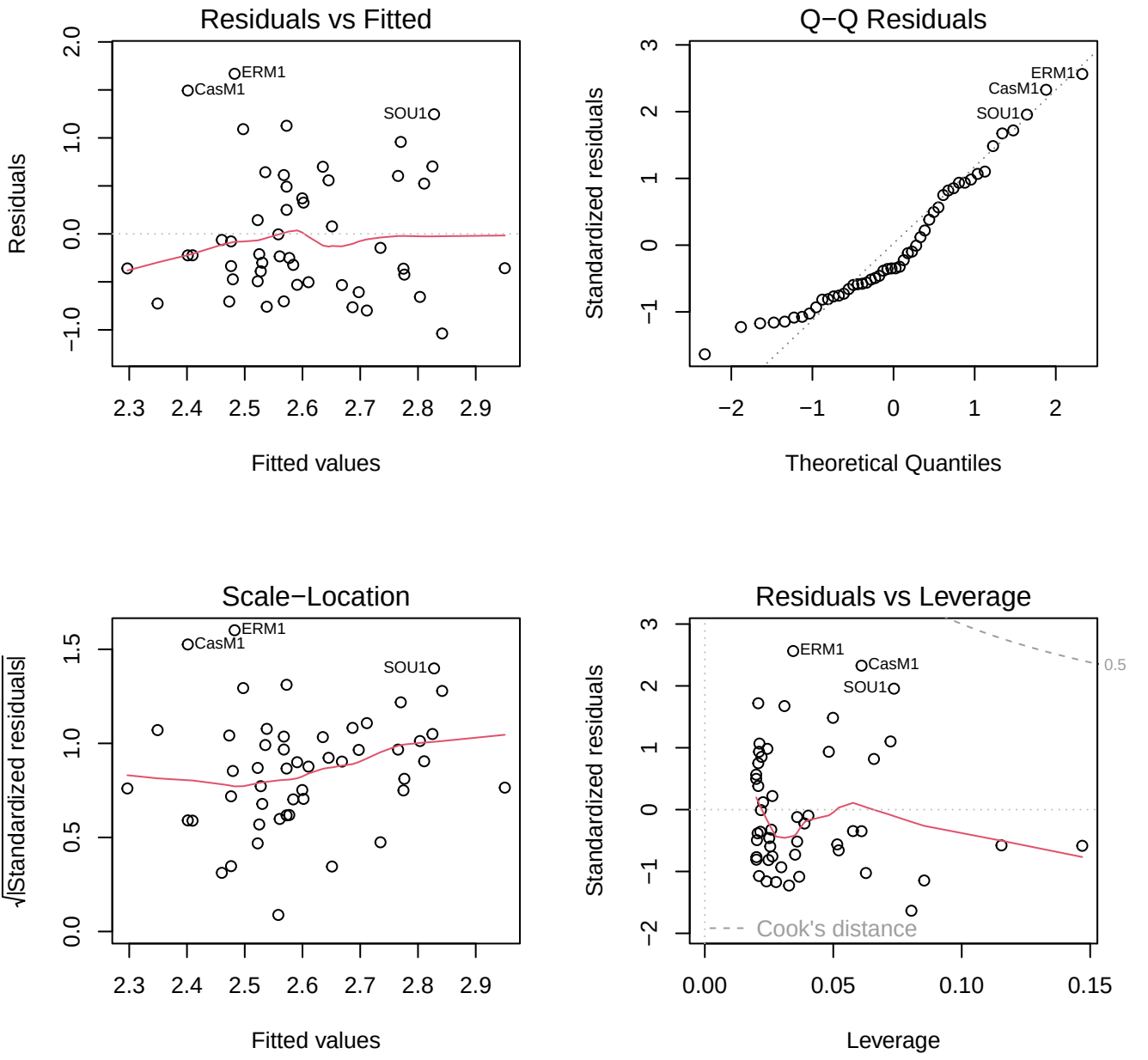

$R^2 = 0.1254976$
p−value: $= 0.0116$
Bacteria_phylum_reads
LUI_500m
2.0
2.5
3.0
3.5
4.0
0
1
2
3
4

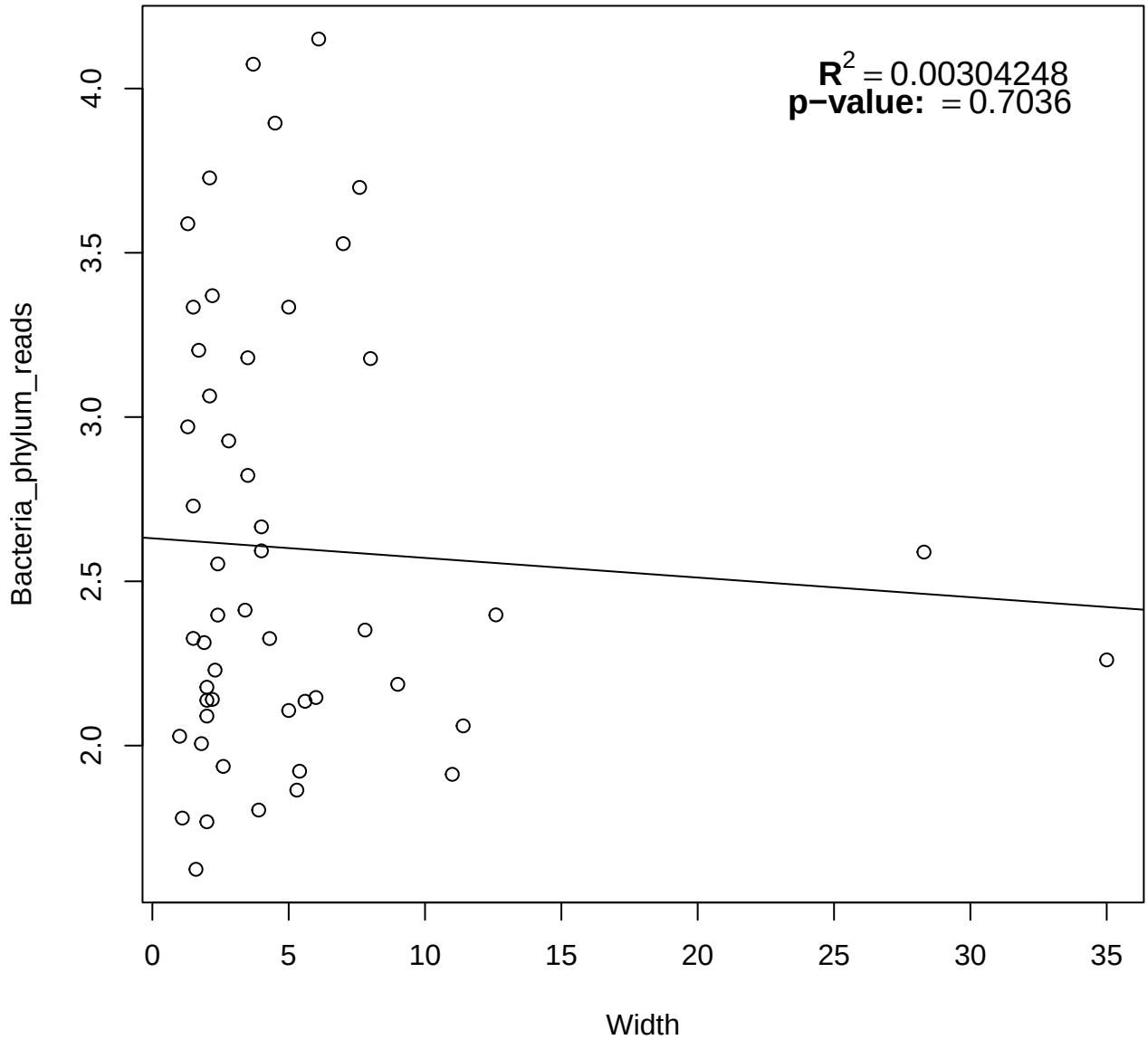

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
SOU1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
SOU1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
SOU1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
HOM1
CasM1
0.5
Cook's distance

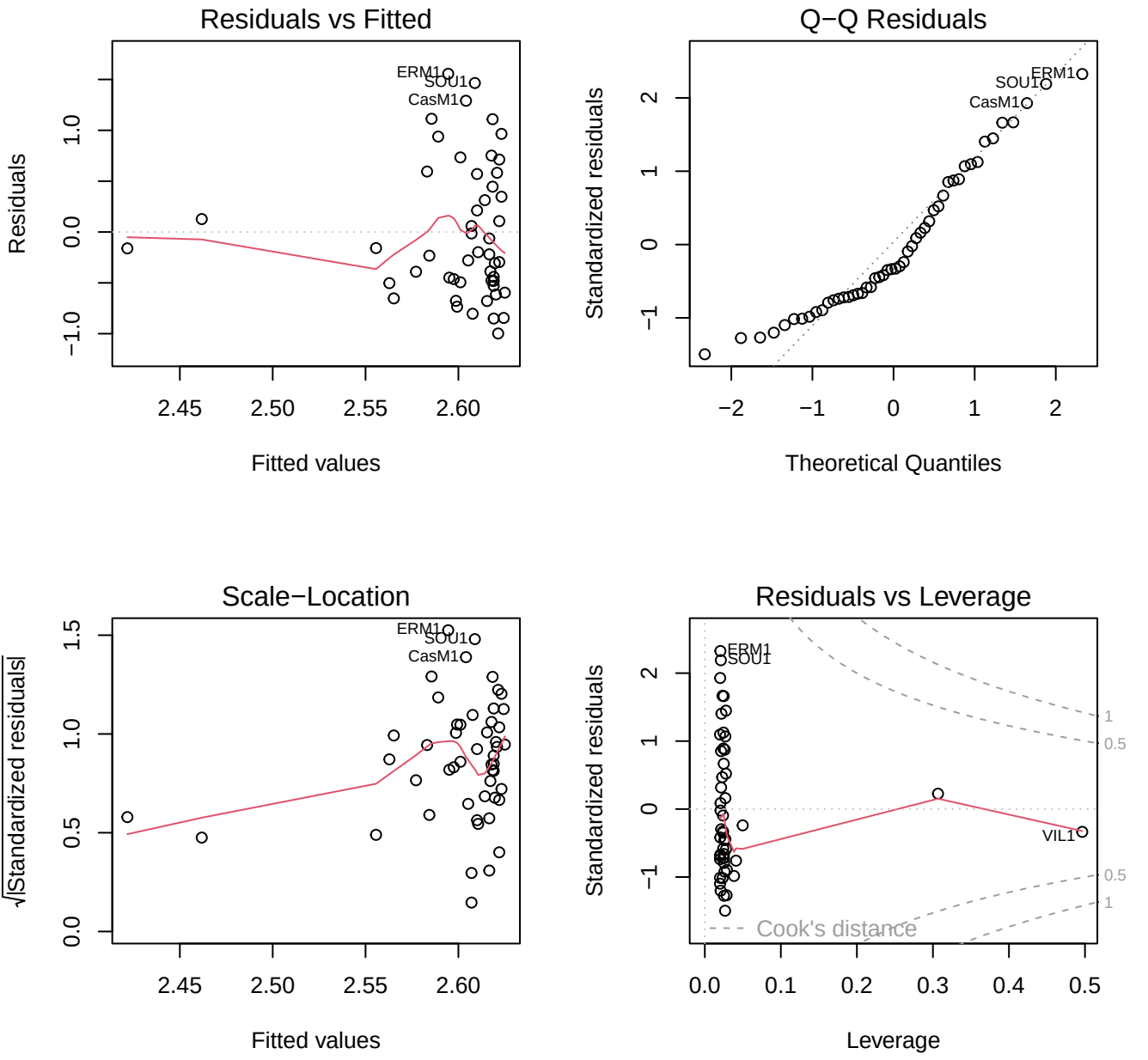

$R^2 = 0.01323625$
p−value: = 0.4263
Bacteria_phylum_reads
mean.Depth
2.0
2.5
3.0
3.5
4.0
1.0
1.5
2.0
2.5
3.0
3.5
4.0

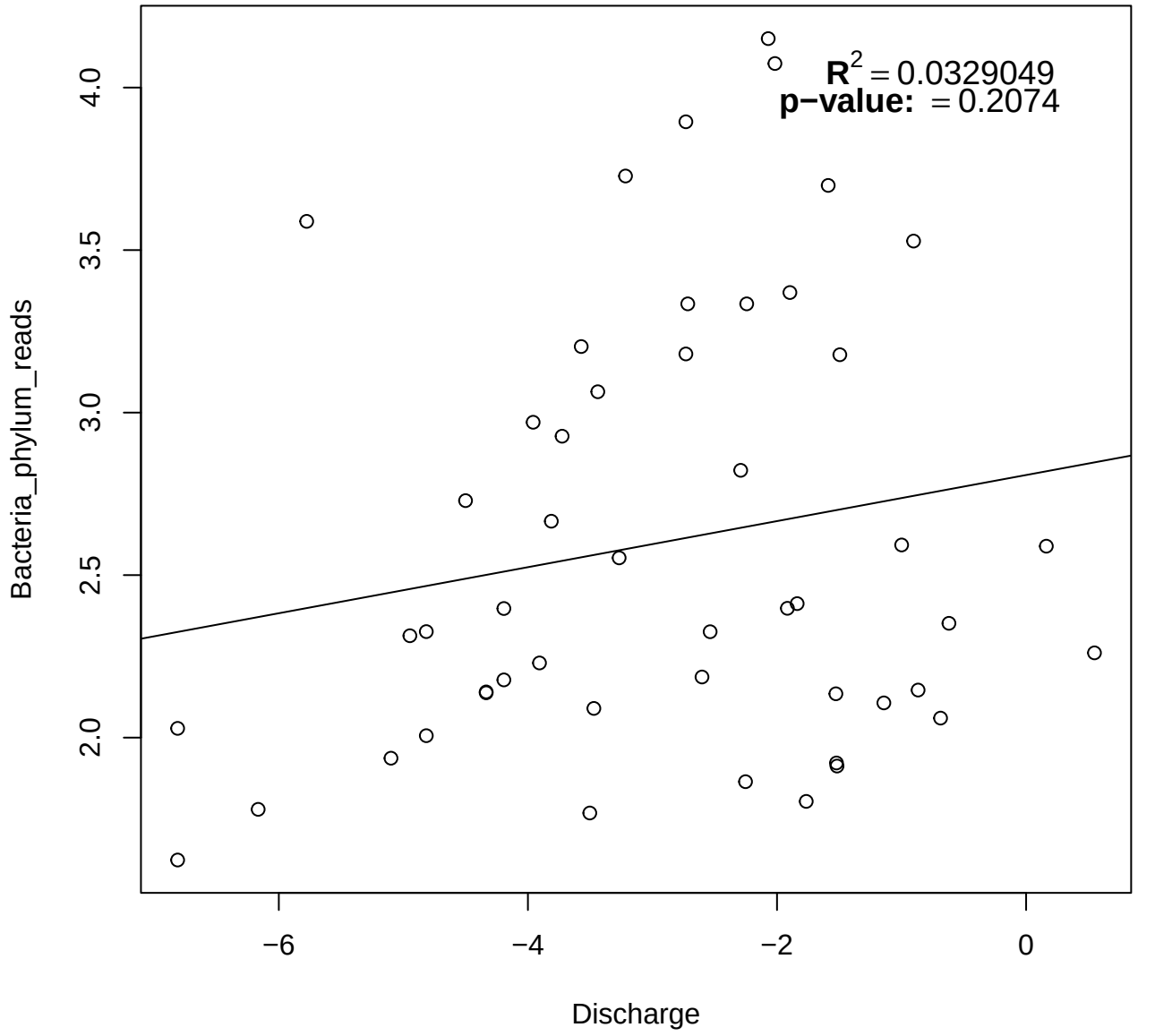

Residuals vs Fitted
Residuals
Fitted values
SOU1
ERM1
CasM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
SOU1
CasM1
Scale−Location
√|Standardized residuals|
Fitted values
SOU1
ERM1
CasM1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
CasM1
EST2
0.5
Cook's distance

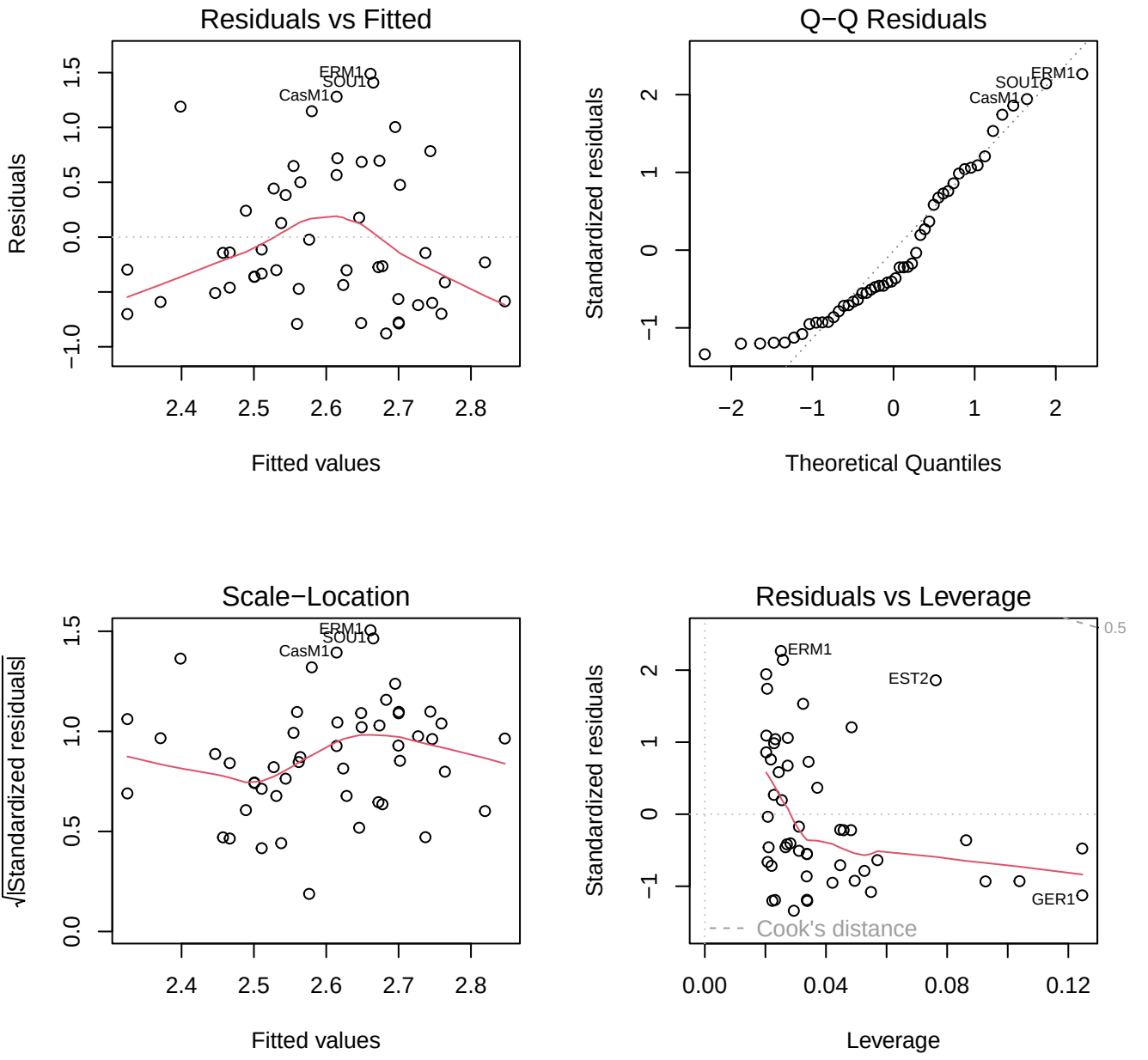

$R^2 = 0.04385685$
p−value: = 0.1444
Bacteria_phylum_reads
mean.Velocity
2.0
2.5
3.0
3.5
4.0
0.1
0.2
0.3
0.4
0.5

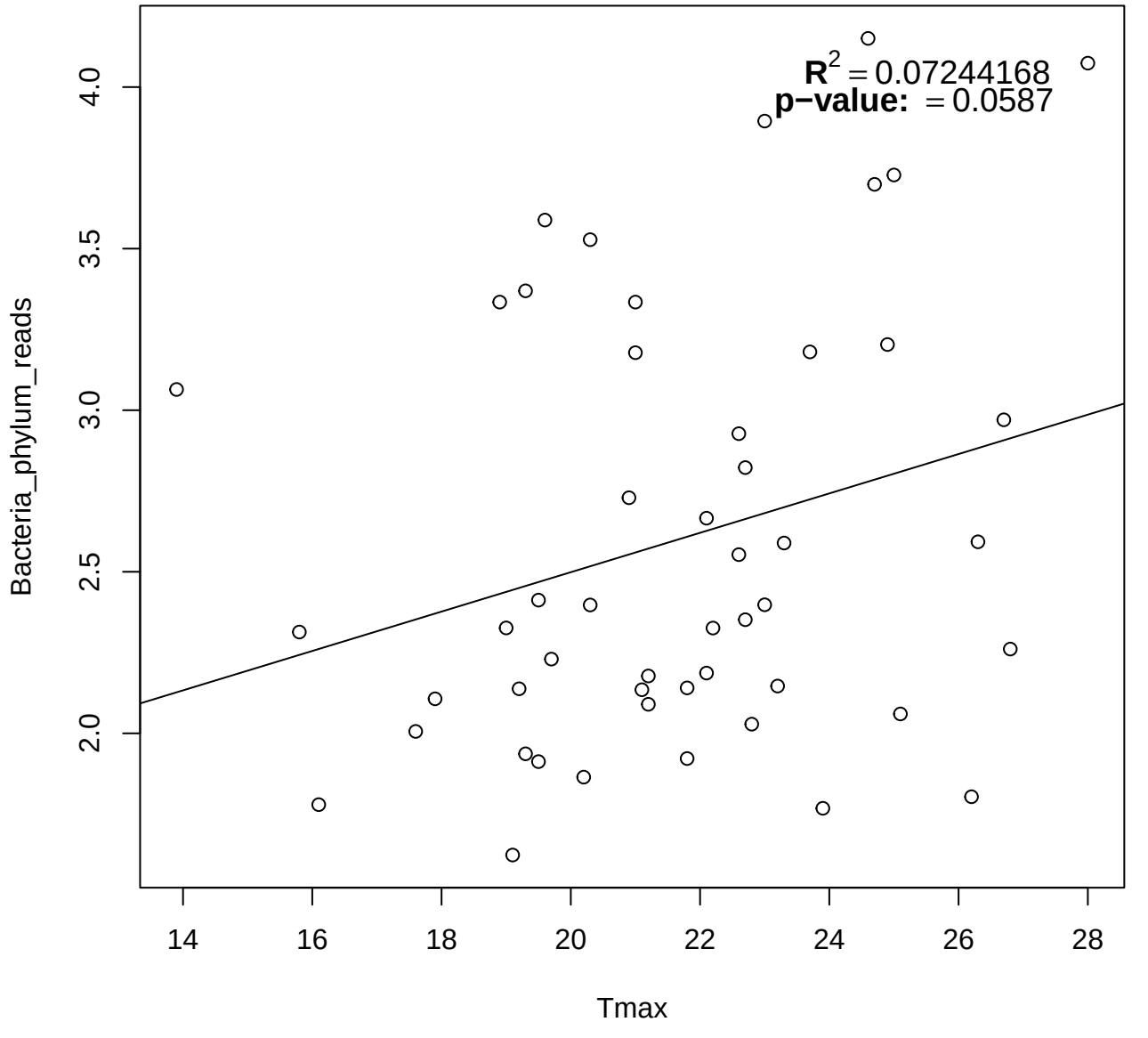

Residuals vs Fitted
Residuals
Fitted values
ERM1
CasM1
SOU1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
CasM1
SOU1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
CasM1
SOU1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
CasM1
SOU1
0.5
Cook's distance

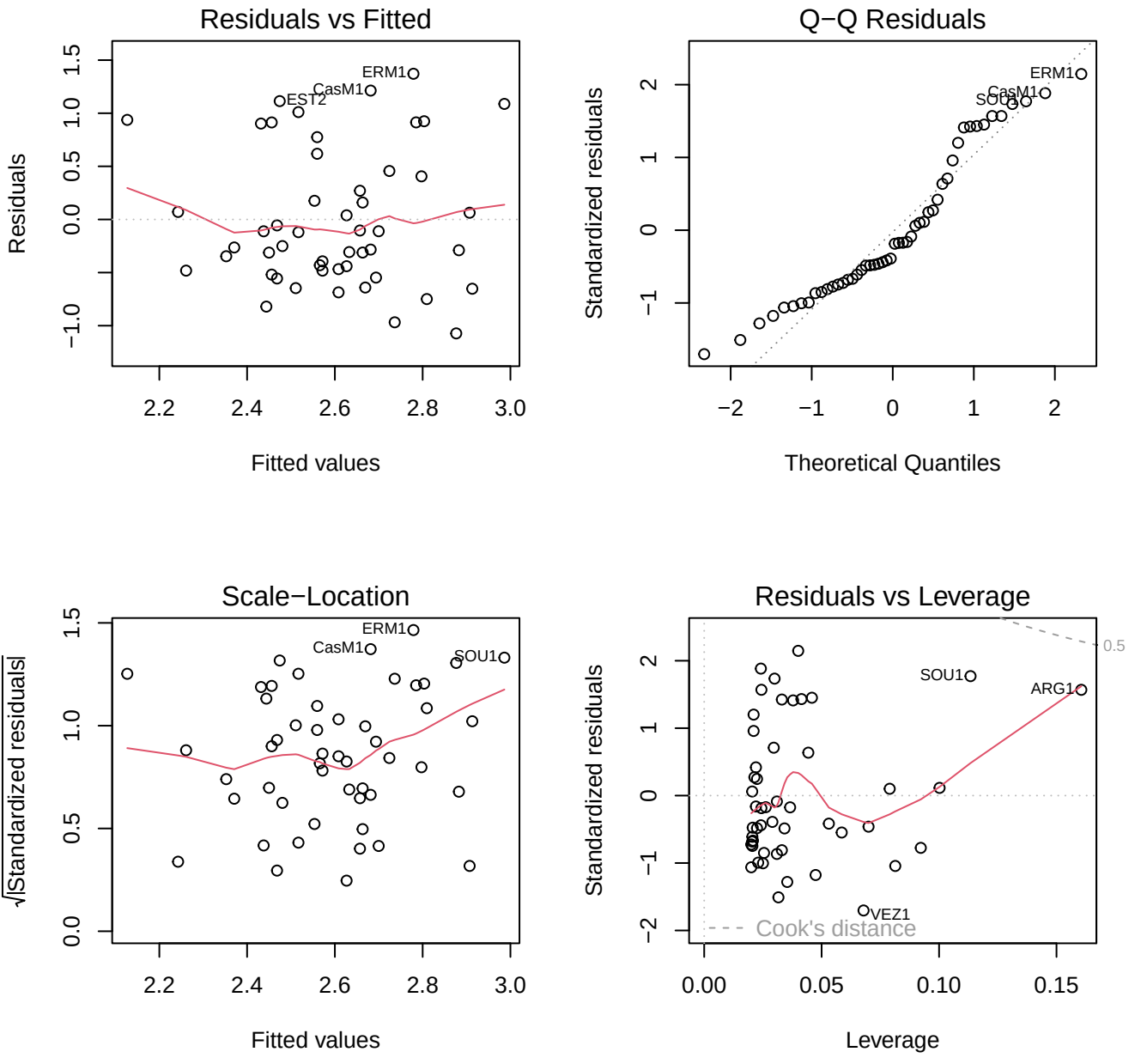

$R^2 = 0.00304248$
p−value: = 0.7036
Bacteria_phylum_reads
Width
2.0
2.5
3.0
3.5
4.0
0
5
10
15
20
25
30
35

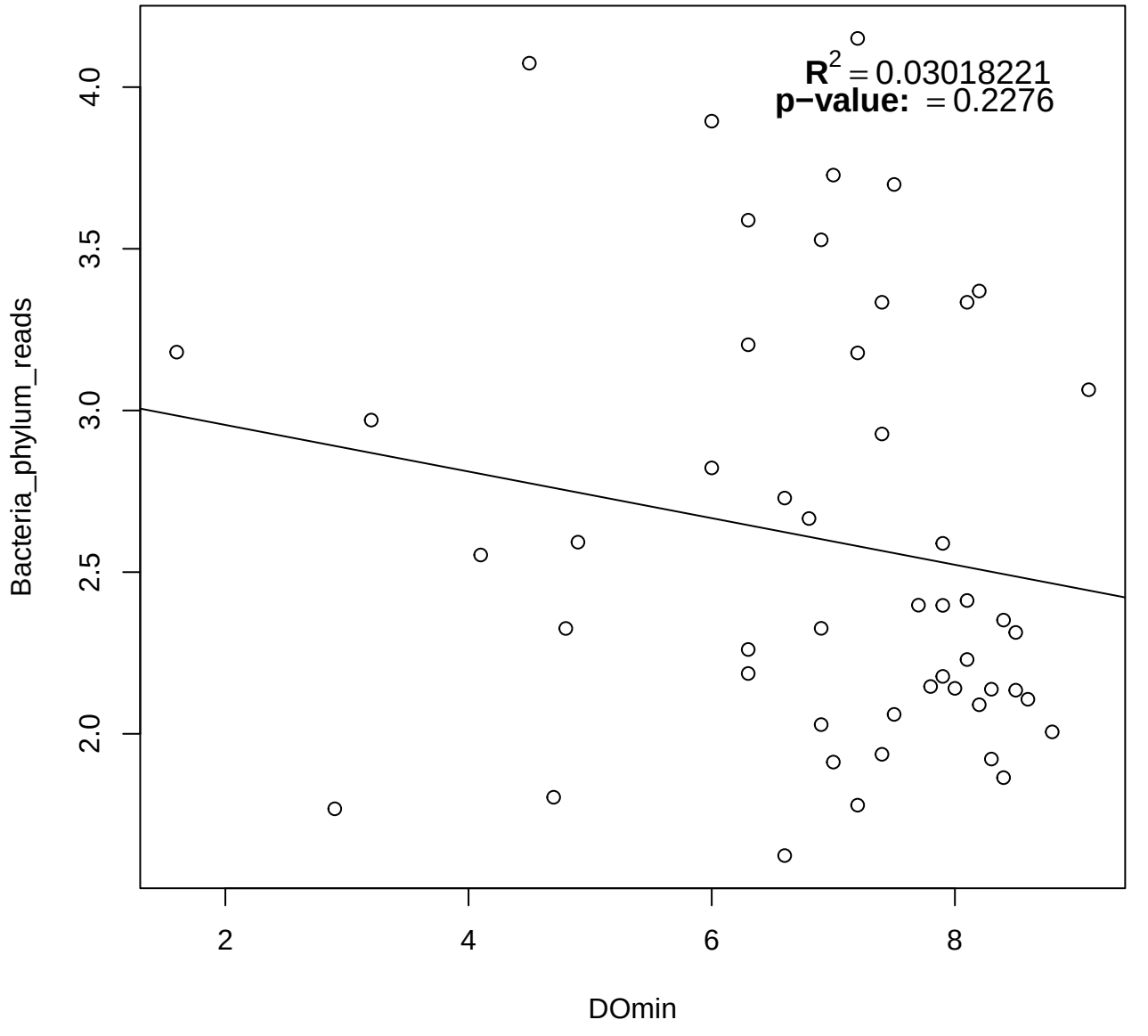

Residuals vs Fitted
Residuals
Fitted values
ERM1
SOU1
CasM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
SOU1
CasM1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
SOU1
CasM1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
SOU1
VIL1
Cook's distance

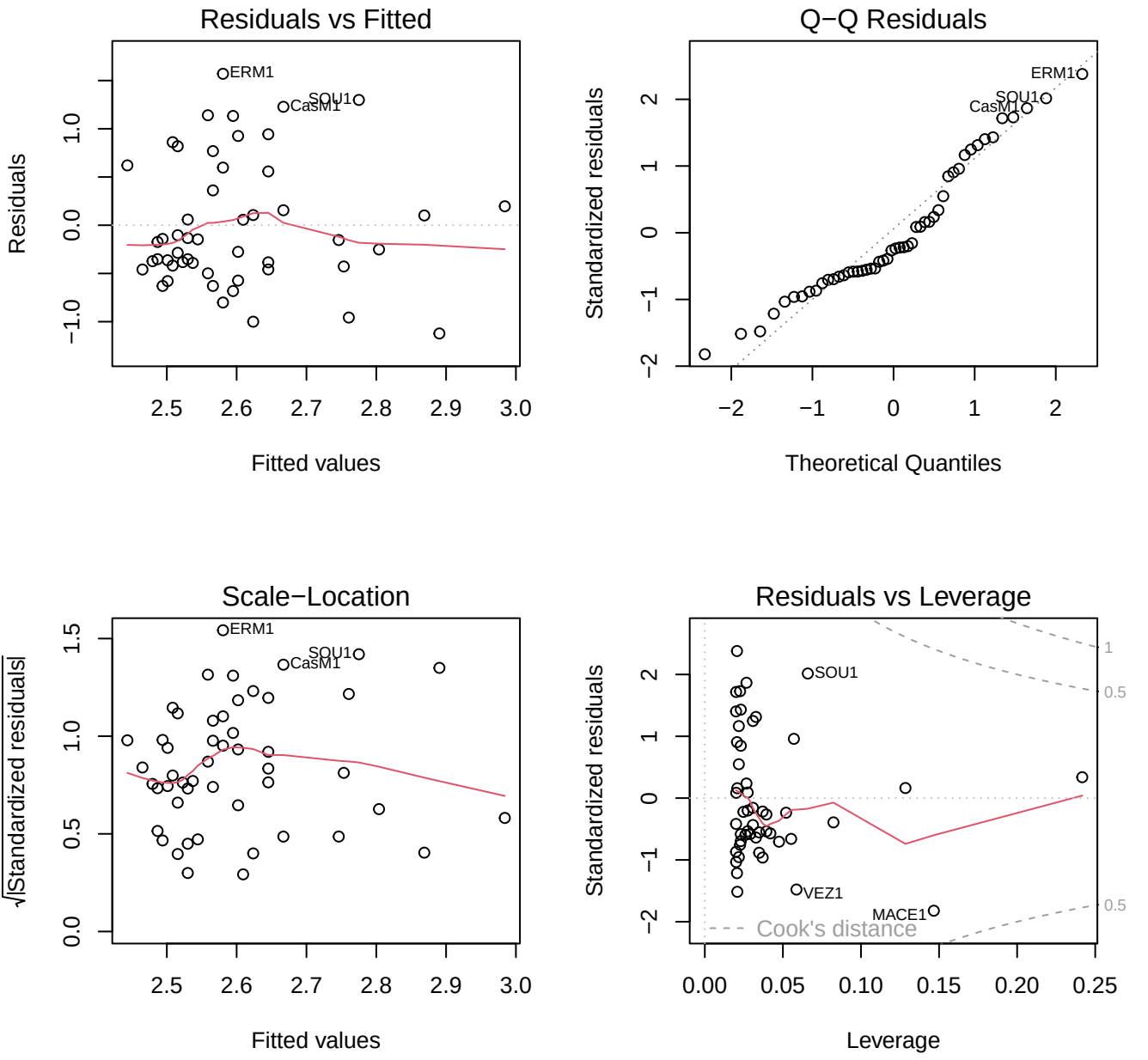

$R^2 = 0.0329049$
p−value: = 0.2074
Bacteria_phylum_reads
2.0
2.5
3.0
3.5
4.0
−6
−4
−2
0
Discharge

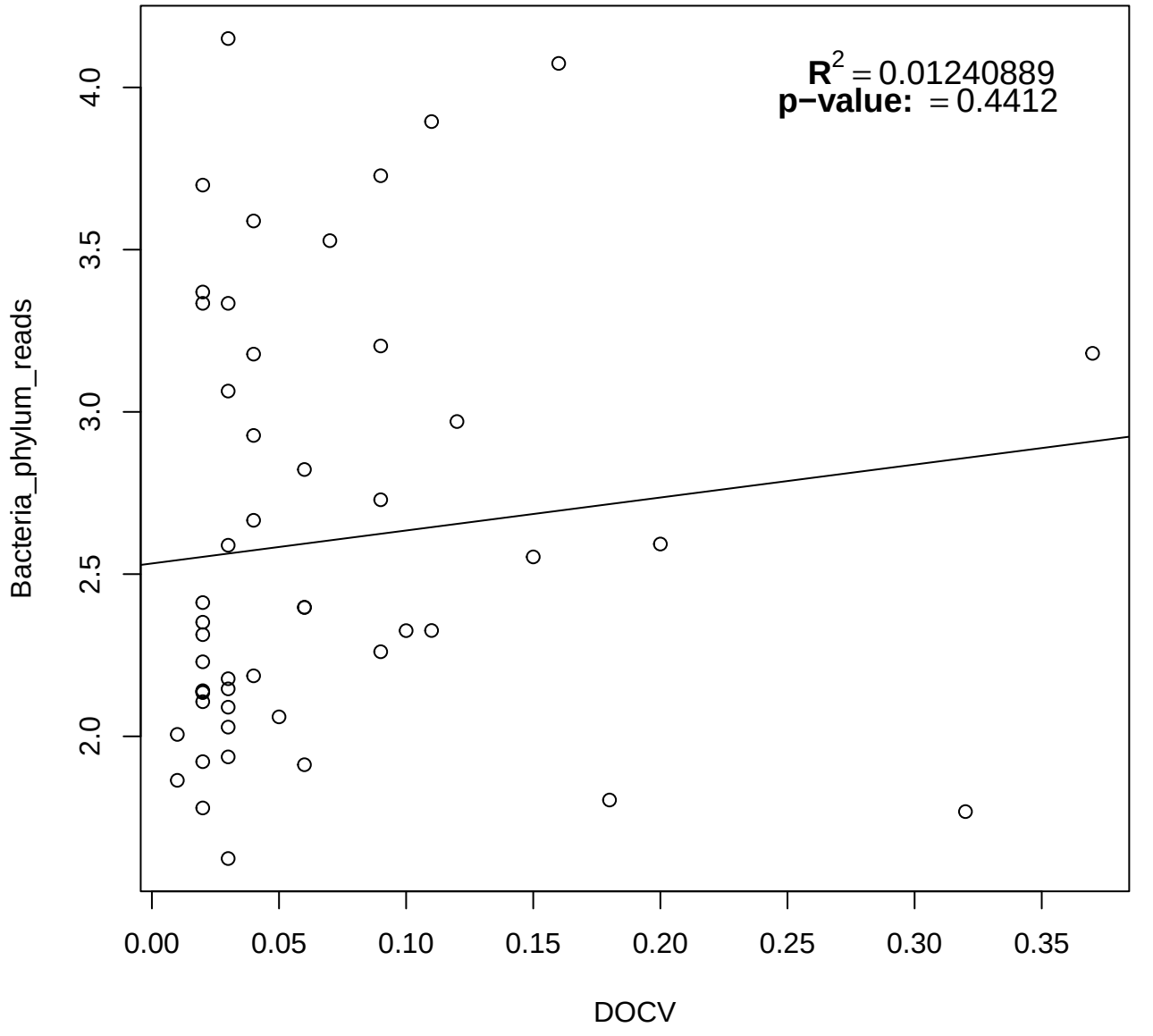

Residuals vs Fitted
Residuals
Fitted values
ERM1
SOU1
CasM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
EST2
GER1
Cook's distance
0.5

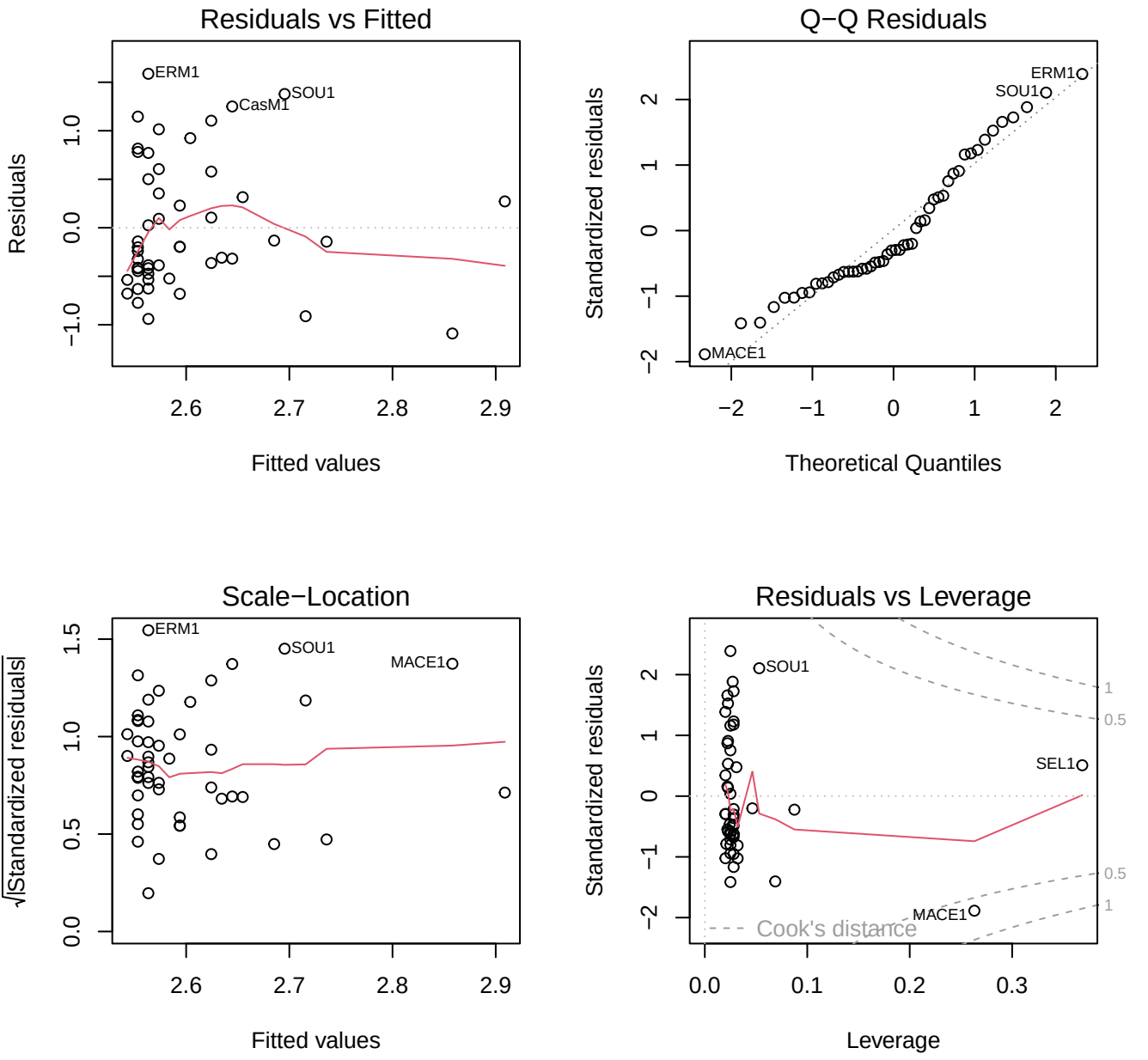

$R^2 = 0.07244168$
p−value: = 0.0587
Bacteria_phylum_reads
2.0
2.5
3.0
3.5
4.0
14
16
18
20
22
24
26
28
Tmax

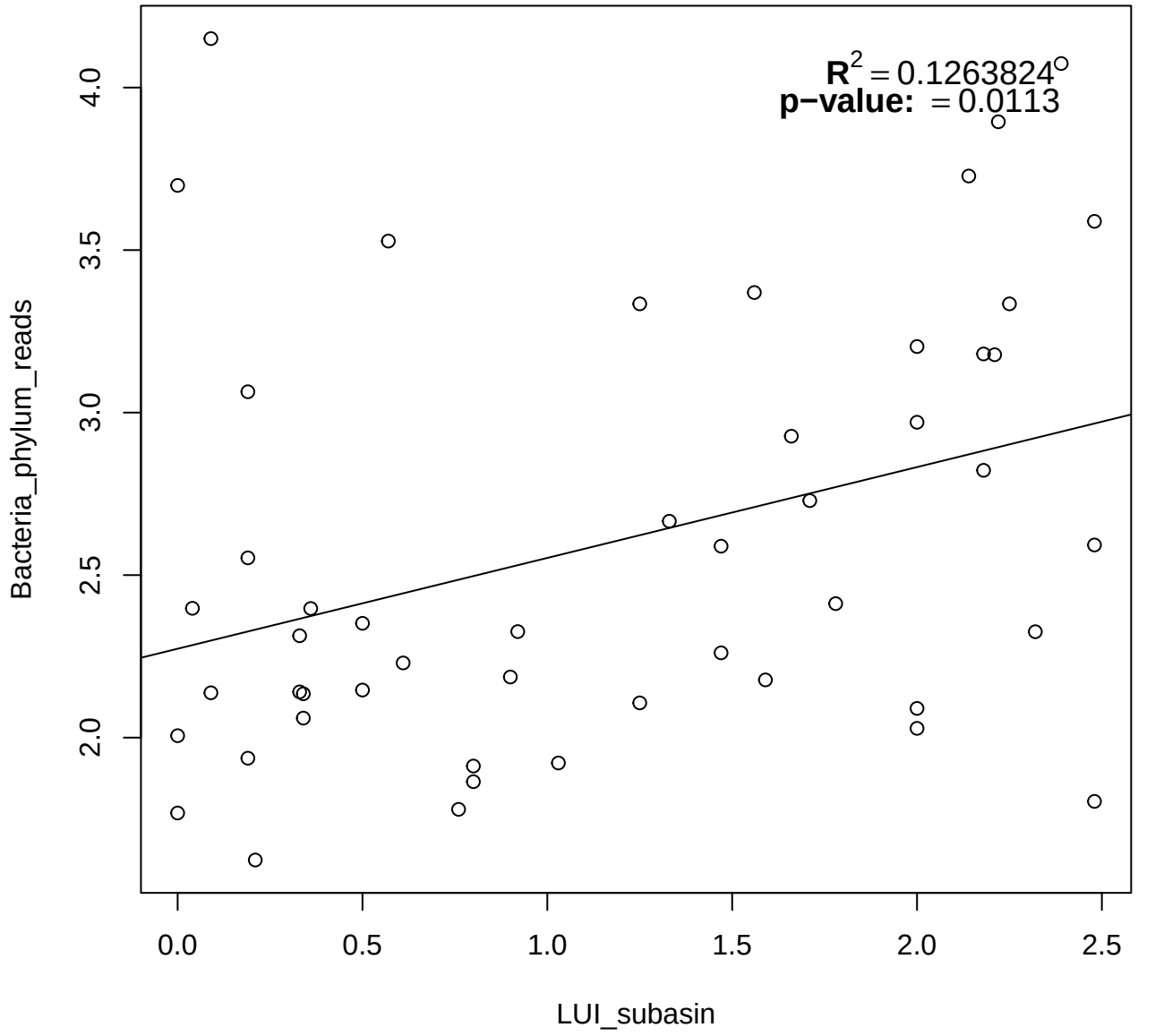

Residuals vs Fitted
Residuals
Fitted values
ERM1
CasM1
EST2
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
CasM1
SOU1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
CasM1
SOU1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
ARG1
VEZ1
Cook's distance
0.5

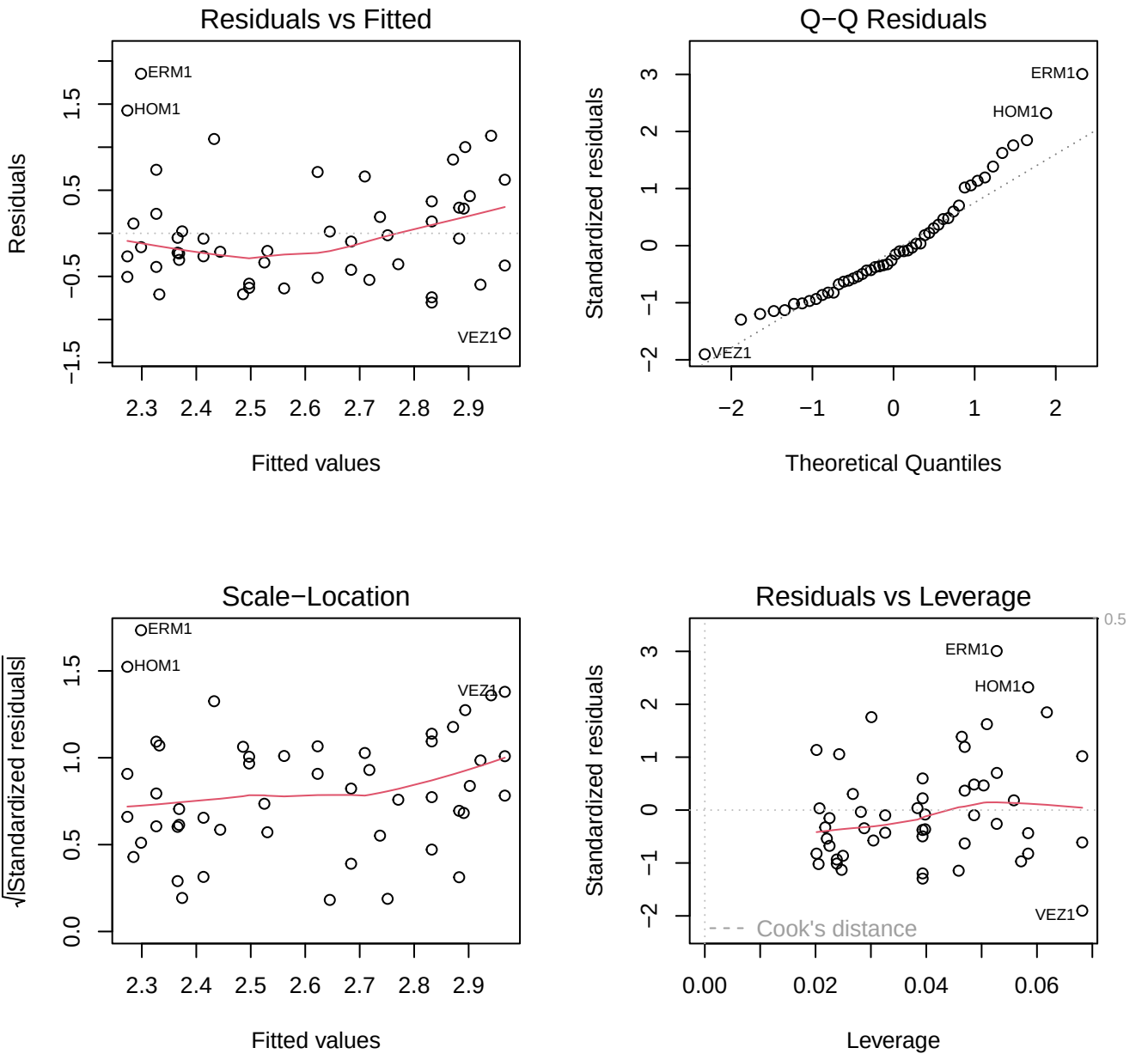

$R^2 = 0.03018221$
p−value: = 0.2276
Bacteria_phylum_reads
DOmin
2.0
2.5
3.0
3.5
4.0
2
4
6
8

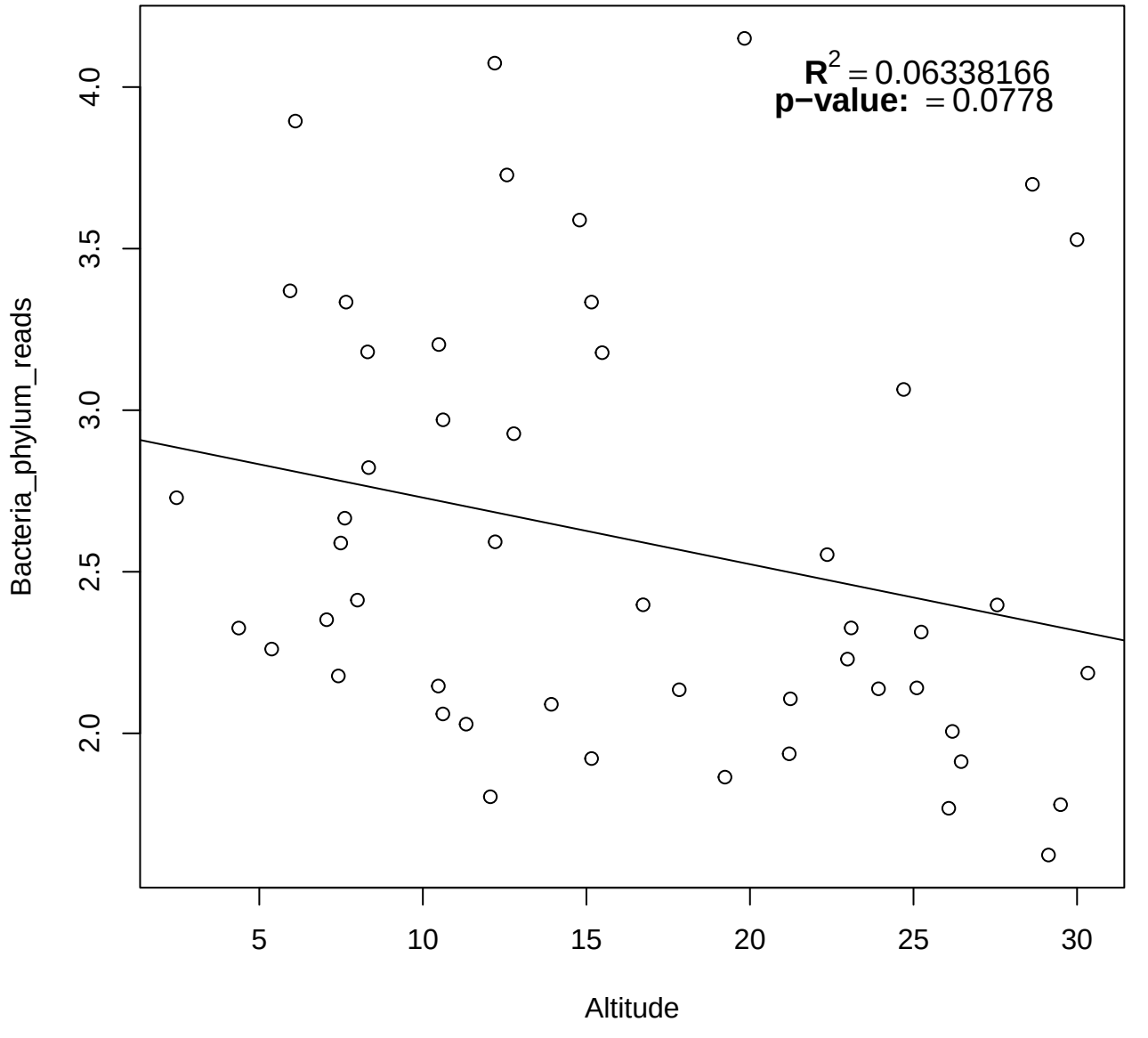

Residuals vs Fitted
Residuals
Fitted values
ERM1
SOU1
CasM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
SOU1
CasM1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
SOU1
CasM1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
VEZ1
MACE1
Cook's distance
1
0.5
0.5

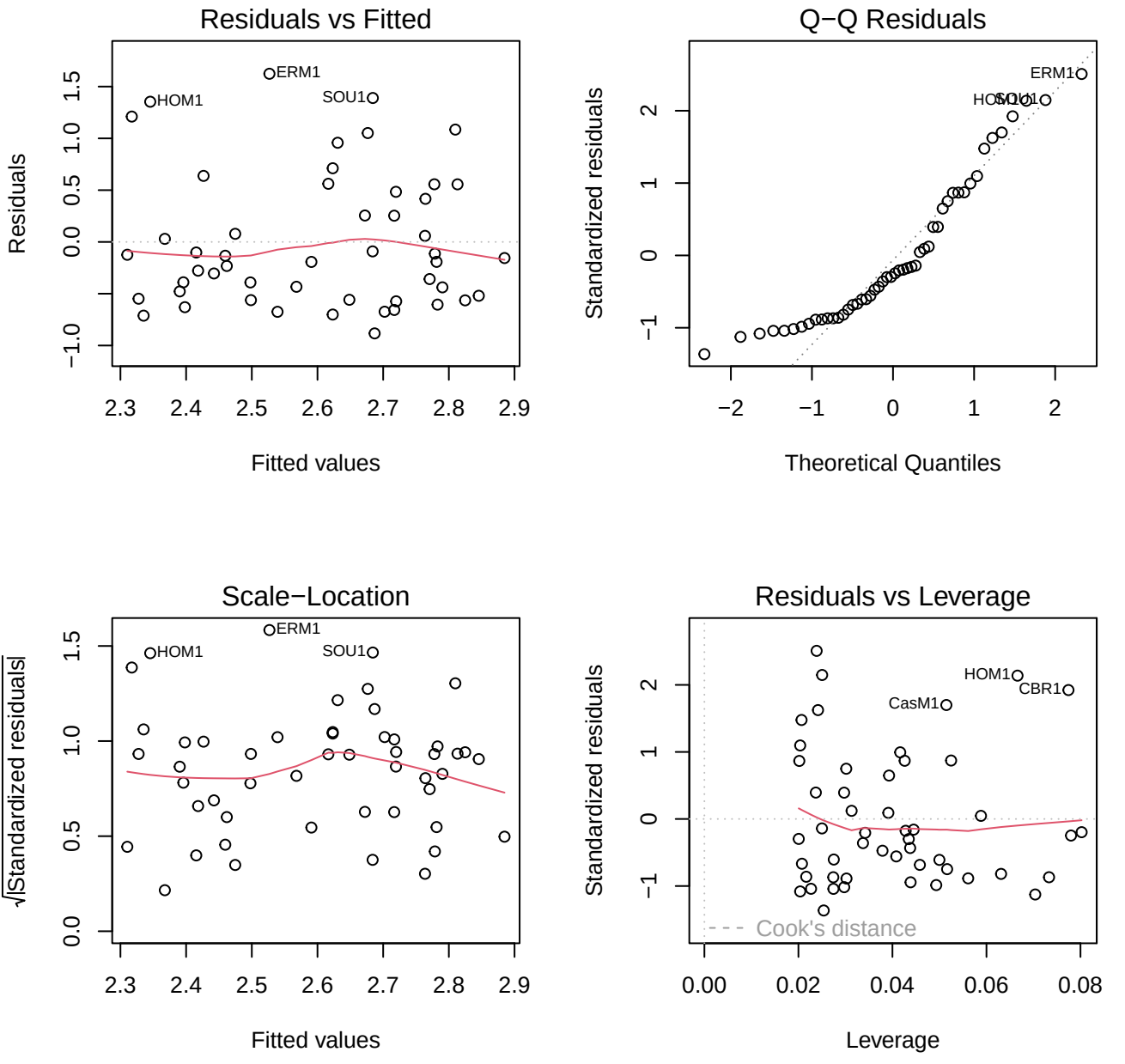

$R^2 = 0.01240889$
p−value: = 0.4412
Bacteria_phylum_reads
DOCV
2.0
2.5
3.0
3.5
4.0
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35

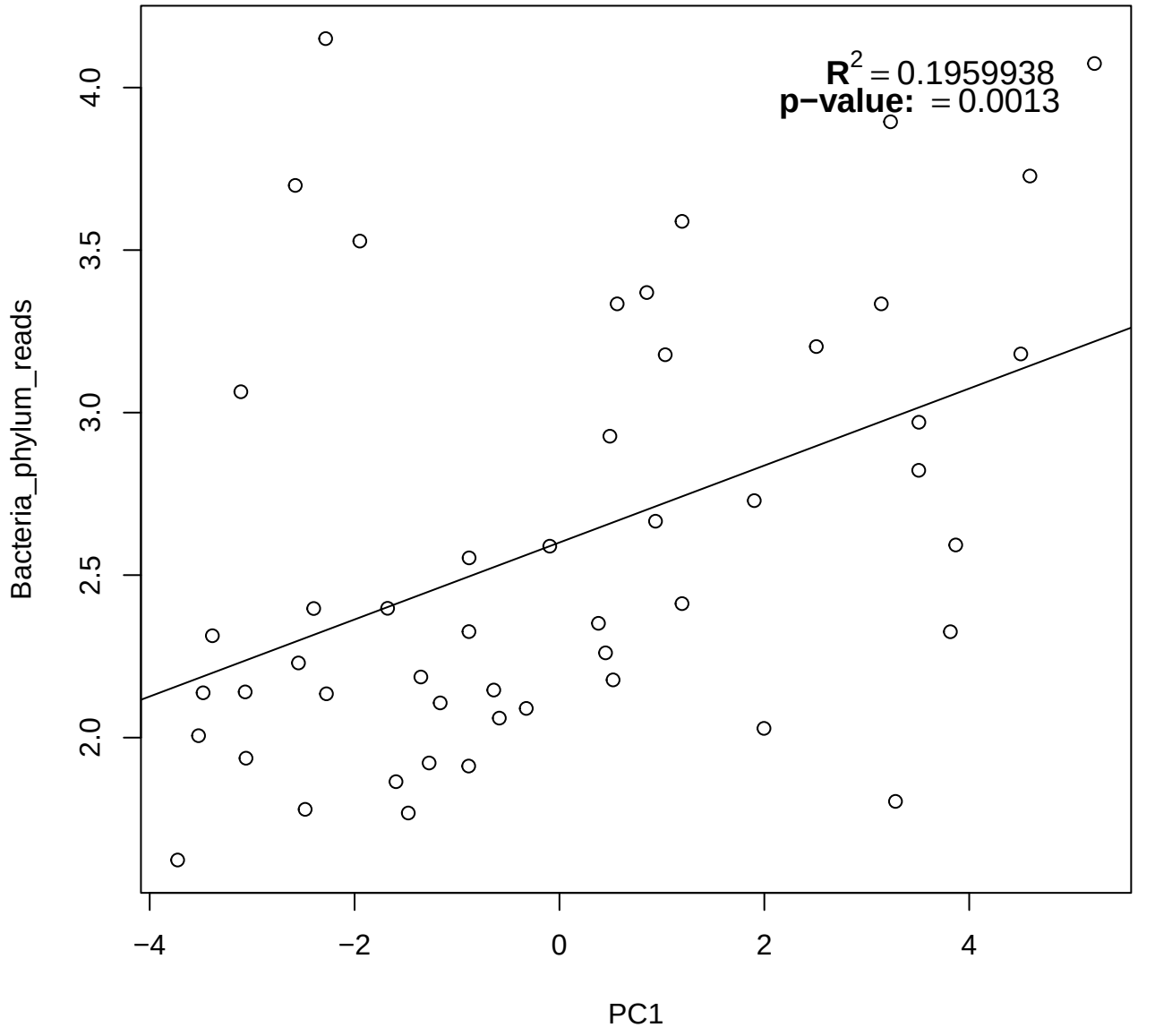

Residuals vs Fitted
Residuals
Fitted values
ERM1
SOU1
CasM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
SOU1
MACE1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
SOU1
MACE1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
SEL1
MACE1
Cook's distance
1
0.5
0.5
1

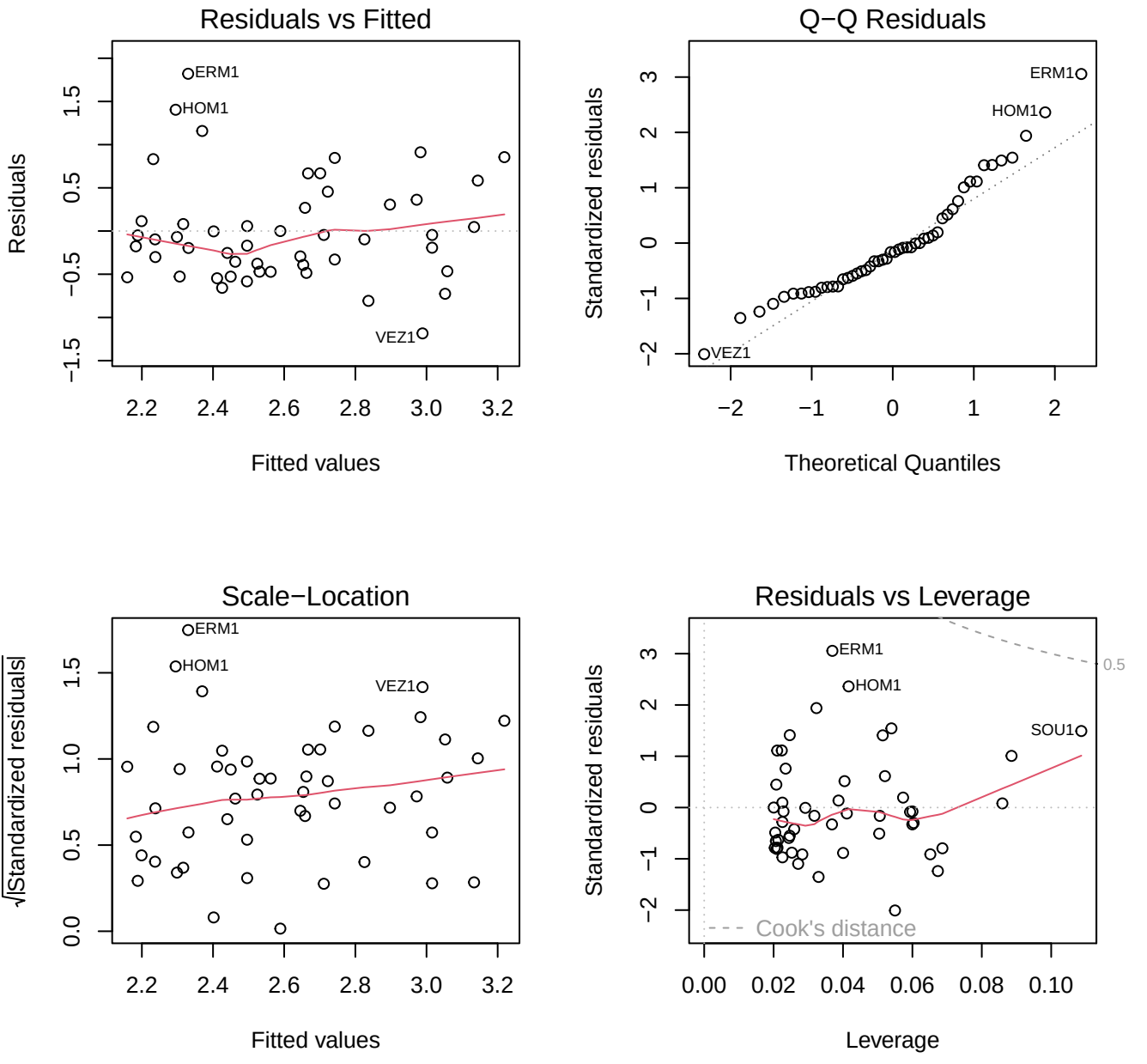

$R^2 = 0.1263824$
p−value: = 0.0113
Bacteria_phylum_reads
LUI_subasin
2.0
2.5
3.0
3.5
4.0
0.0
0.5
1.0
1.5
2.0
2.5

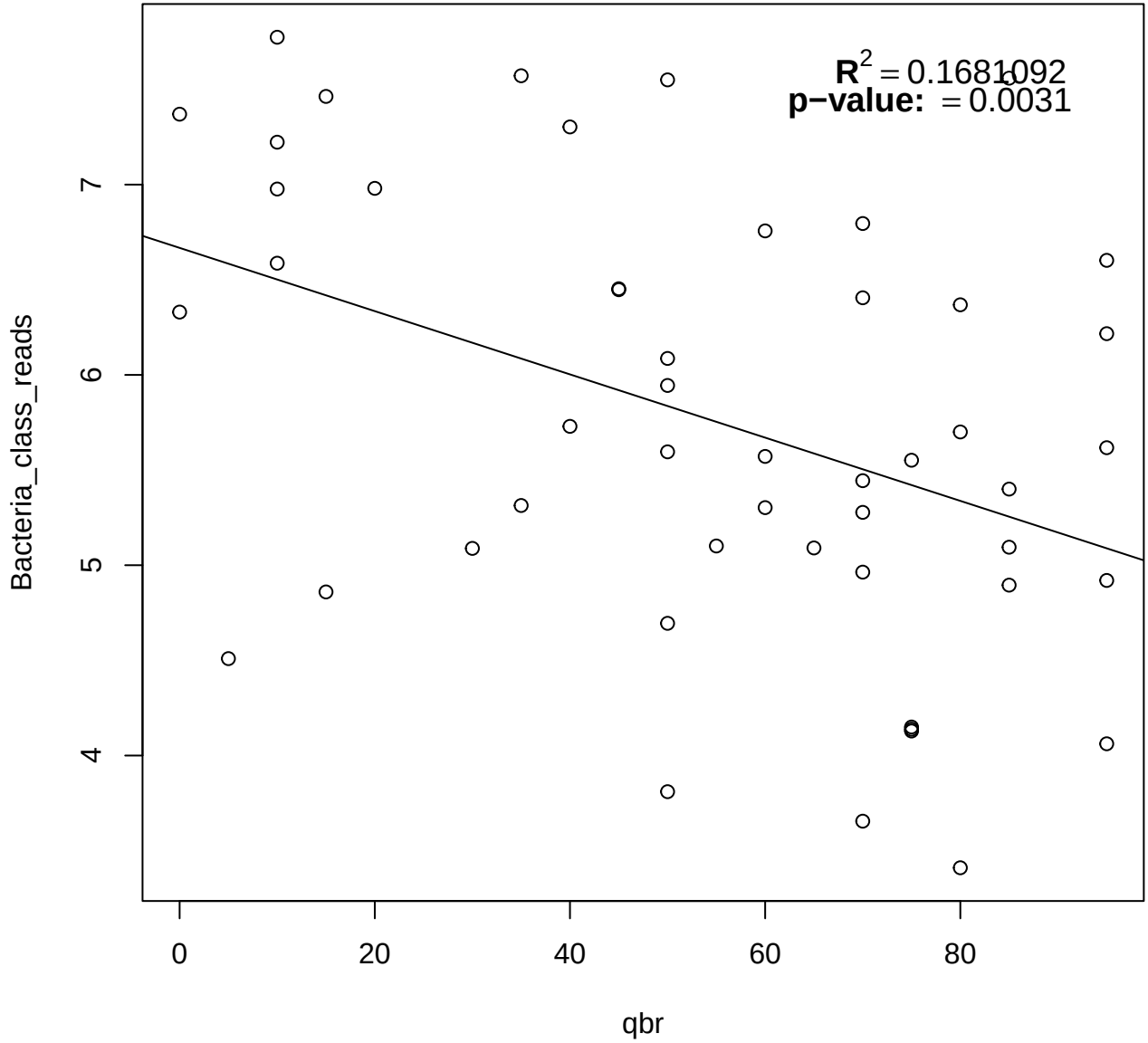

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
HOM1
VEZ1
Cook's distance
0.5

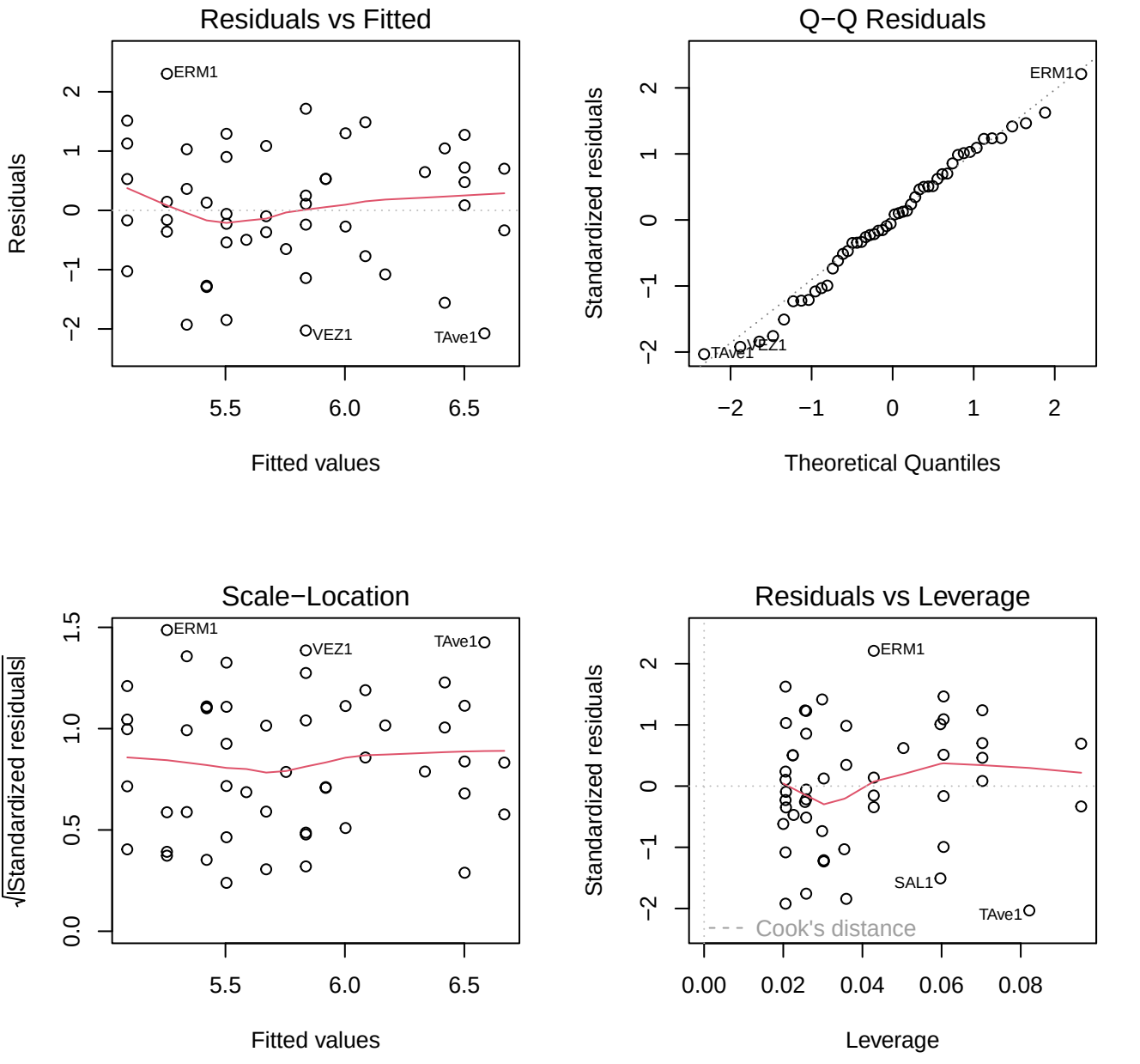

$R^2 = 0.06338166$
p−value: $= 0.0778$
Bacteria_phylum_reads
2.0
2.5
3.0
3.5
4.0
5
10
15
20
25
30
Altitude

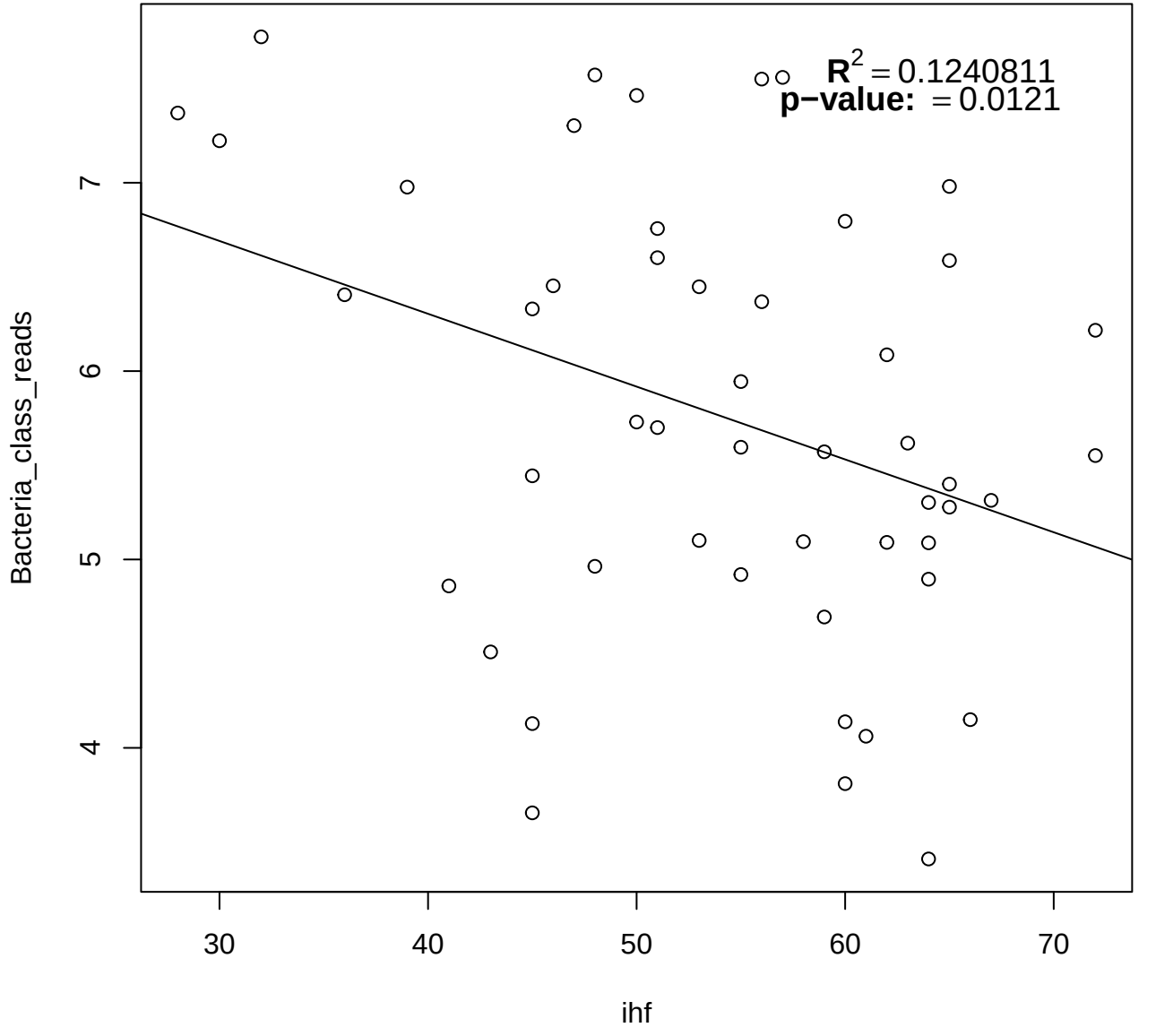

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
SOU1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
SOU1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
SOU1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
CBR1
CasM1
Cook's distance

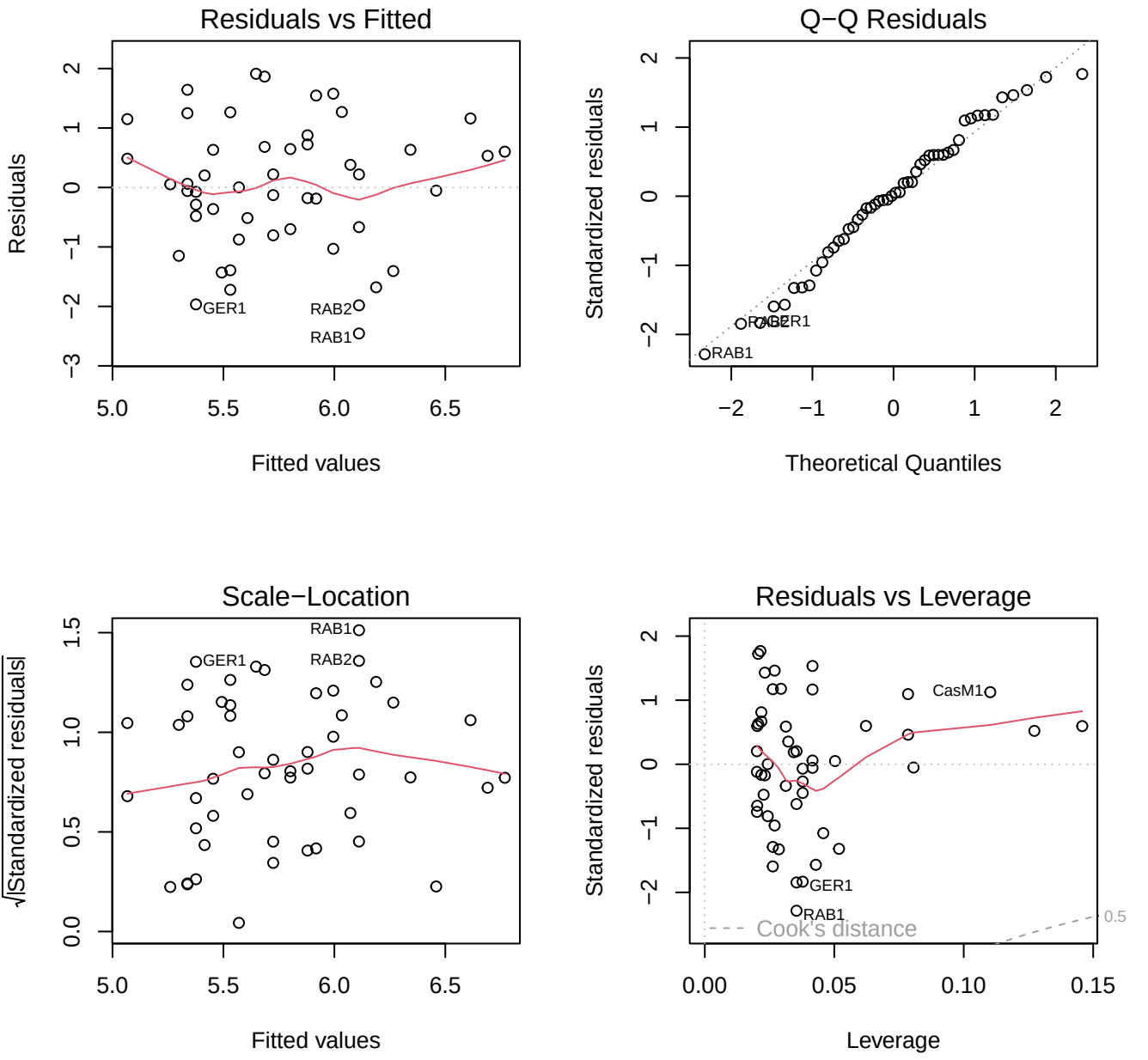

$R^2 = 0.1959938$
p−value: = 0.0013
Bacteria_phylum_reads
2.0
2.5
3.0
3.5
4.0
−4
−2
0
2
4
PC1

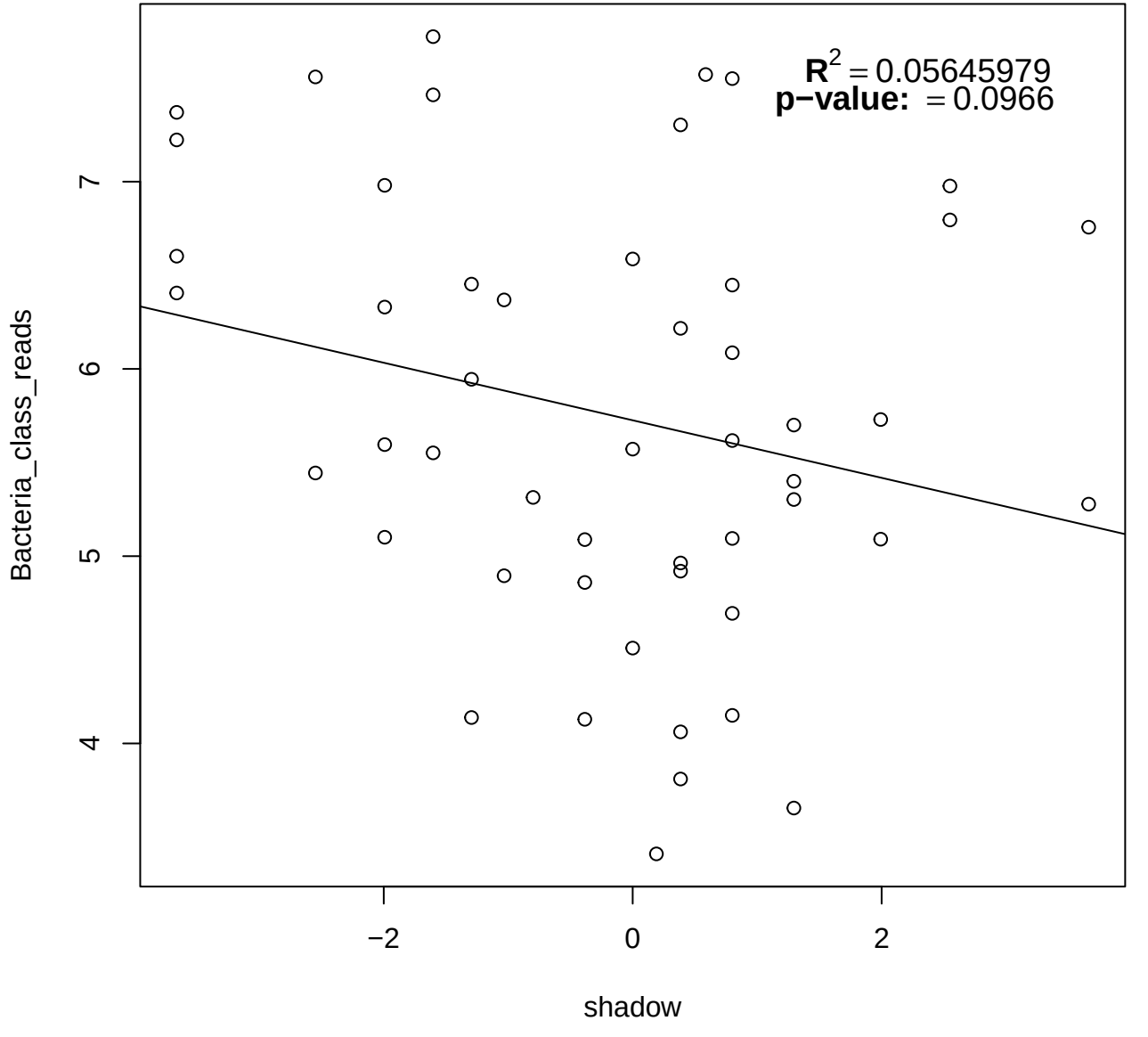

Residuals vs Fitted
Residuals
Fitted values
ERM1
HOM1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
HOM1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
HOM1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
HOM1
SOU1
0.5
Cook's distance

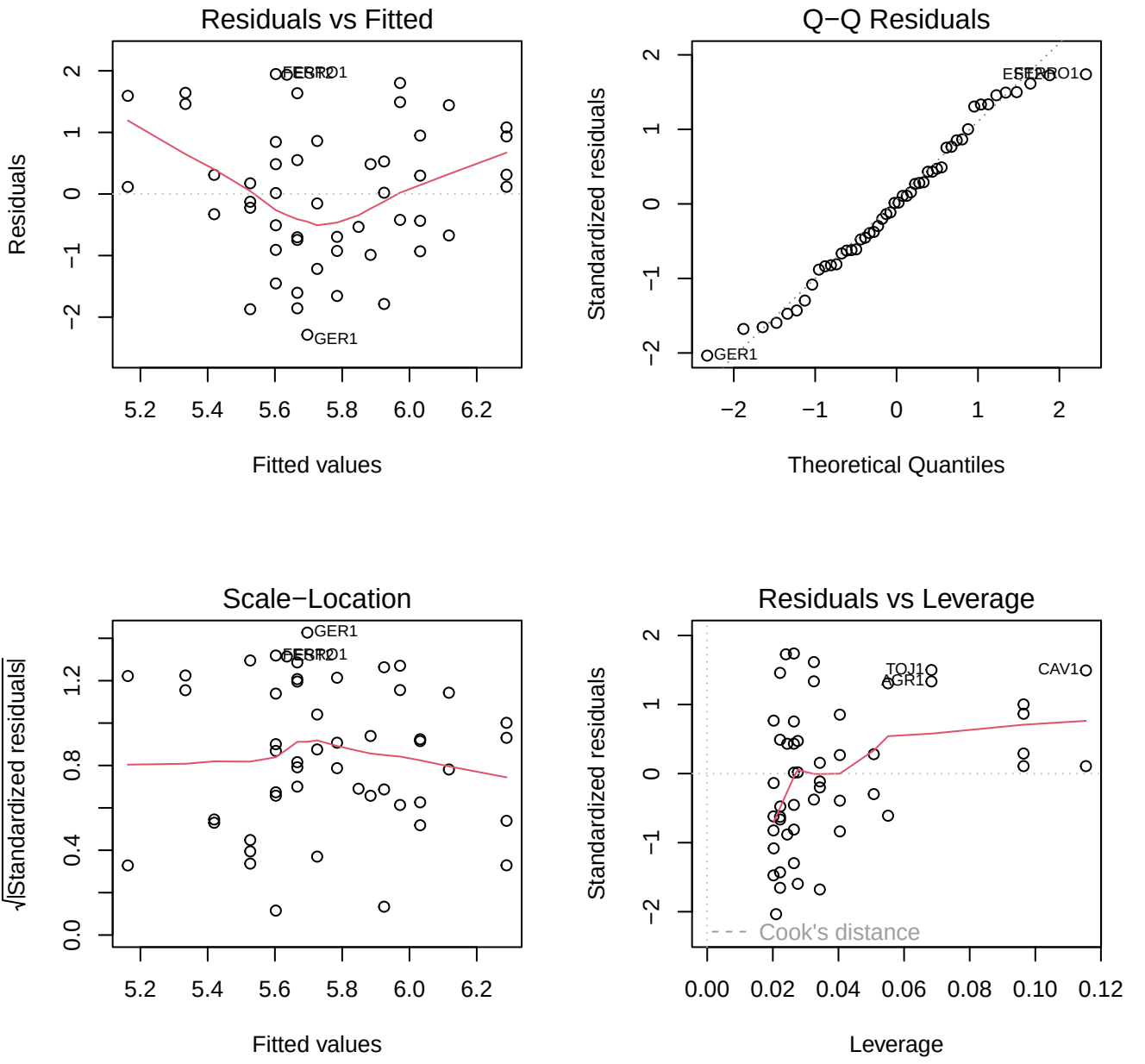

$R^2 = 0.1681092$
p−value: = 0.0031
Bacteria_class_reads
qbr
4
5
6
7
0
20
40
60
80

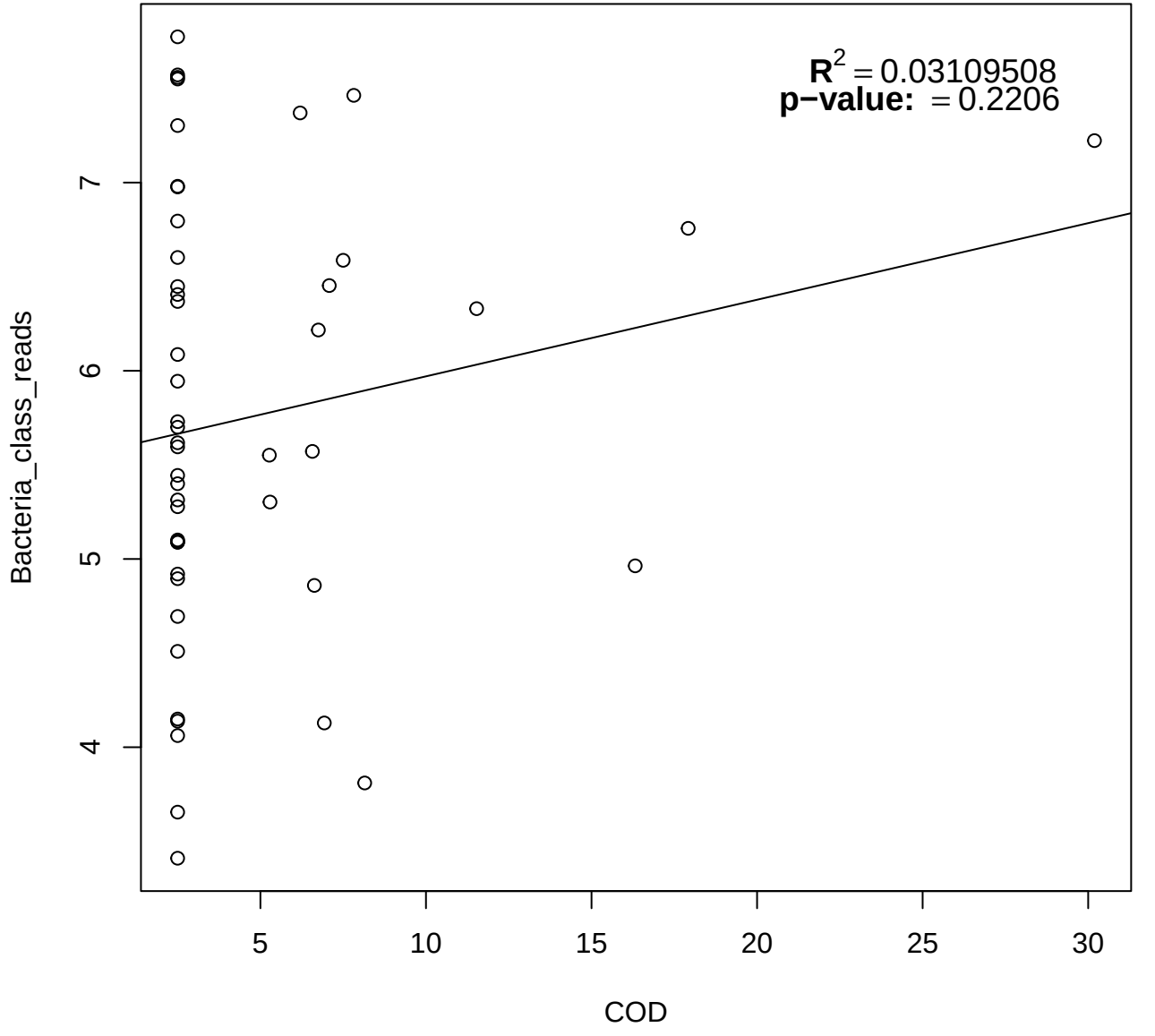

Residuals vs Fitted
Residuals
Fitted values
ERM1
VEZ1
TAve1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
TAve1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
VEZ1
TAve1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
SAL1
TAve1
Cook's distance

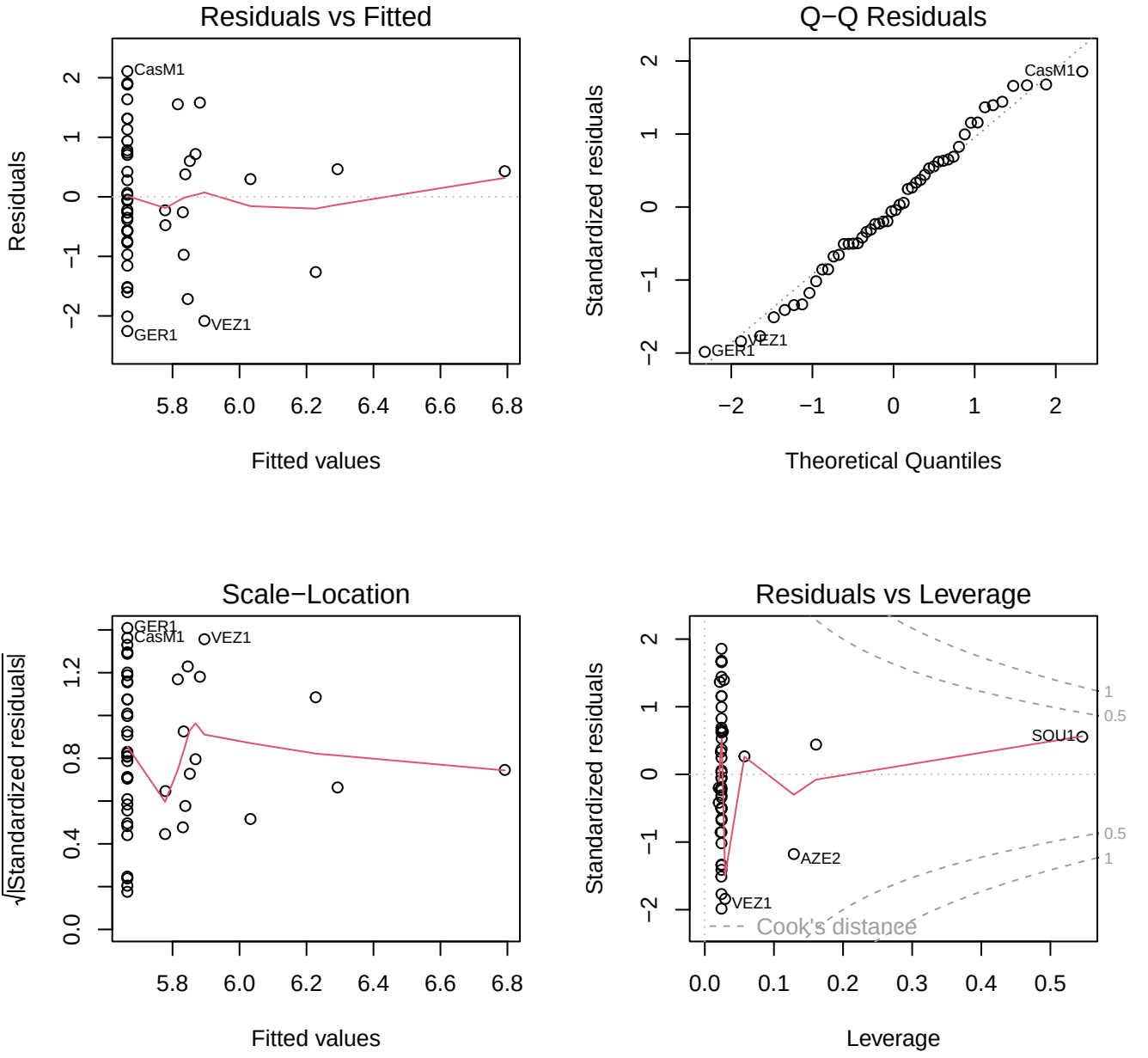

$R^2 = 0.1240811$
p−value: = 0.0121
Bacteria_class_reads
ihf
4
5
6
7
30
40
50
60
70

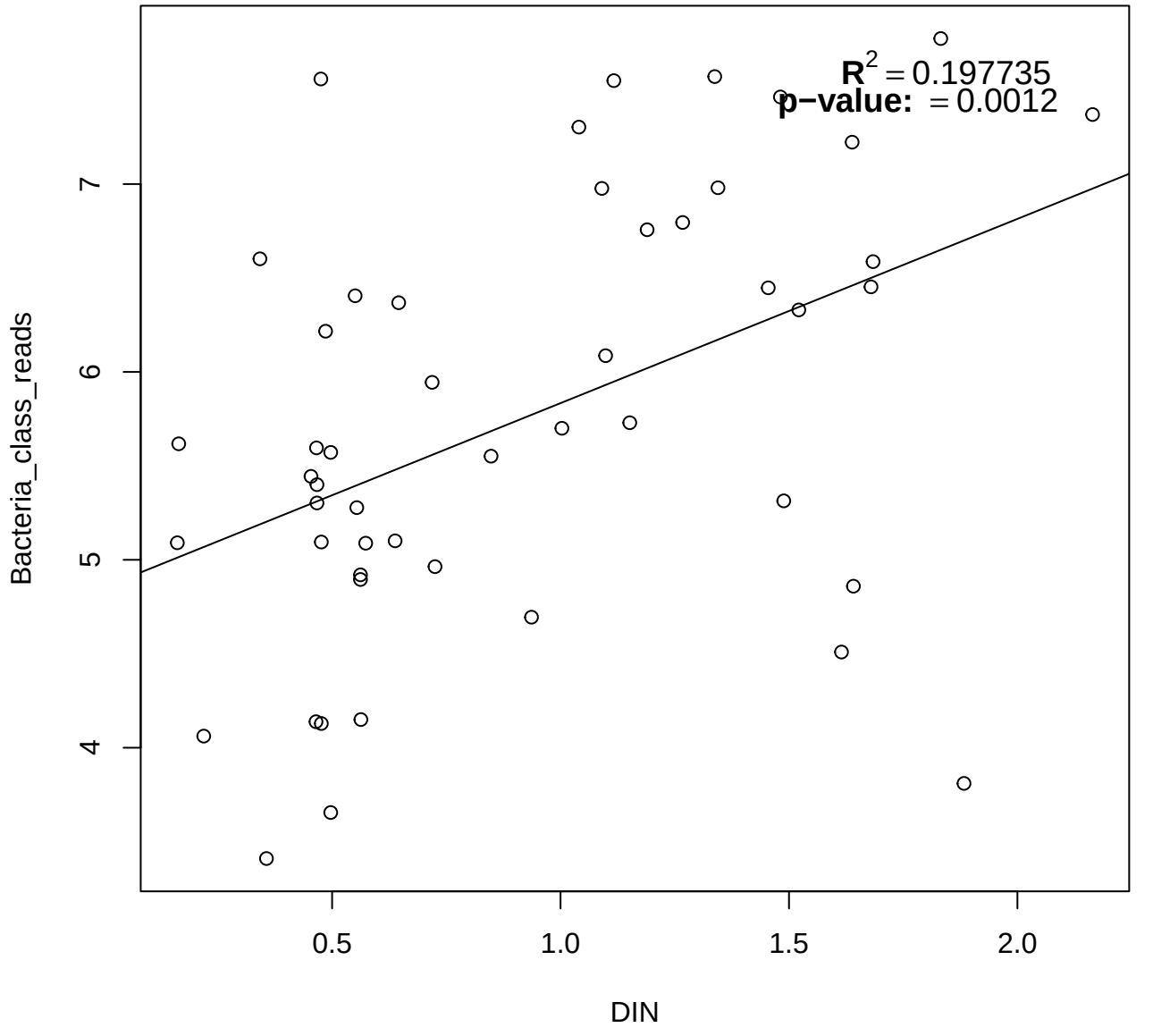

Residuals vs Fitted
Residuals
Fitted values
GER1
RAB2
RAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
RAB1
Scale−Location
√|Standardized residuals|
Fitted values
RAB1
GER1
RAB2
Residuals vs Leverage
Standardized residuals
Leverage
CasM1
GER1
RAB1
Cook's distance
0.5

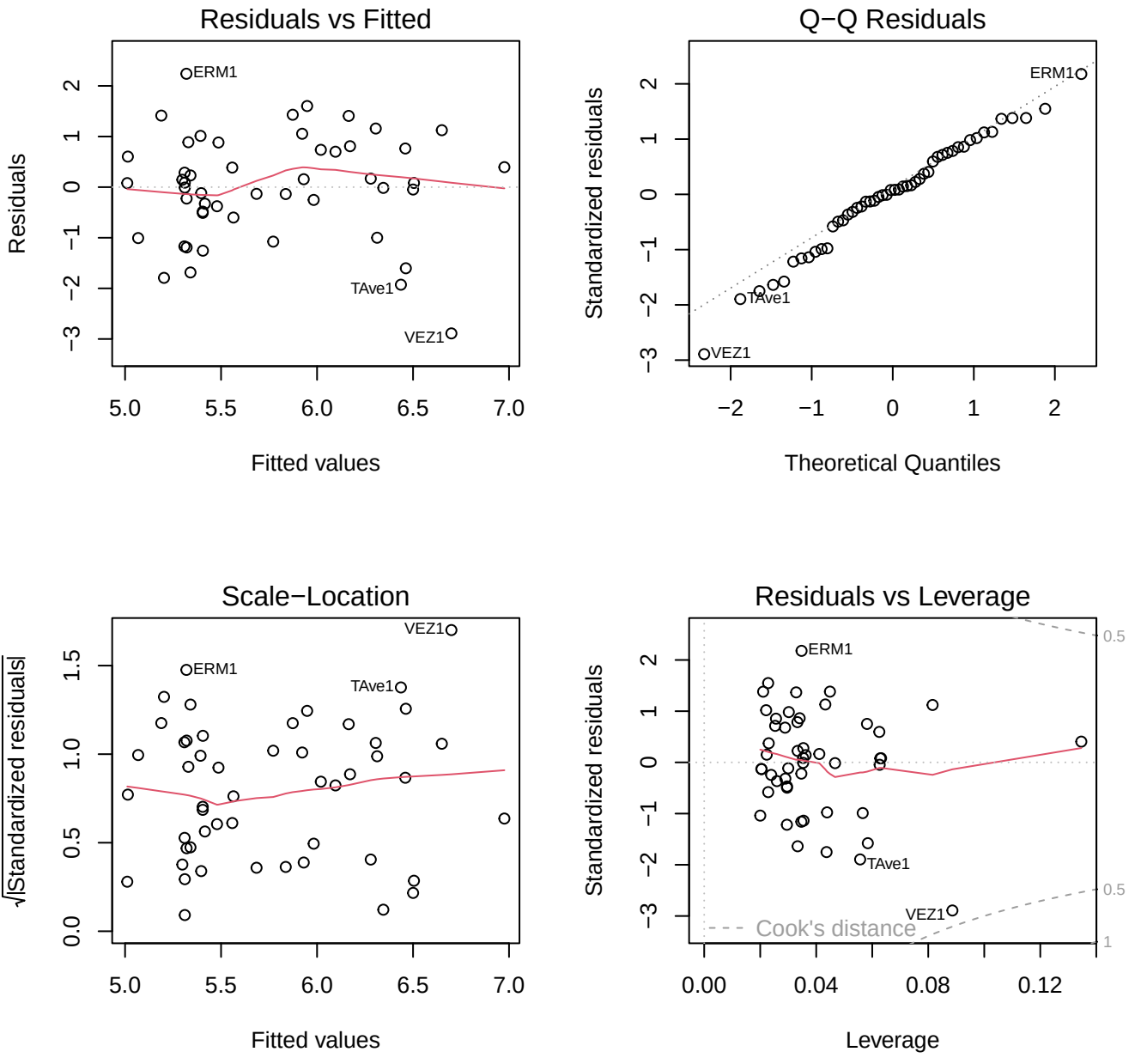

$R^2 = 0.05645979$
p−value: = 0.0966
Bacteria_class_reads
shadow
4
5
6
7
−2
0
2

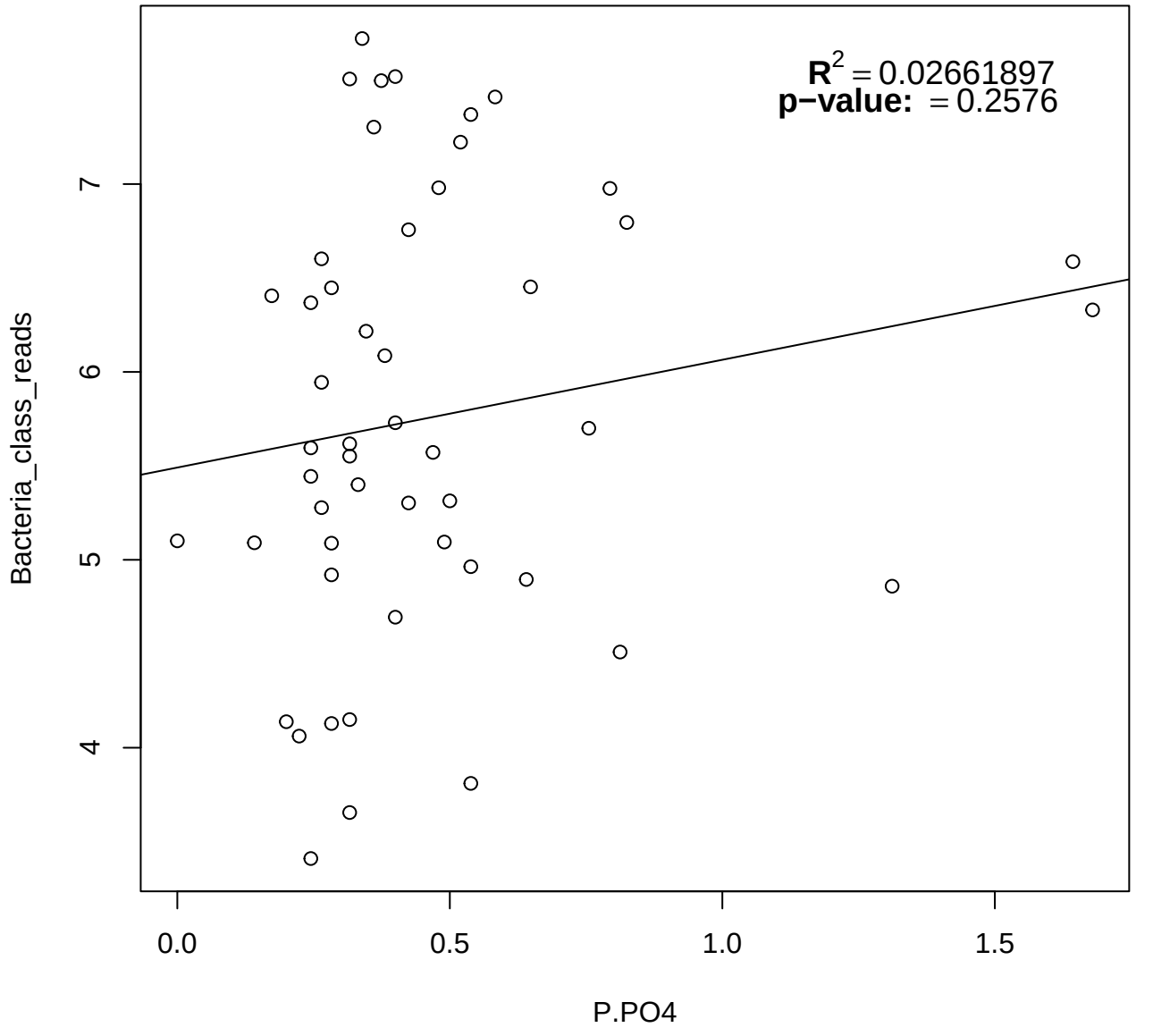

Residuals vs Fitted
Residuals
Fitted values
GER1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
GER1
Scale−Location
√|Standardized residuals|
Fitted values
GER1
Residuals vs Leverage
Standardized residuals
Leverage
TOJ1
AGR1
CAV1
Cook's distance

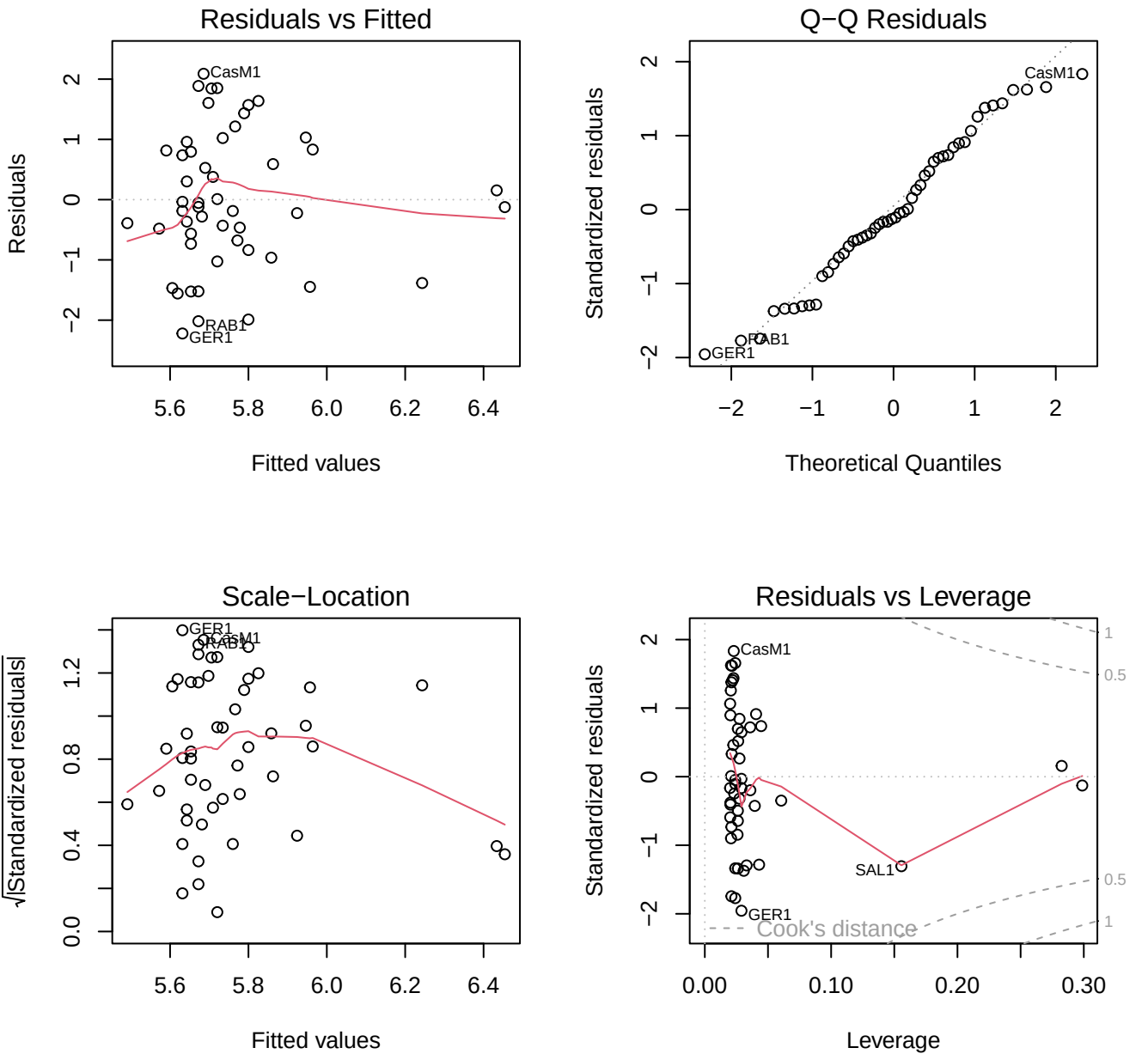

$R^2 = 0.03109508$
p−value: = 0.2206
Bacteria_class_reads
COD
4
5
6
7
5
10
15
20
25
30

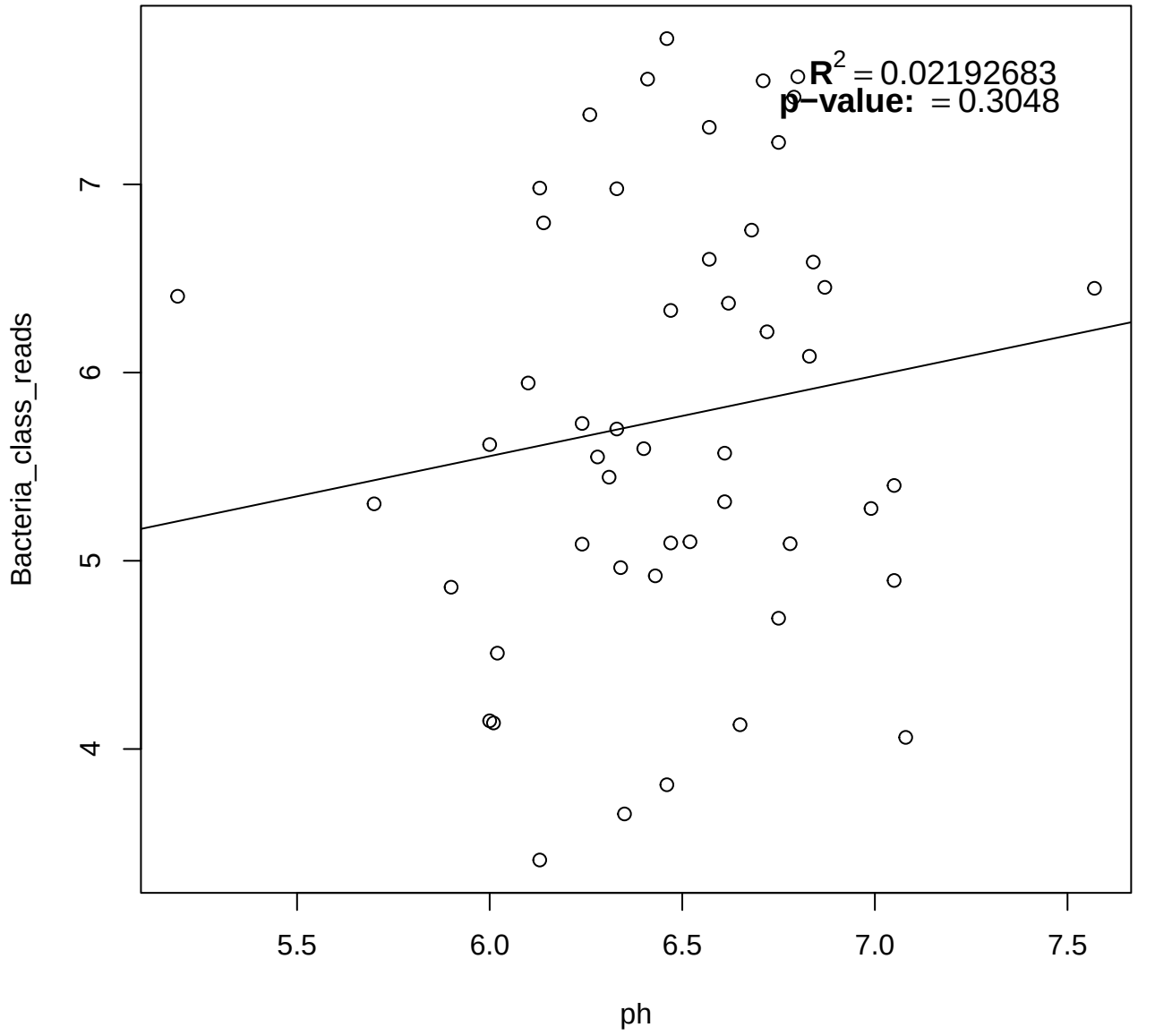

Residuals vs Fitted
Residuals
Fitted values
CasM1
GER1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
CasM1
GER1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
GER1
CasM1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
SOU1
AZE2
VEZ1
Cook's distance

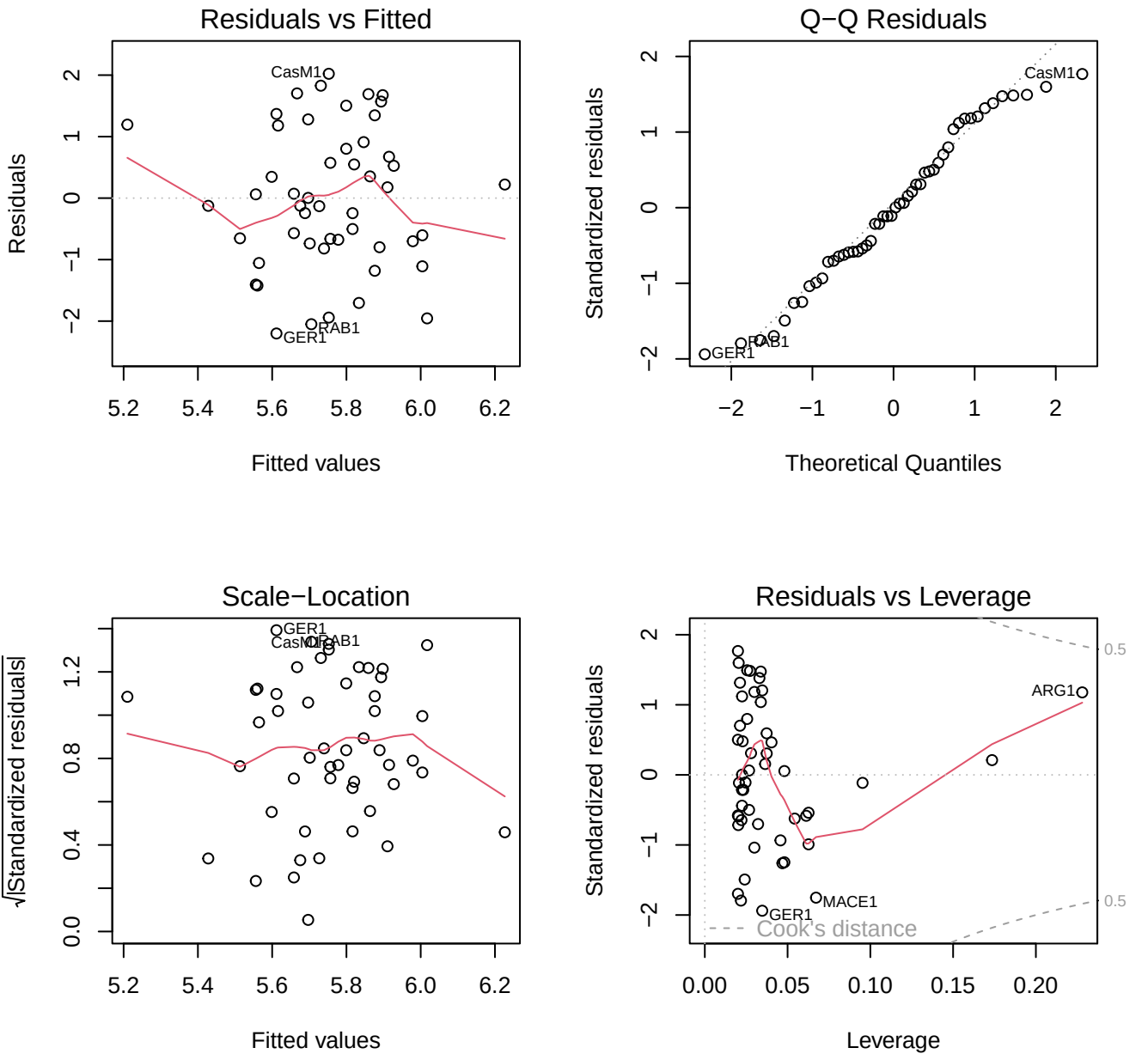

$R^2 = 0.197735$
p−value: = 0.0012
Bacteria_class_reads
DIN
4
5
6
7
0.5
1.0
1.5
2.0

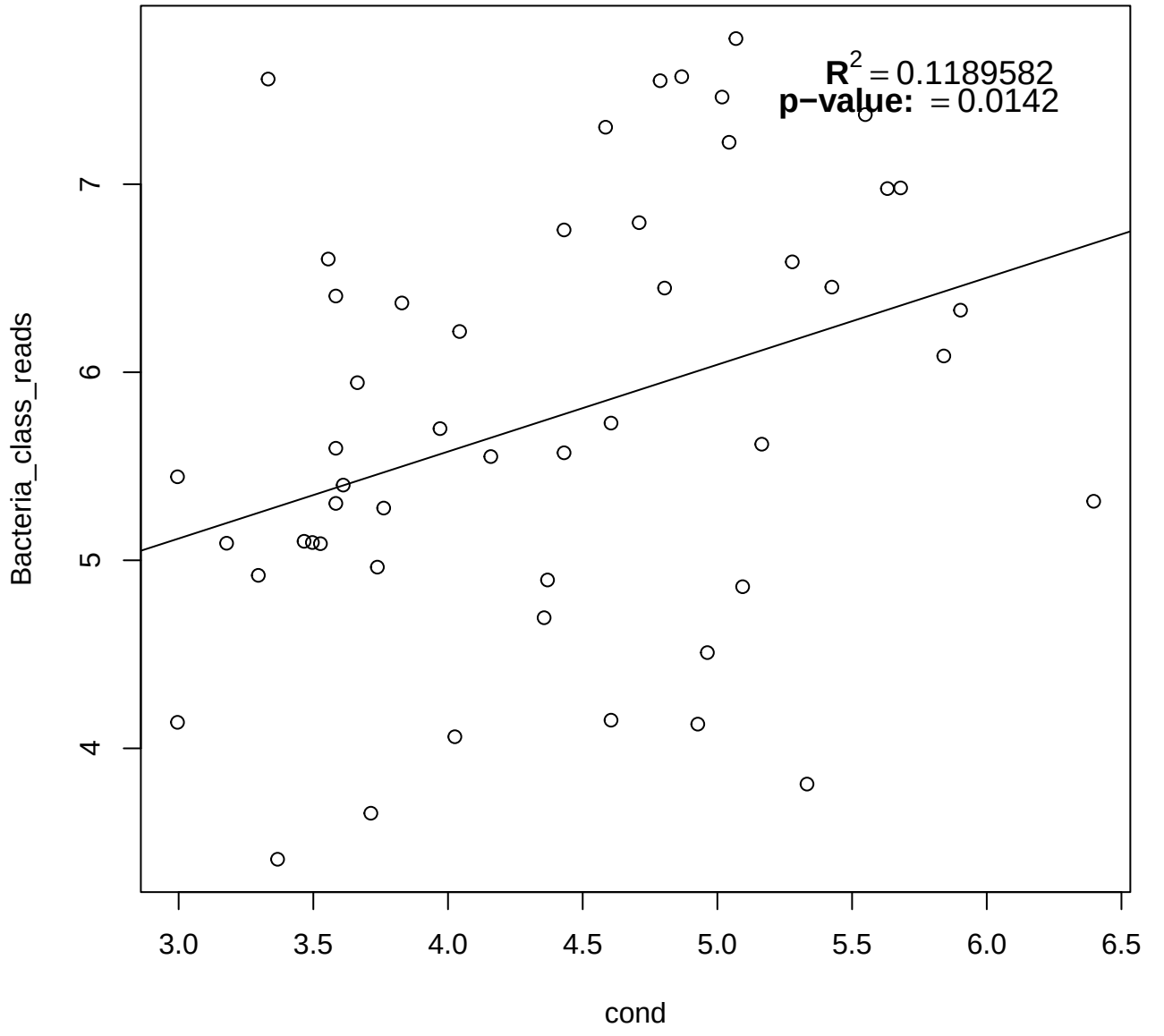

Residuals vs Fitted
Residuals
Fitted values
ERM1
TAve1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
TAve1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
VEZ1
ERM1
TAve1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
TAve1
VEZ1
Cook's distance
0.5
0.5
1

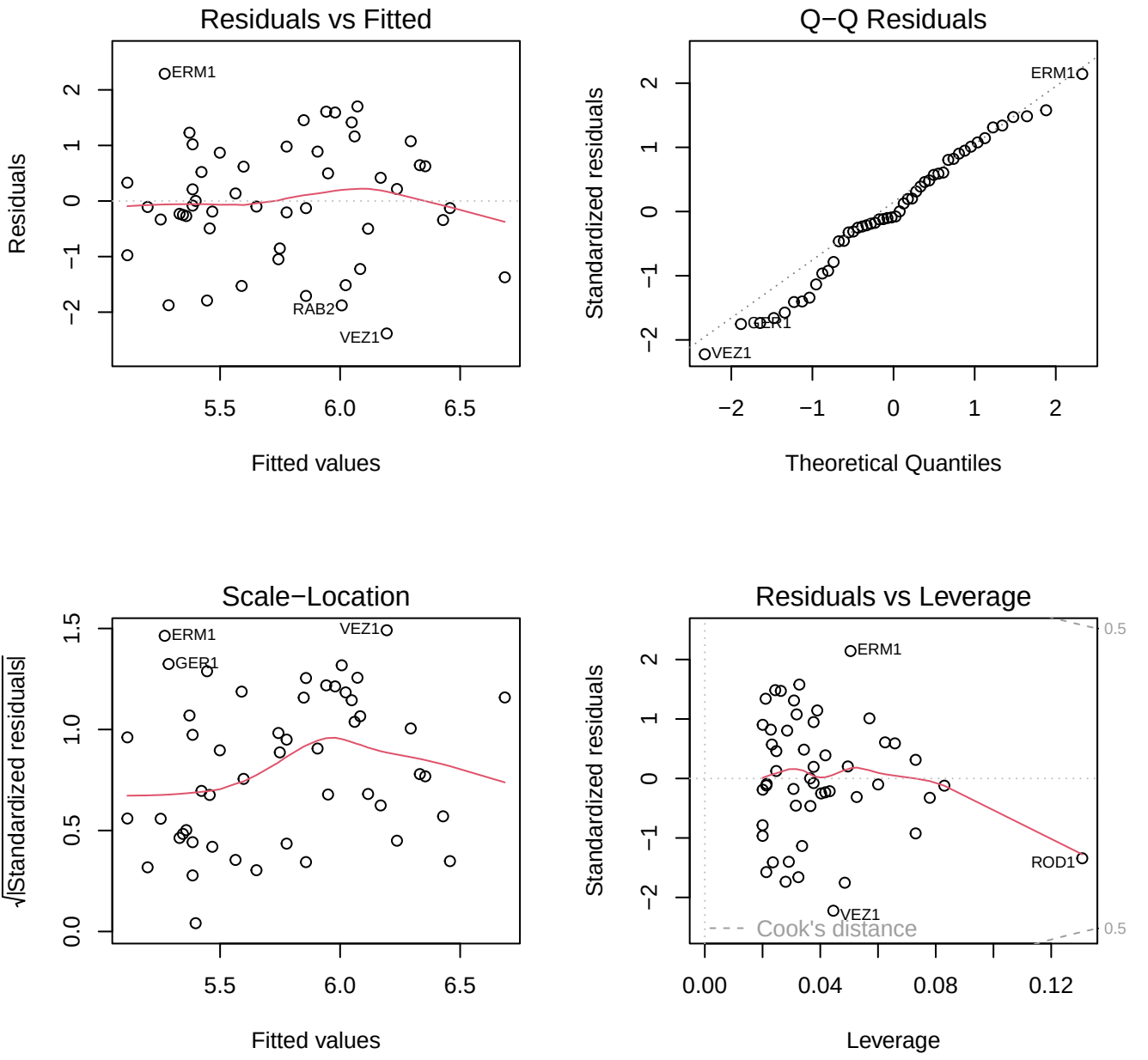

$R^2 = 0.02661897$
p−value: = 0.2576
Bacteria_class_reads
4
5
6
7
0.0
0.5
1.0
1.5
P.PO4

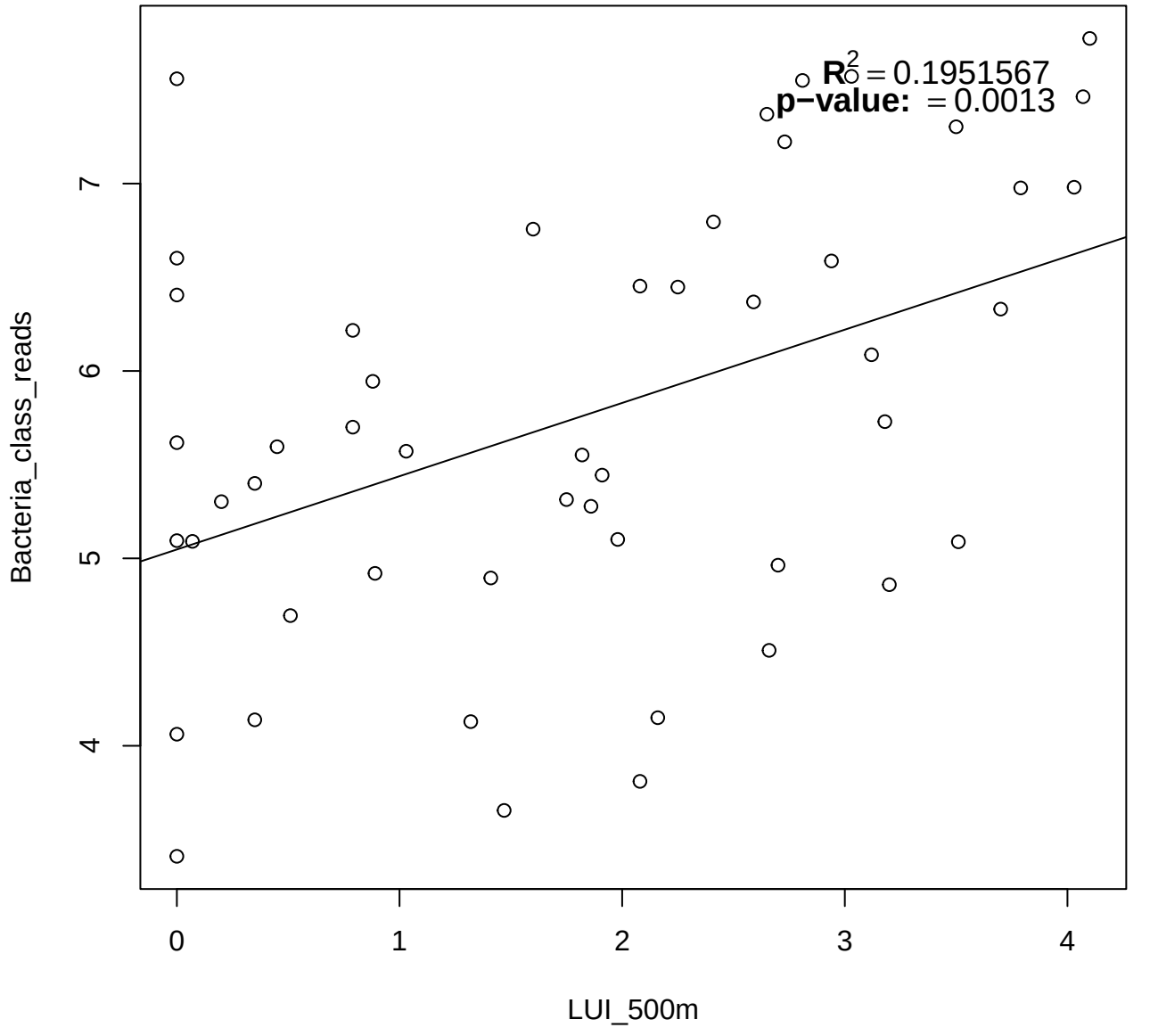

Residuals vs Fitted
Residuals
Fitted values
CasM1
RAB1
GER1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
CasM1
RAB1
GER1
Scale−Location
√|Standardized residuals|
Fitted values
GER1
CasM1
RAB1
Residuals vs Leverage
Standardized residuals
Leverage
CasM1
SAL1
GER1
Cook's distance

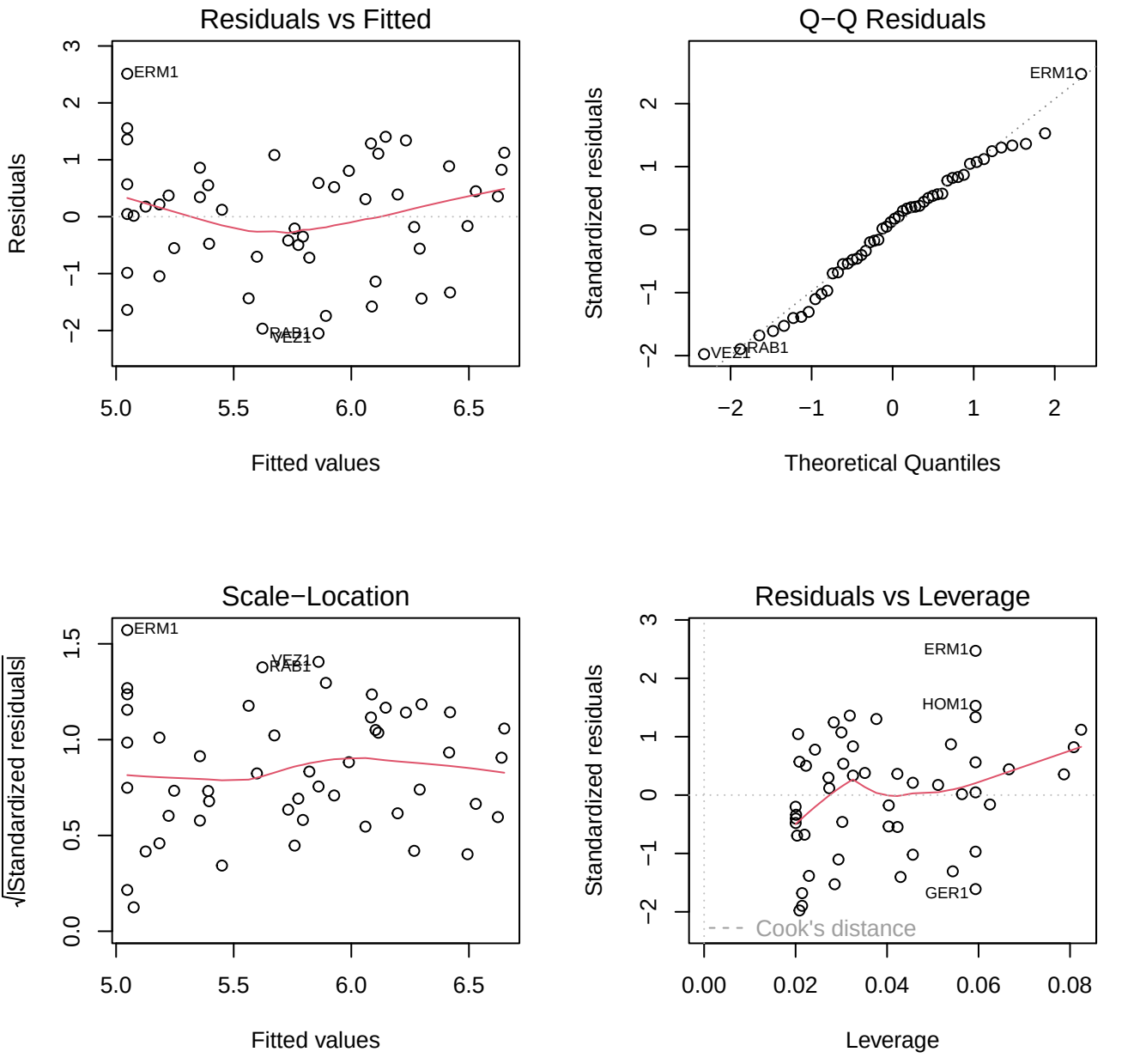

$R^2 = 0.02192683$
p−value: $= 0.3048$
Bacteria_class_reads
ph
4
5
6
7
5.5
6.0
6.5
7.0
7.5

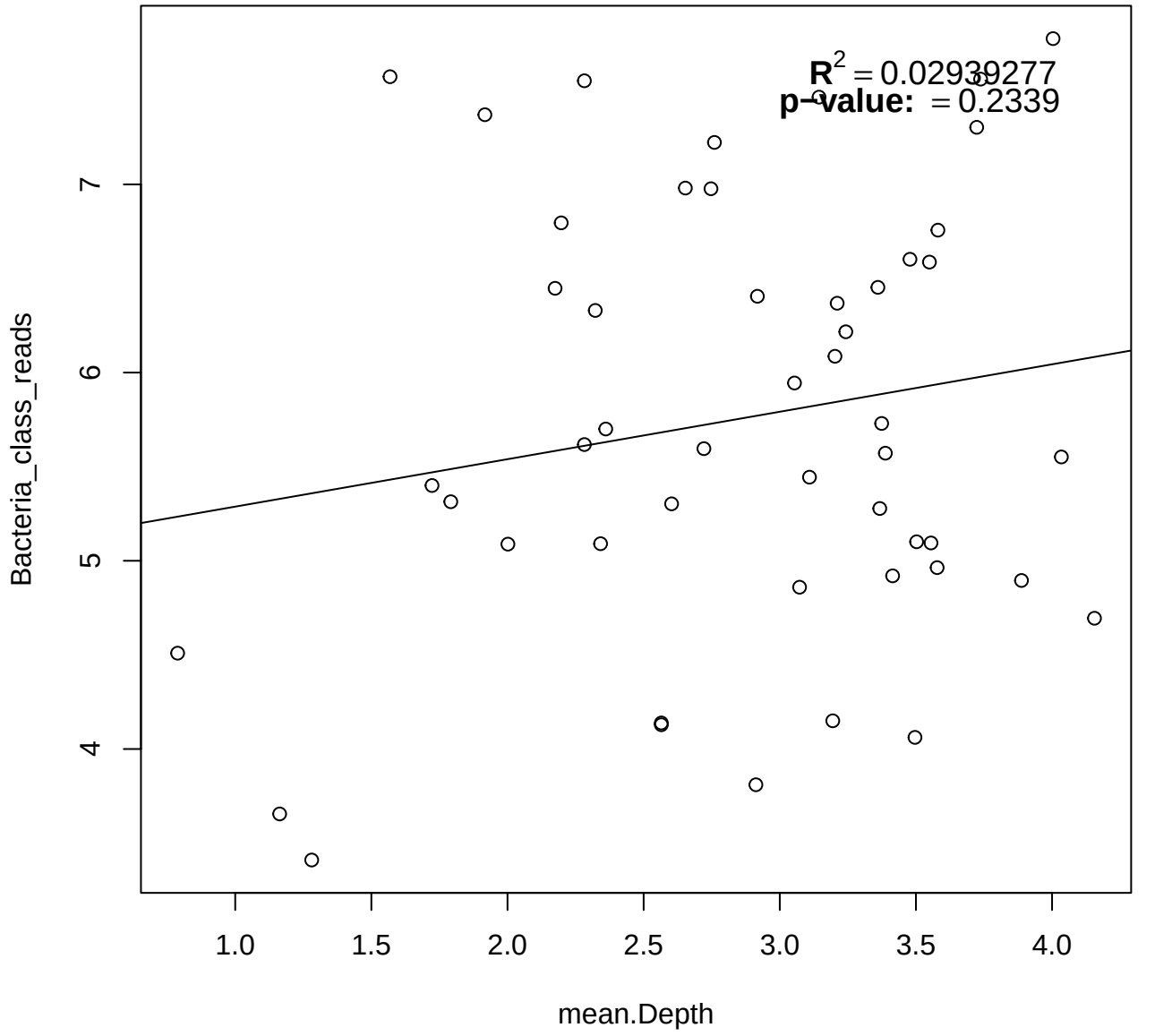

Residuals vs Fitted
Residuals
Fitted values
CasM1
GER1
RAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
CasM1
GER1
RAB1
Scale−Location
√|Standardized residuals|
Fitted values
GER1
CasM1
RAB1
Residuals vs Leverage
Standardized residuals
Leverage
ARG1
MACE1
GER1
Cook's distance
0.5
0.5

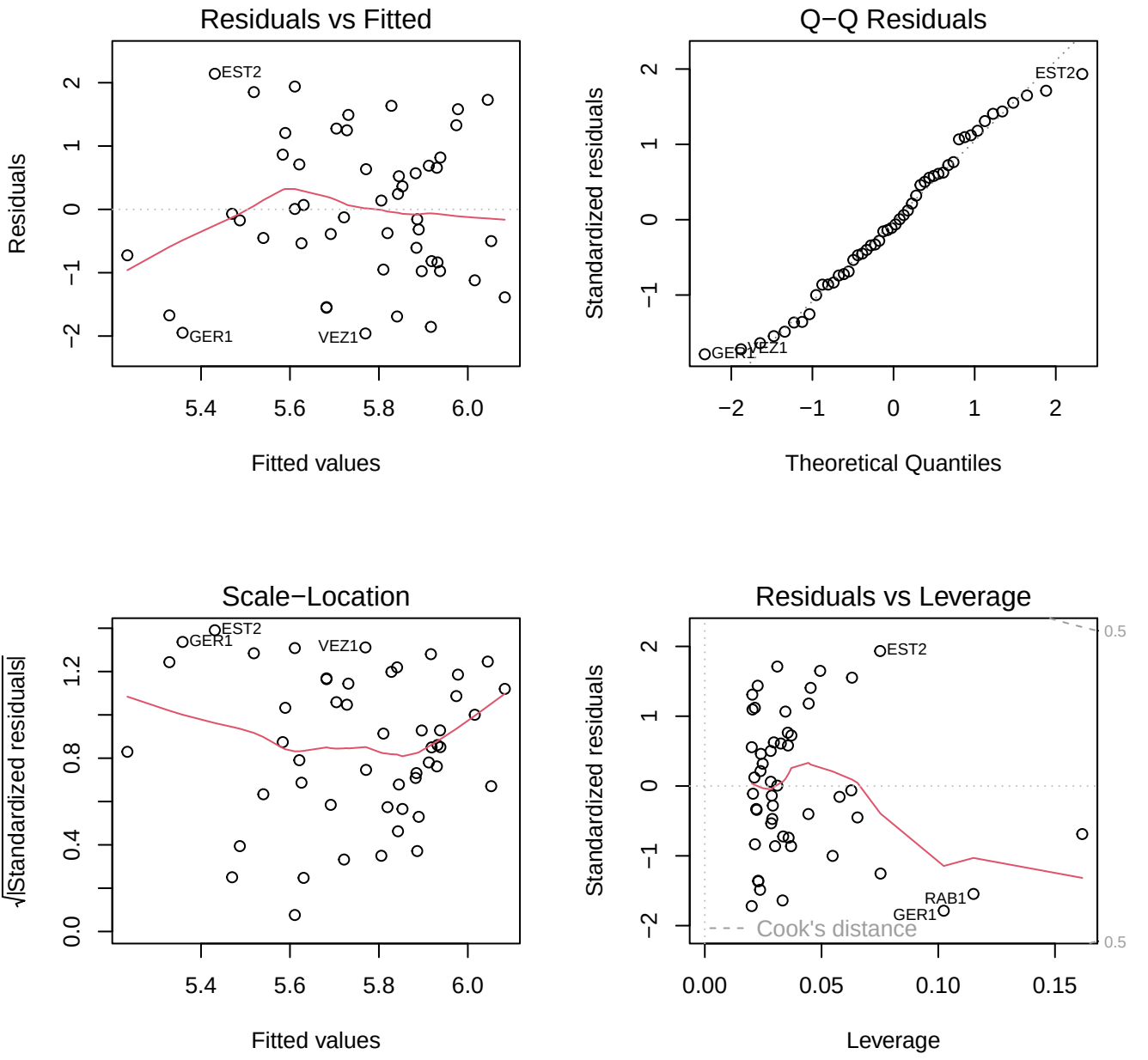

$R^2 = 0.1189582$
p−value: = 0.0142
Bacteria_class_reads
cond
4
5
6
7
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5

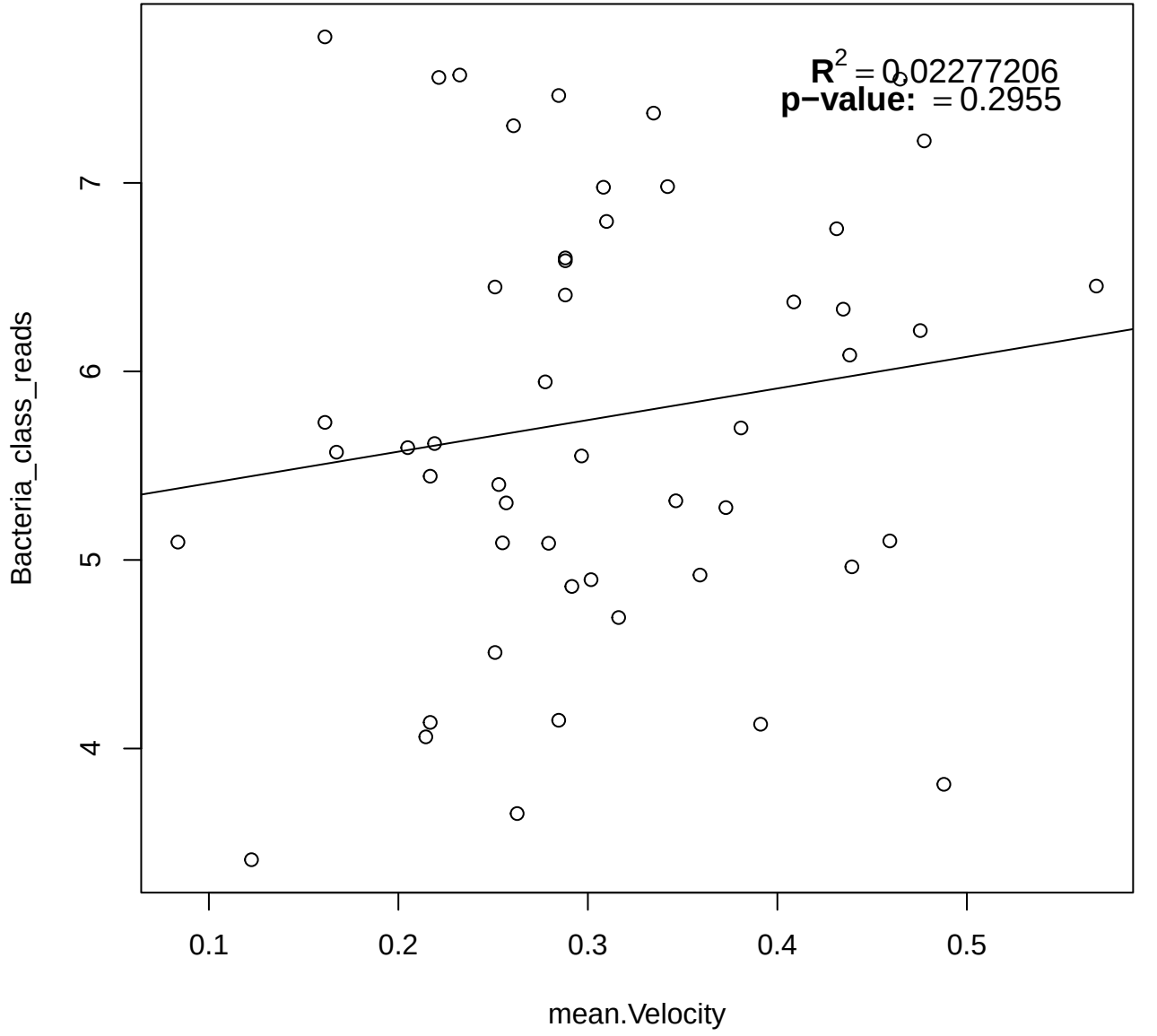

Residuals vs Fitted
Residuals
Fitted values
ERM1
RAB2
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
GER1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
GER1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
ROD1
VEZ1
Cook's distance
0.5

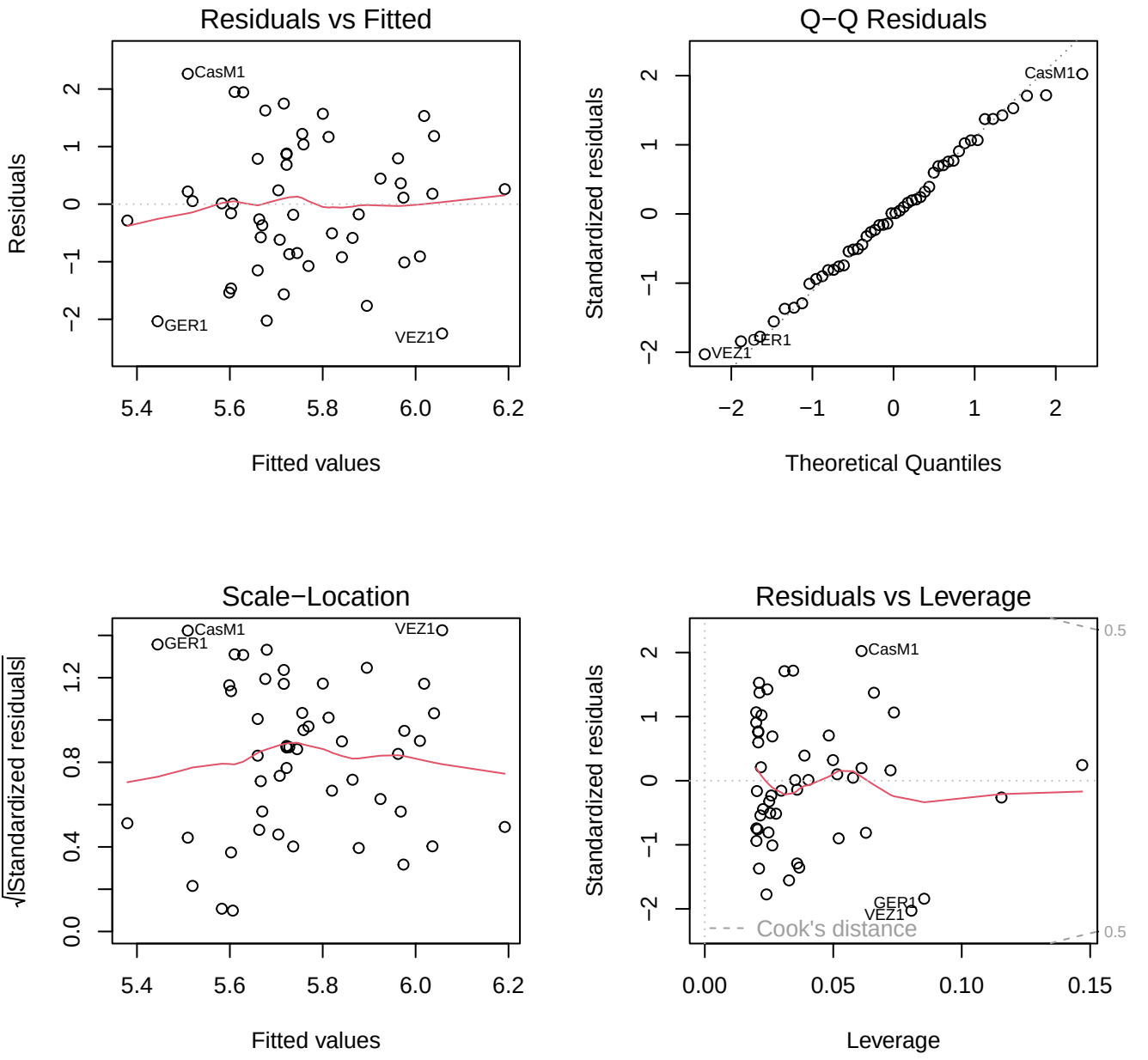

$R^2 = 0.1951567$
p−value: = 0.0013
Bacteria_class_reads
LUI_500m
4
5
6
7
0
1
2
3
4

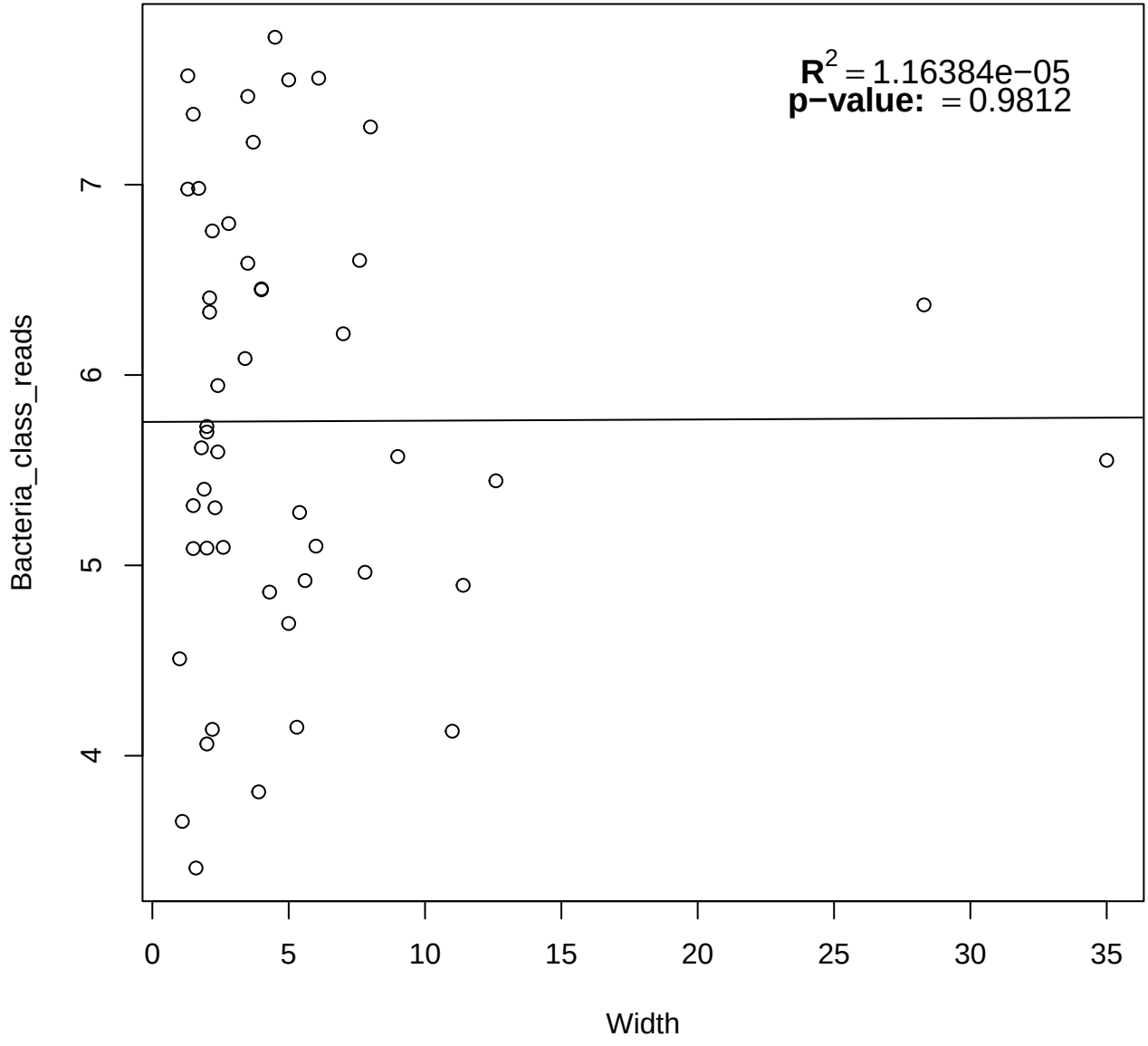

Residuals vs Fitted
Residuals
Fitted values
ERM1
RAB1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
VEZ1
RAB1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
VEZ1
RAB1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
HOM1
GER1
Cook's distance

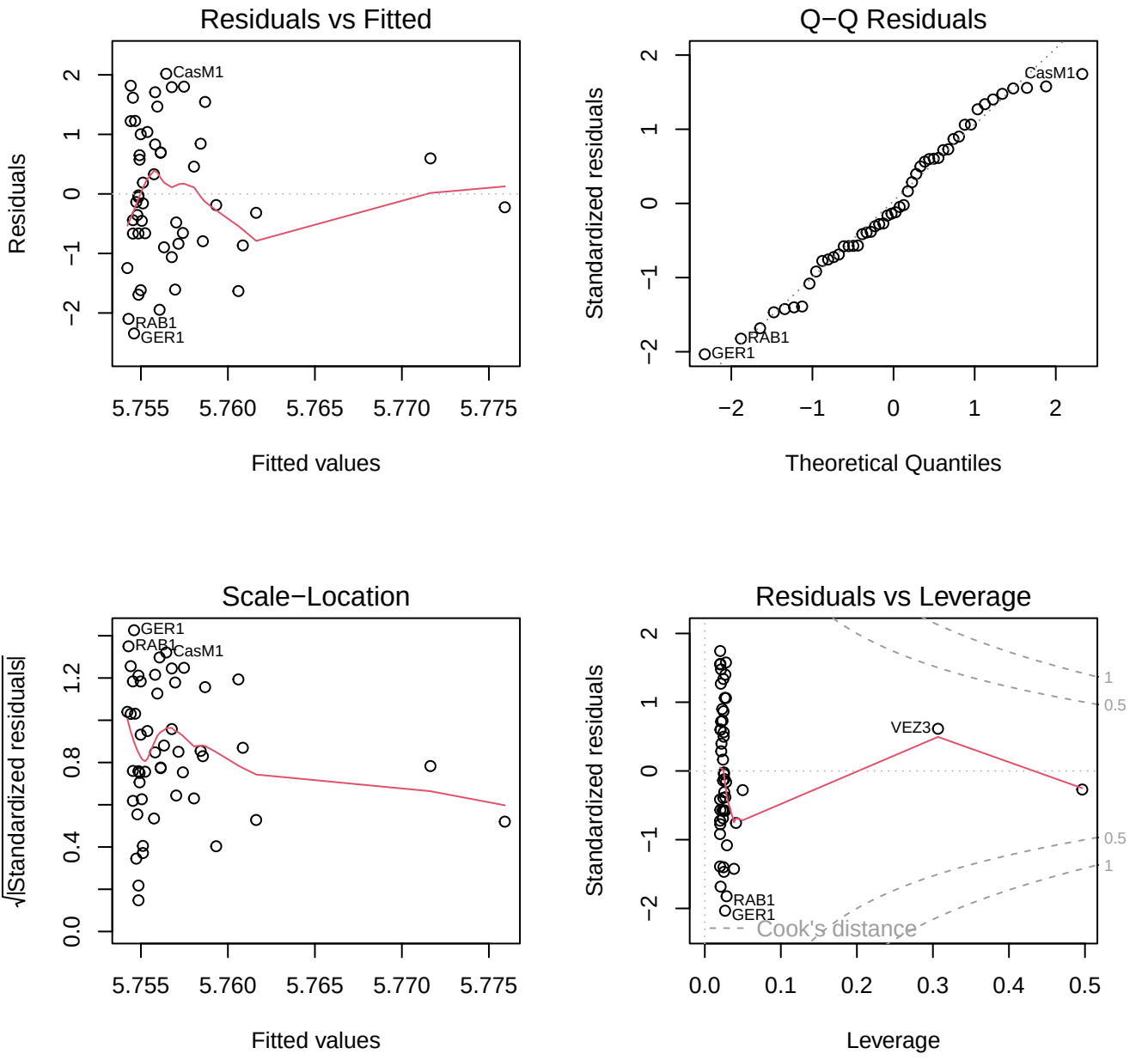

$R^2 = 0.02939277$
p-value: = 0.2339
Bacteria_class_reads
4
5
6
7
1.0
1.5
2.0
2.5
3.0
3.5
4.0
mean.Depth

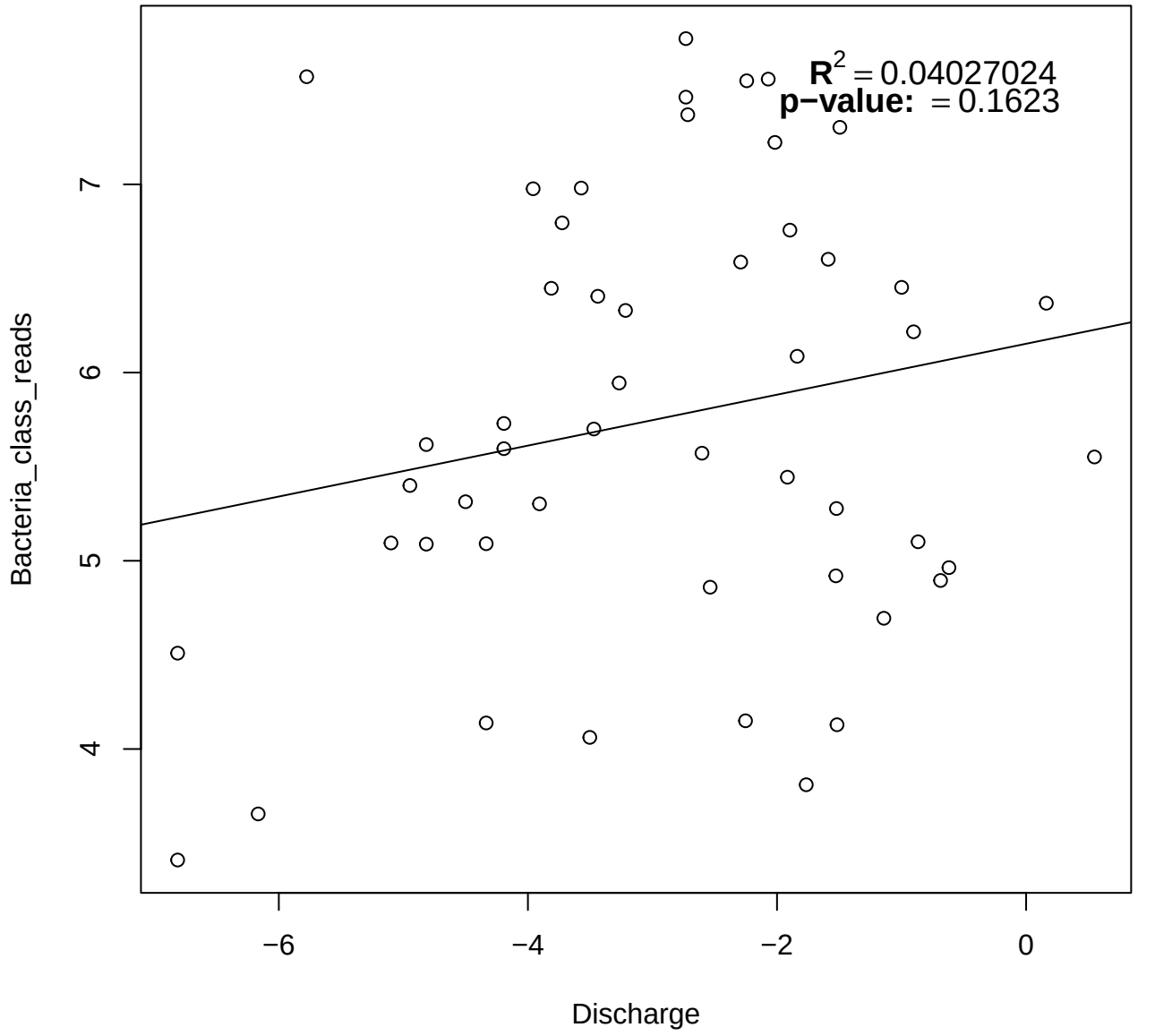

Residuals vs Fitted
Residuals
Fitted values
EST2
GER1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
EST2
GER1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
EST2
GER1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
EST2
RAB1
GER1
Cook's distance
0.5
0.5

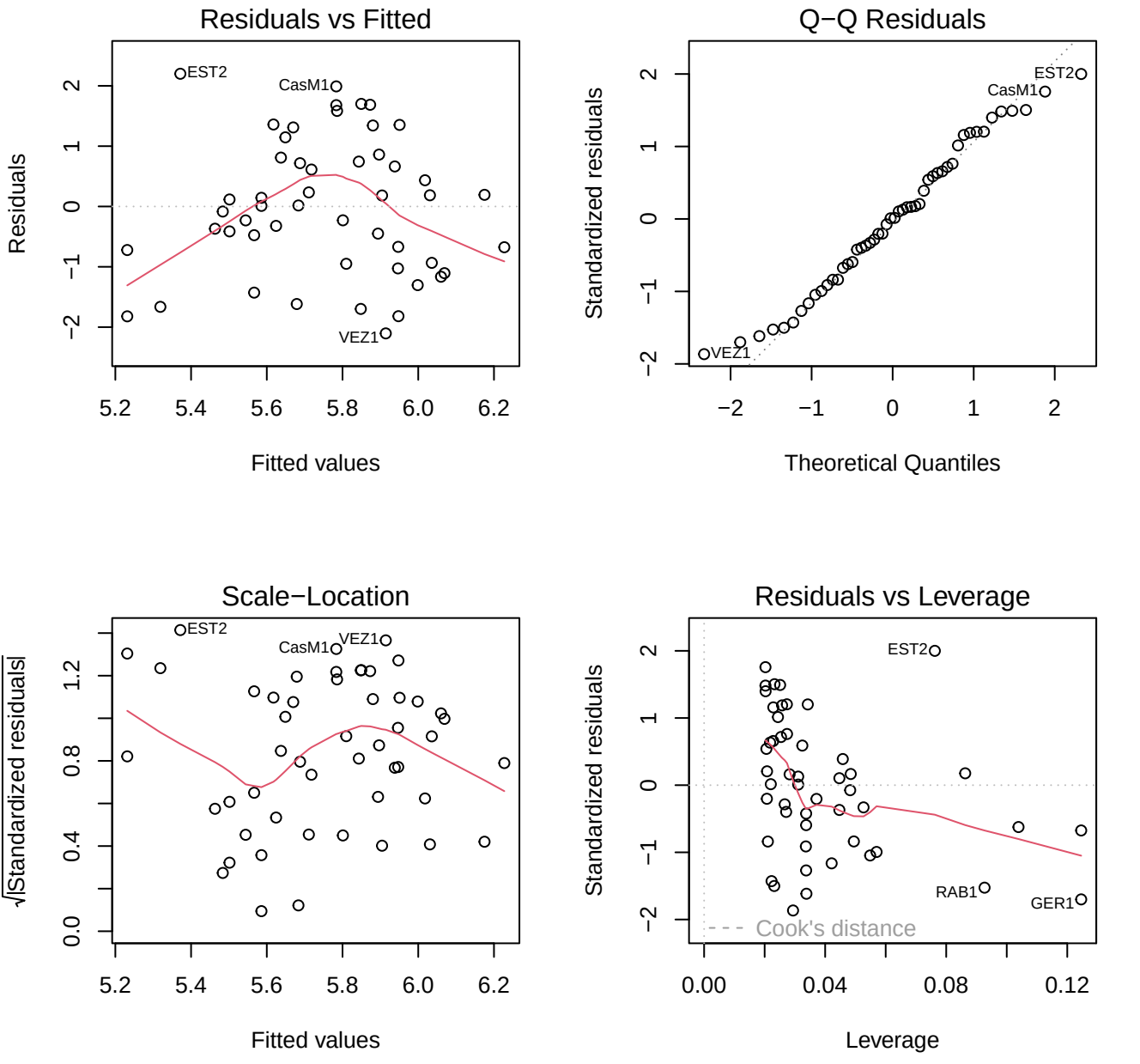

$R^2 = 0.02277206$
p−value: = 0.2955
Bacteria_class_reads
4
5
6
7
0.1
0.2
0.3
0.4
0.5
mean.Velocity

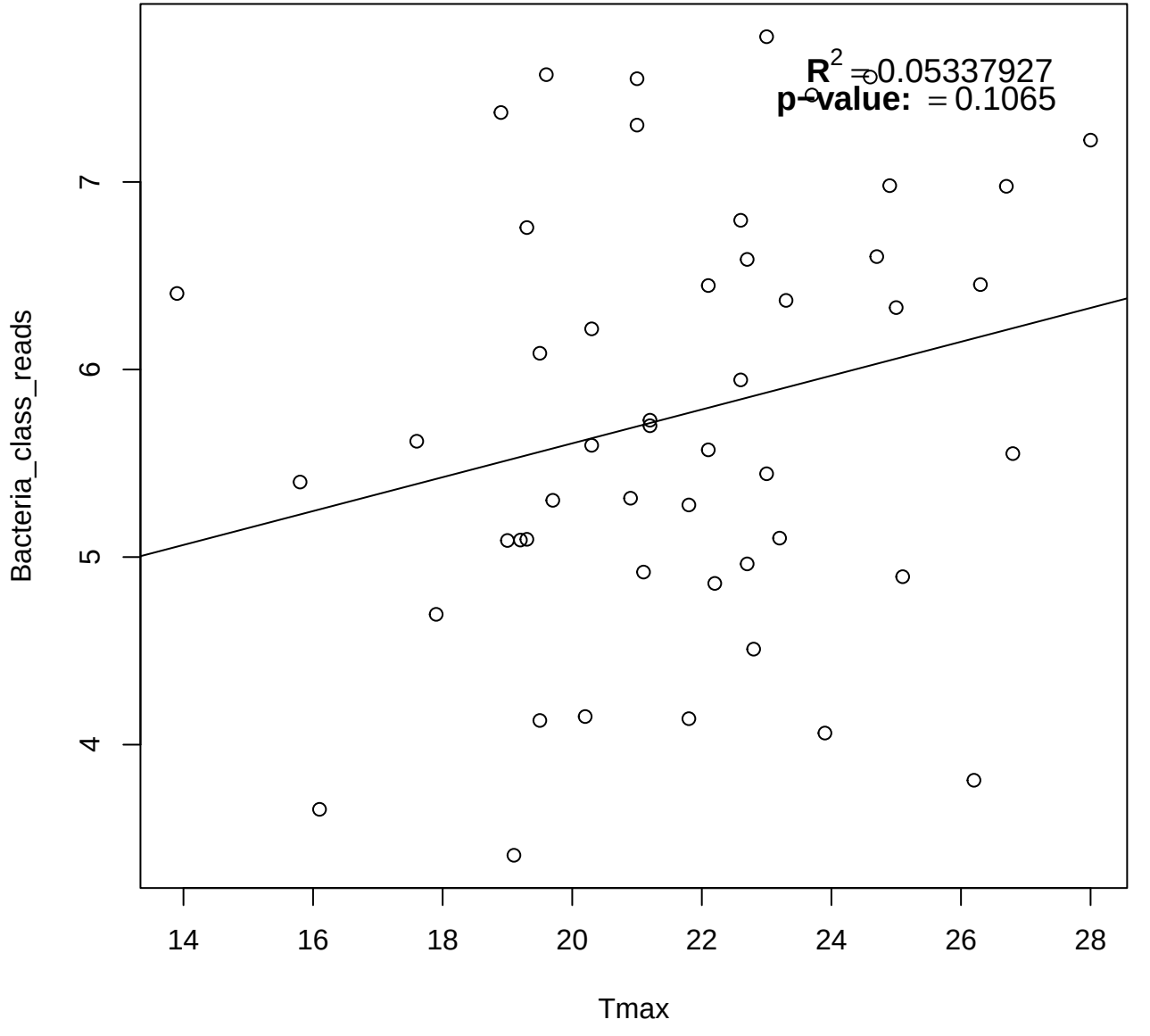

Residuals vs Fitted
Residuals
Fitted values
CasM1
GER1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
CasM1
GER1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
CasM1
GER1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
CasM1
GER1
VEZ1
Cook's distance
0.5
0.5

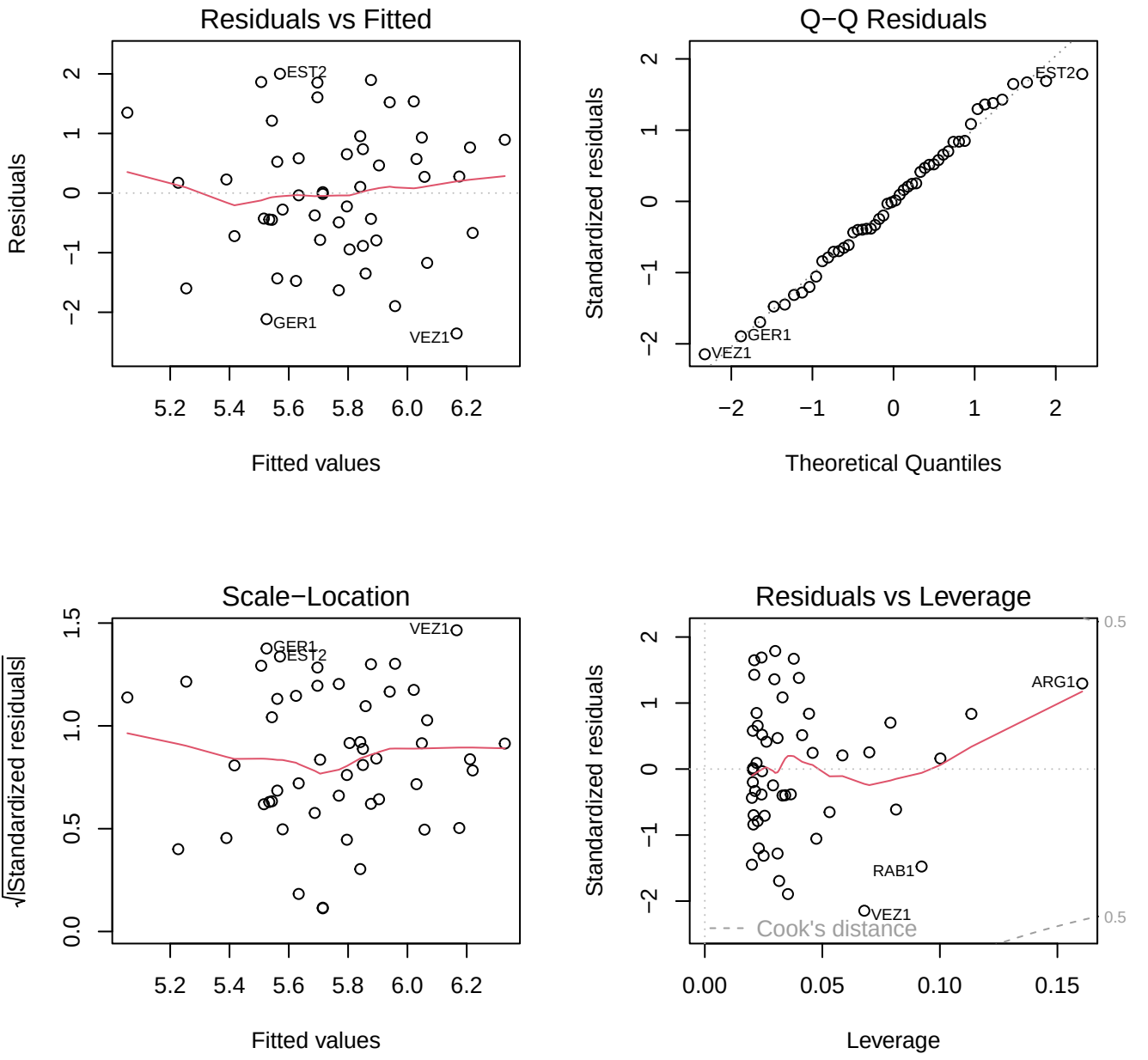

$R^2 = 1.16384e-05$
p−value: = 0.9812
Bacteria_class_reads
Width
4
5
6
7
0
5
10
15
20
25
30
35

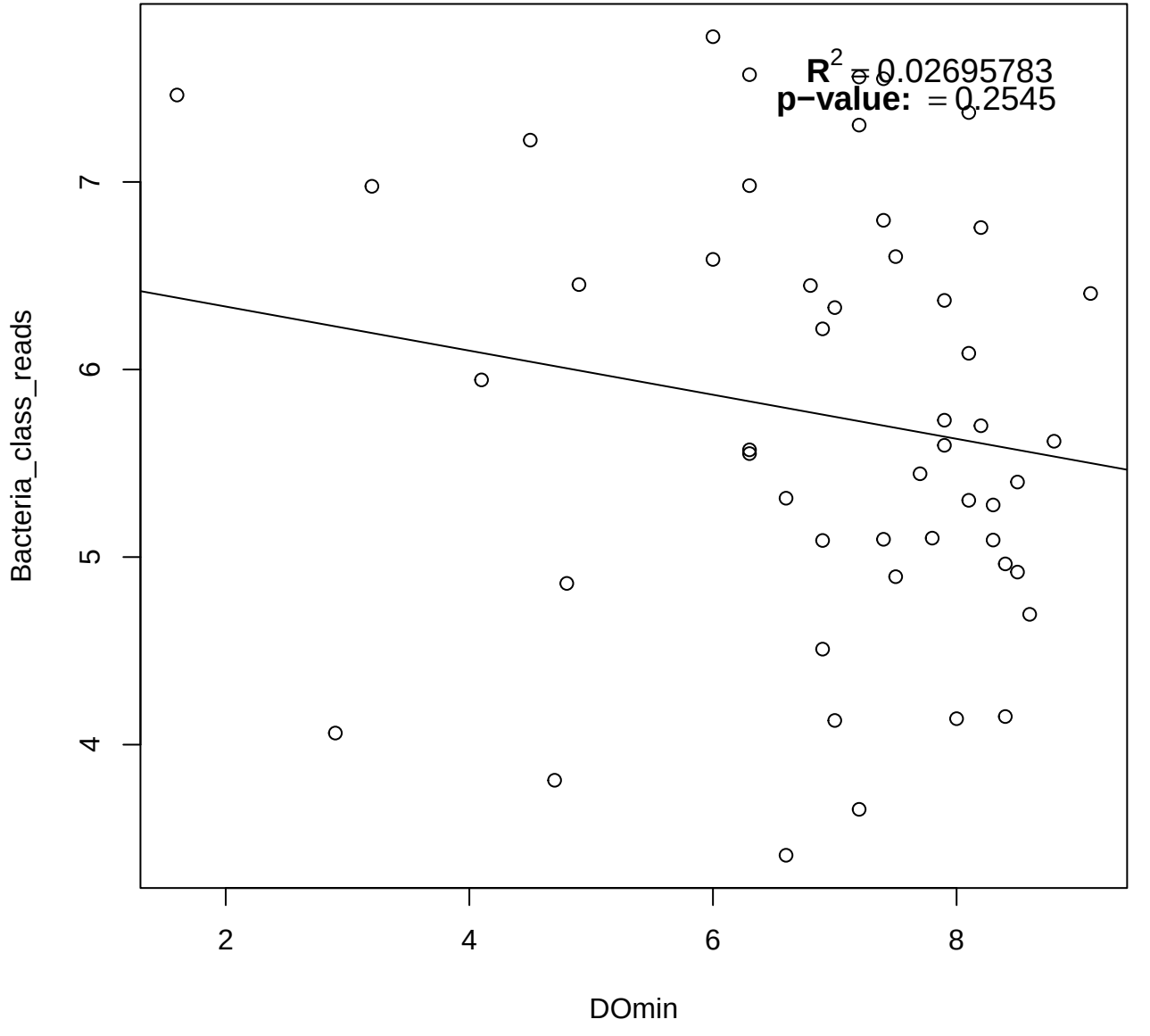

Residuals vs Fitted
Residuals
Fitted values
CasM1
RAB1
GER1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
CasM1
RAB1
GER1
Scale−Location
√|Standardized residuals|
Fitted values
GER1
RAB1
CasM1
Residuals vs Leverage
Standardized residuals
Leverage
VEZ3
RAB1
GER1
Cook's distance

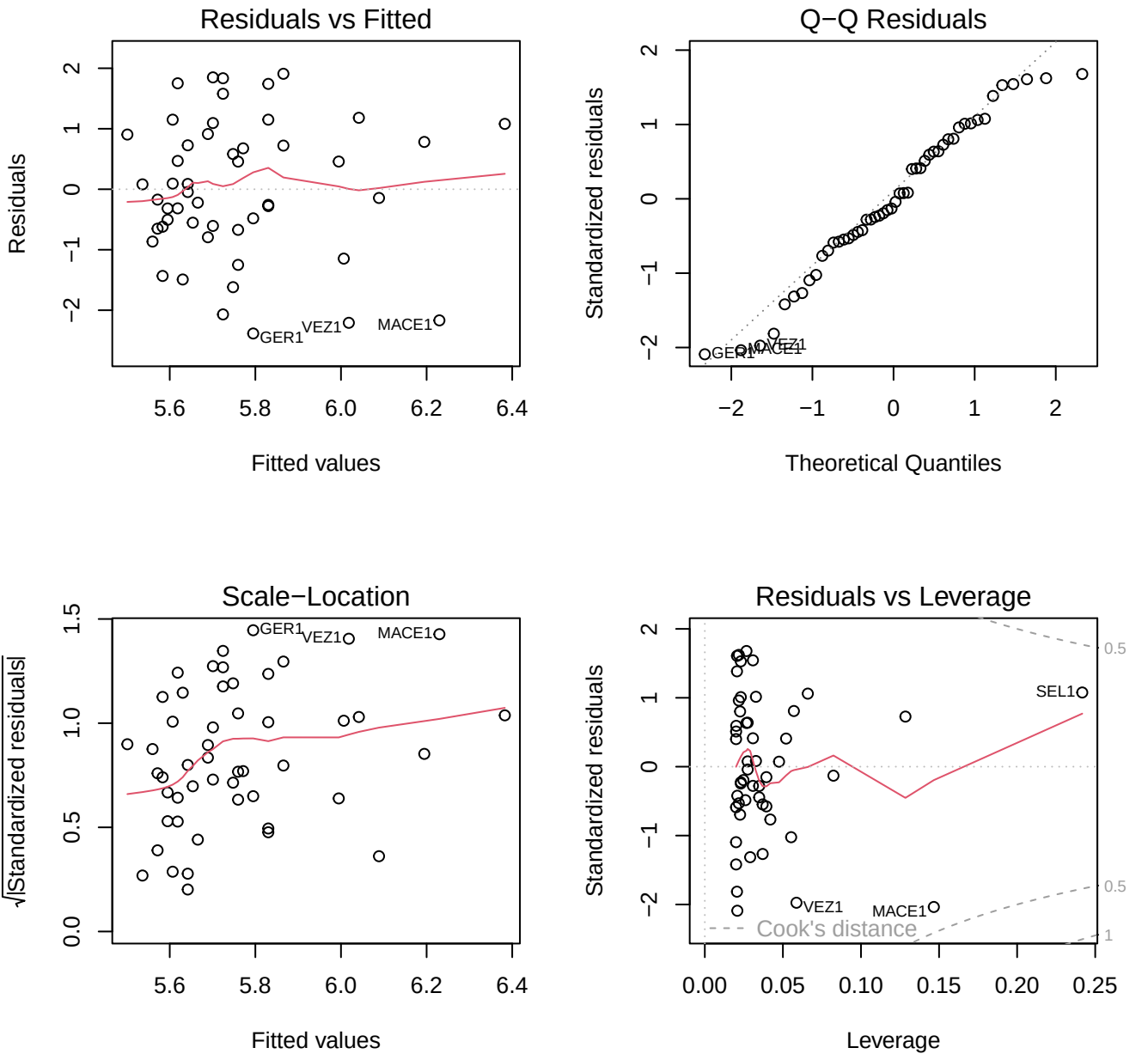

$R^2 = 0.04027024$
p−value: = 0.1623
Bacteria_class_reads
4
5
6
7
−6
−4
−2
0
Discharge

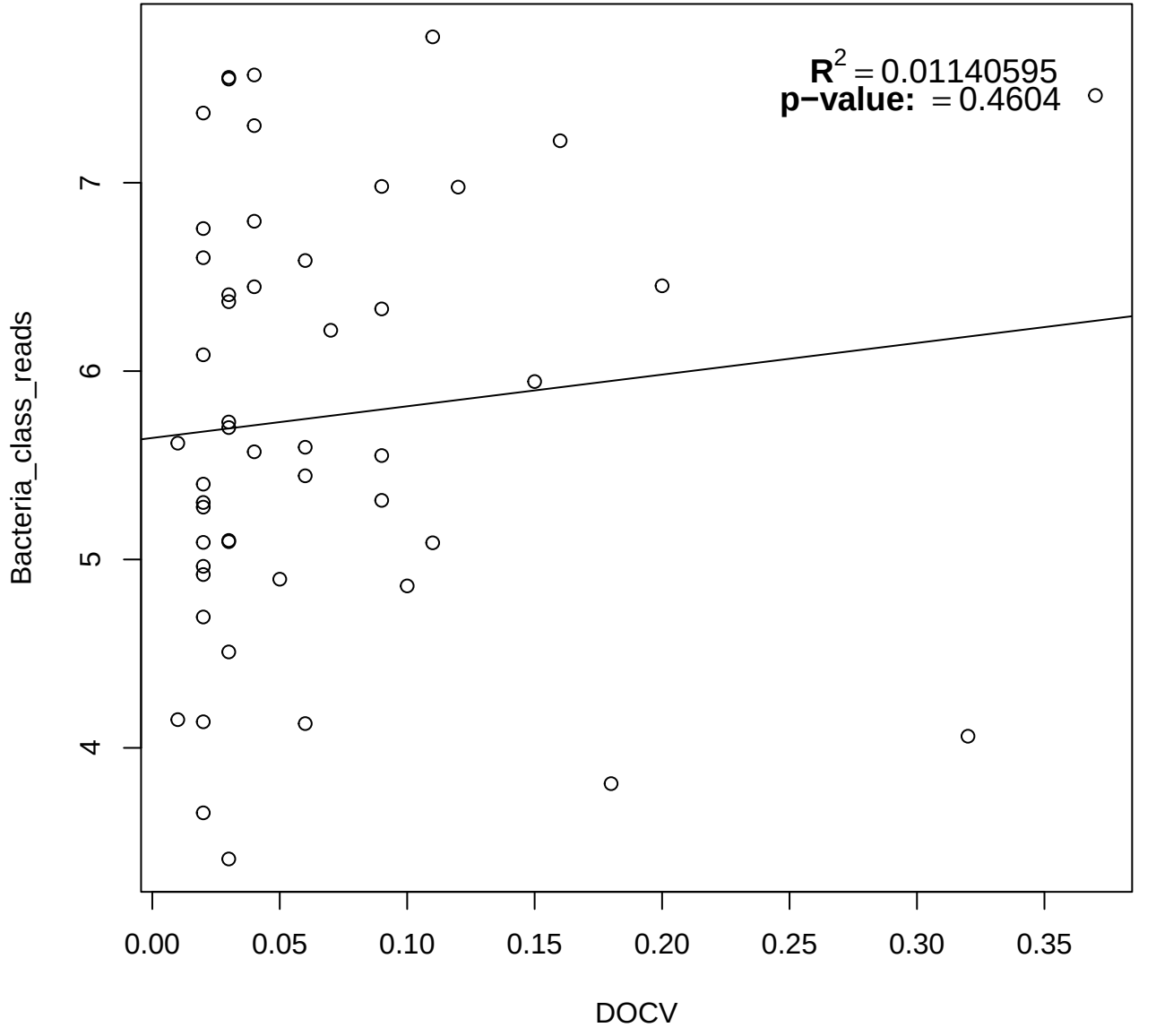

Residuals vs Fitted
Residuals
Fitted values
EST2
CasM1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
EST2
CasM1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
EST2
CasM1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
EST2
RAB1
GER1
Cook's distance

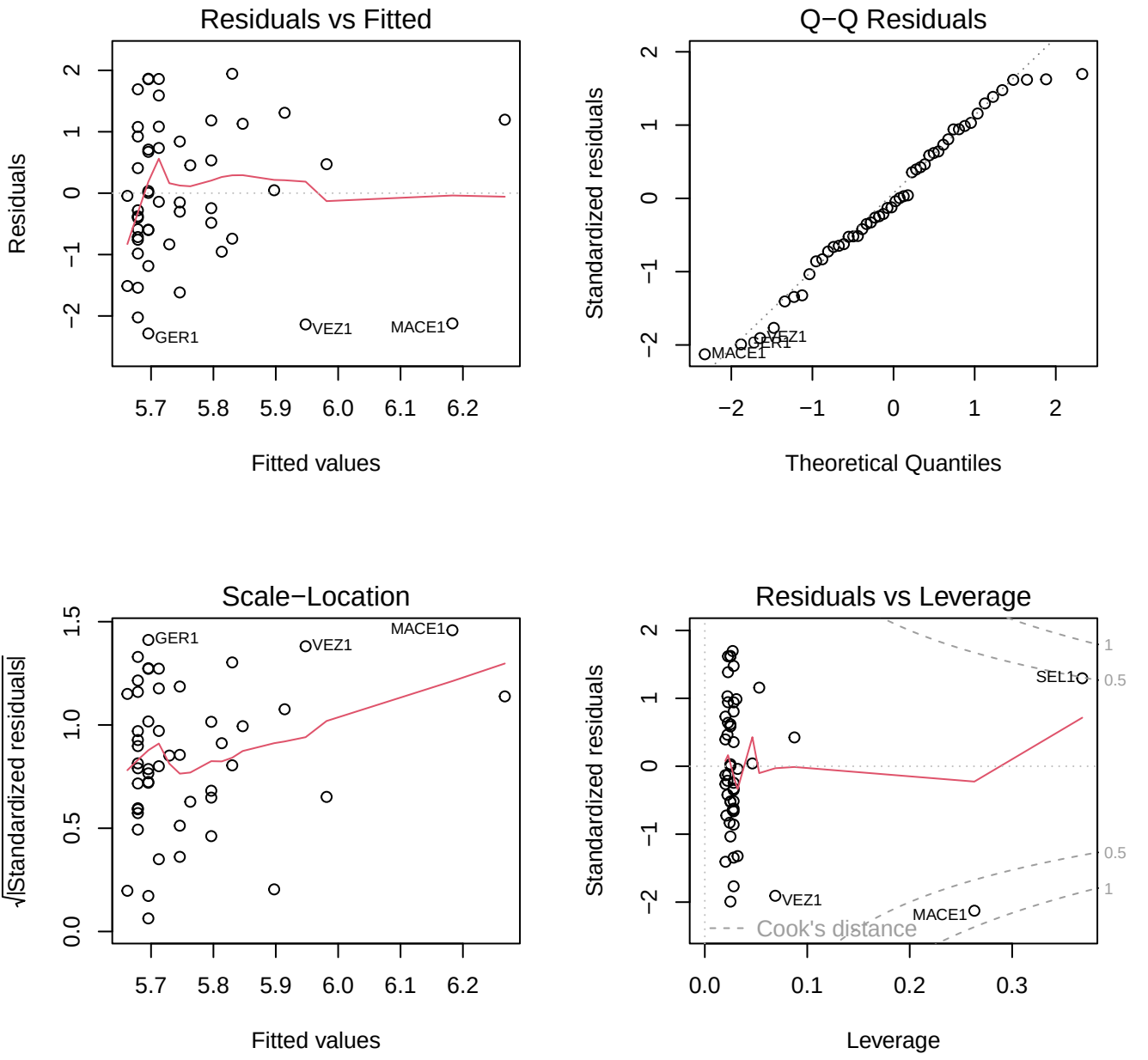

R^2 = 0.05337927
p-value: = 0.1065
Bacteria_class_reads
Tmax
4
5
6
7
14
16
18
20
22
24
26
28

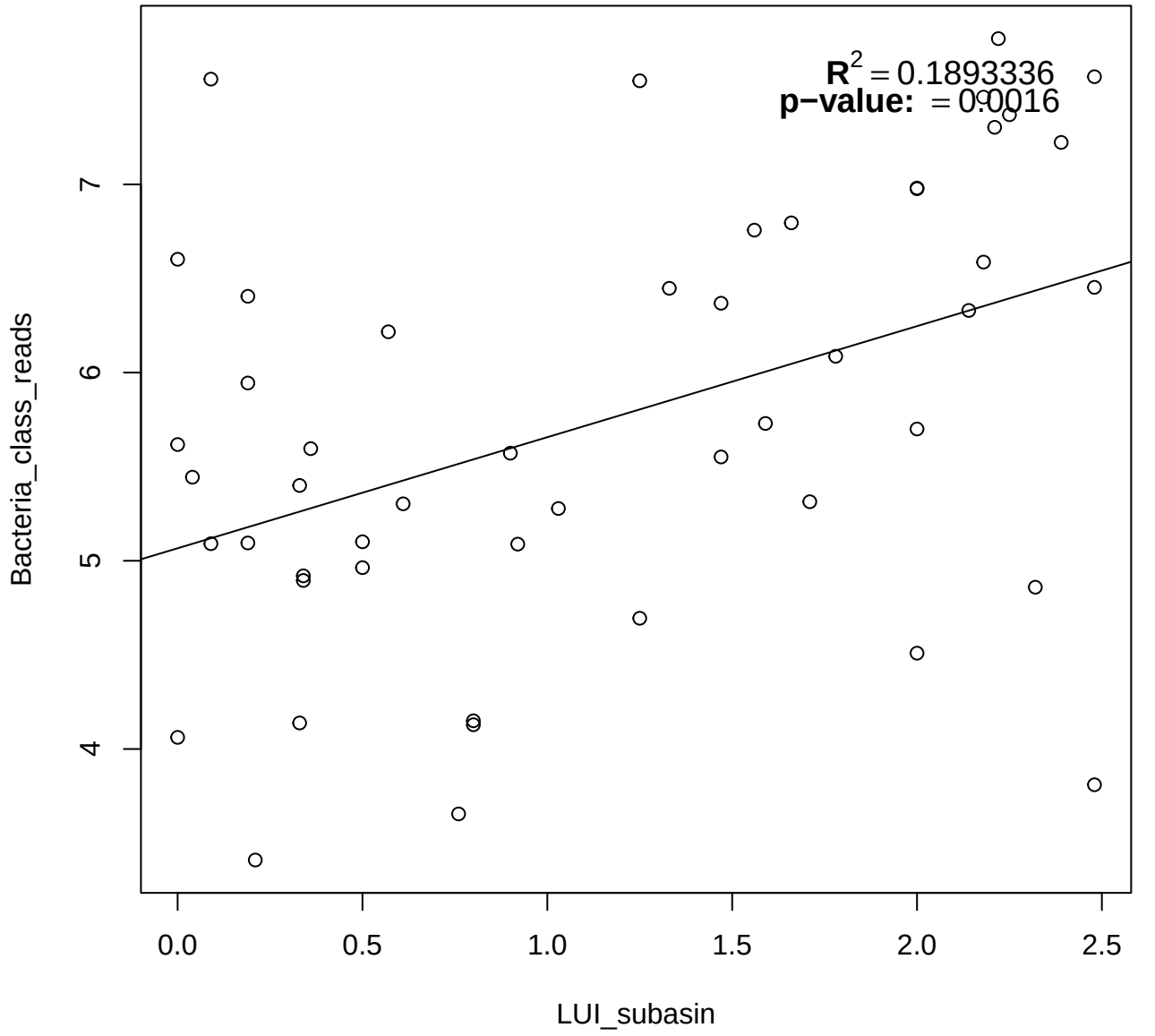

Residuals vs Fitted
Residuals
Fitted values
EST2
GER1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
EST2
GER1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
VEZ1
GER1
EST2
Residuals vs Leverage
Standardized residuals
Leverage
ARG1
RAB1
VEZ1
Cook's distance
0.5
0.5

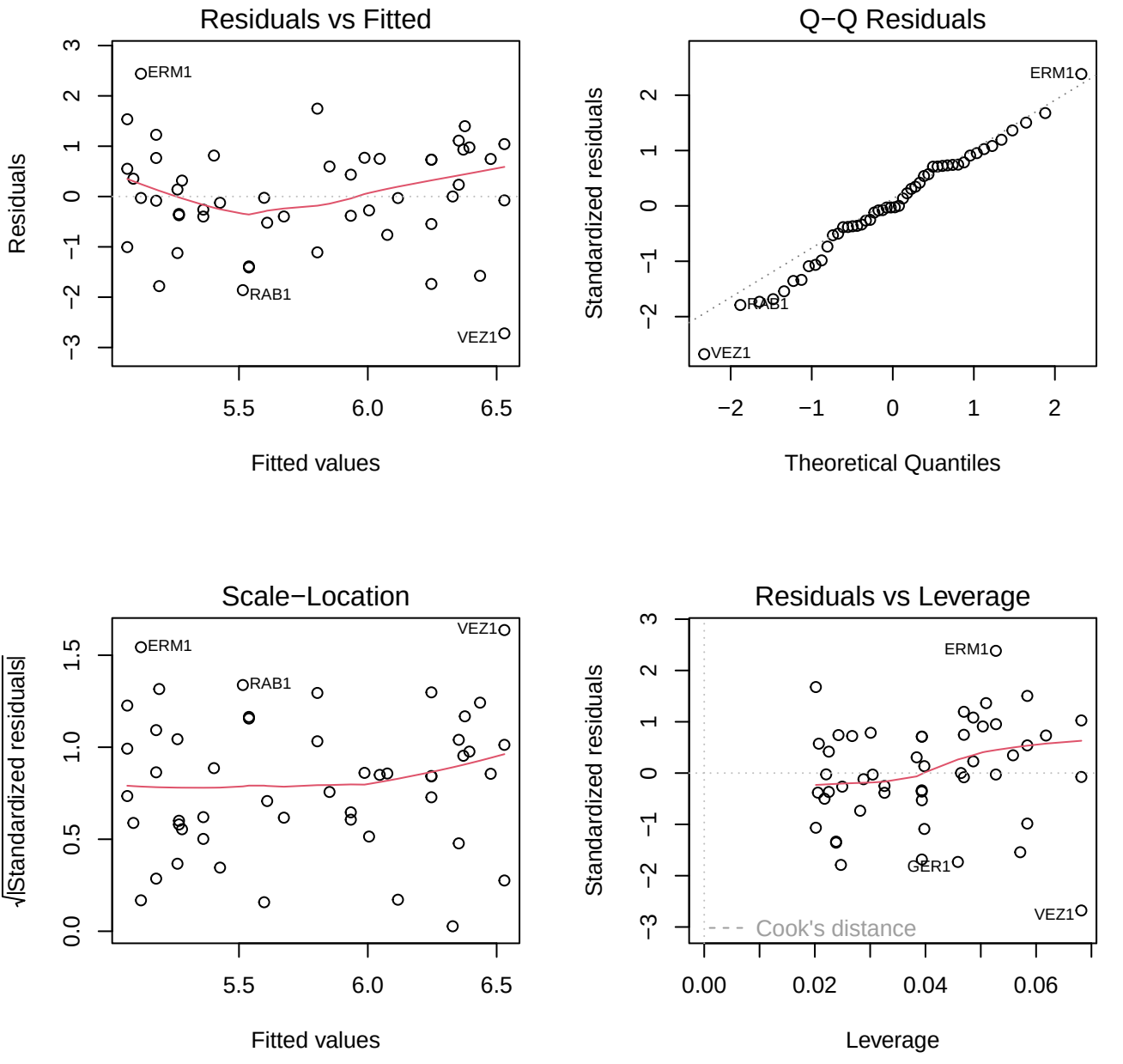

$R^2 = 0.02695783$
p−value: = 0.2545
Bacteria_class_reads
DOmin
4
5
6
7
2
4
6
8

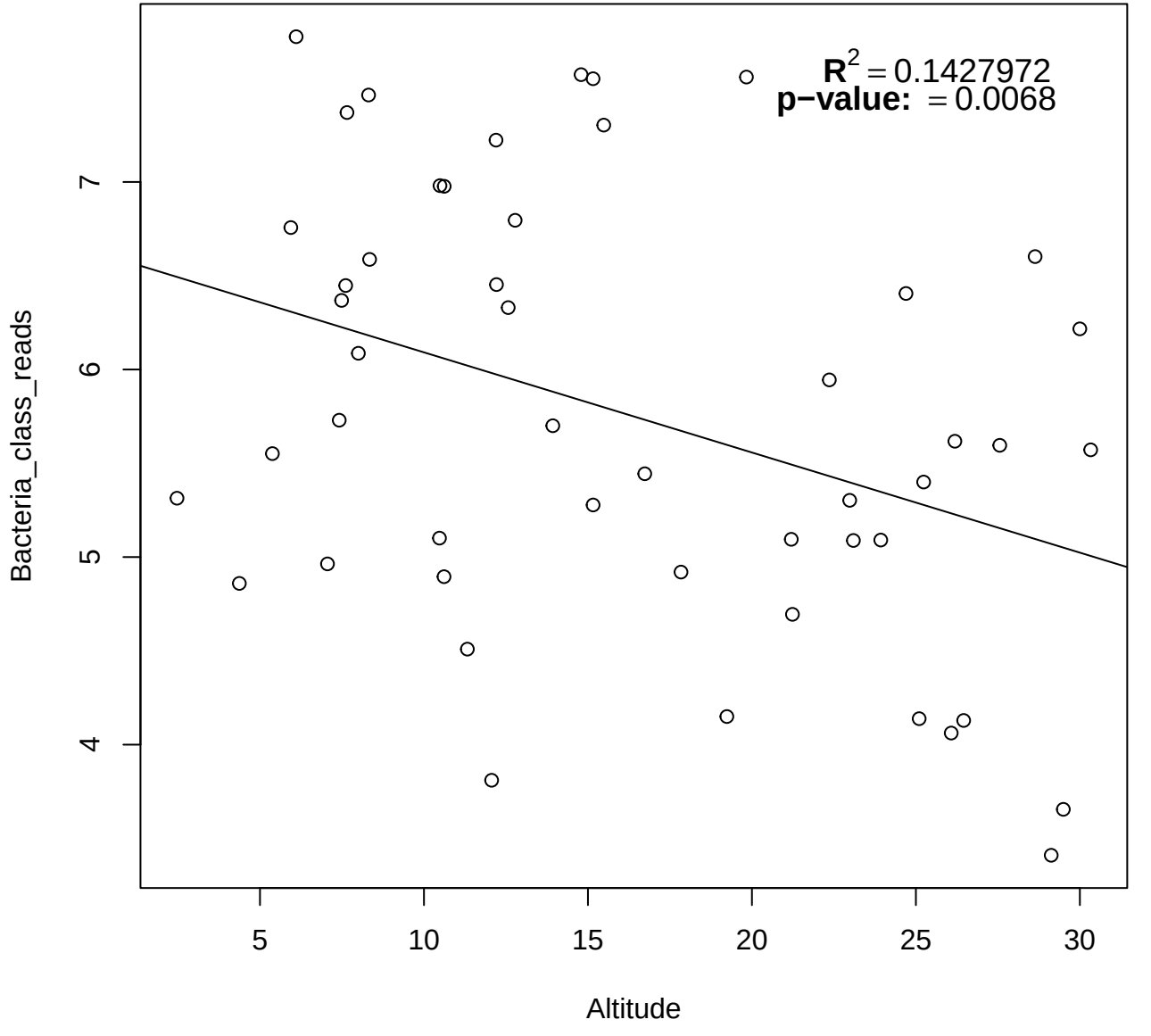

Residuals vs Fitted
Residuals
Fitted values
GER1
VEZ1
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
GER1
VEZ1
MACE1
Scale−Location
√|Standardized residuals|
Fitted values
GER1
VEZ1
MACE1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
VEZ1
MACE1
Cook's distance
0.5
0.5
1

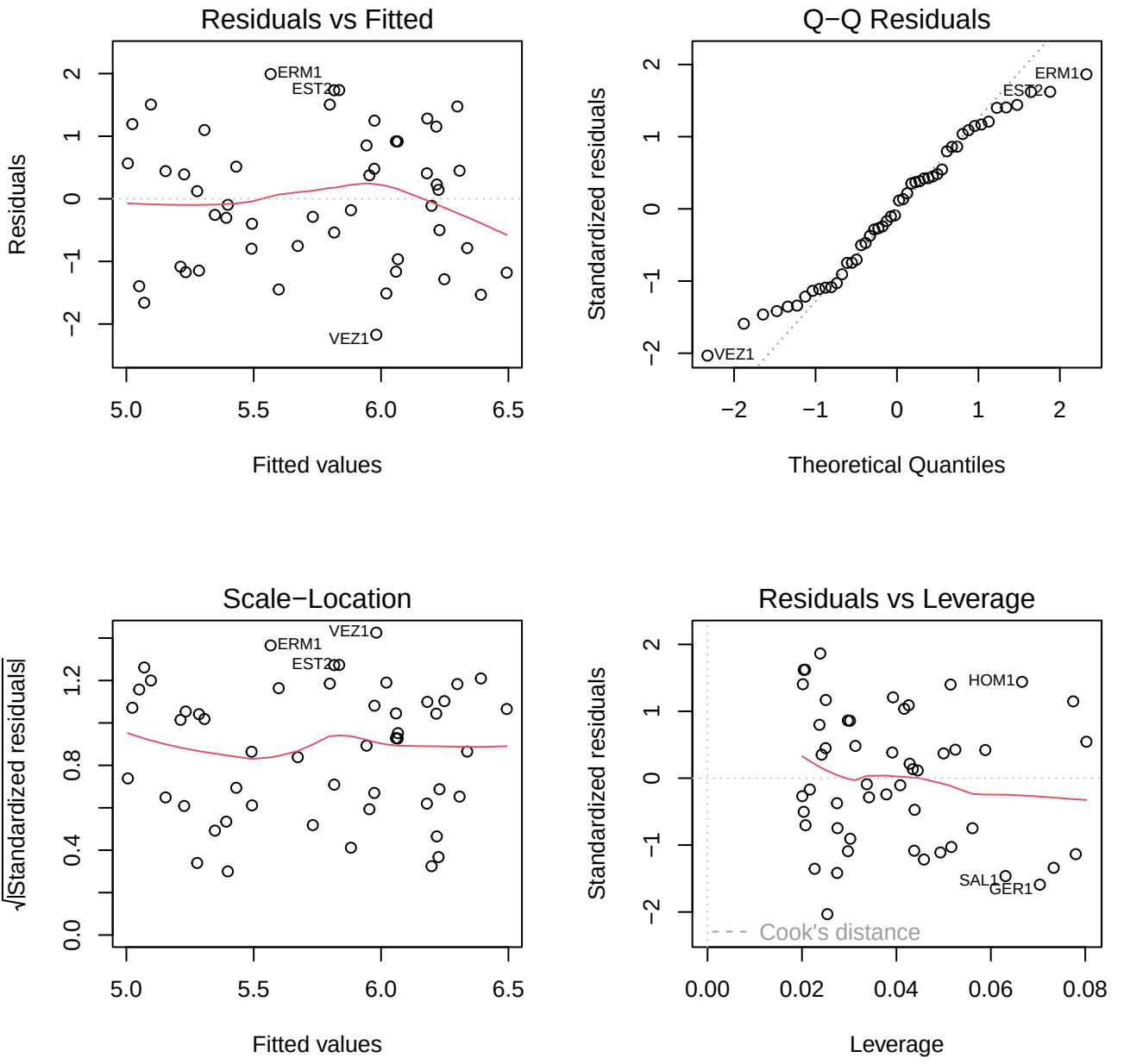

$R^2 = 0.01140595$
p−value: = 0.4604
Bacteria_class_reads
DOCV
4
5
6
7
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35

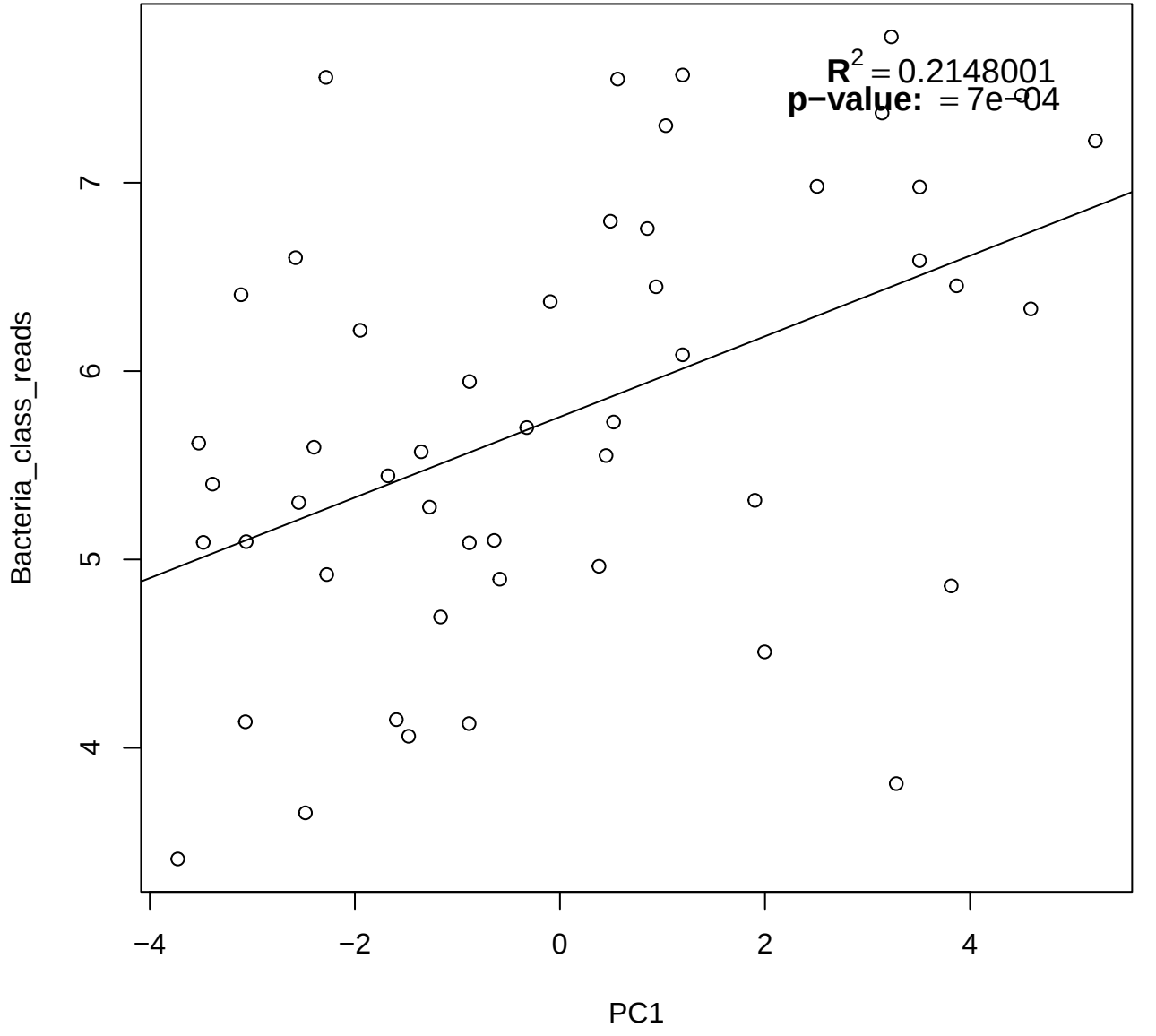

Residuals vs Fitted
Residuals
Fitted values
GER1
VEZ1
MACE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
MACE1
VEZ1
GER1
Scale−Location
√|Standardized residuals|
Fitted values
GER1
VEZ1
MACE1
Residuals vs Leverage
Standardized residuals
Leverage
SEL1
VEZ1
MACE1
Cook's distance
1
0.5
0.5
1

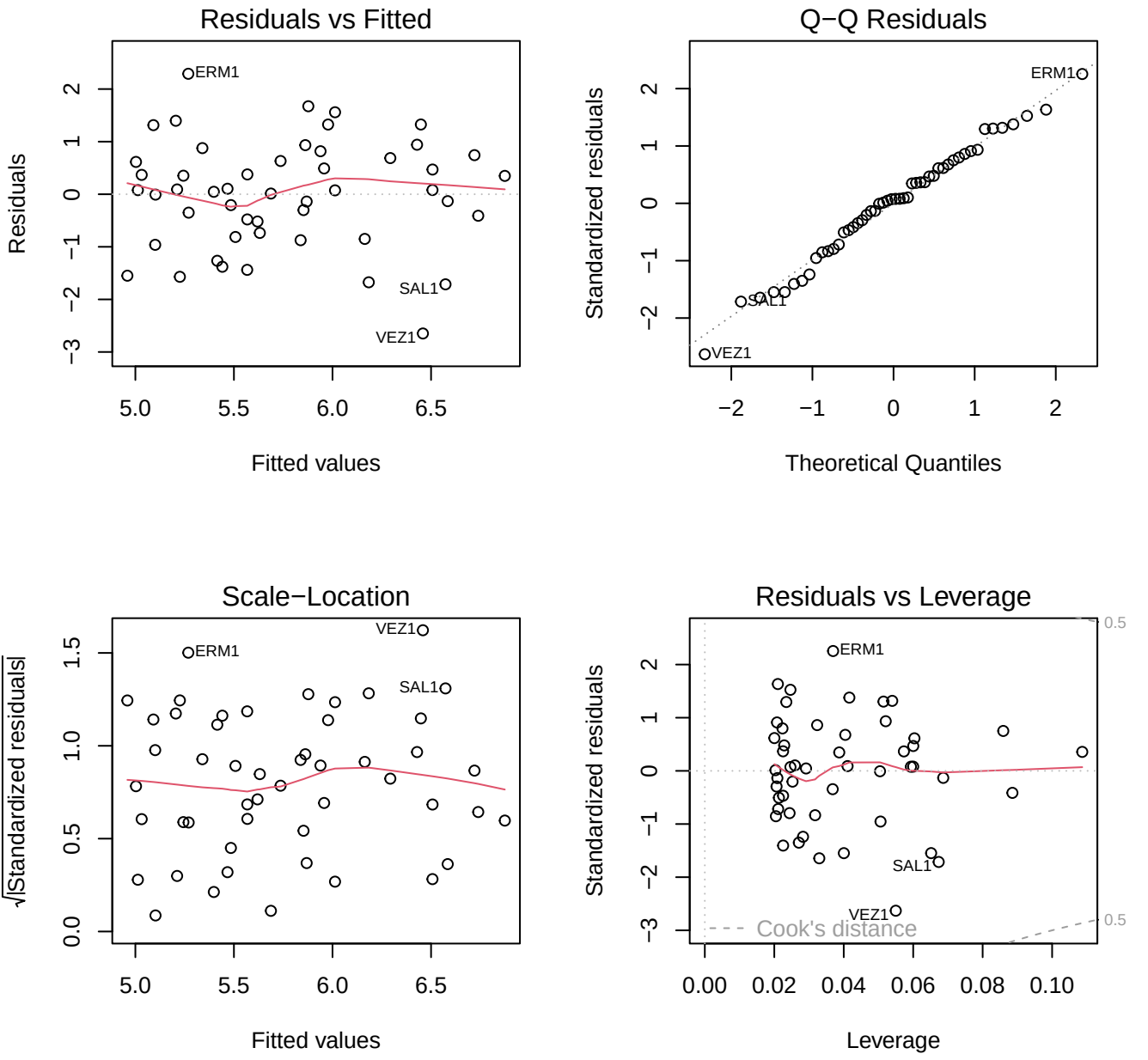

$R^2 = 0.1893336$
p−value: = 0.0016
Bacteria_class_reads
LUI_subasin
4
5
6
7
0.0
0.5
1.0
1.5
2.0
2.5

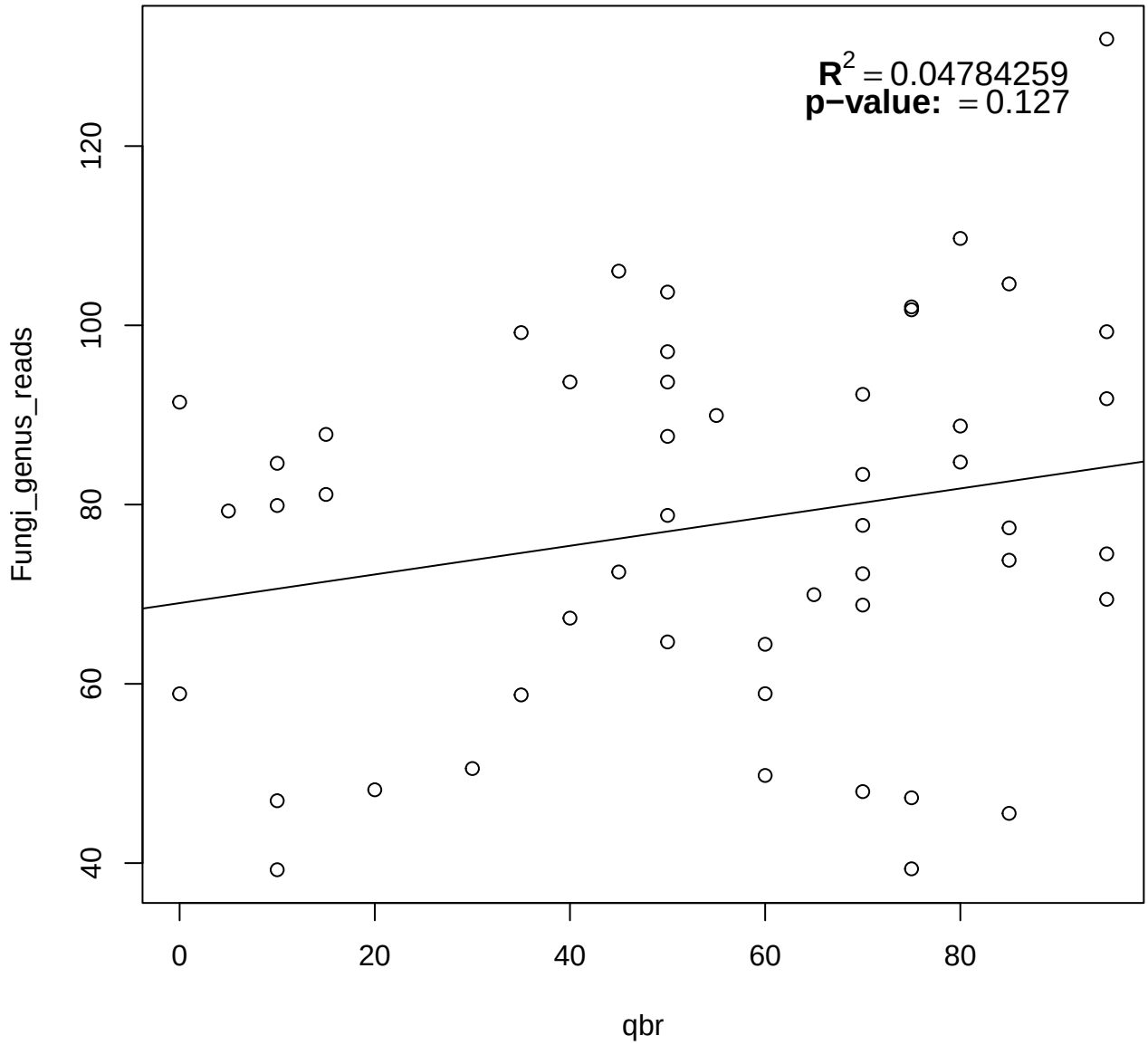

Residuals vs Fitted
Residuals
Fitted values
ERM1
RAB1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
RAB1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
RAB1
VEZ1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
GER1
VEZ1
Cook's distance

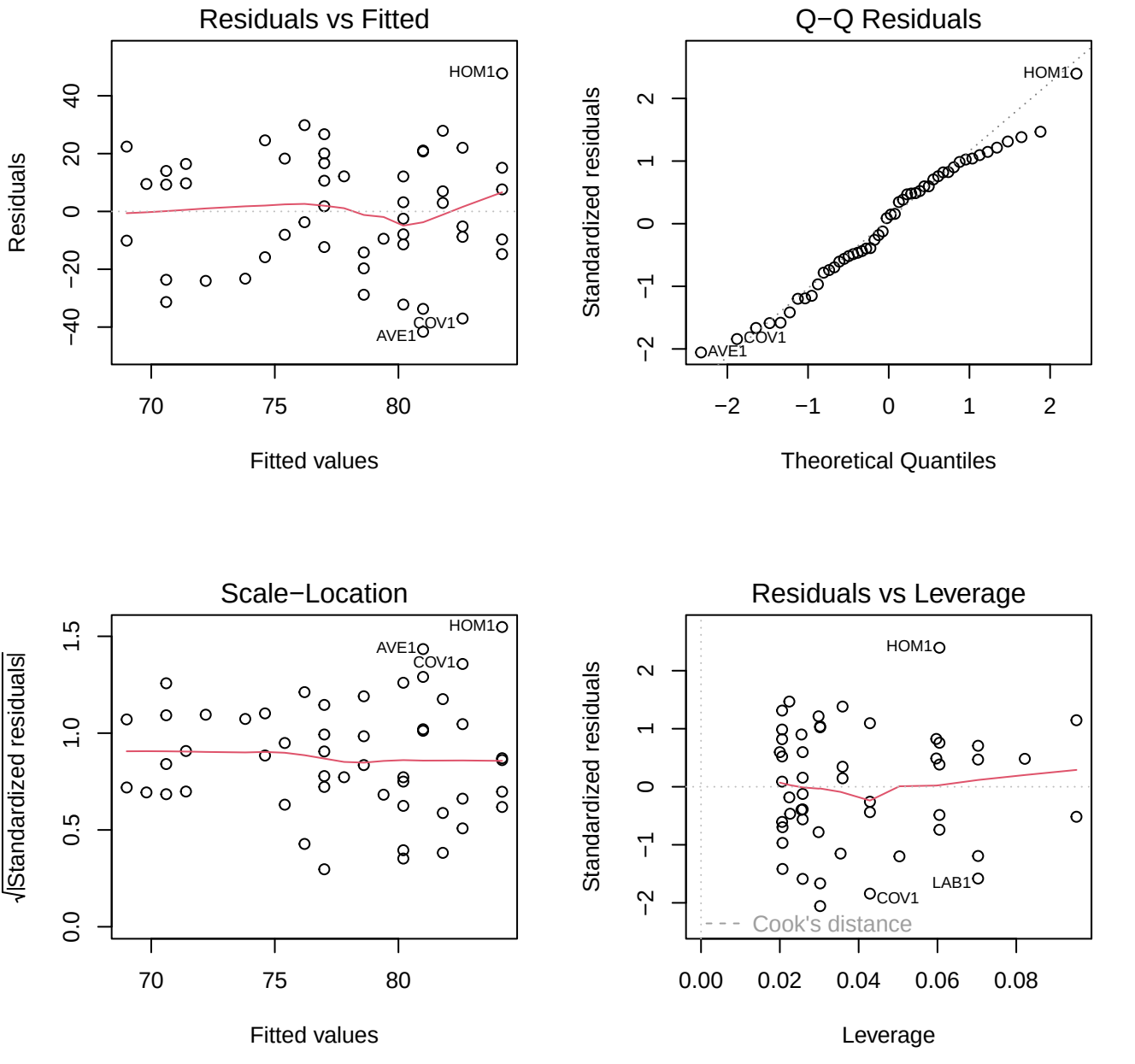

$R^2 = 0.1427972$
p−value: = 0.0068
Bacteria_class_reads
Altitude
4
5
6
7
5
10
15
20
25
30

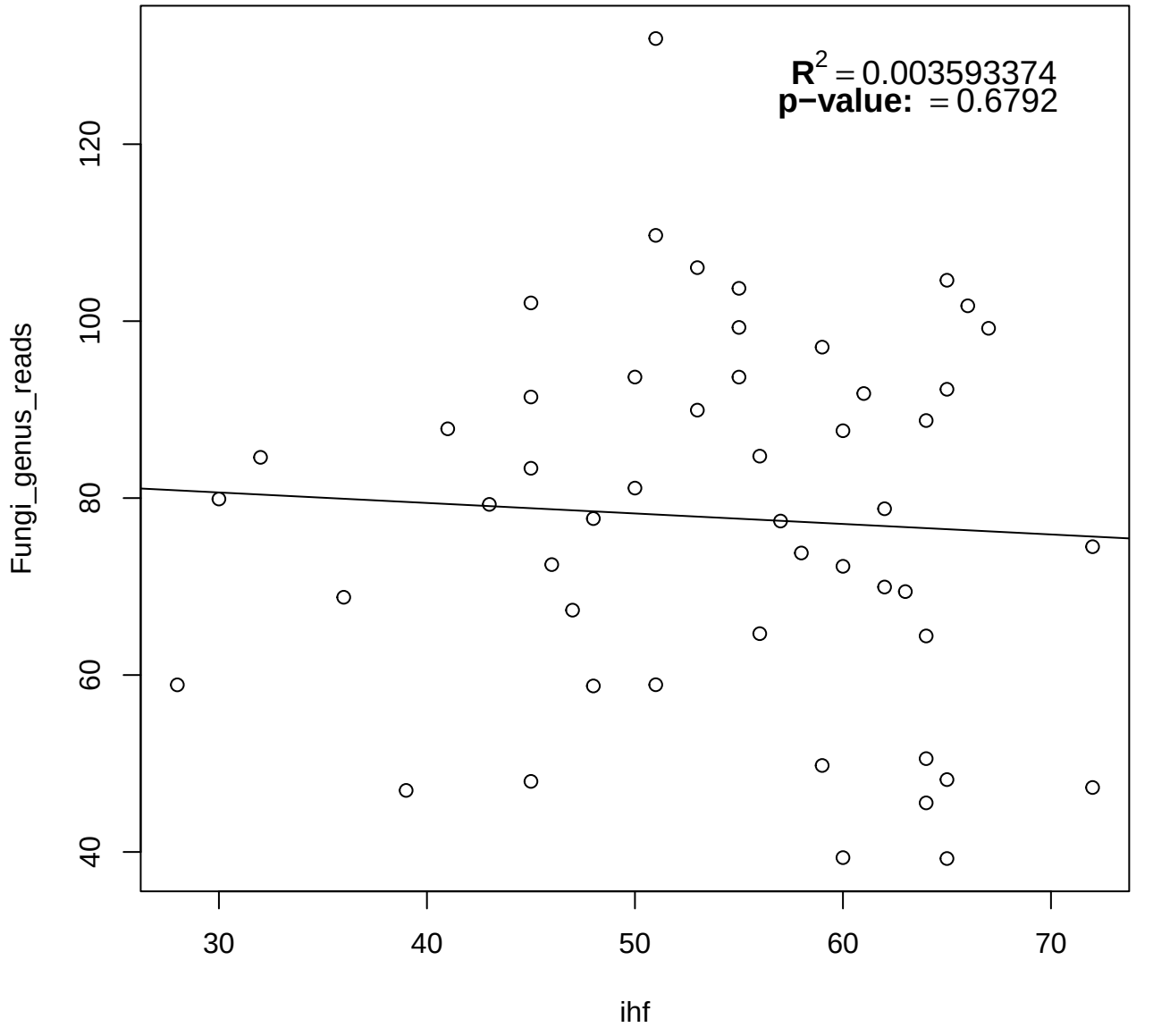

Residuals vs Fitted
Residuals
Fitted values
ERM1
EST2
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
EST2
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
VEZ1
ERM1
EST2
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
SAL1
GER1
Cook's distance

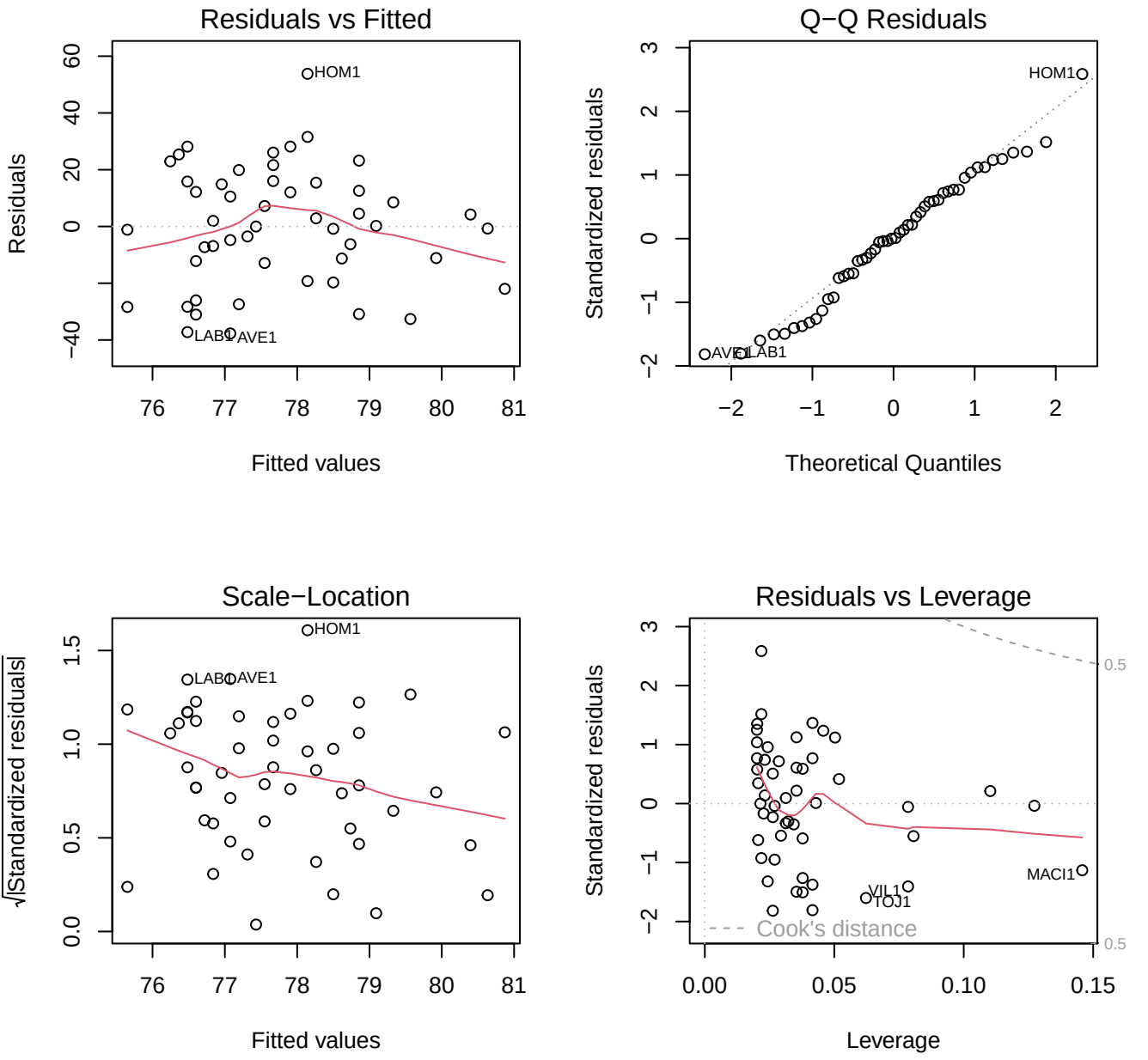

$R^2 = 0.2148001$
p−value: = 7e−04
Bacteria_class_reads
PC1
4
5
6
7
−4
−2
0
2
4

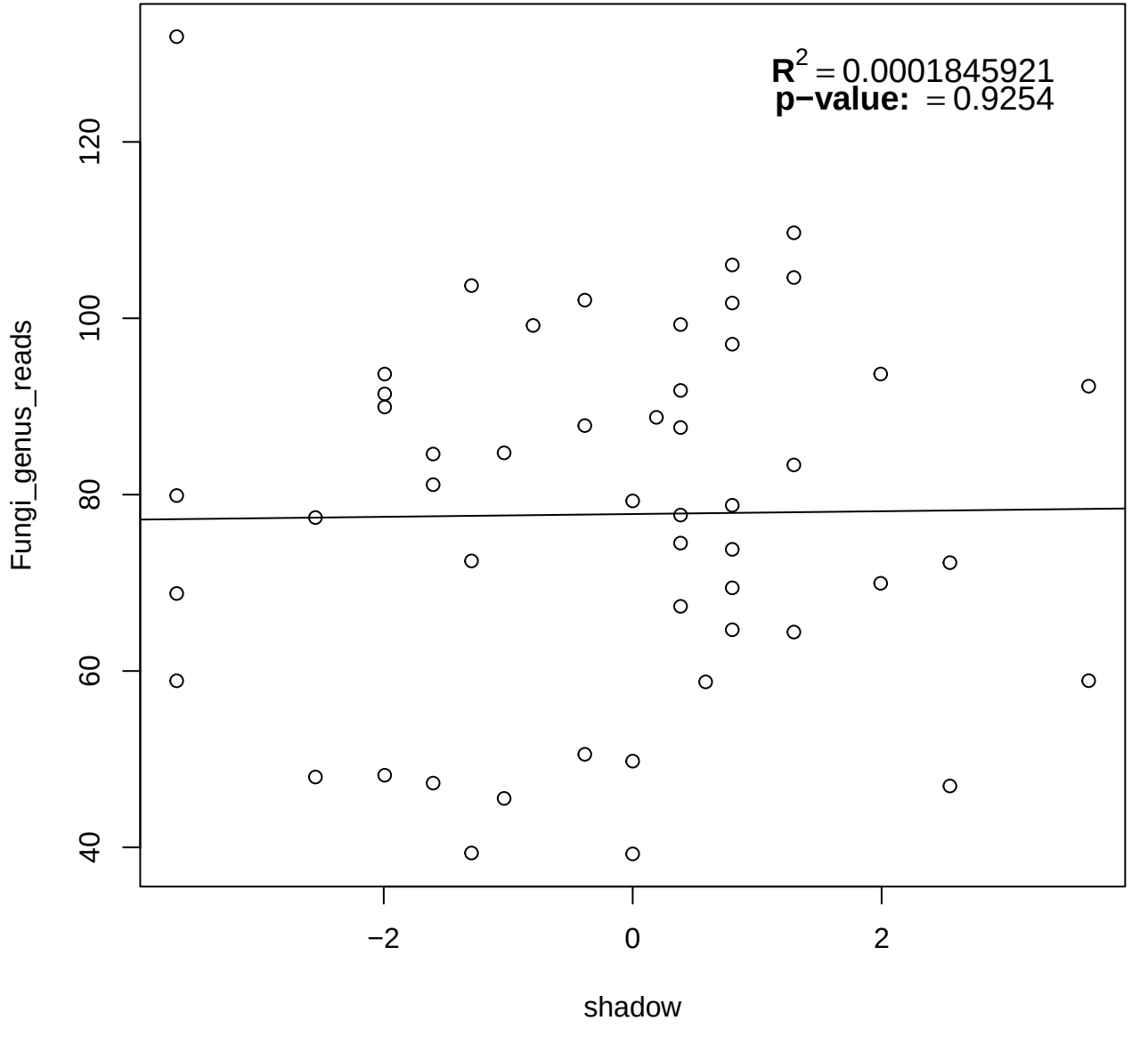

Residuals vs Fitted
Residuals
Fitted values
ERM1
SAL1
VEZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
SAL1
VEZ1
Scale−Location
√|Standardized residuals|
Fitted values
VEZ1
ERM1
SAL1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
SAL1
VEZ1
Cook's distance
0.5
0.5

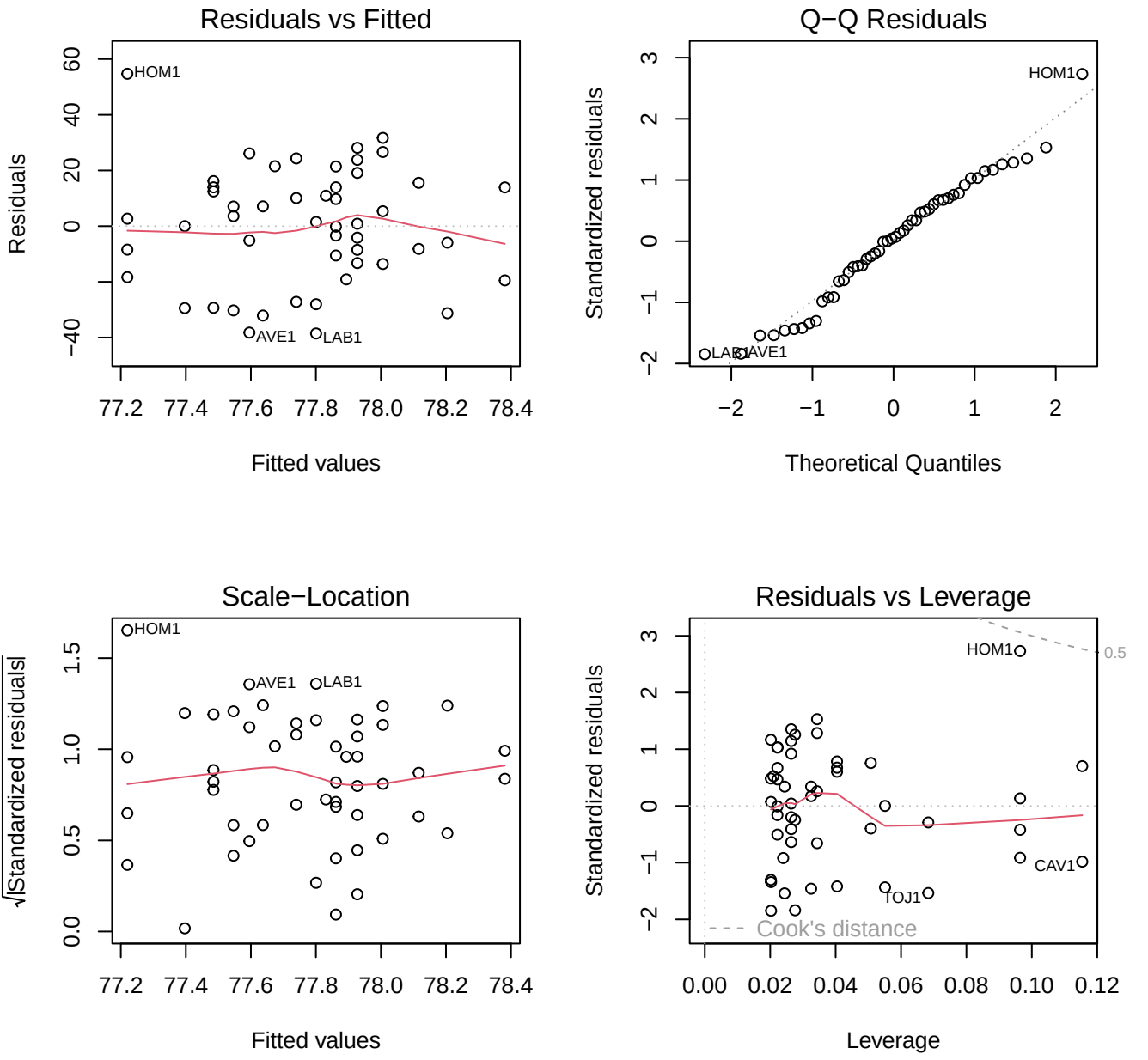

$R^2 = 0.04784259$
p−value: $= 0.127$
Fungi_genus_reads
qbr
40
60
80
100
120
0
20
40
60
80

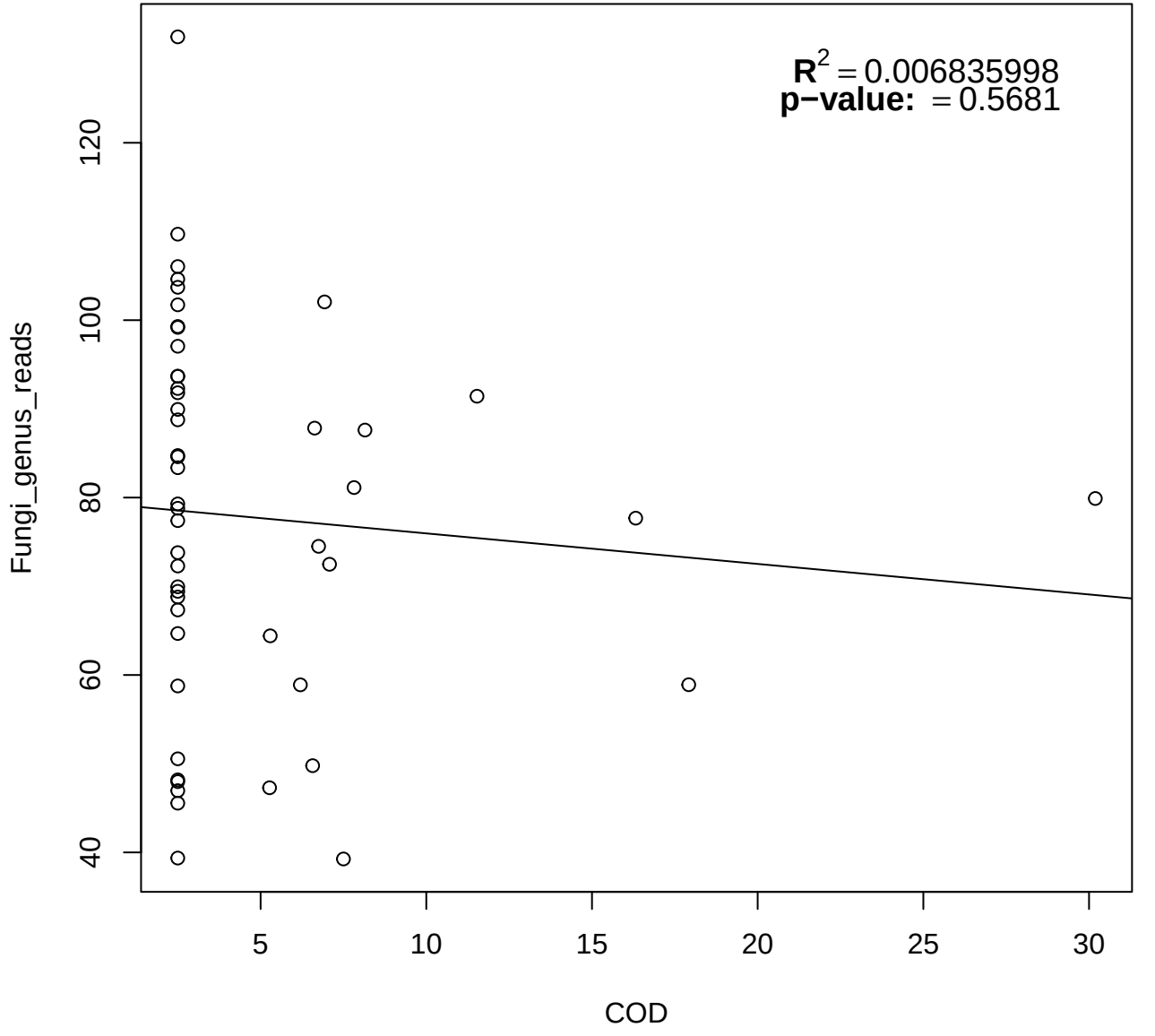

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
LAB1
COV1
Cook's distance

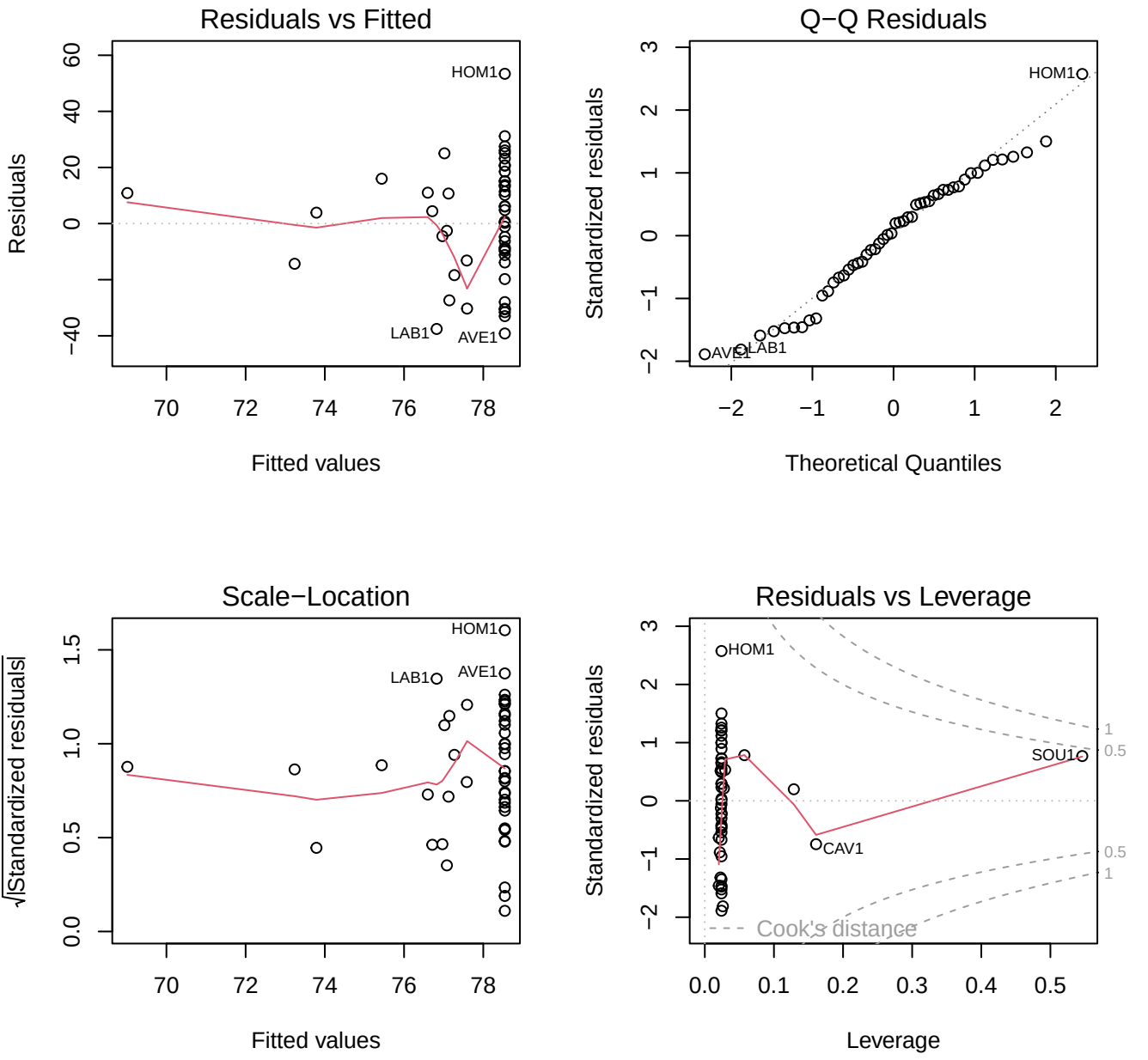

$R^2 = 0.003593374$
p−value: = 0.6792
Fungi_genus_reads
ihf
40
60
80
100
120
30
40
50
60
70

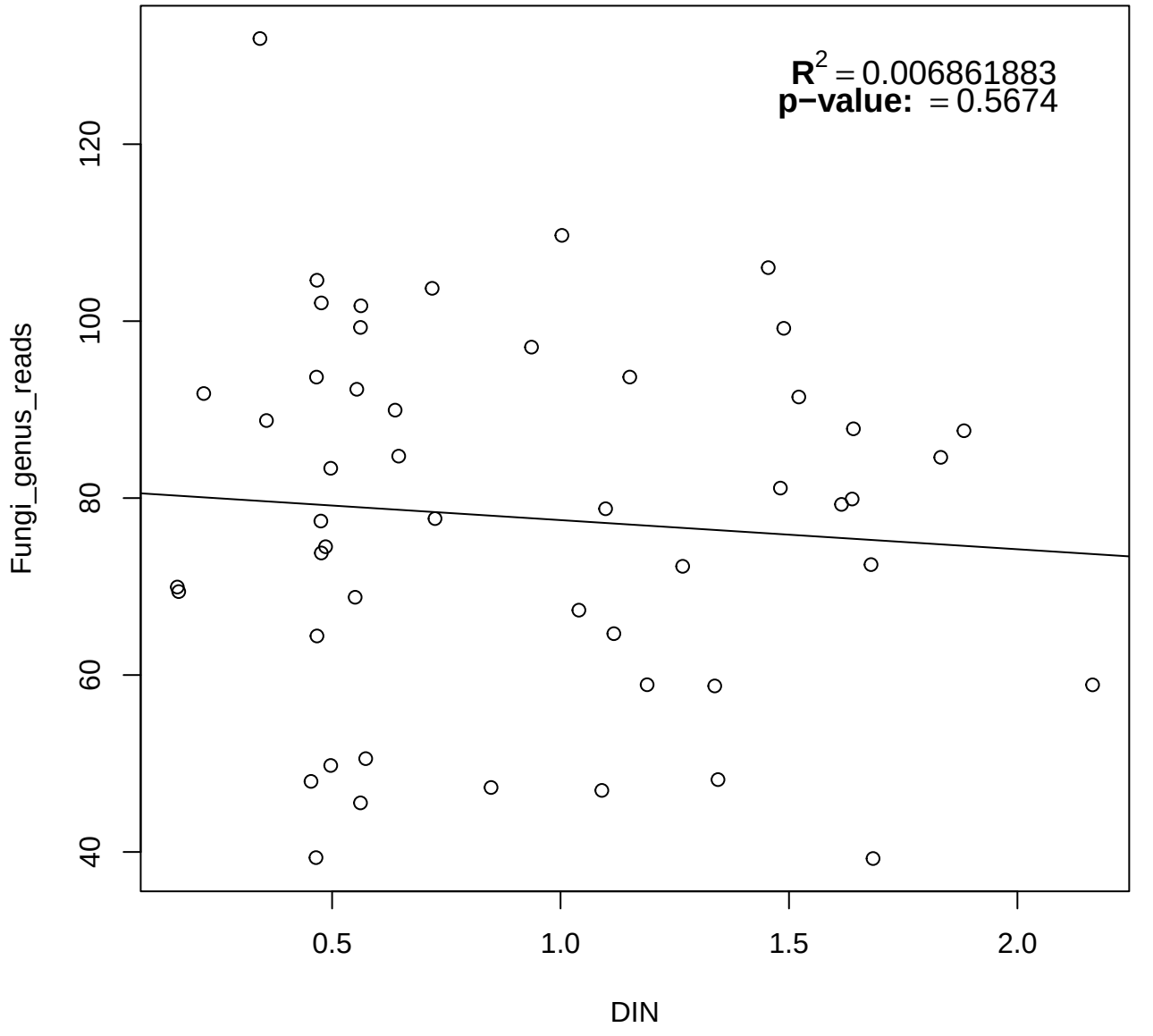

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
AVE1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
MACI1
VIL1
TOJ1
Cook's distance
0.5
0.5

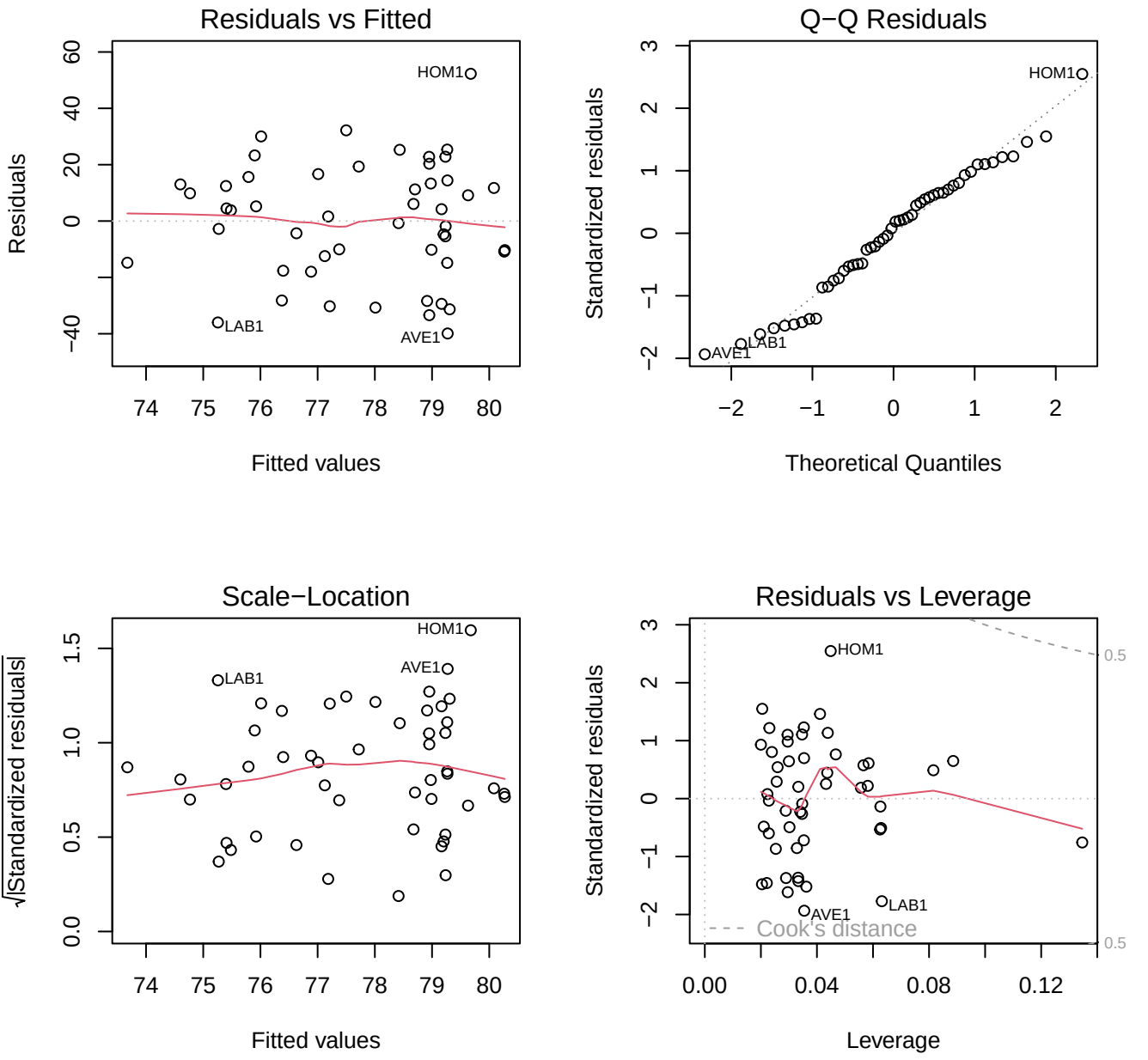

$R^2 = 0.0001845921$
p−value: = 0.9254
Fungi_genus_reads
40
60
80
100
120
−2
0
2
shadow

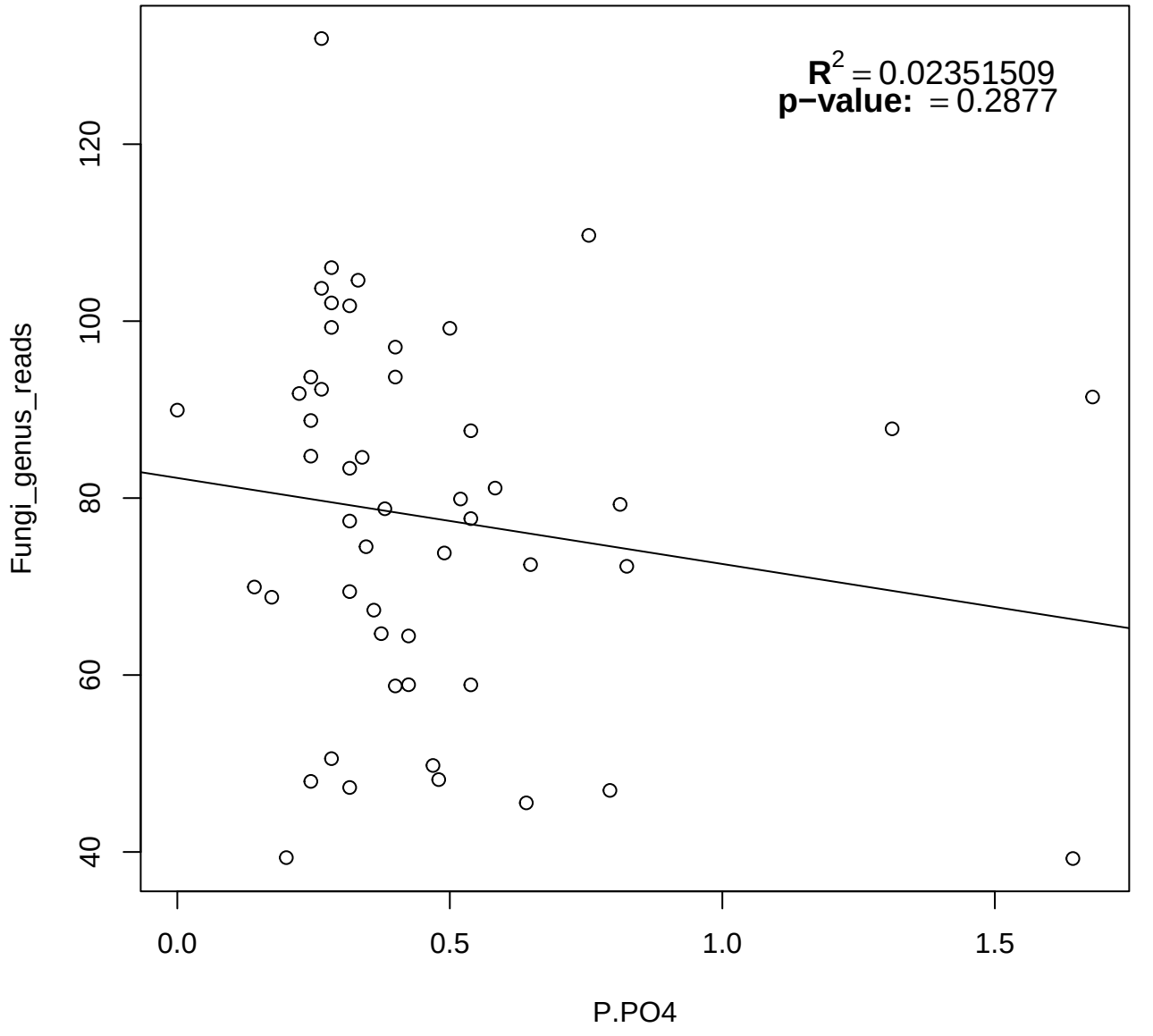

Residuals vs Fitted
Residuals
Fitted values
HOM1
AVE1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
CAV1
TOJ1
0.5
Cook's distance

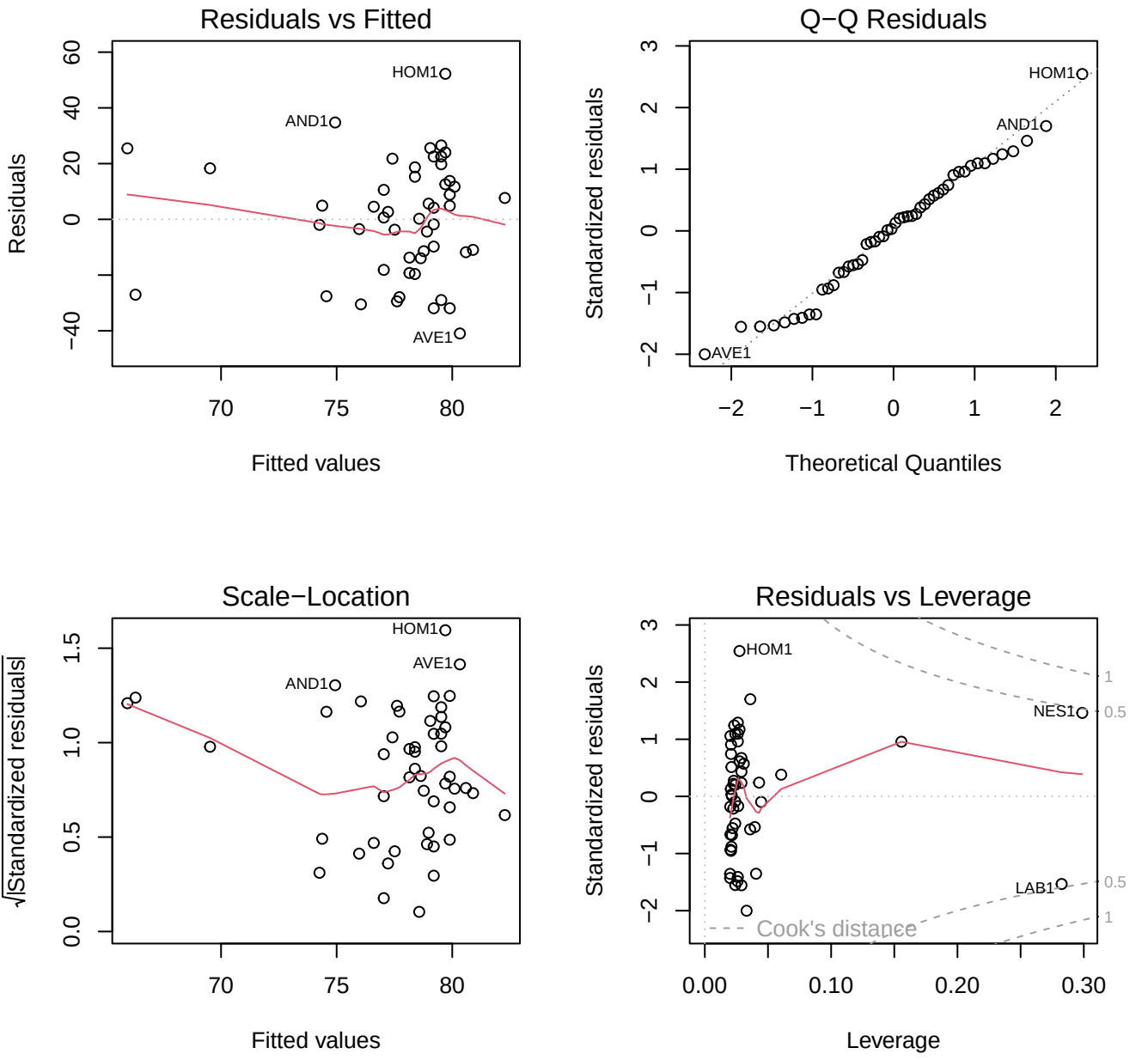

$R^2 = 0.006835998$
p−value: = 0.5681
Fungi_genus_reads
40
60
80
100
120
5
10
15
20
25
30
COD

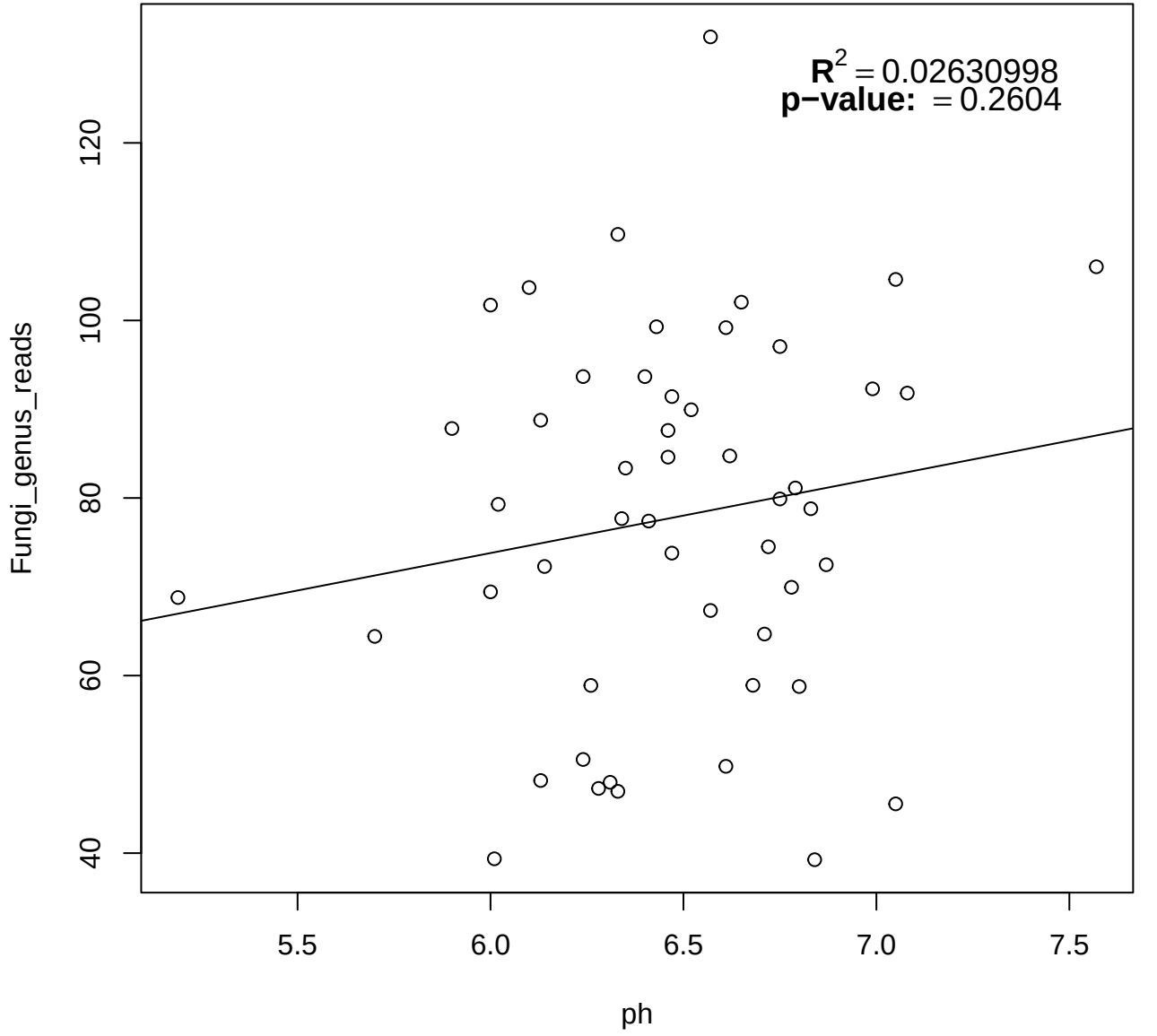

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
AVE1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
SOU1
CAV1
Cook's distance

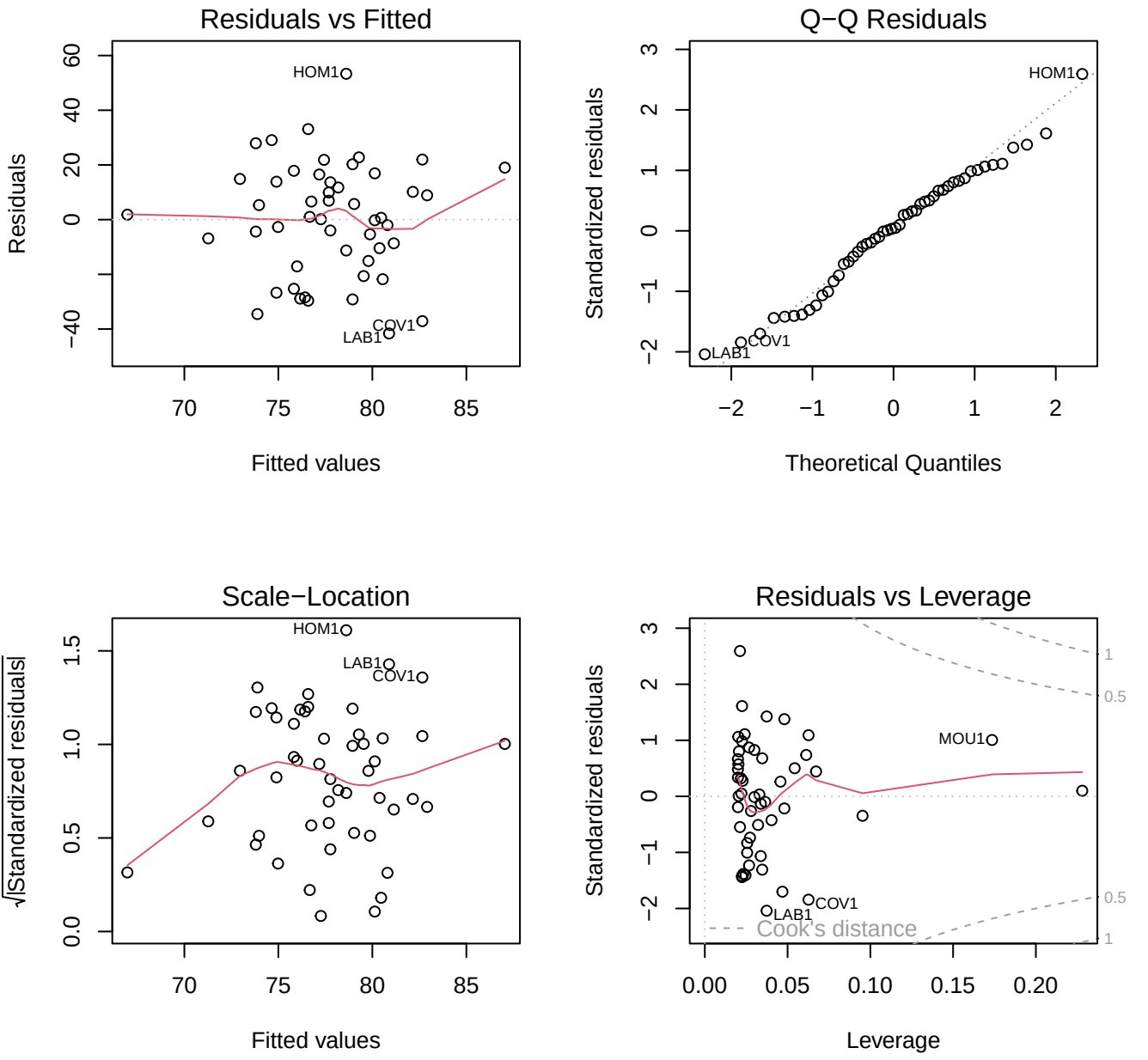

$R^2 = 0.006861883$
p−value: = 0.5674
Fungi_genus_reads
40
60
80
100
120
0.5
1.0
1.5
2.0
DIN

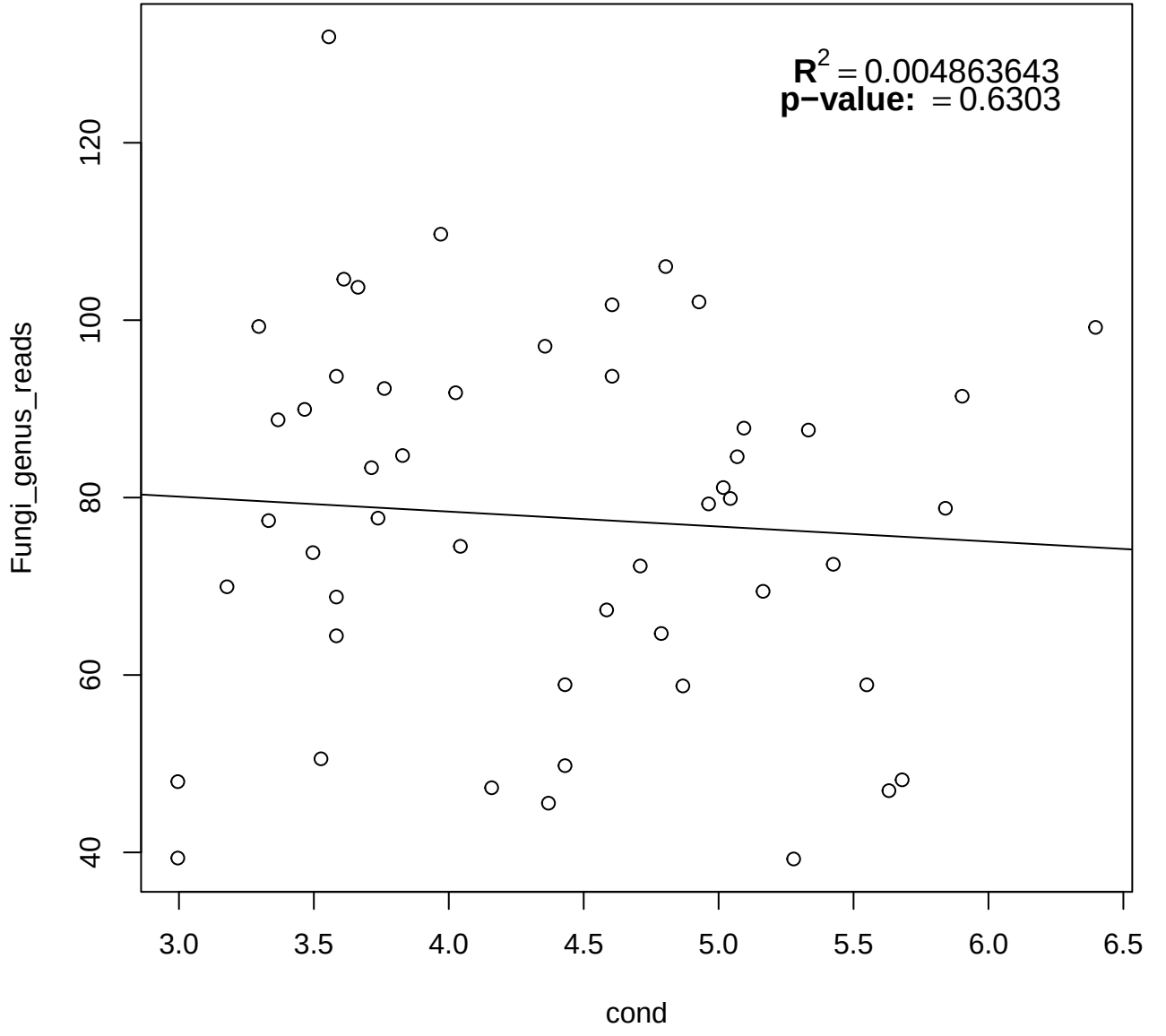

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
AVE1
LAB1
Cook's distance
0.5
0.5

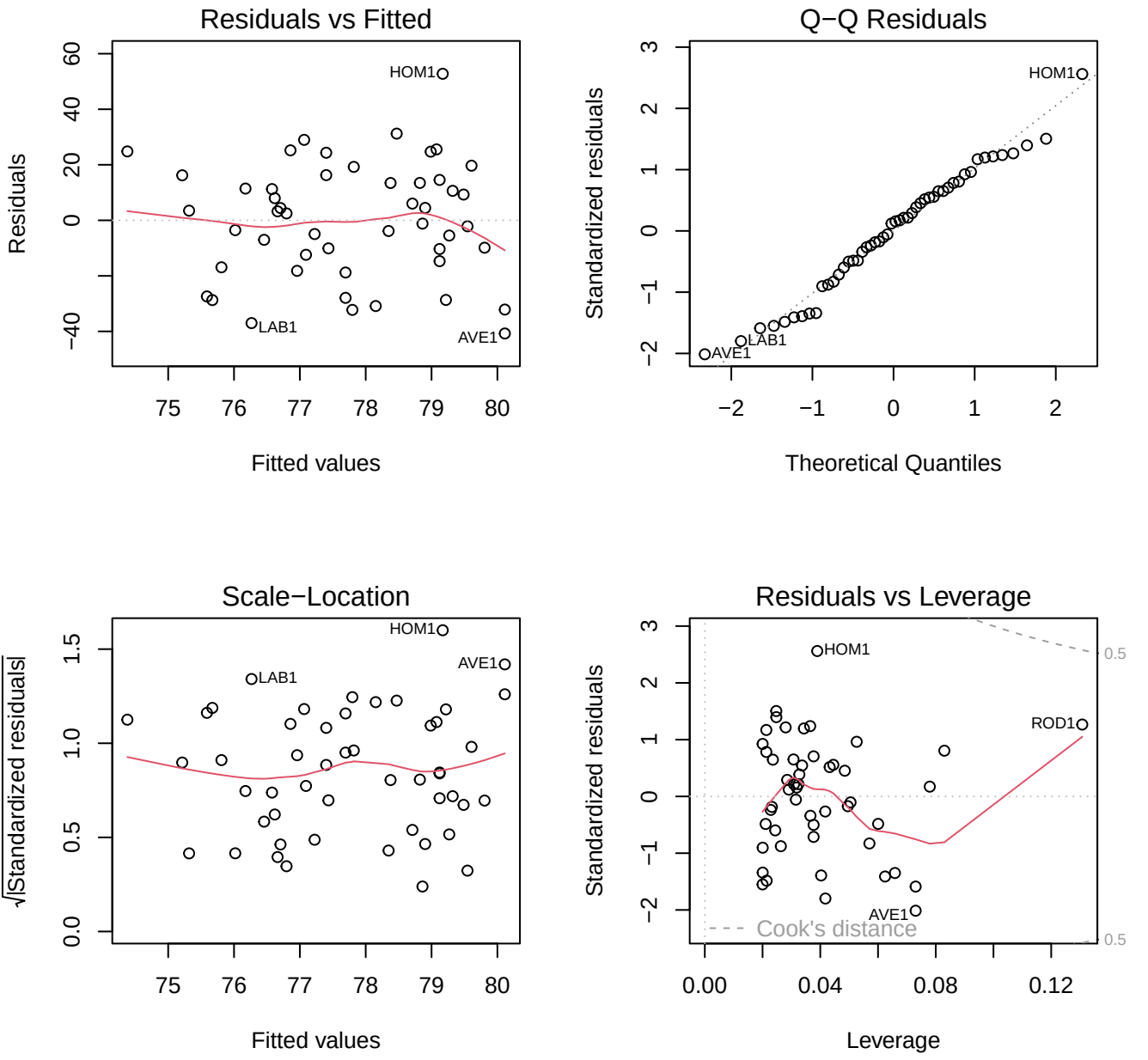

$R^2 = 0.02351509$
p−value: = 0.2877
Fungi_genus_reads
40
60
80
100
120
0.0
0.5
1.0
1.5
P.PO4

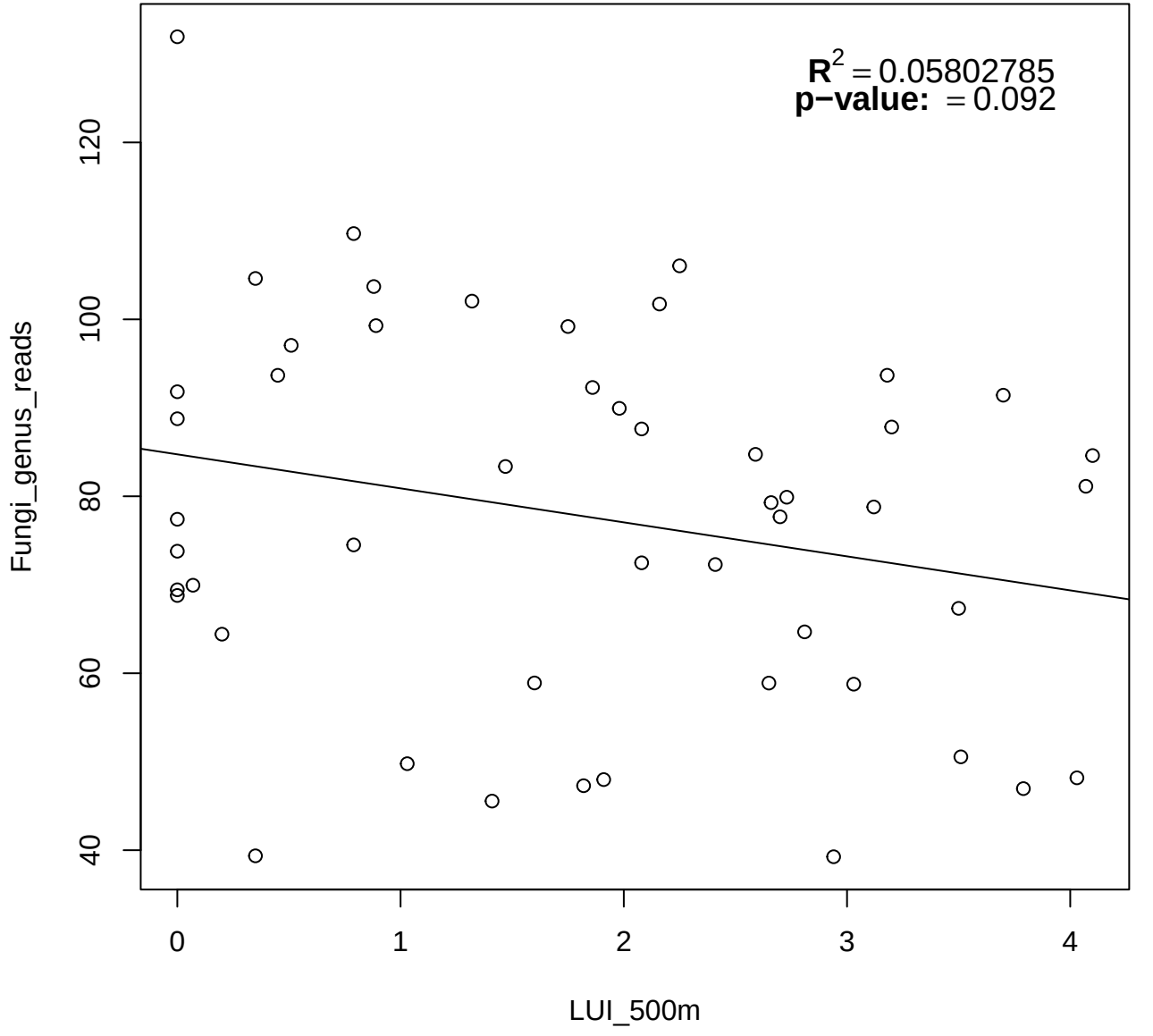

Residuals vs Fitted
Residuals
Fitted values
HOM1
AND1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
AND1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
AND1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
NES1
LAB1
Cook's distance

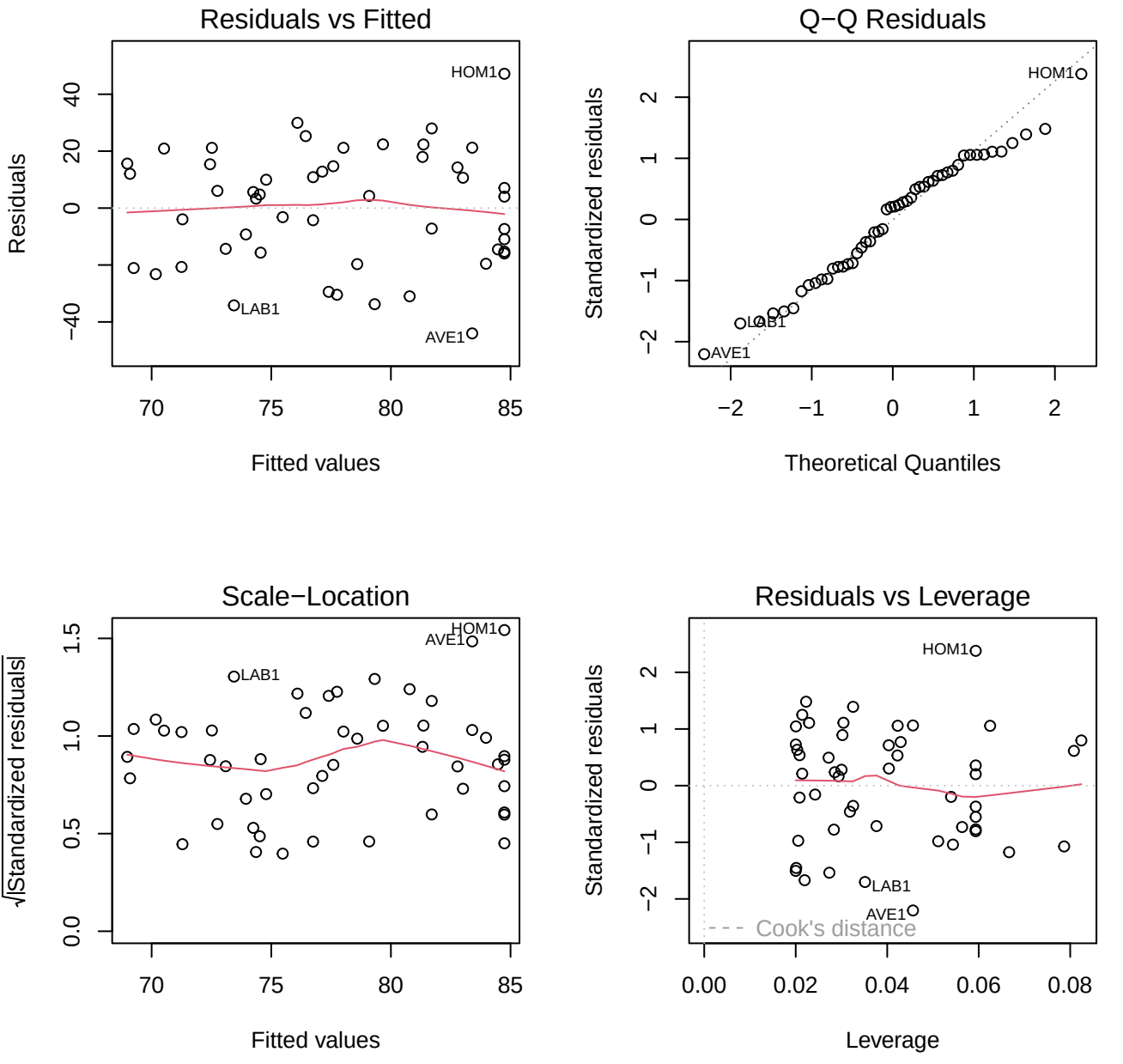

$R^2 = 0.02630998$
p−value: = 0.2604
Fungi_genus_reads
40
60
80
100
120
5.5
6.0
6.5
7.0
7.5
ph

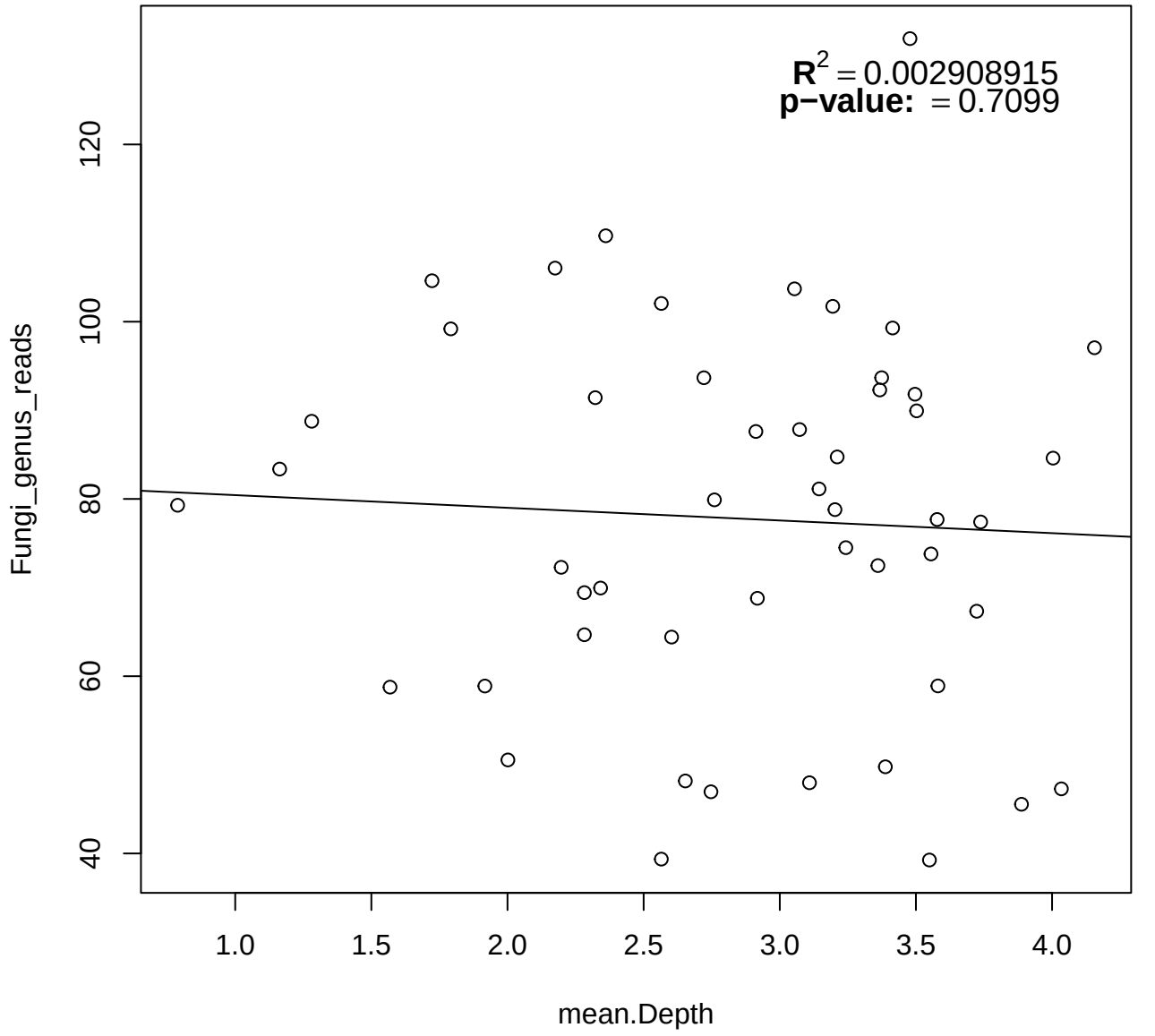

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
MOU1
COV1
LAB1
Cook's distance

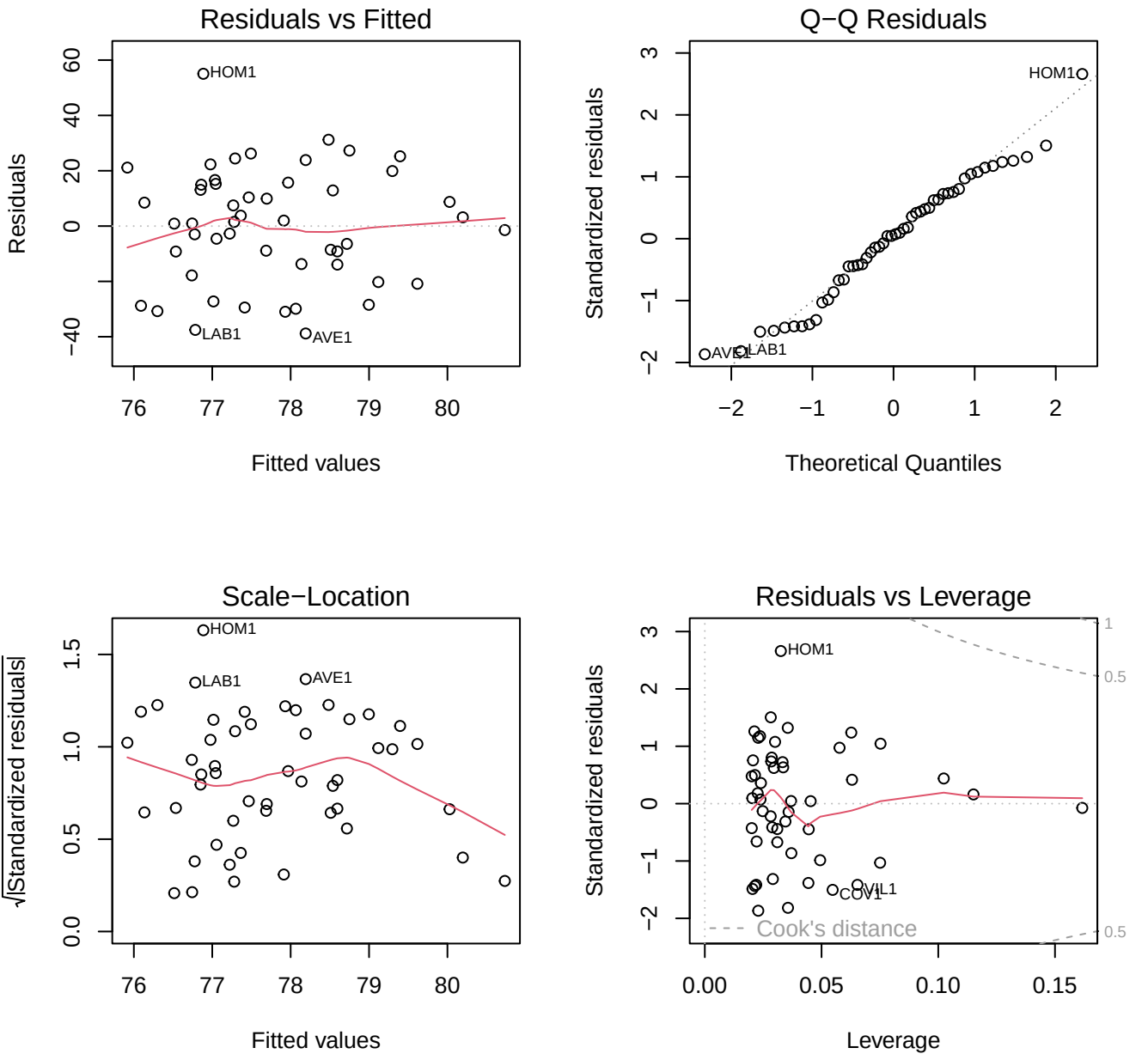

$R^2 = 0.004863643$
p−value: = 0.6303
Fungi_genus_reads
40
60
80
100
120
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
cond

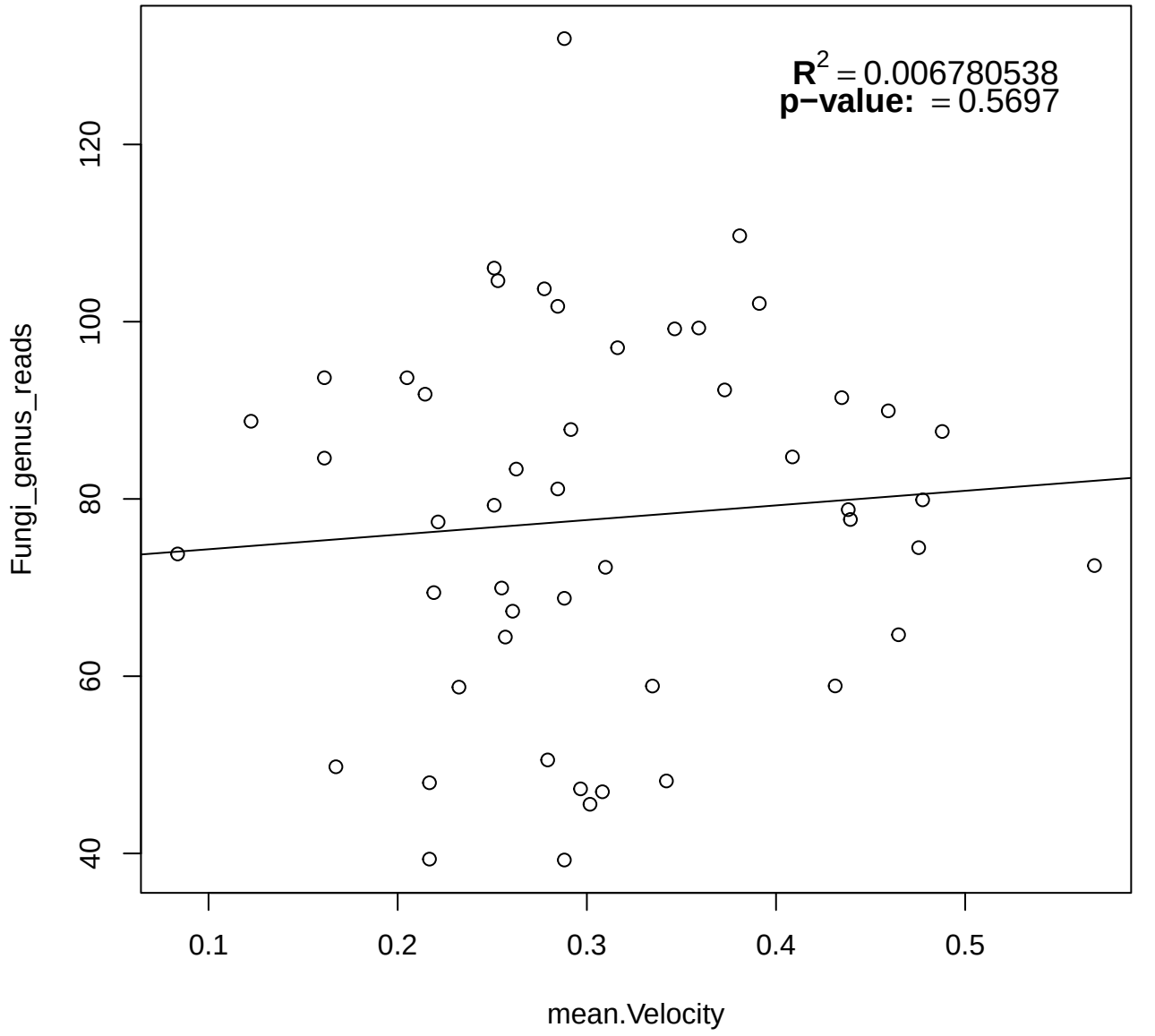

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
ROD1
AVE1
Cook's distance
0.5
0.5

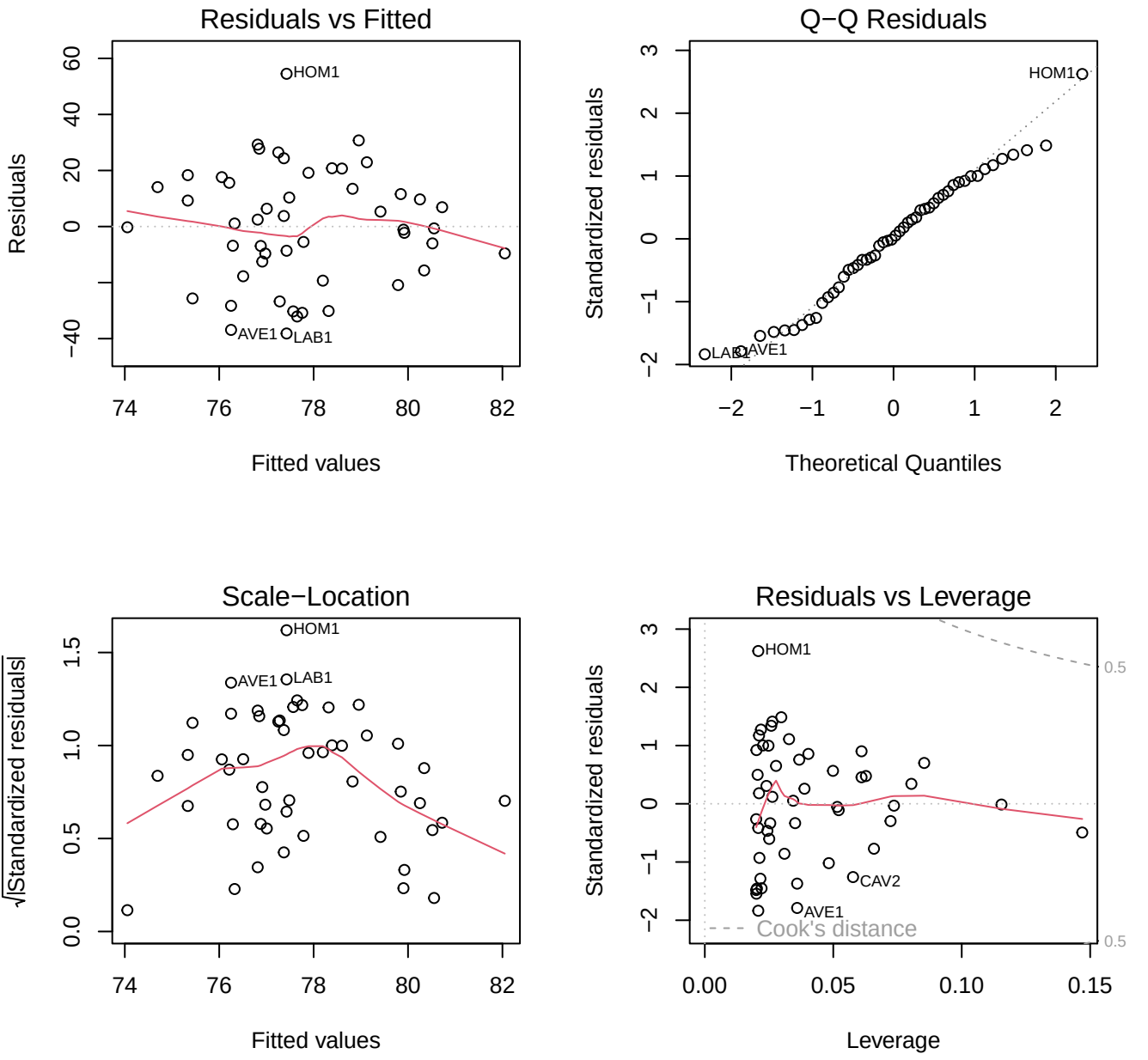

$R^2 = 0.05802785$
p−value: = 0.092
Fungi_genus_reads
40
60
80
100
120
0
1
2
3
4
LUI_500m

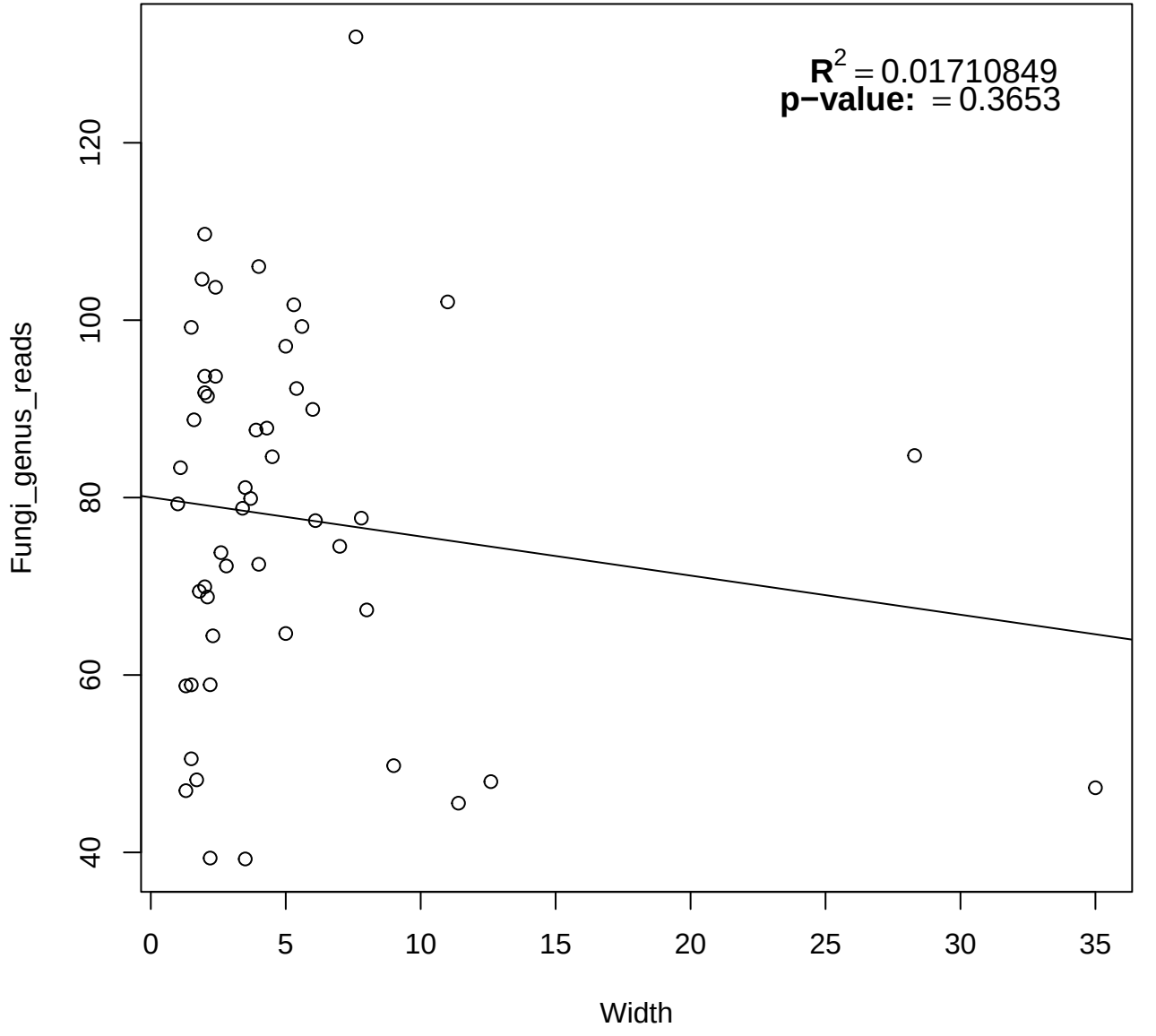

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
LAB1
AVE1
Cook's distance

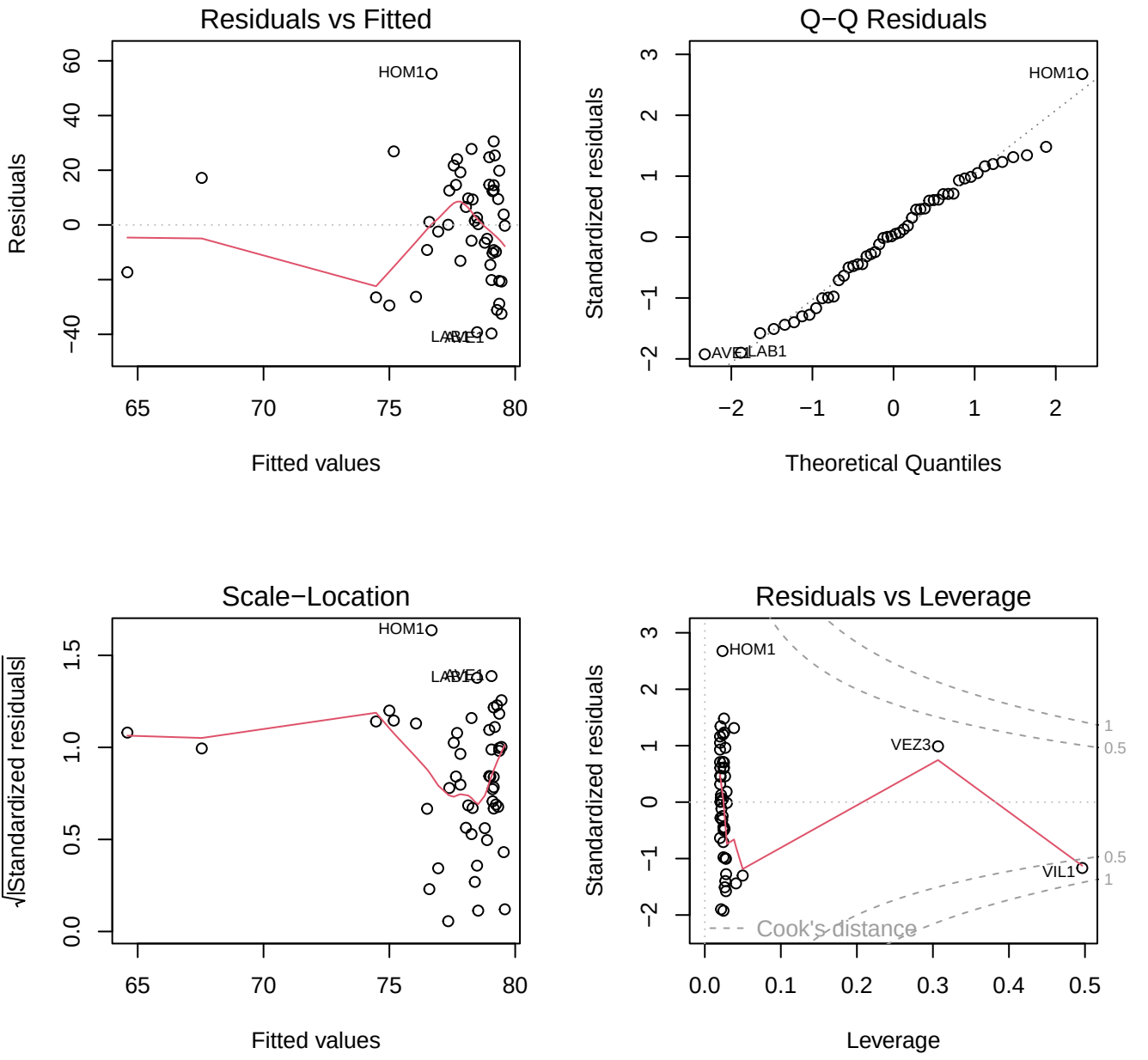

$R^2 = 0.002908915$
p−value: = 0.7099
Fungi_genus_reads
40
60
80
100
120
1.0
1.5
2.0
2.5
3.0
3.5
4.0
mean.Depth

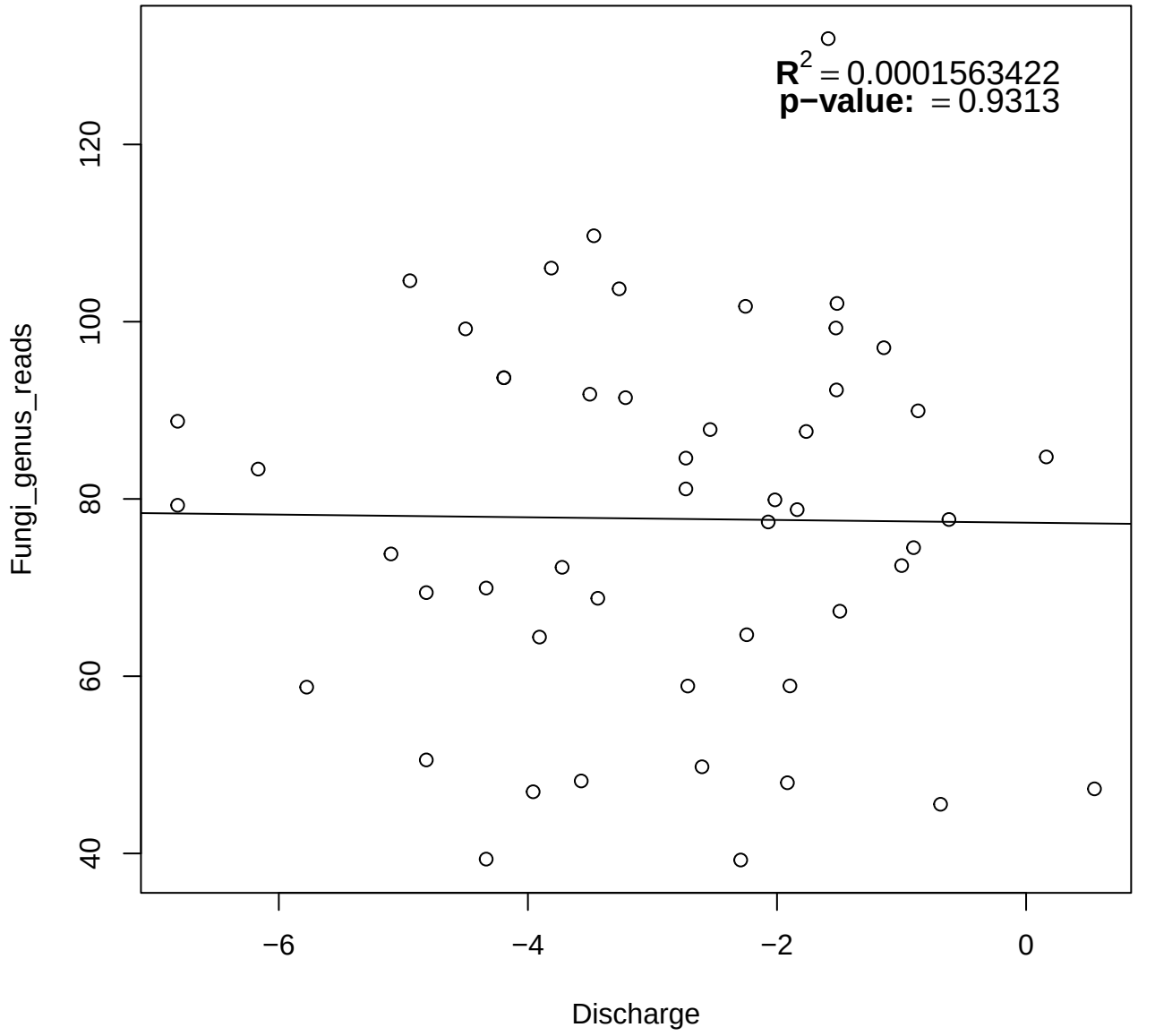

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
AVE1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
COV1
VIL1
Cook's distance

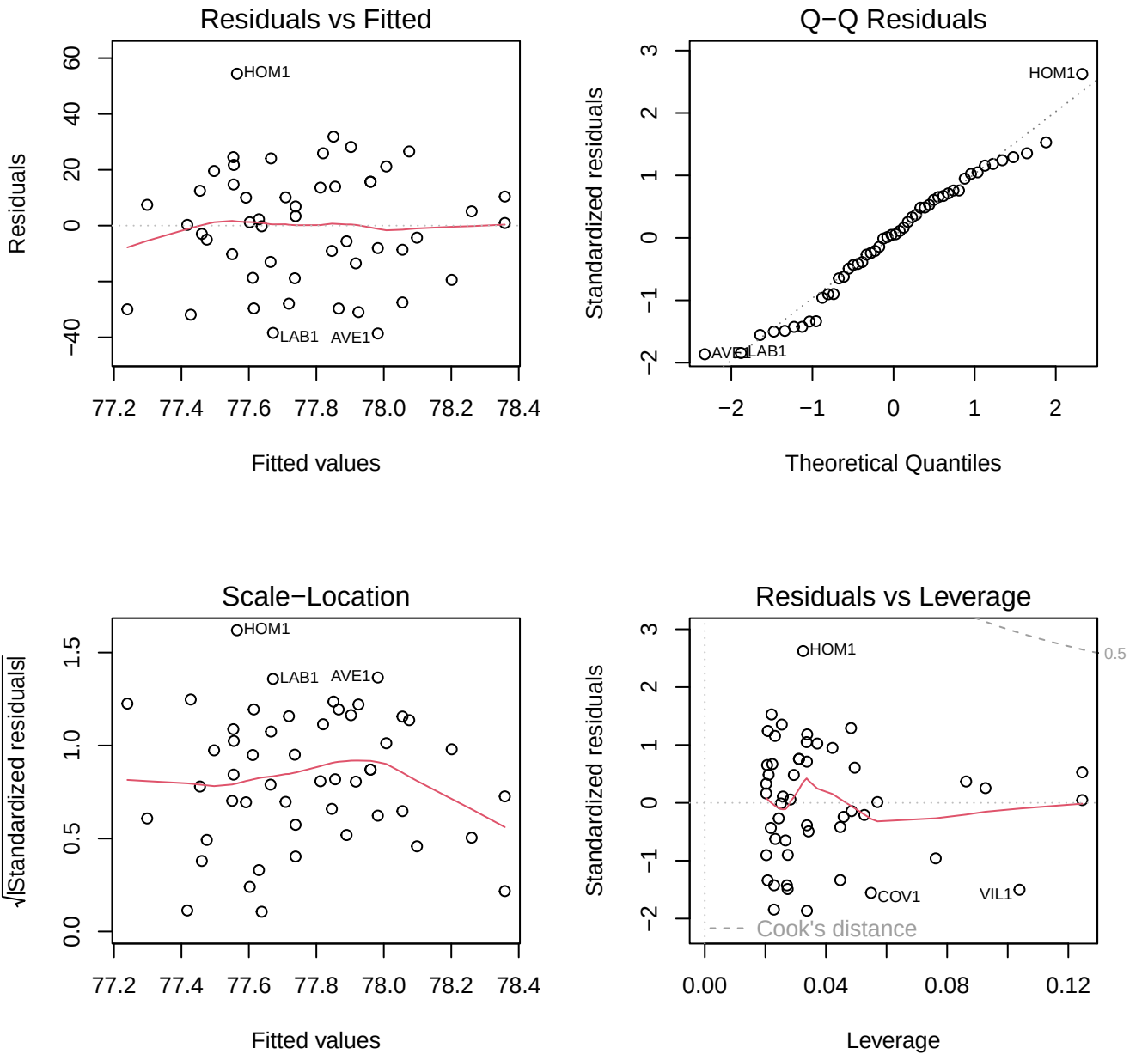

$R^2 = 0.006780538$
p−value: = 0.5697
Fungi_genus_reads
40
60
80
100
120
0.1
0.2
0.3
0.4
0.5
mean.Velocity

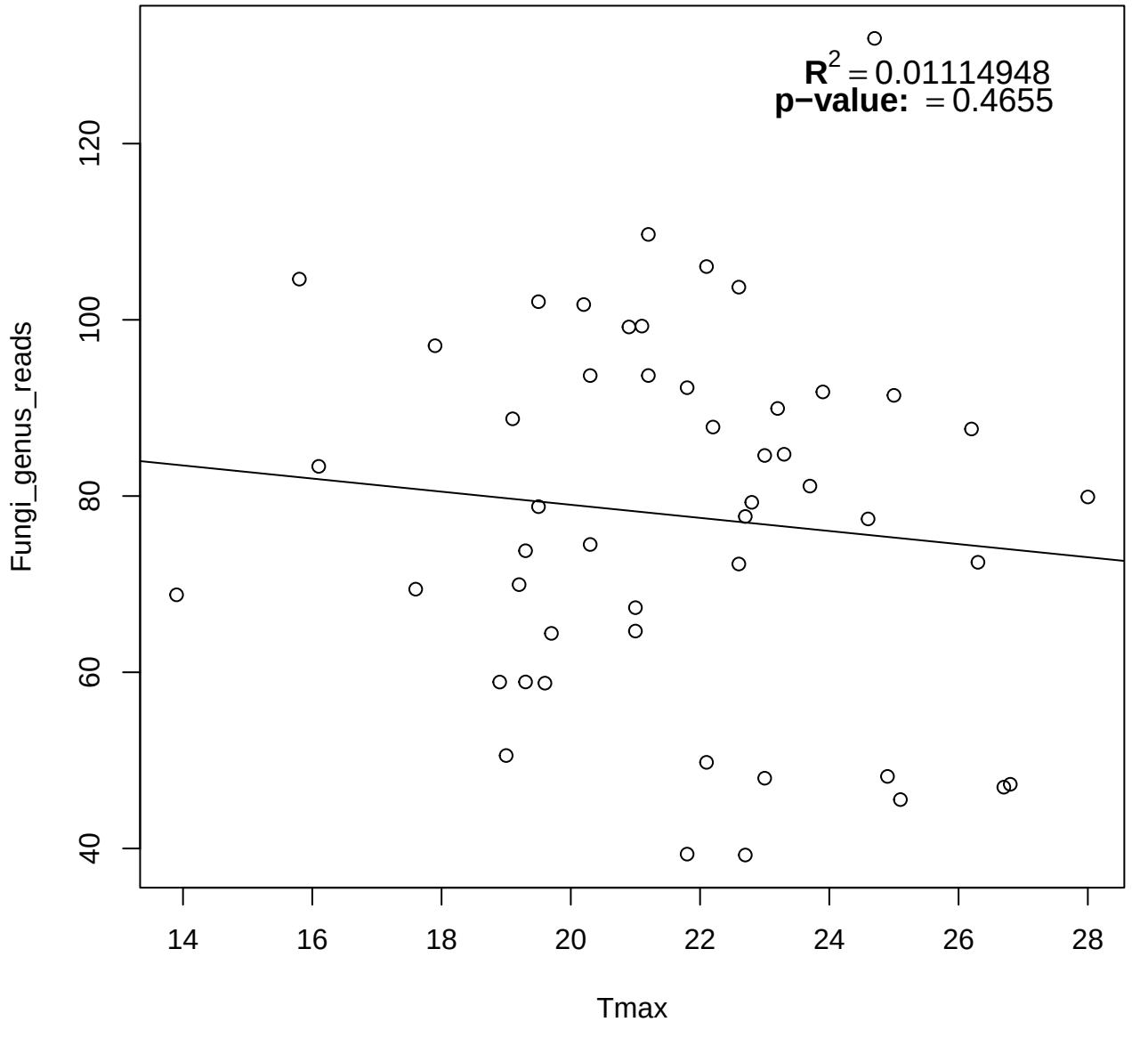

Residuals vs Fitted
Residuals
Fitted values
HOM1
AVE1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
CAV2
AVE1
Cook's distance
0.5
0.5

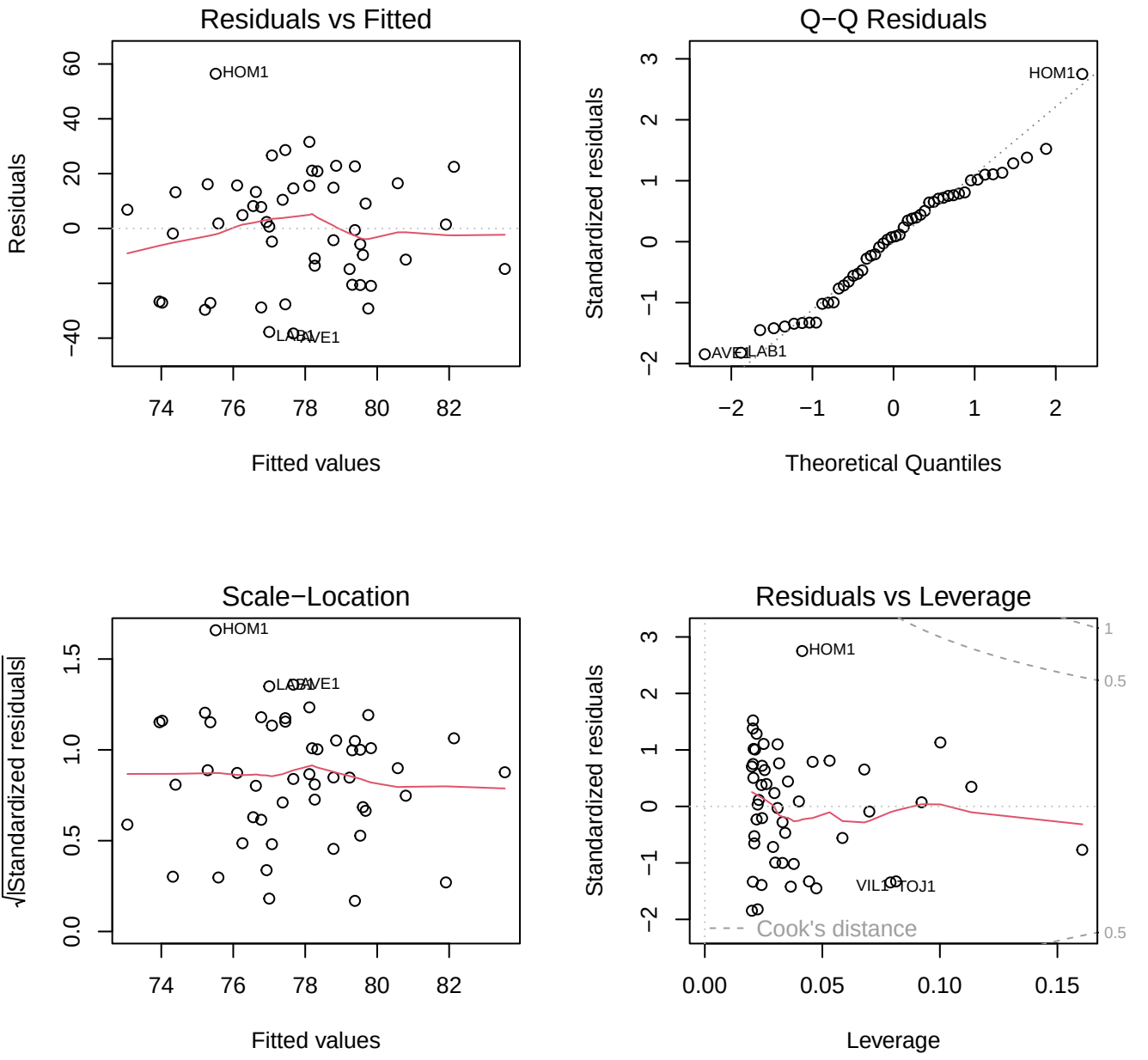

$R^2 = 0.01710849$
p−value: = 0.3653
Fungi_genus_reads
Width
40
60
80
100
120
0
5
10
15
20
25
30
35

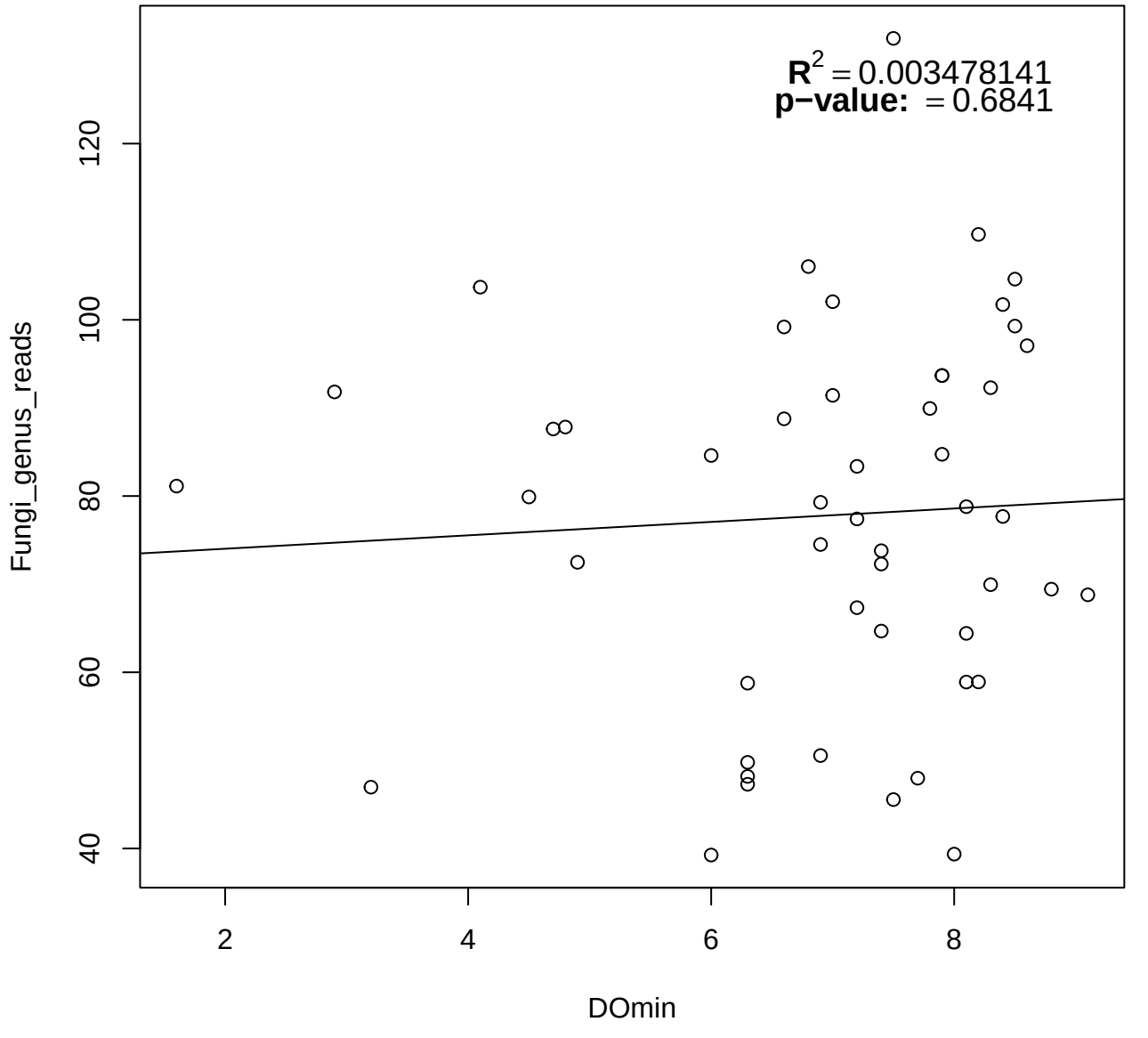

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
AVE1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
VEZ3
VIL1
Cook's distance

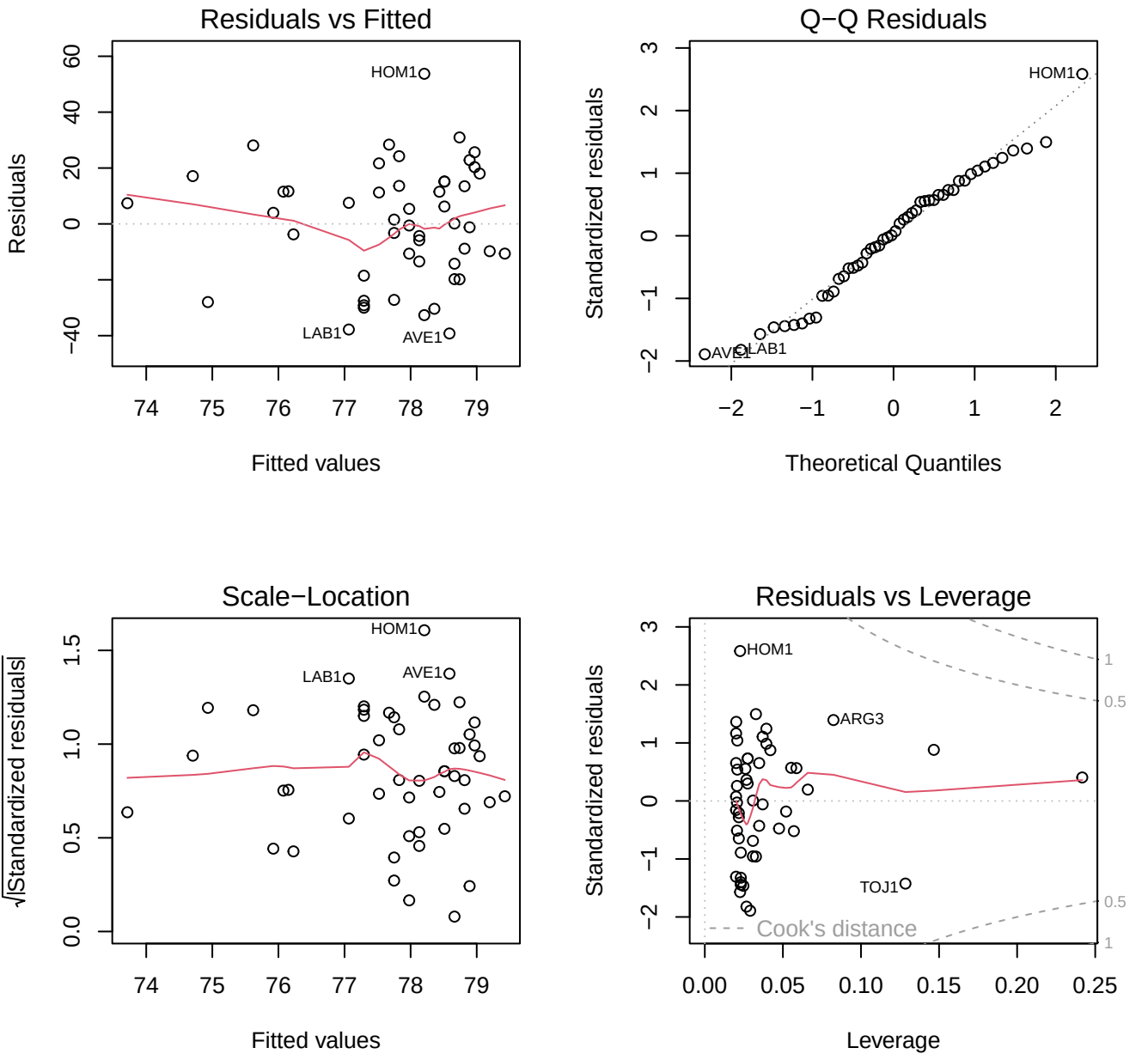

$R^2 = 0.0001563422$
p−value: = 0.9313
Fungi_genus_reads
40
60
80
100
120
−6
−4
−2
0
Discharge

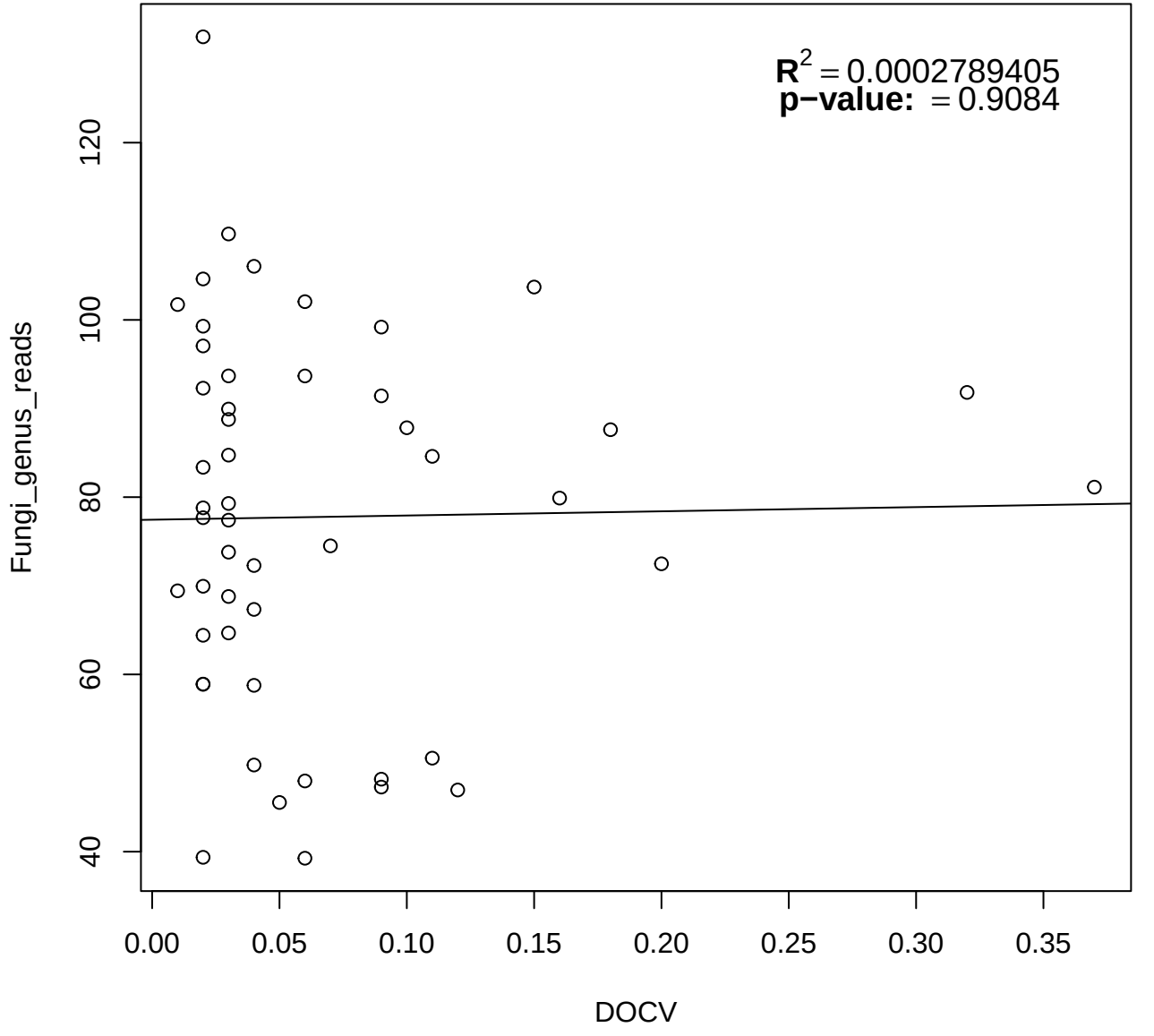

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
AVE1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
COV1
VIL1
0.5
Cook's distance

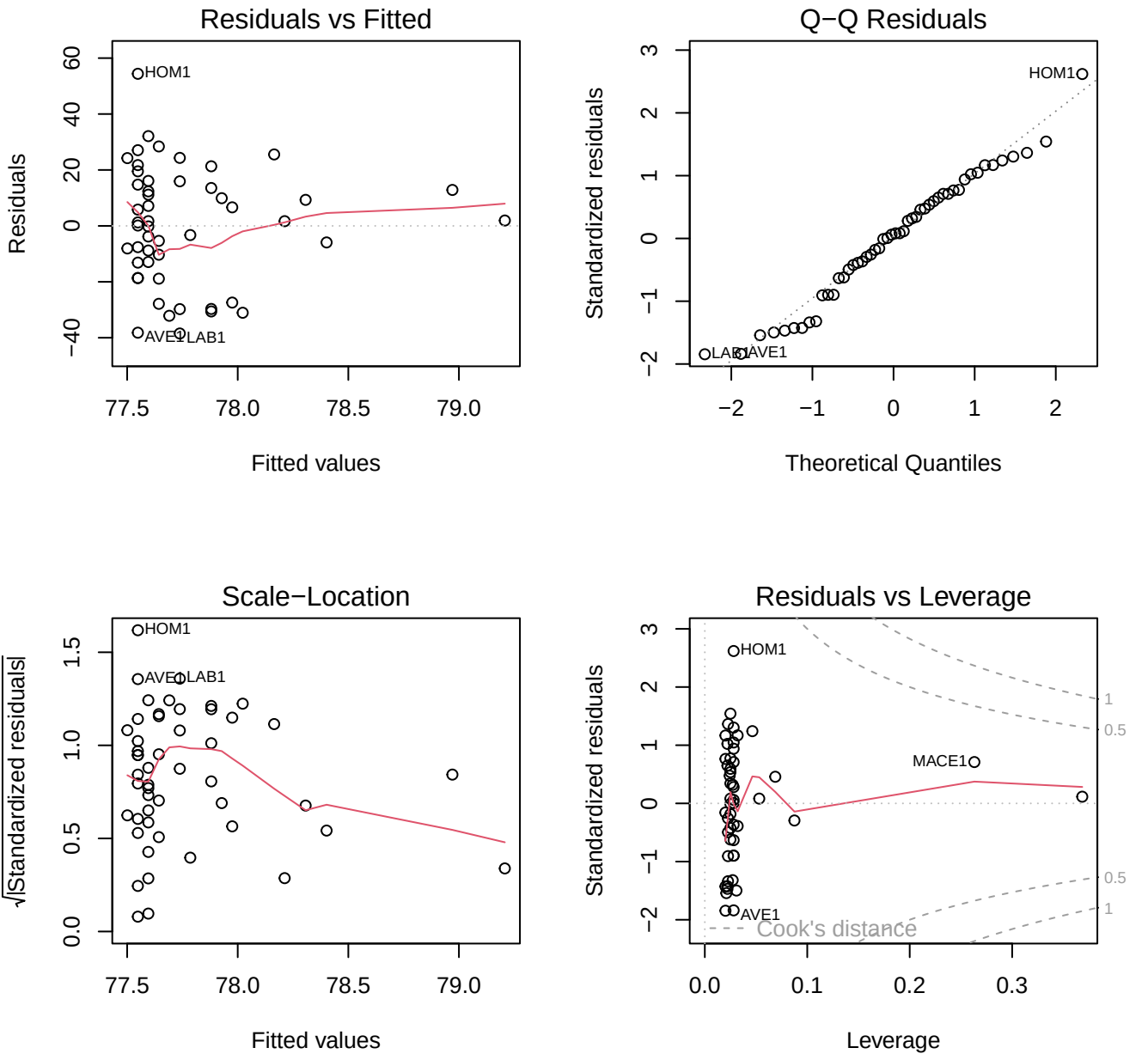

$R^2 = 0.01114948$
p−value: = 0.4655
Fungi_genus_reads
Tmax
40
60
80
100
120
14
16
18
20
22
24
26
28

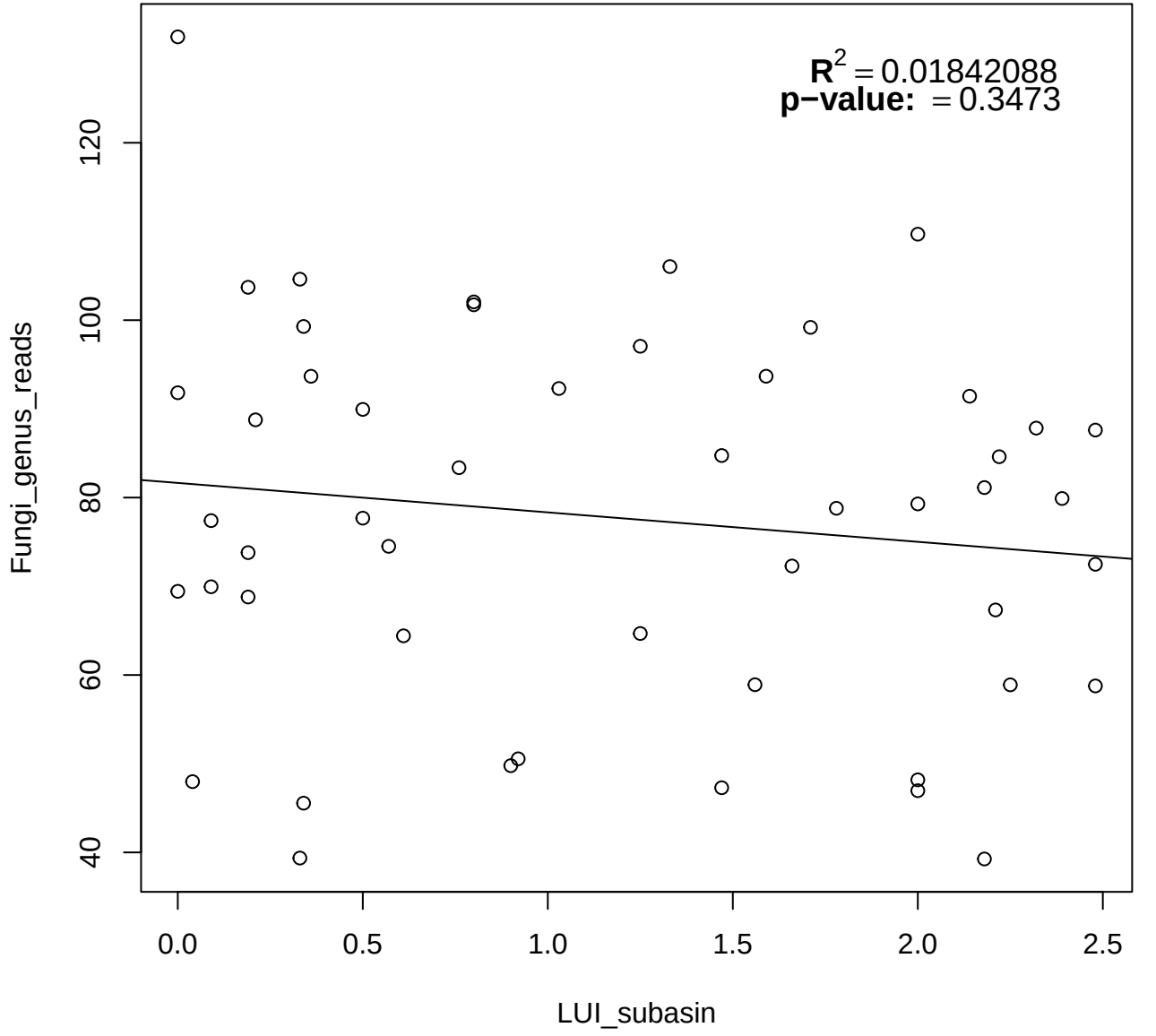

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
AVE1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
VIL1
TOJ1
Cook's distance

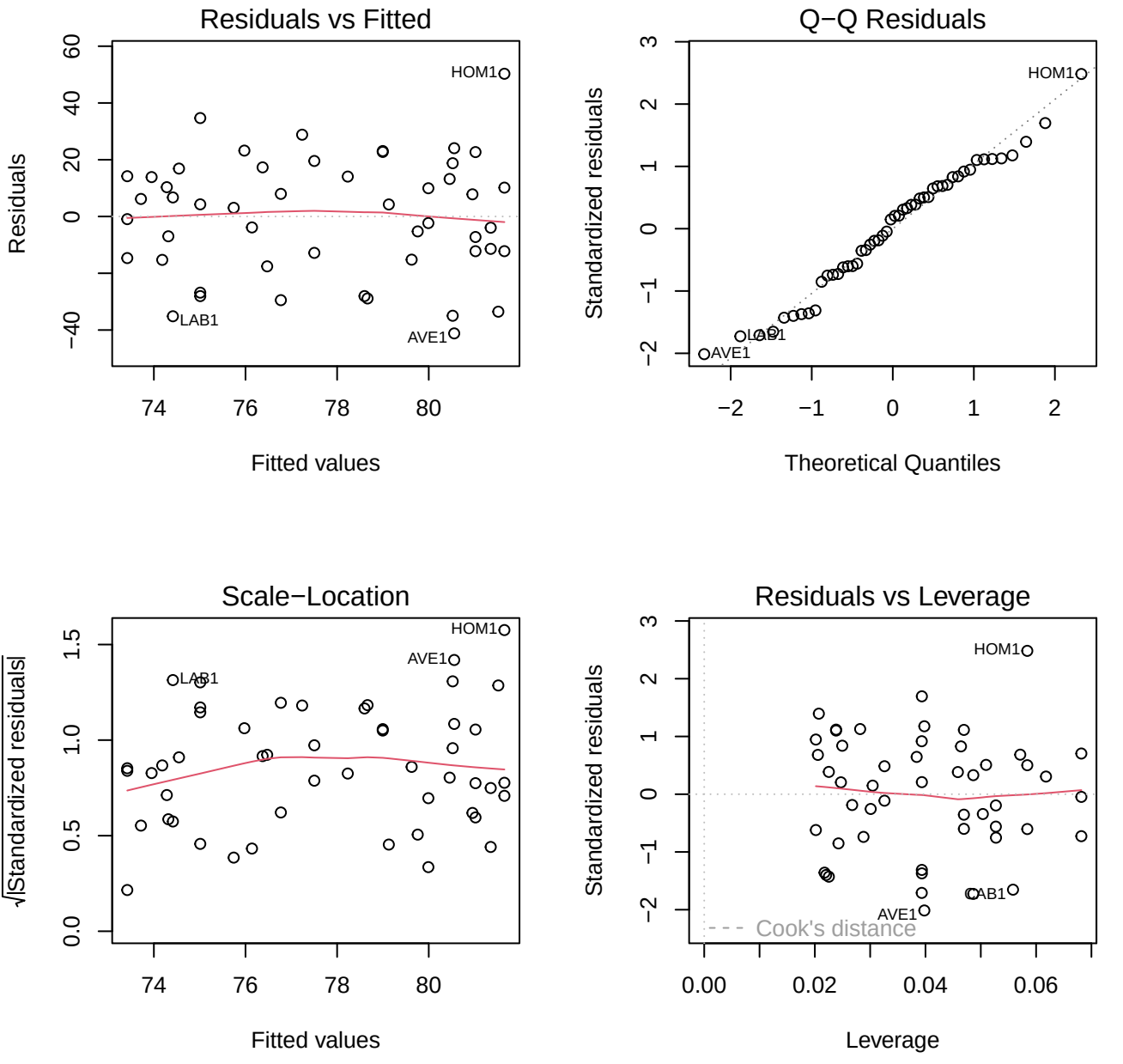

$R^2 = 0.003478141$
p−value: = 0.6841
Fungi_genus_reads
DOmin
40
60
80
100
120
2
4
6
8

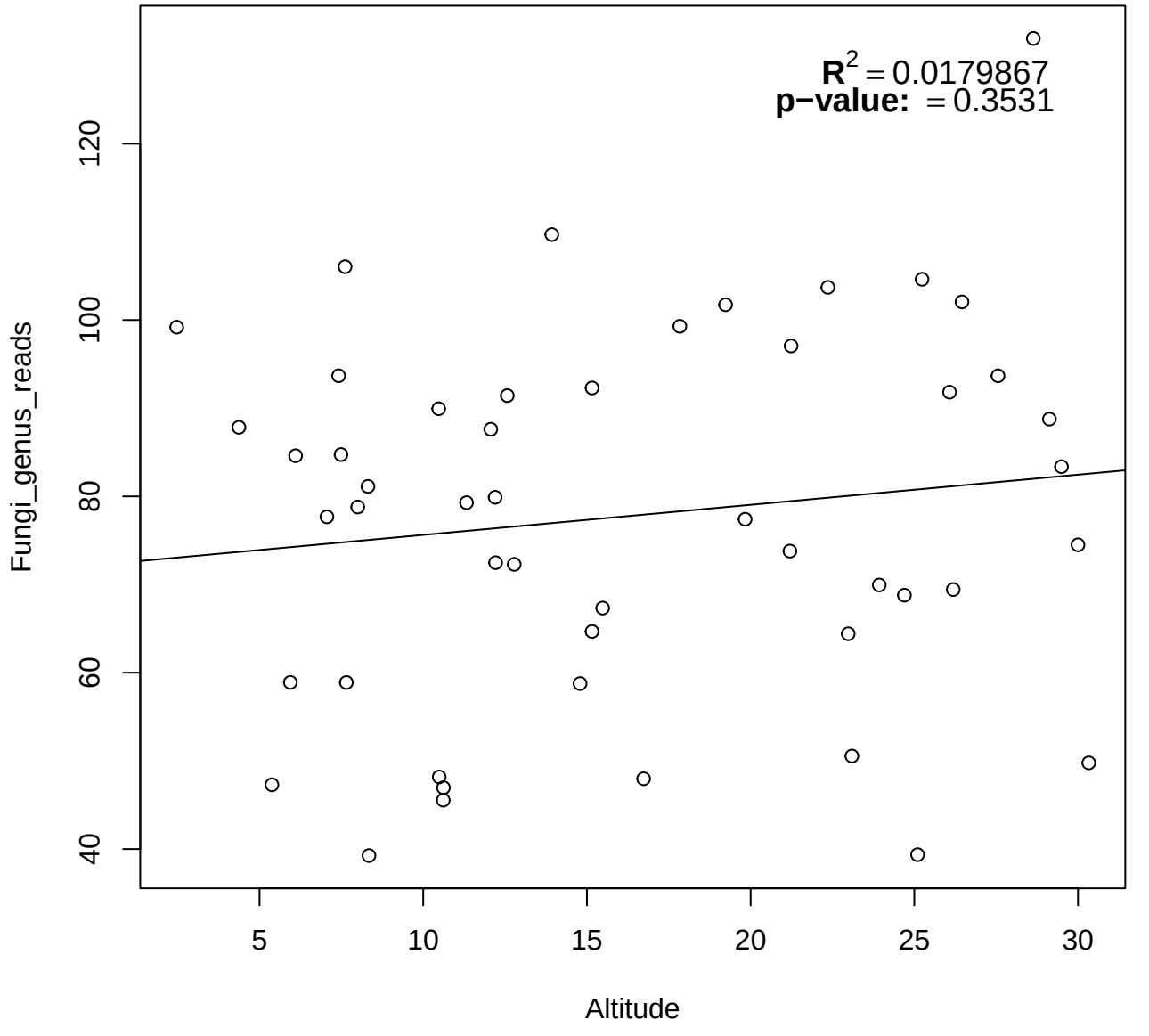

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
AVE1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
ARG3
TOJ1
Cook's distance

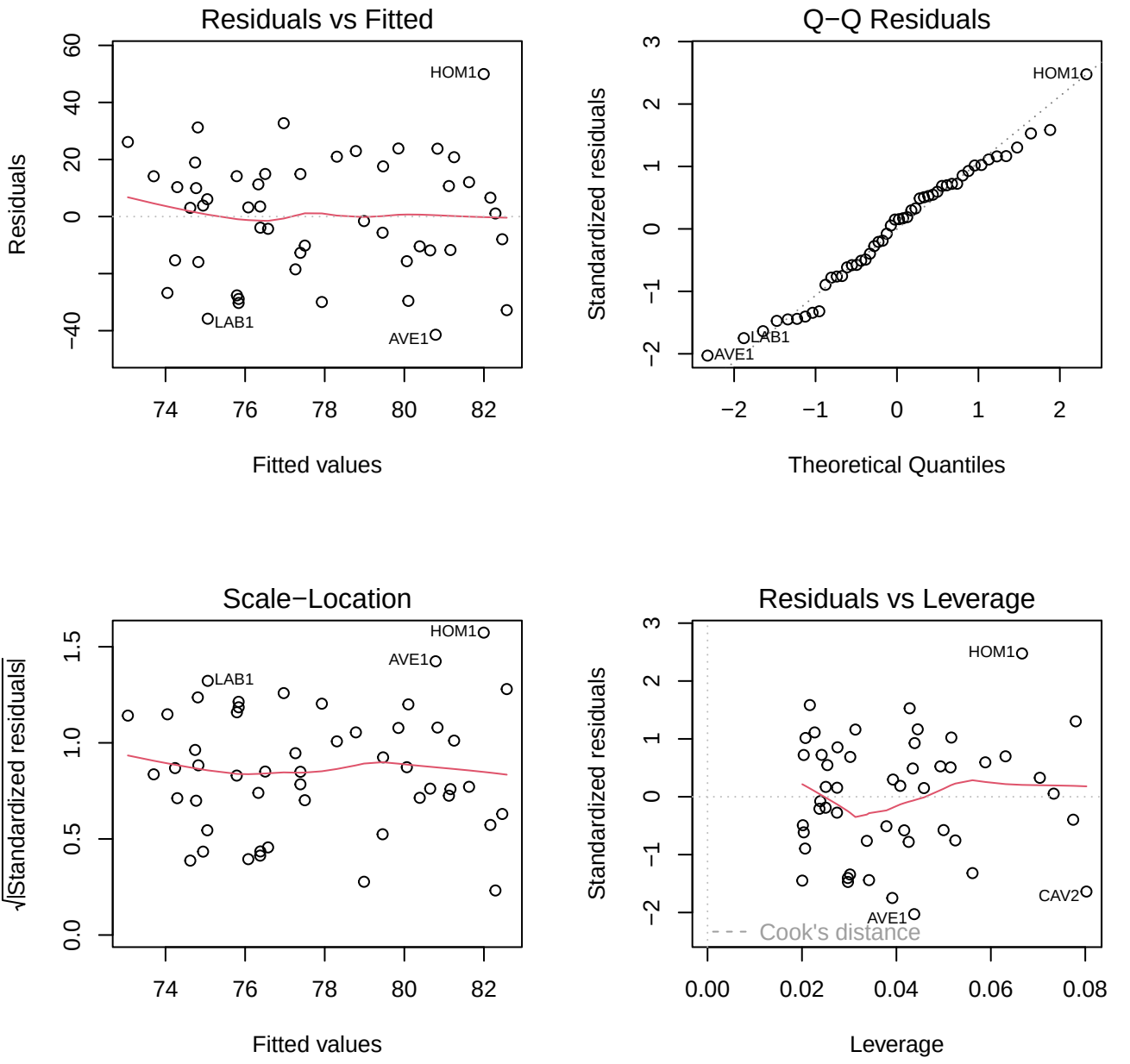

$R^2 = 0.0002789405$
p−value: = 0.9084
Fungi_genus_reads
DOCV
40
60
80
100
120
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35

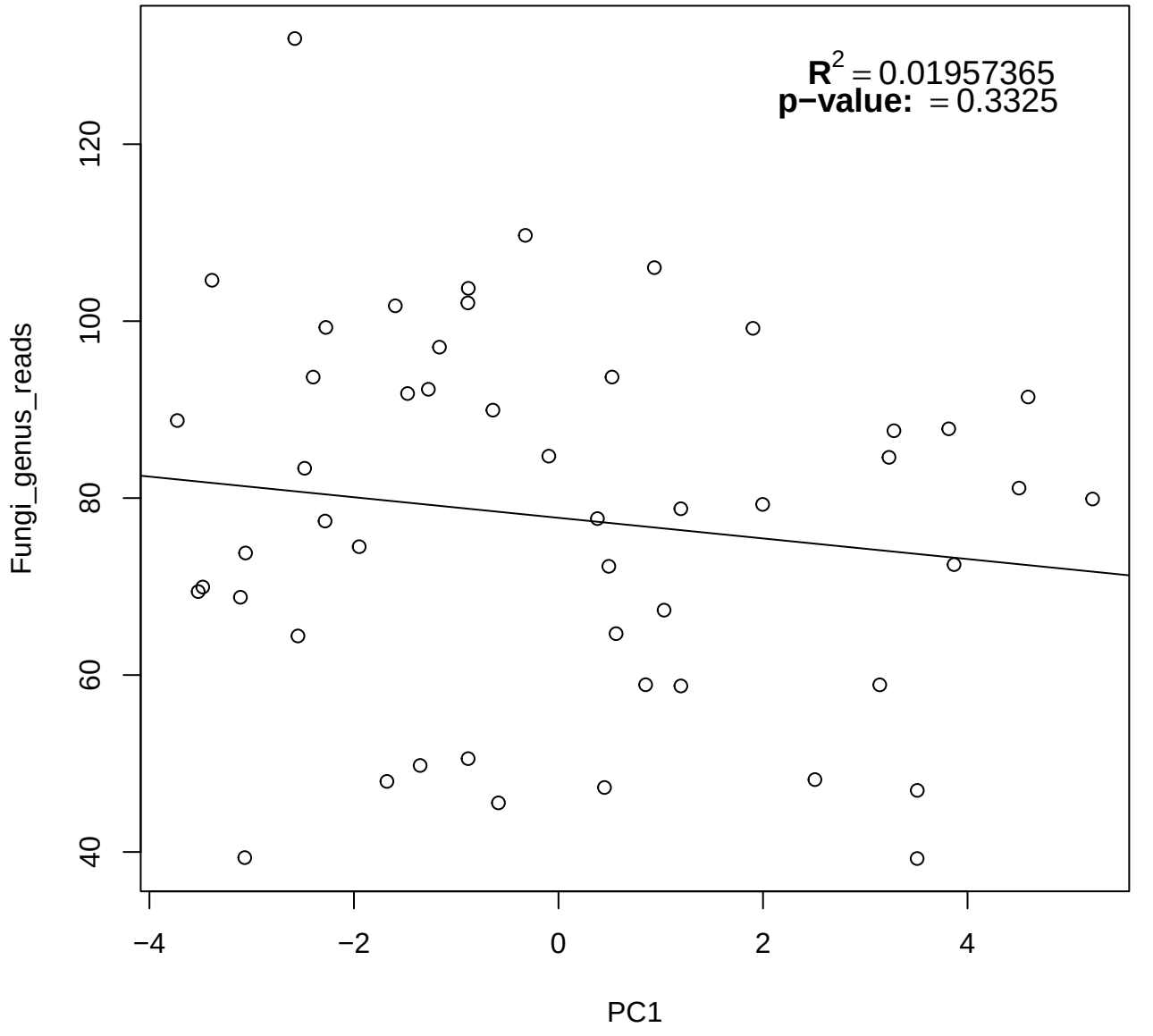

Residuals vs Fitted
Residuals
Fitted values
HOM1
AVE1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
MACE1
AVE1
Cook's distance

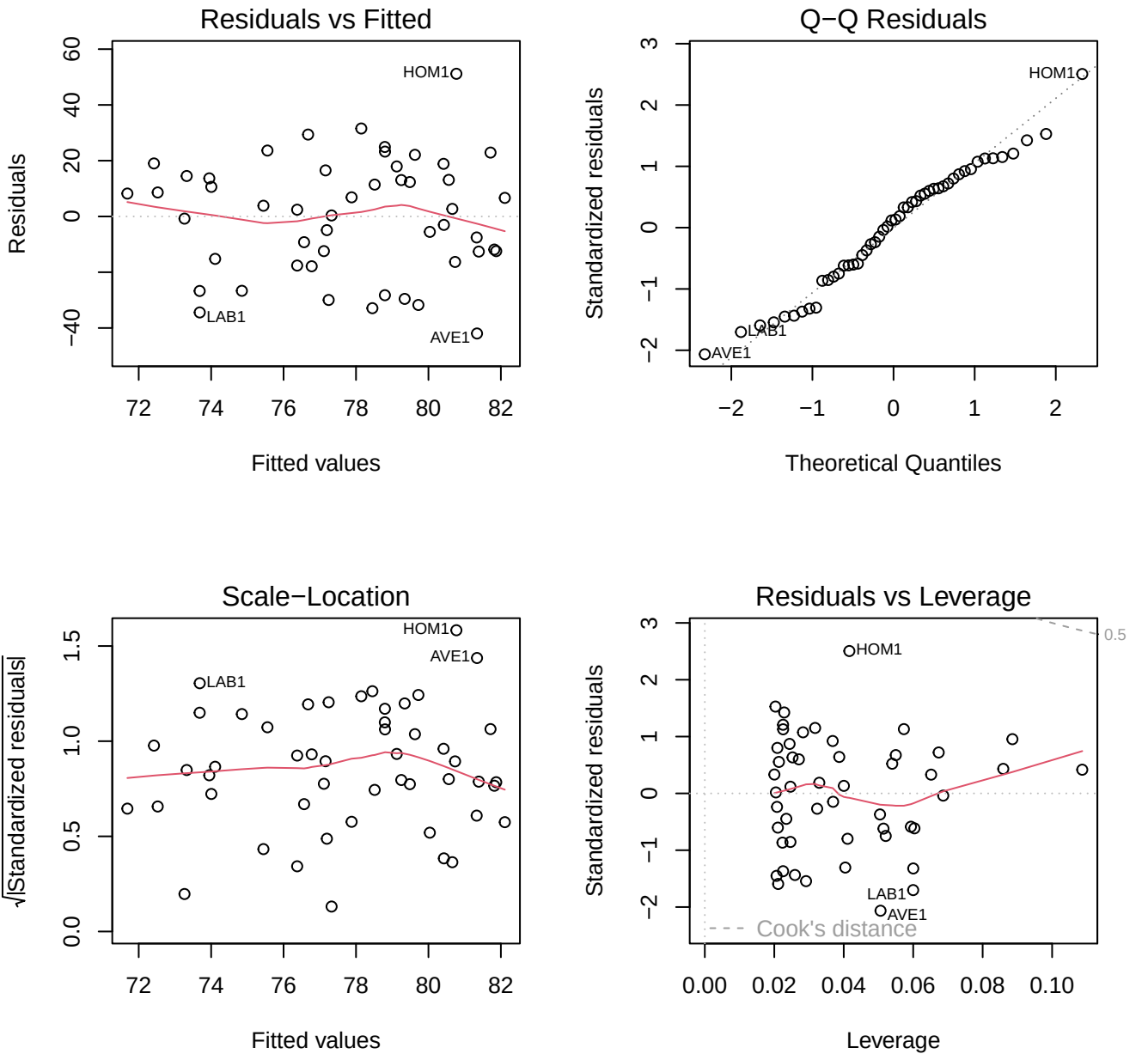

$R^2 = 0.01842088$
p−value: = 0.3473
Fungi_genus_reads
40
60
80
100
120
0.0
0.5
1.0
1.5
2.0
2.5
LUI_subasin

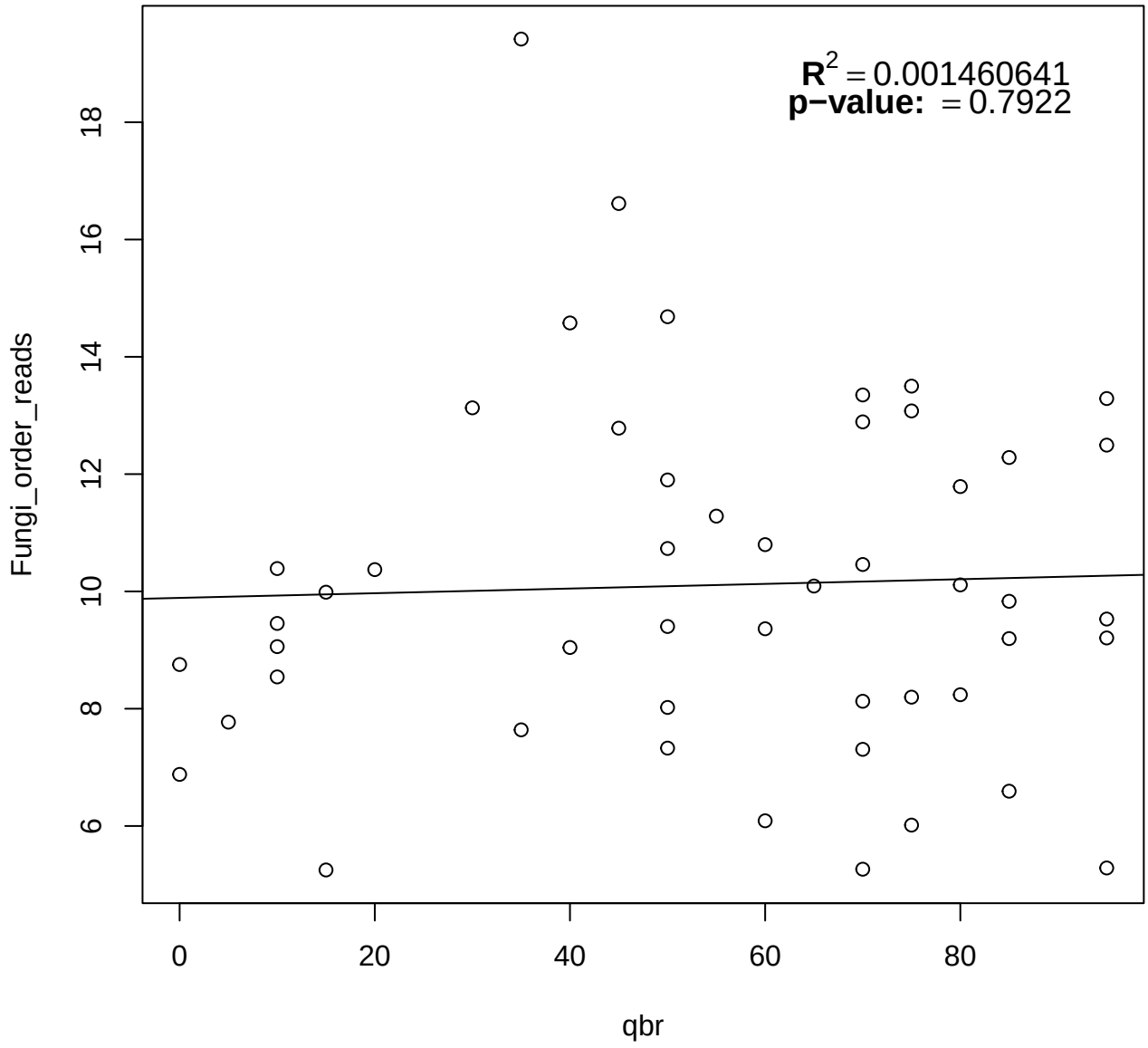

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
LAB1
AVE1
Cook's distance

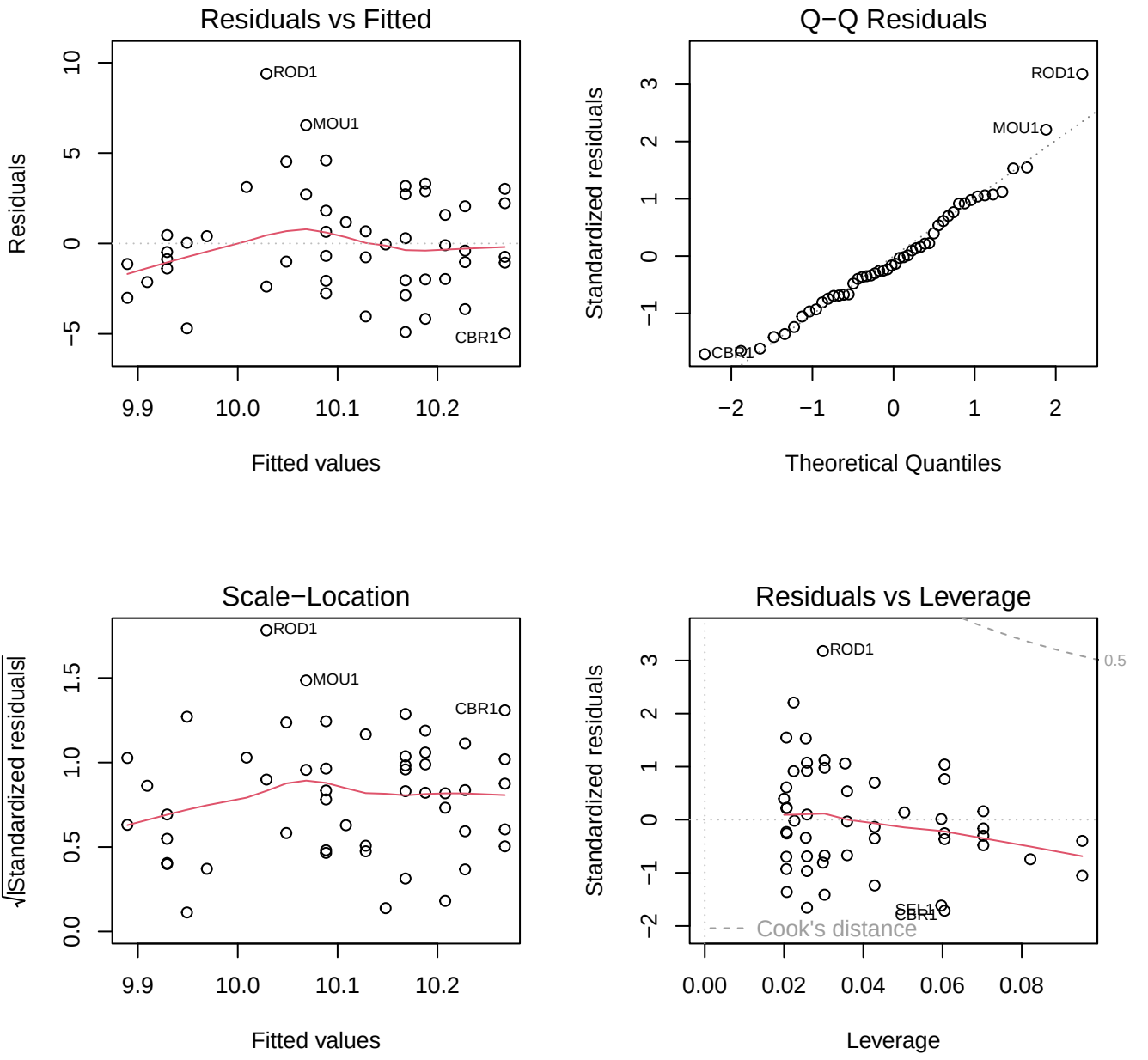

$R^2 = 0.0179867$
p−value: = 0.3531
Fungi_genus_reads
40
60
80
100
120
5
10
15
20
25
30
Altitude

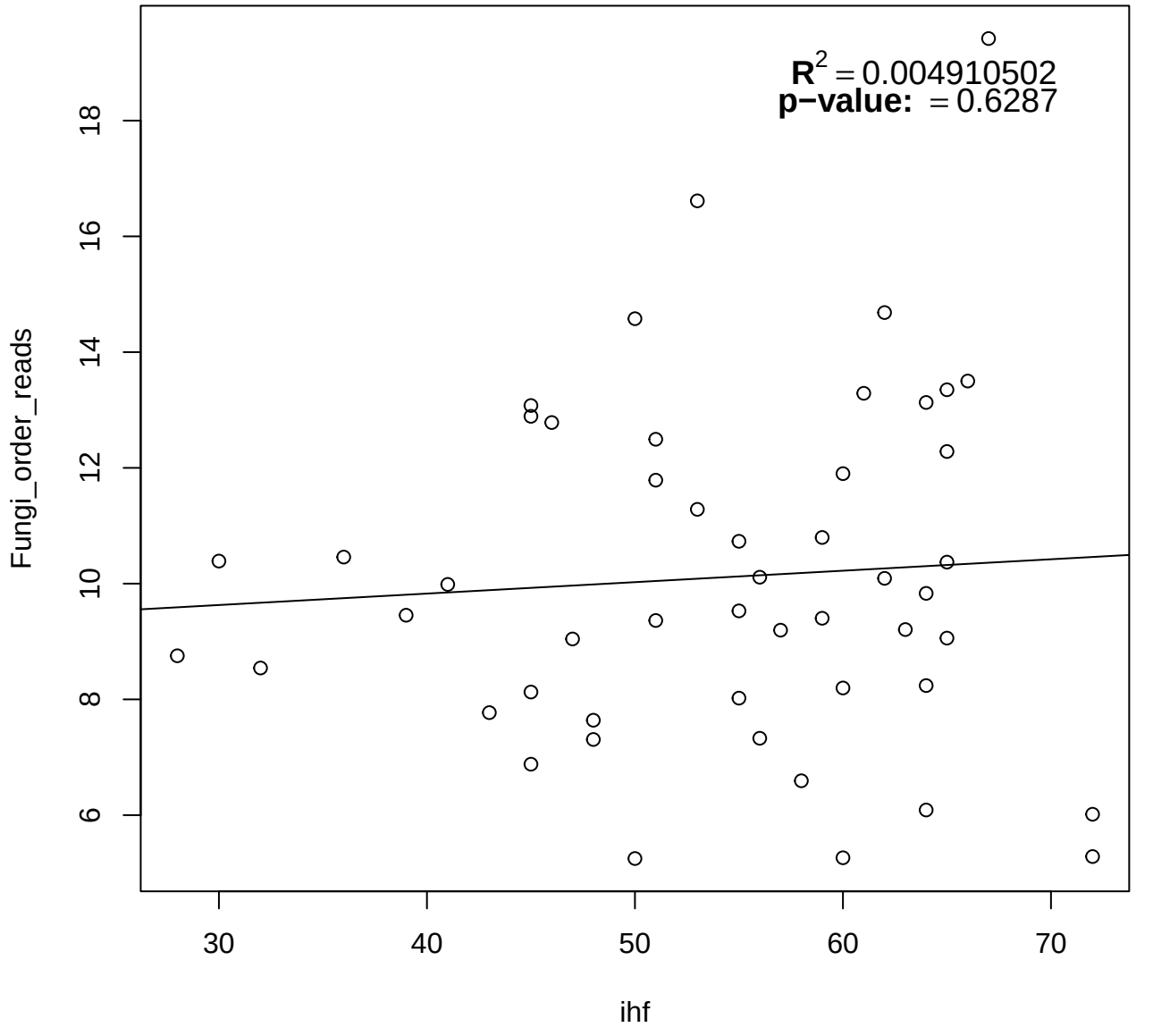

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
CAV2
AVE1
Cook's distance

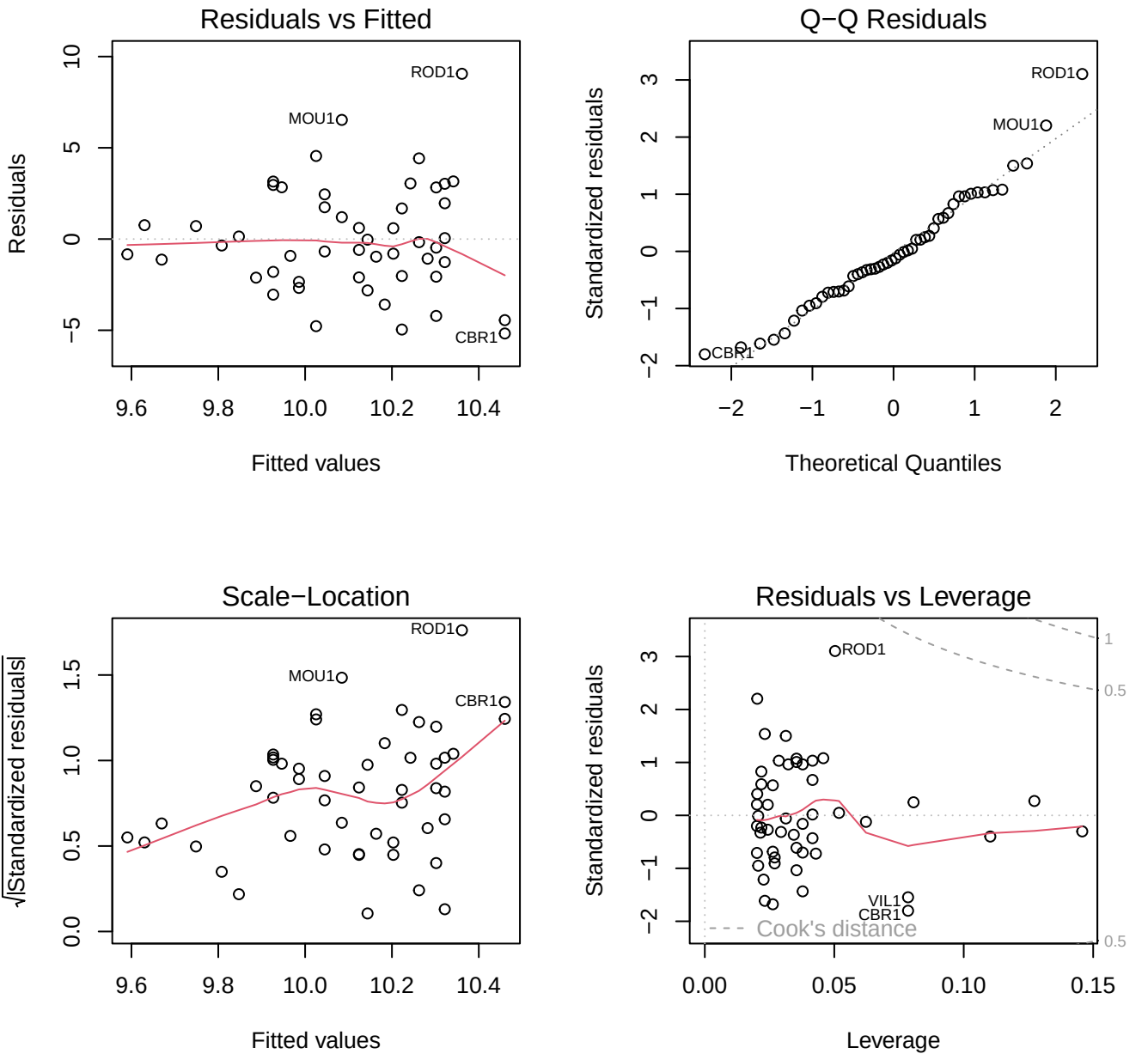

$R^2 = 0.01957365$
p−value: = 0.3325
Fungi_genus_reads
PC1
40
60
80
100
120
−4
−2
0
2
4

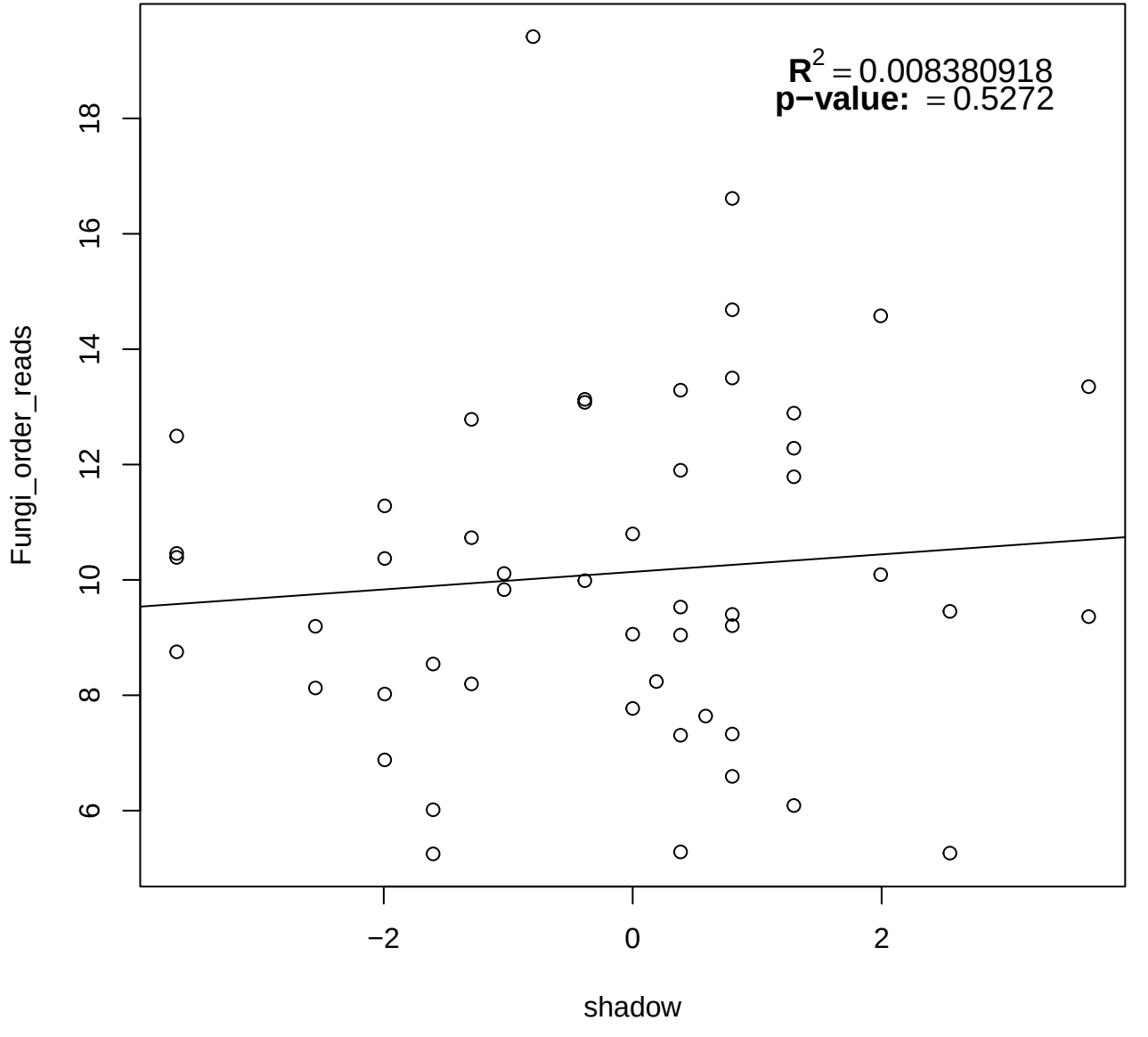

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
LAB1
AVE1
Cook's distance
0.5

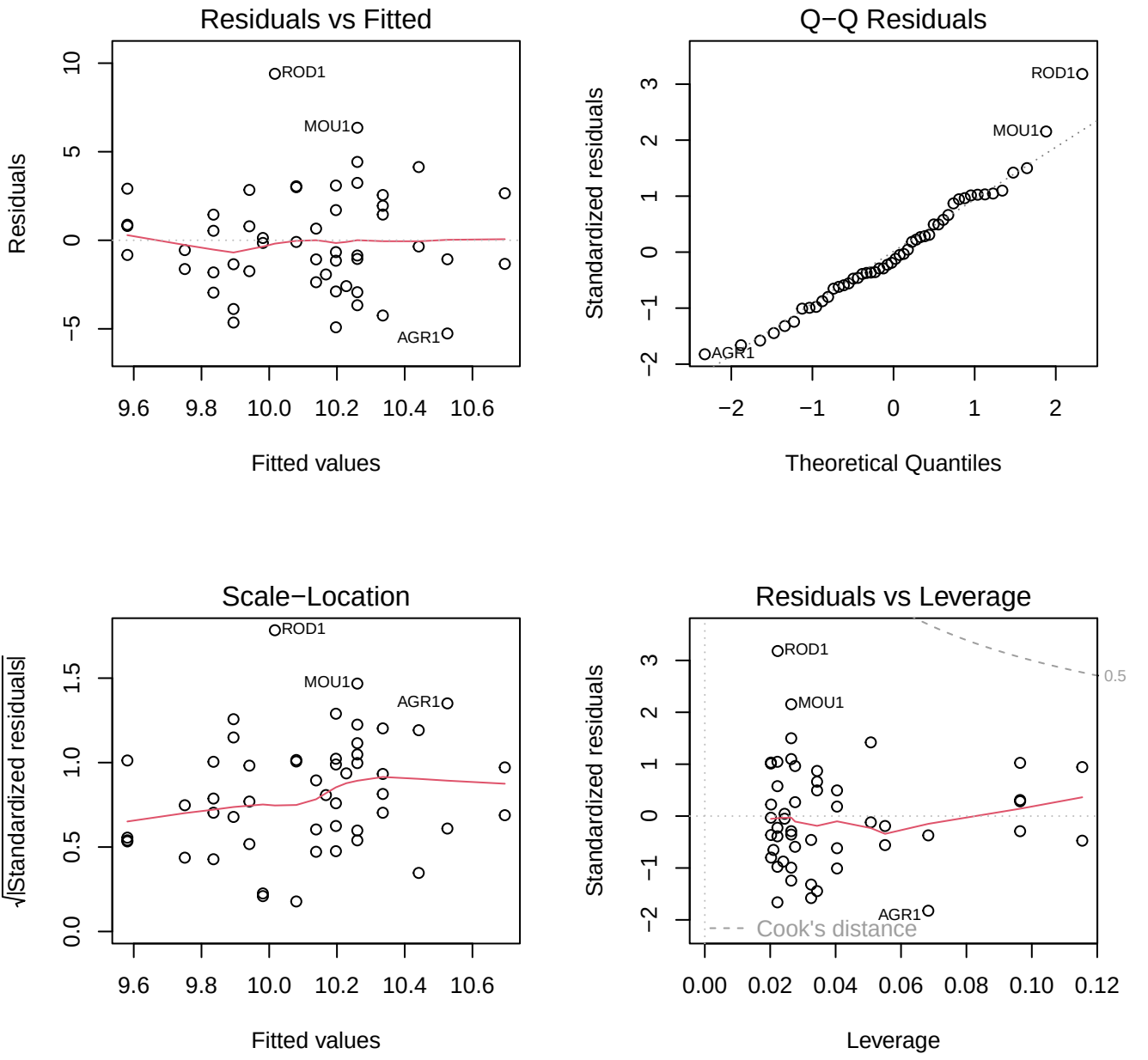

$R^2 = 0.001460641$
p−value: = 0.7922
Fungi_order_reads
qbr
6
8
10
12
14
16
18
0
20
40
60
80

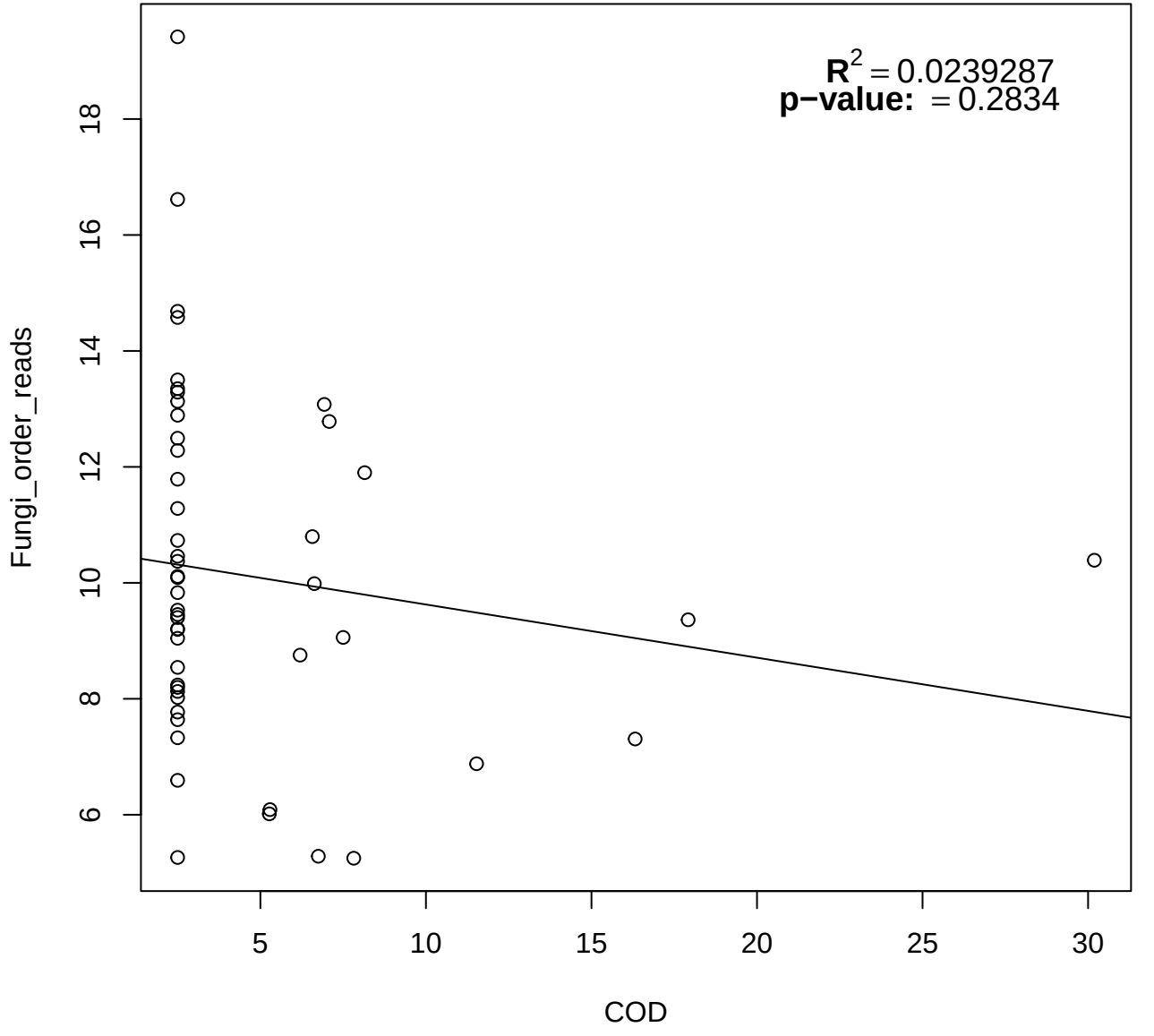

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
CBR1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
CBR1
SEL1
0.5
Cook's distance

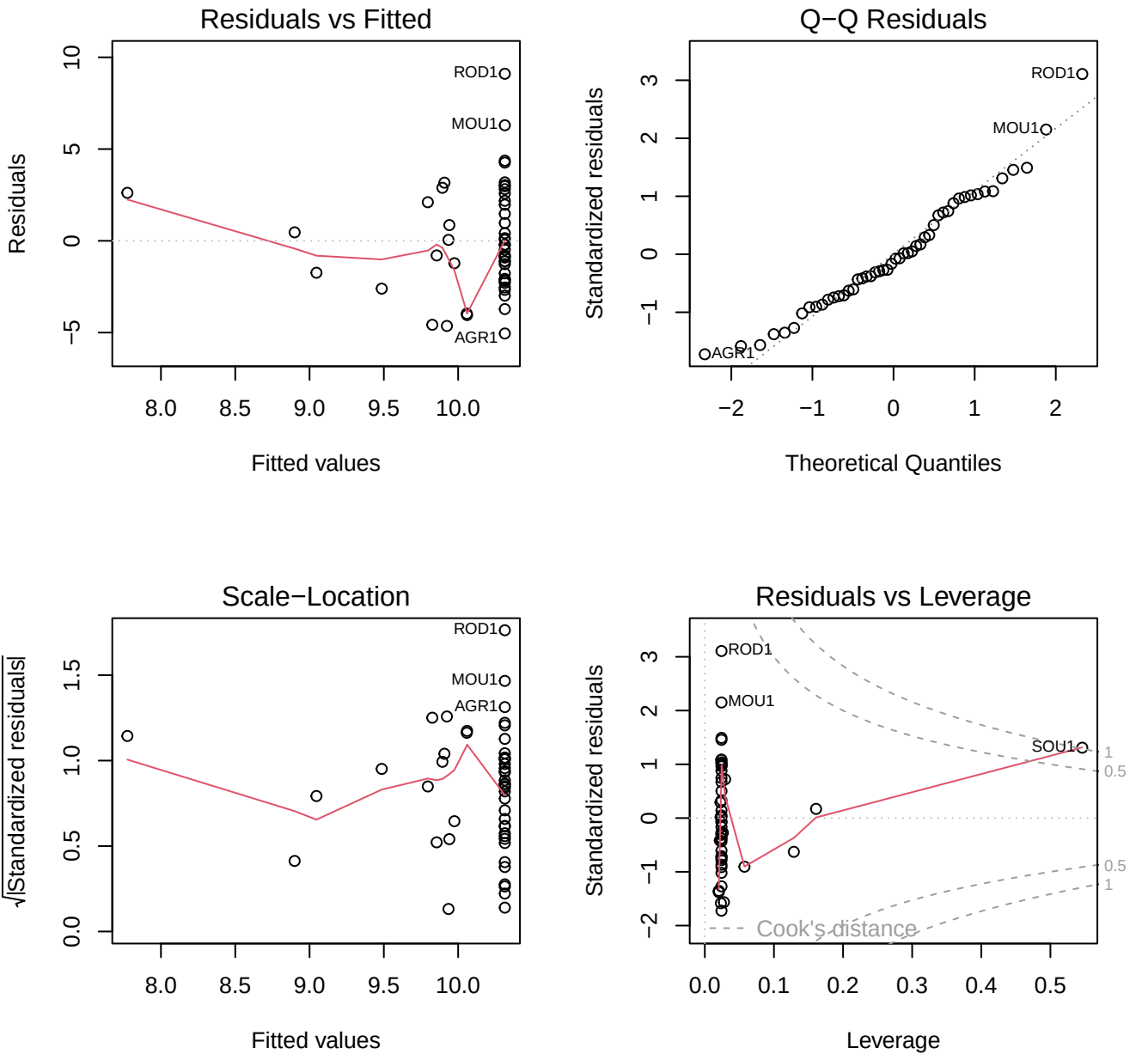

$R^2 = 0.004910502$
p−value: = 0.6287
Fungi_order_reads
ihf
6
8
10
12
14
16
18
30
40
50
60
70

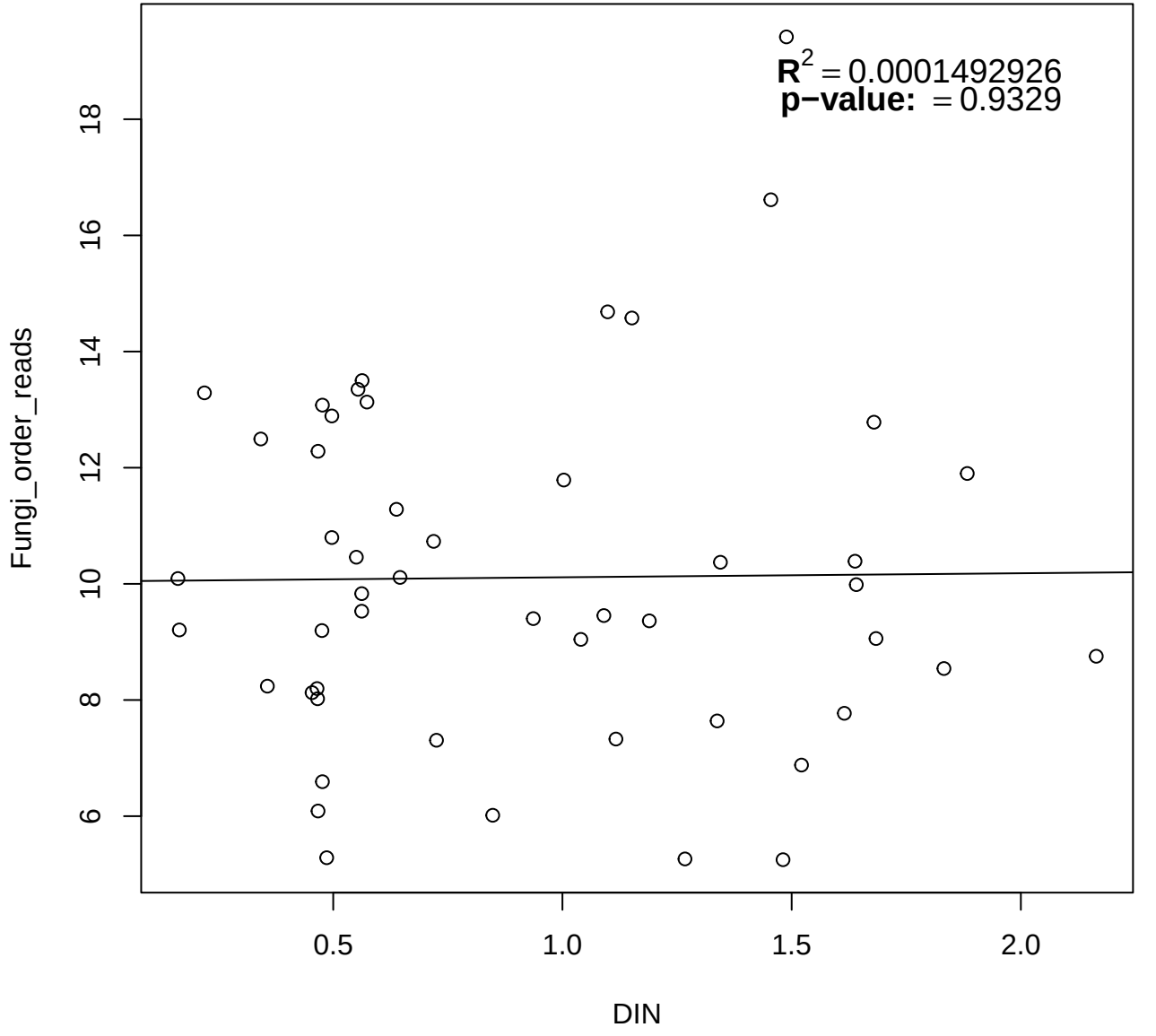

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
CBR1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
VIL1
CBR1
Cook's distance
1
0.5
0.5

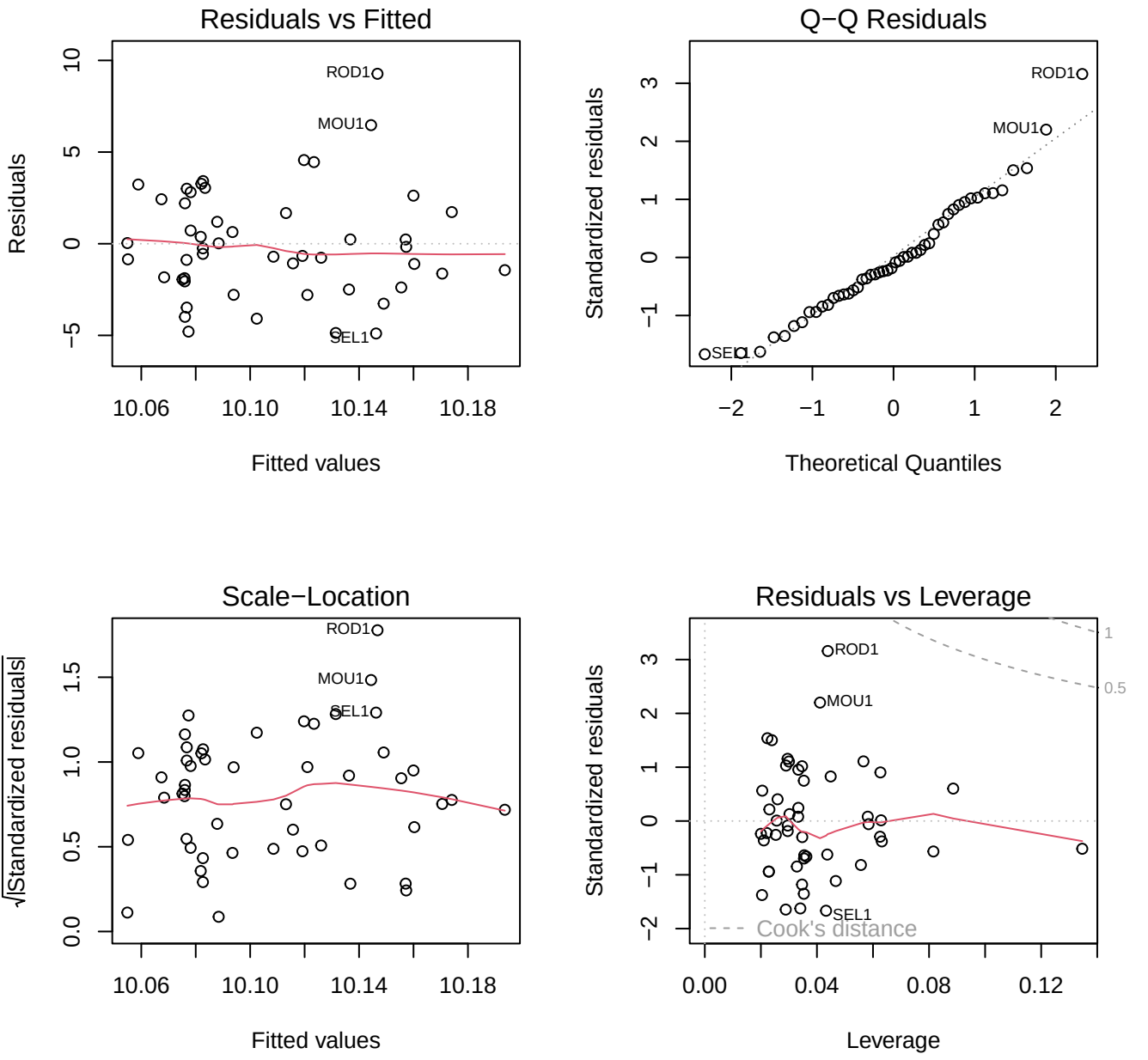

$R^2 = 0.008380918$
p−value: = 0.5272
Fungi_order_reads
shadow
6
8
10
12
14
16
18
−2
0
2

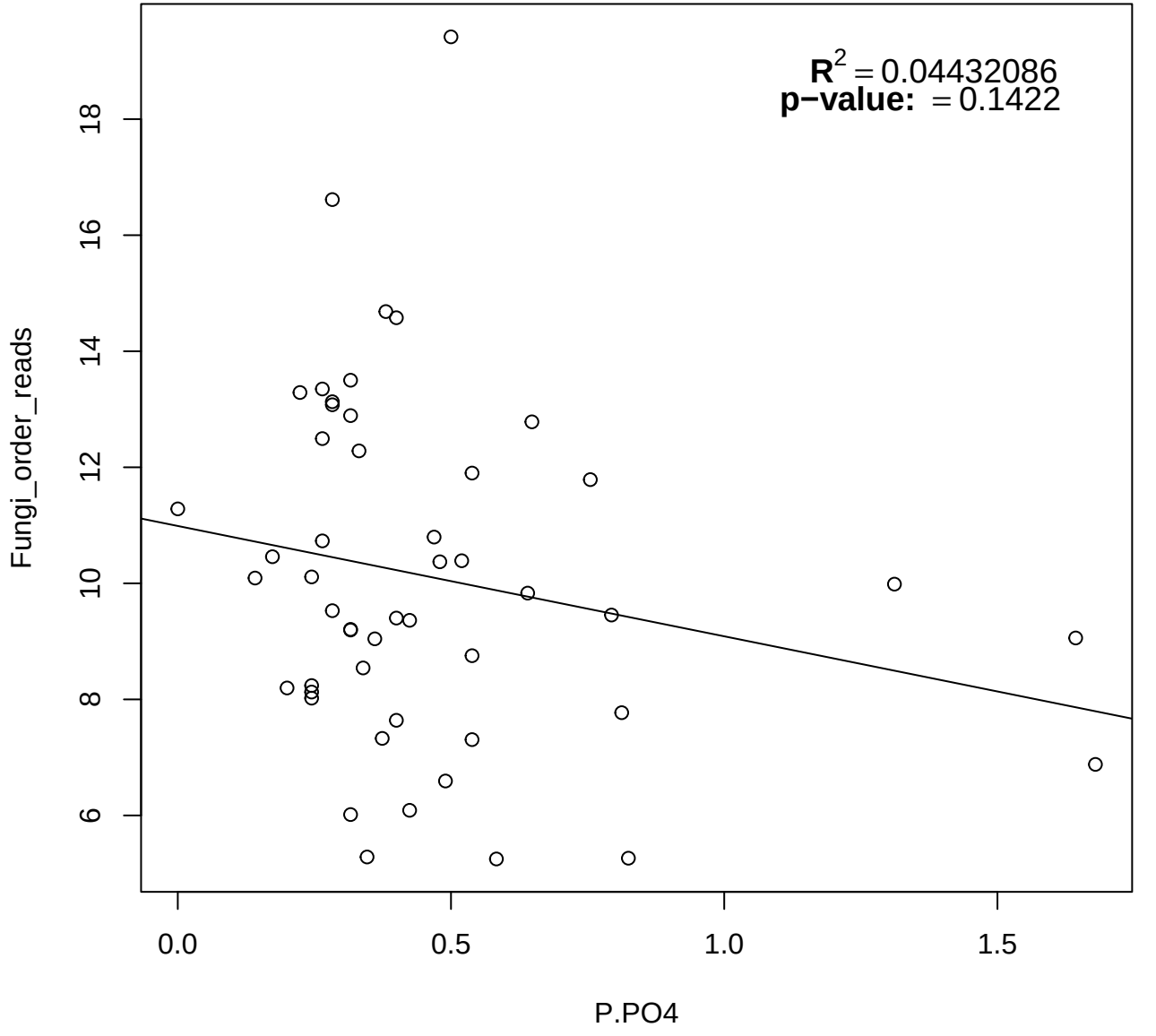

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
AGR1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MOU1
AGR1
0.5
Cook's distance

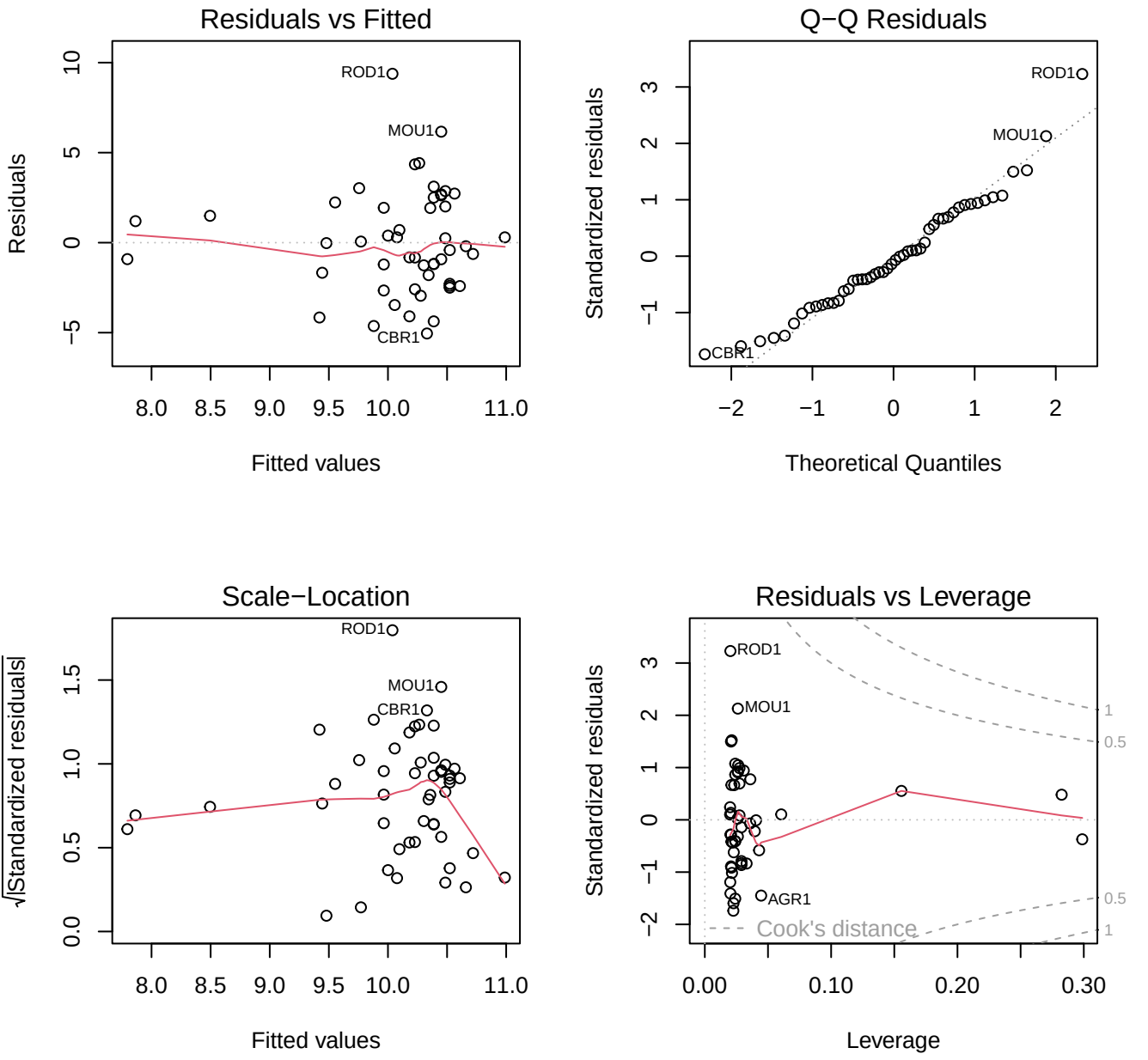

$R^2 = 0.0239287$
p−value: = 0.2834
Fungi_order_reads
COD
6
8
10
12
14
16
18
5
10
15
20
25
30

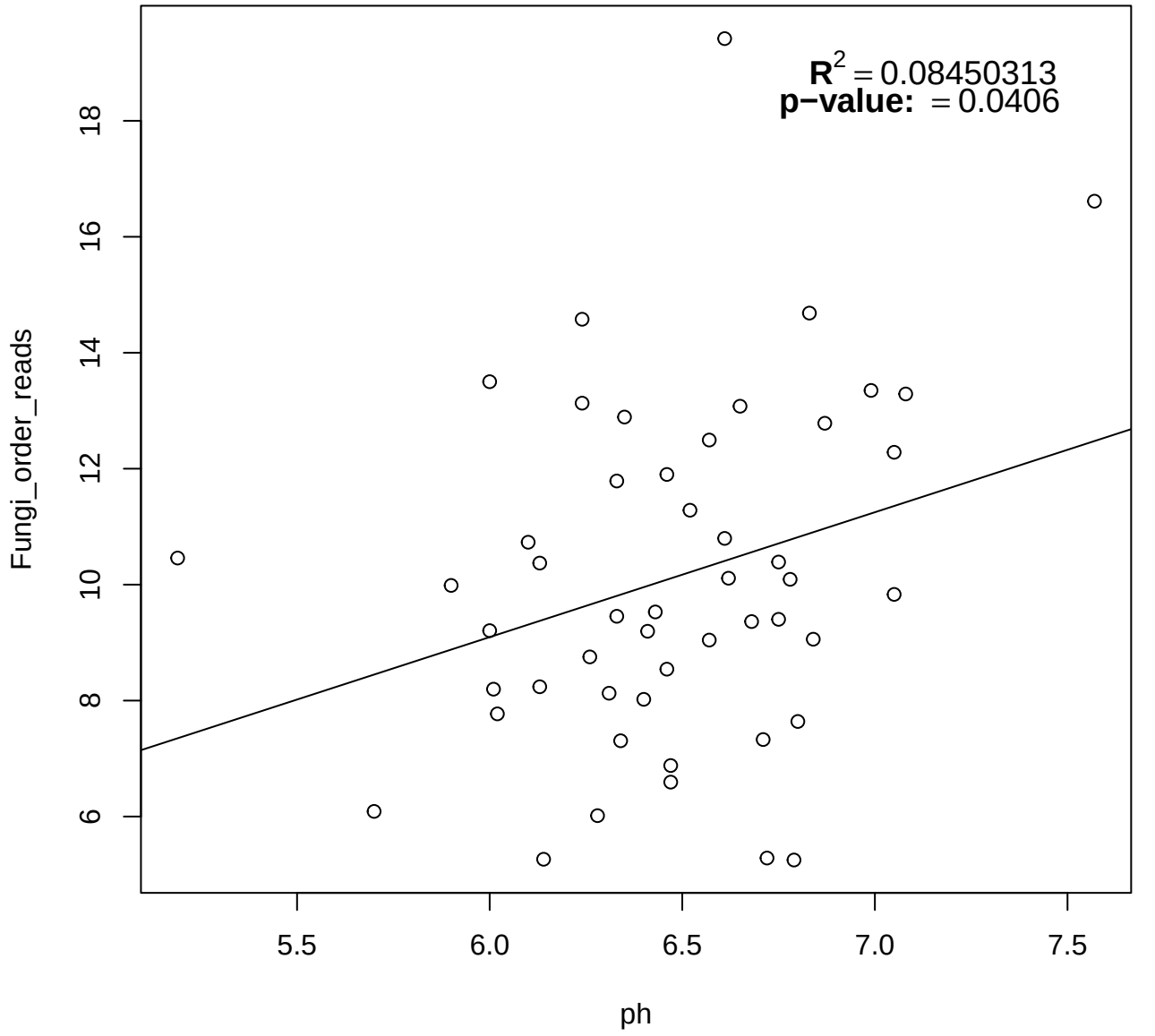

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
AGR1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MOU1
SOU1
Cook's distance

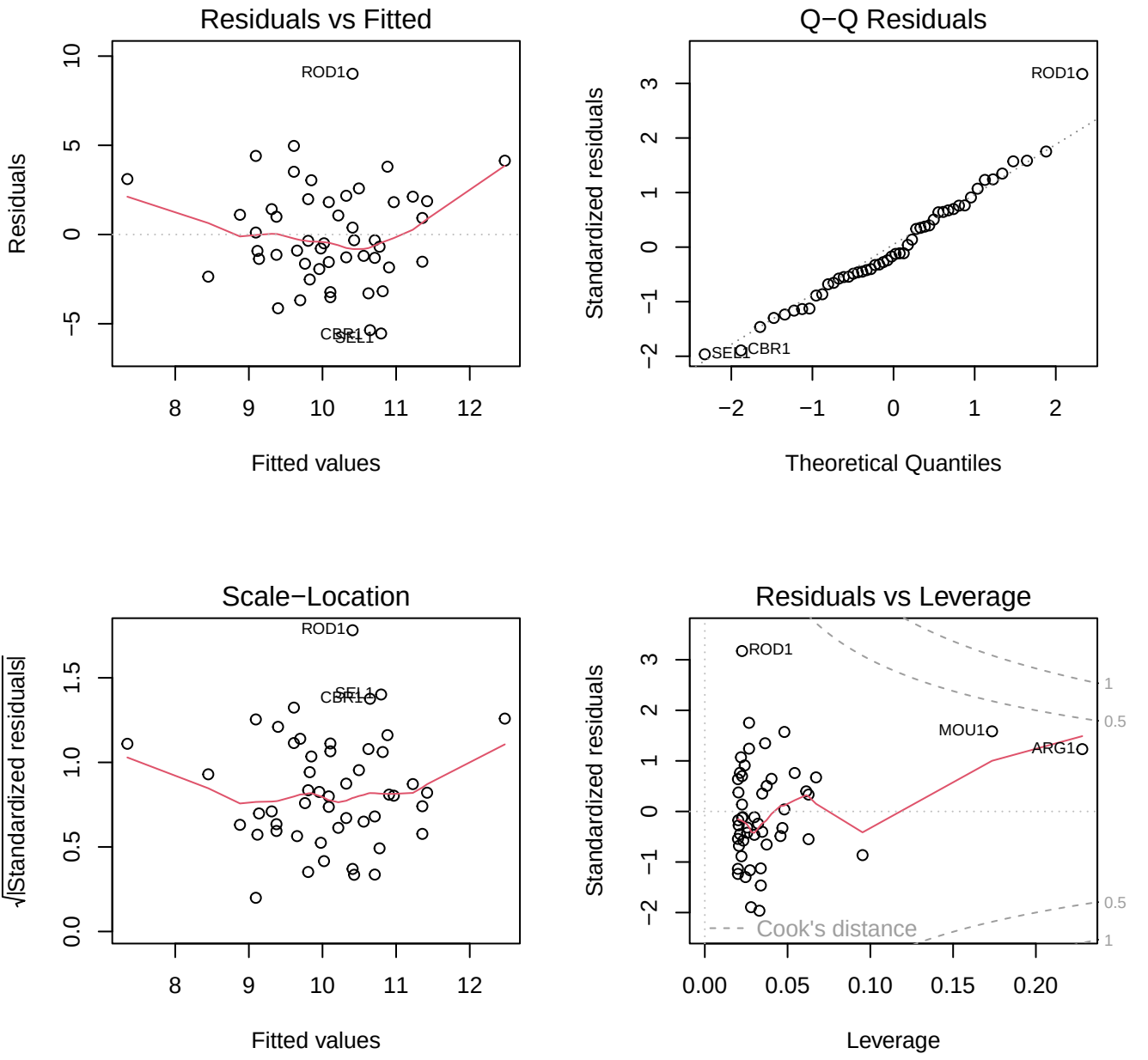

$R^2 = 0.0001492926$
p−value: = 0.9329
Fungi_order_reads
DIN
6
8
10
12
14
16
18
0.5
1.0
1.5
2.0

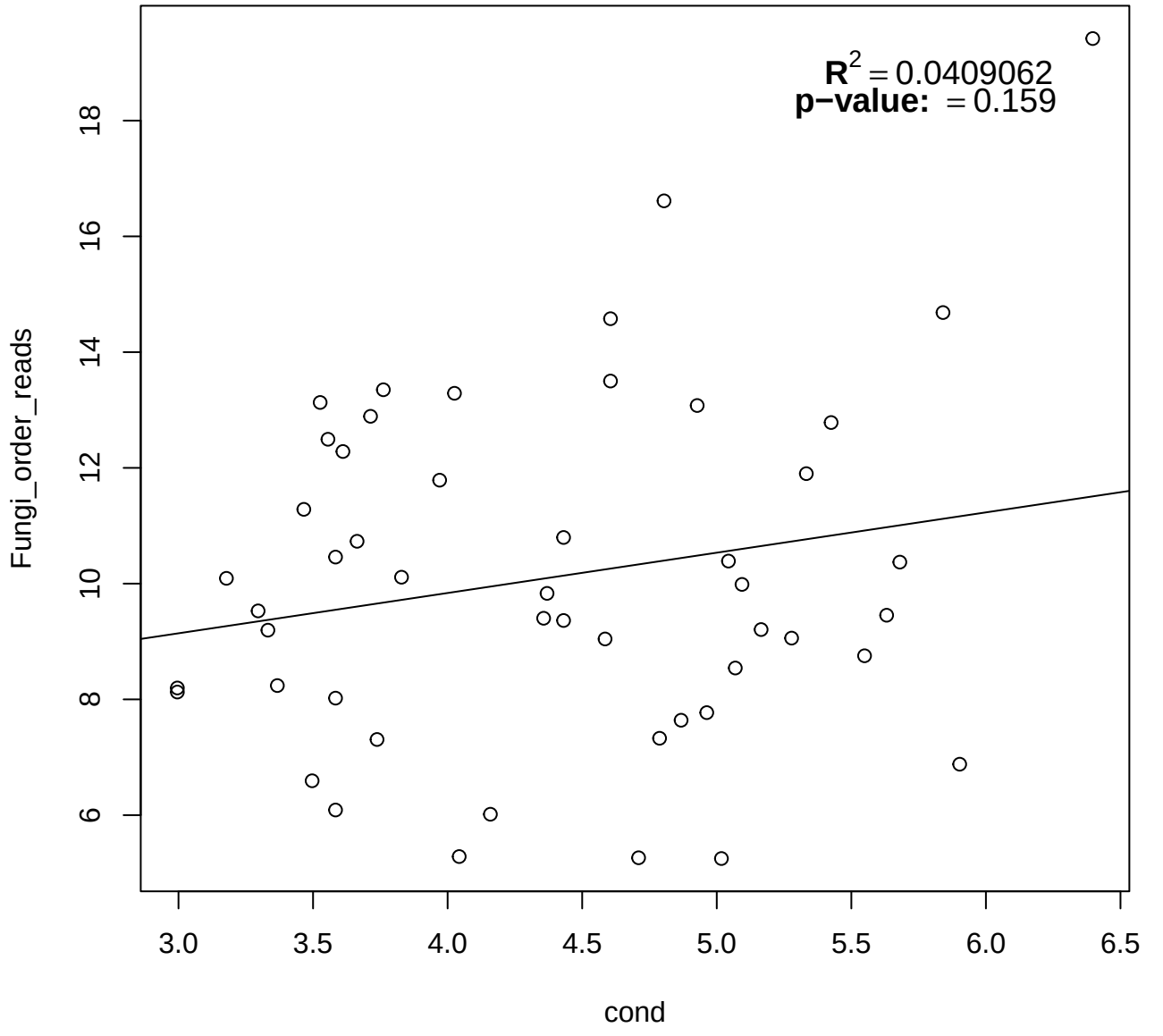

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
SEL1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
SEL1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MOU1
SEL1
Cook's distance
1
0.5

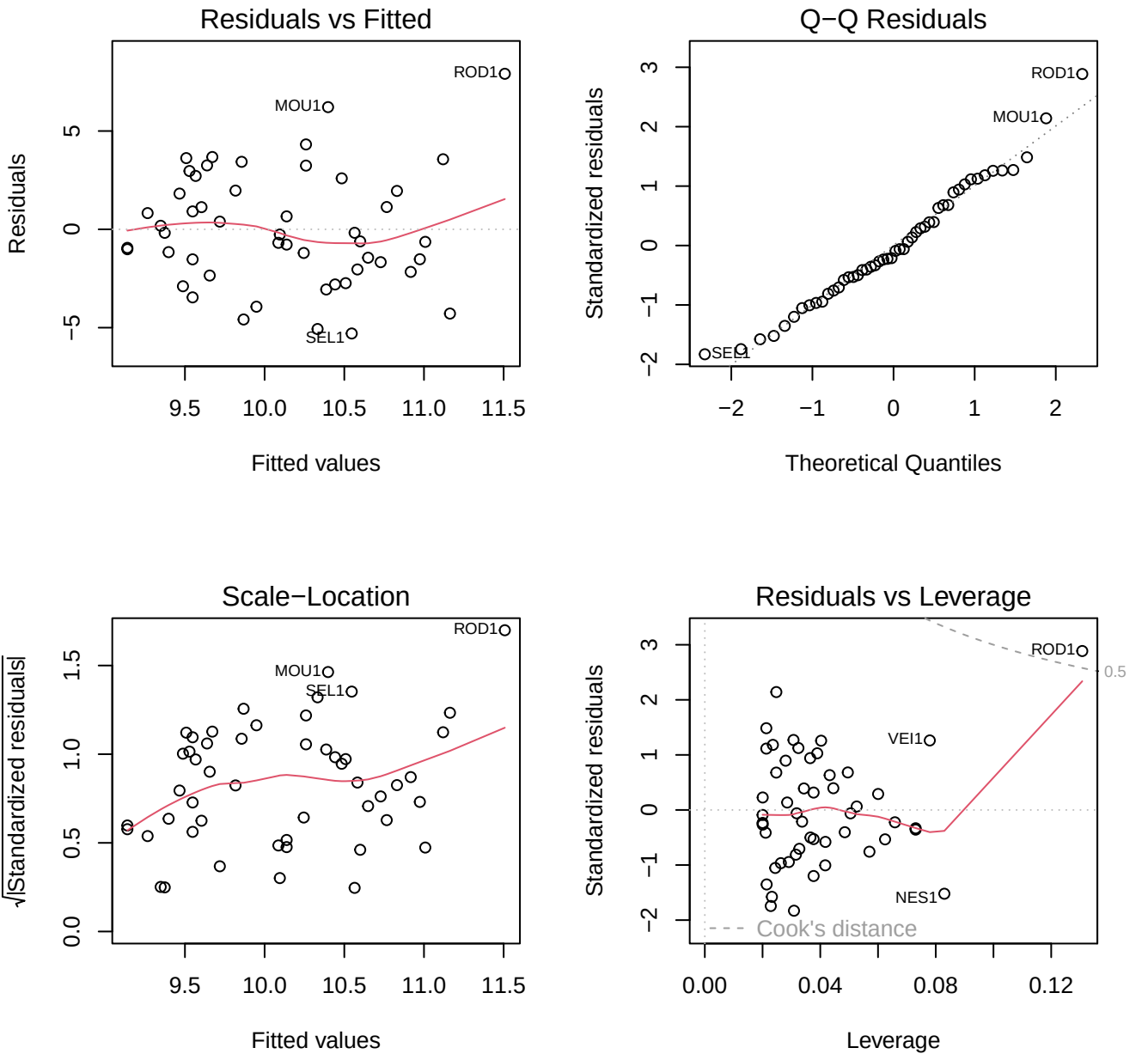

$R^2 = 0.04432086$
p−value: = 0.1422
Fungi_order_reads
P.PO4
6
8
10
12
14
16
18
0.0
0.5
1.0
1.5

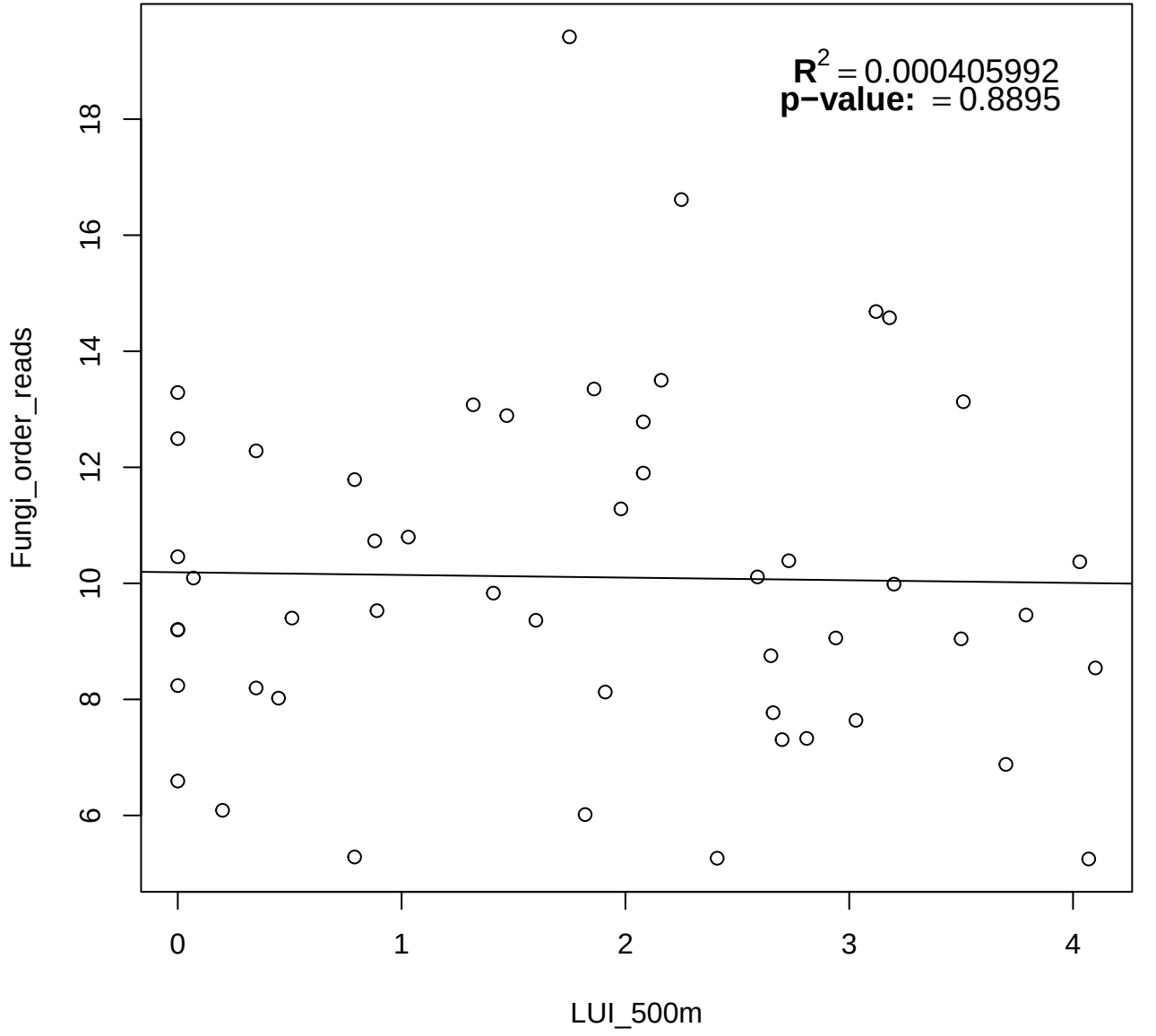

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
CBR1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MOU1
AGR1
Cook's distance
1
0.5
0.5
1

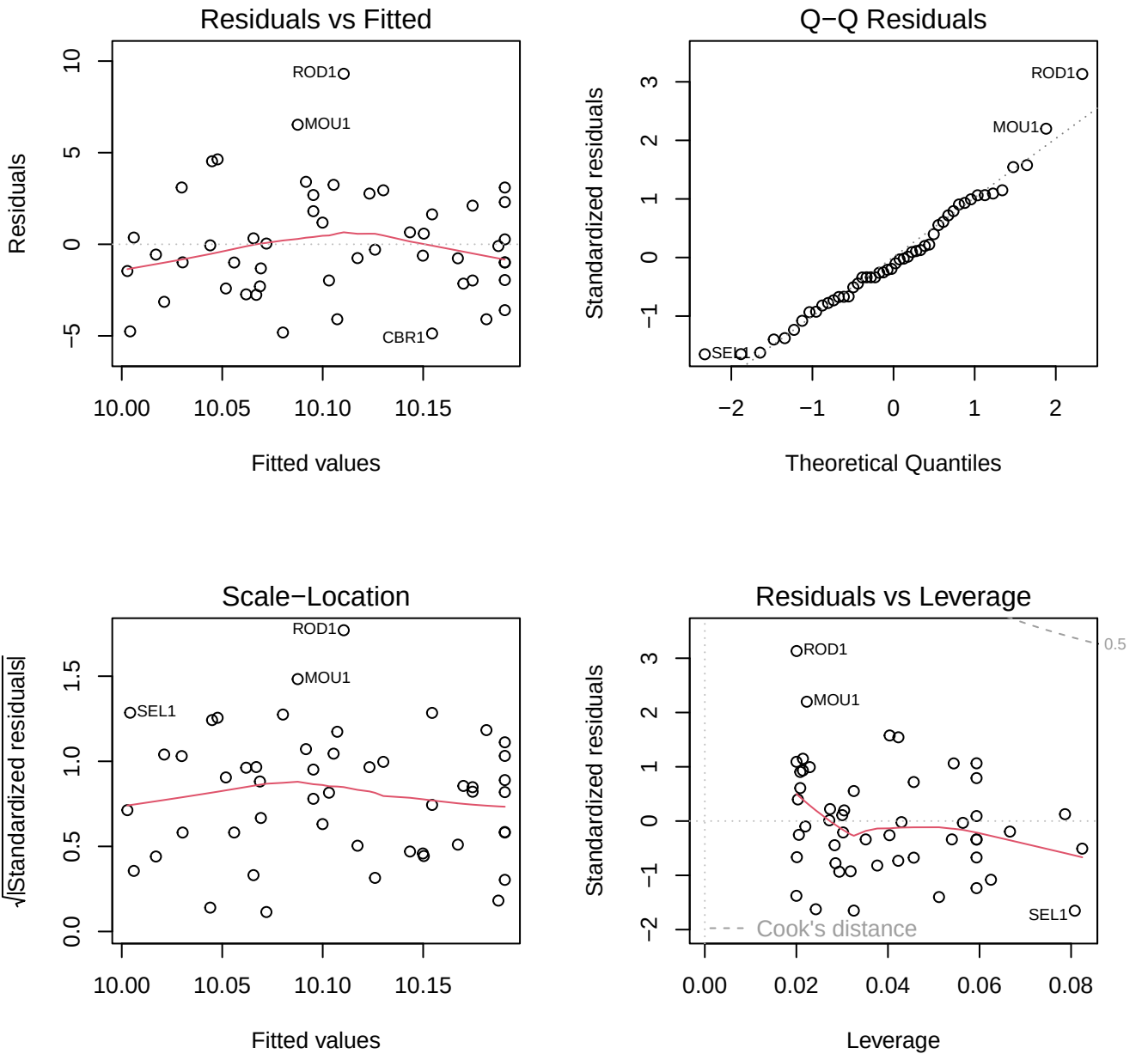

$R^2 = 0.08450313$
p−value: = 0.0406
Fungi_order_reads
ph
6
8
10
12
14
16
18
5.5
6.0
6.5
7.0
7.5

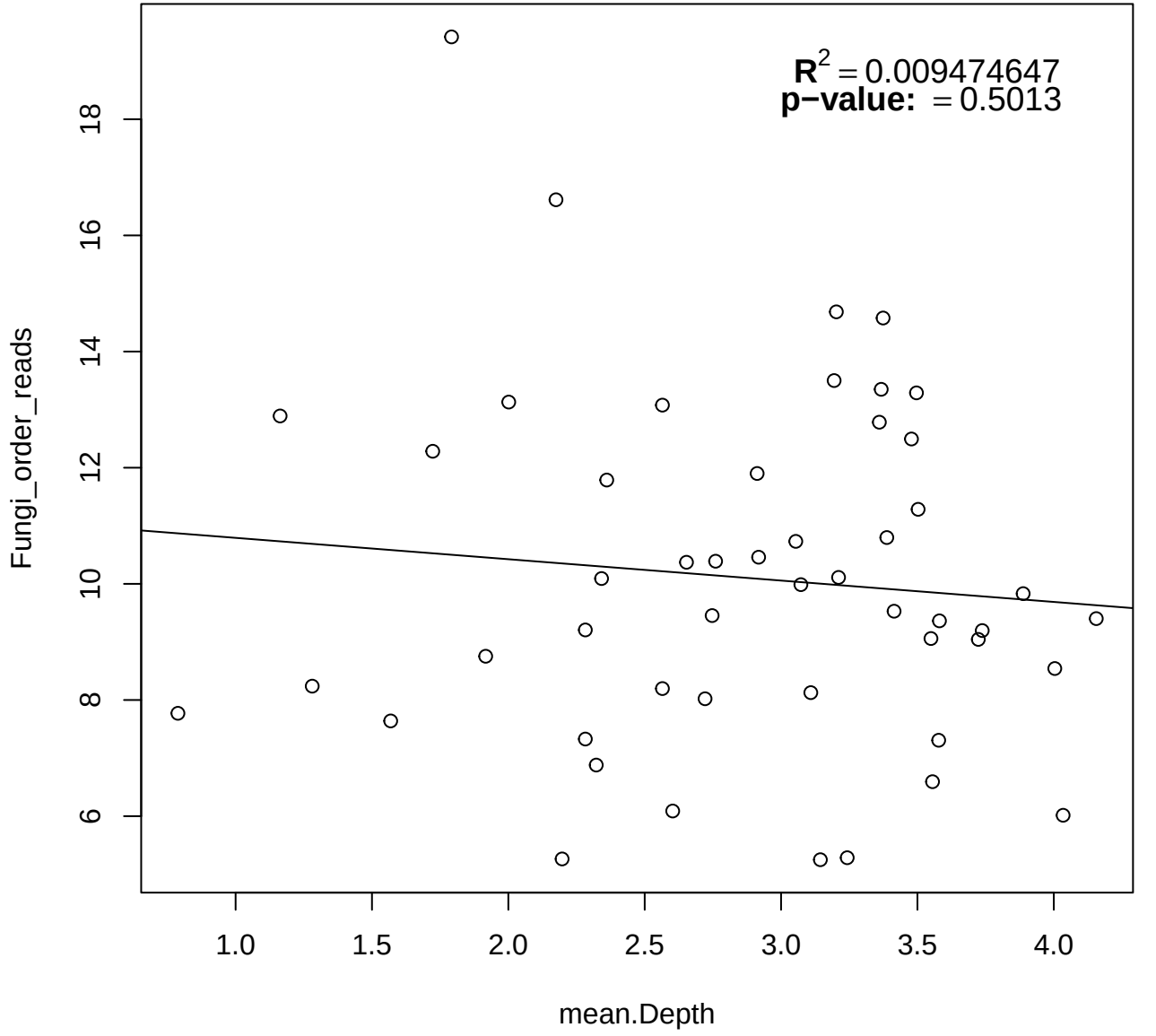

Residuals vs Fitted
Residuals
Fitted values
ROD1
CBR1
SEL1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
SEL1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
CBR1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MOU1
ARG1
Cook's distance

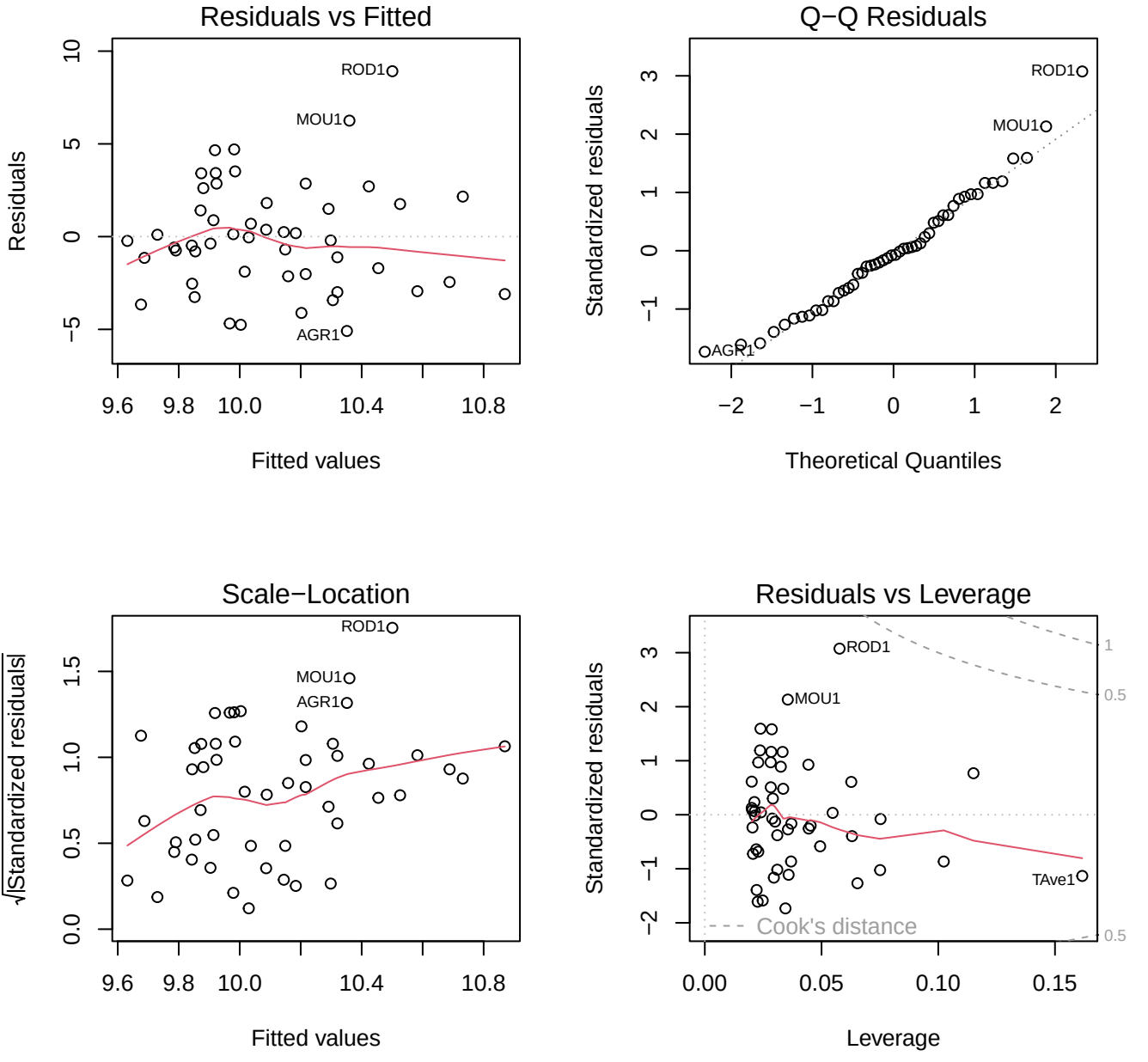

$R^2 = 0.0409062$
p−value: = 0.159
Fungi_order_reads
cond
6
8
10
12
14
16
18
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5

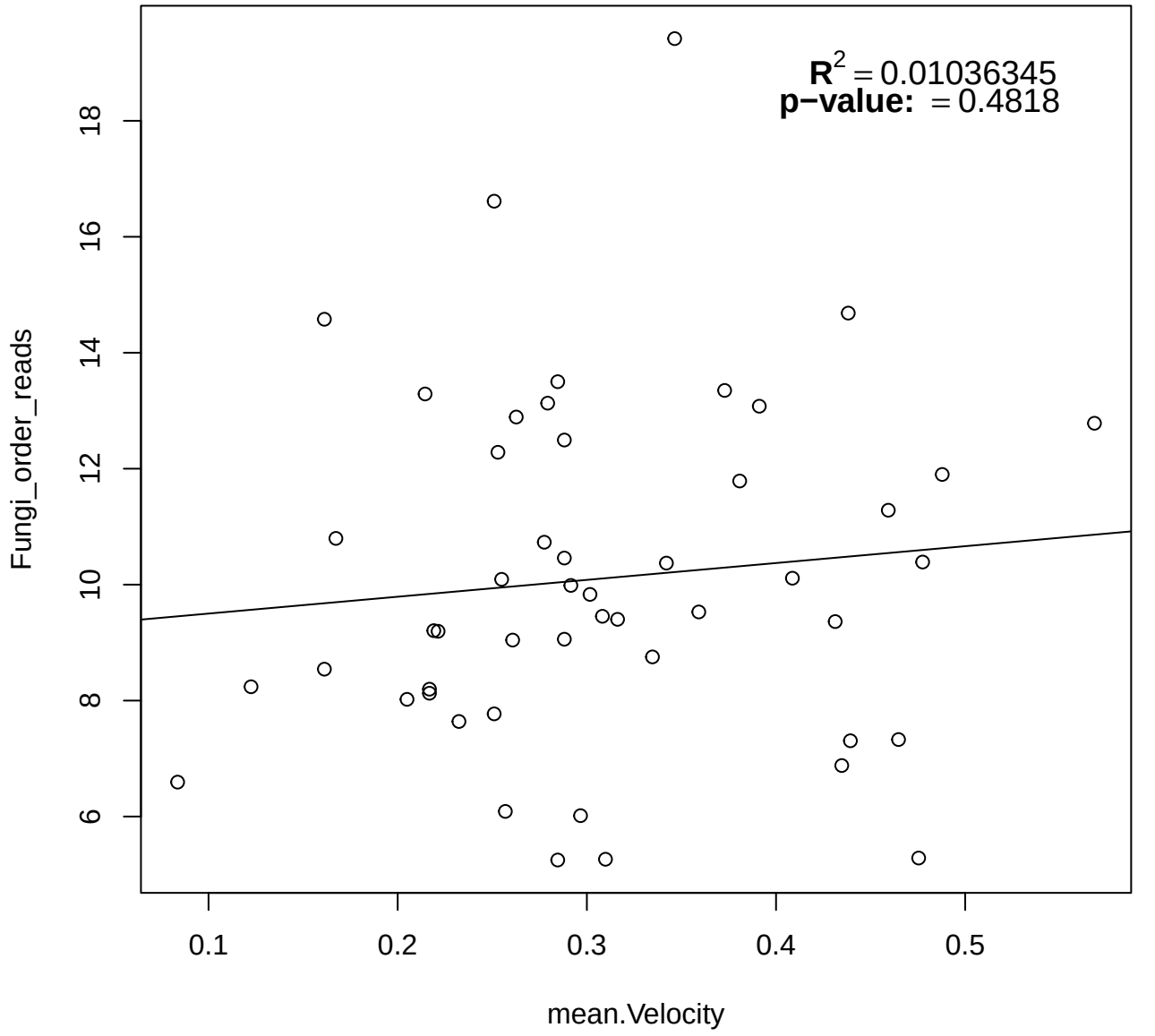

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
SEL1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
SEL1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
VEI1
NES1
0.5
Cook's distance

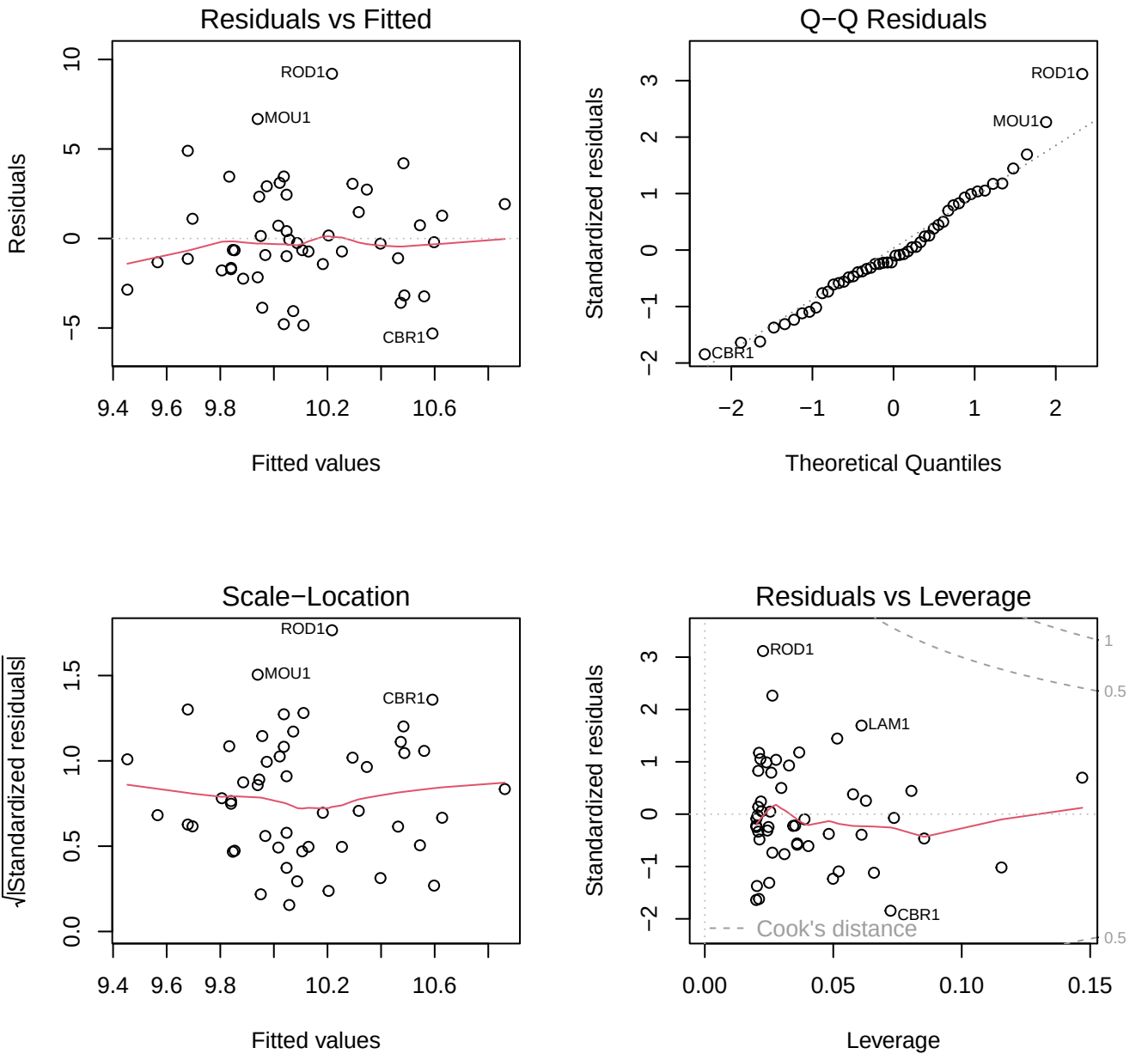

$R^2 = 0.000405992$
p−value: = 0.8895
Fungi_order_reads
LUI_500m
6
8
10
12
14
16
18
0
1
2
3
4

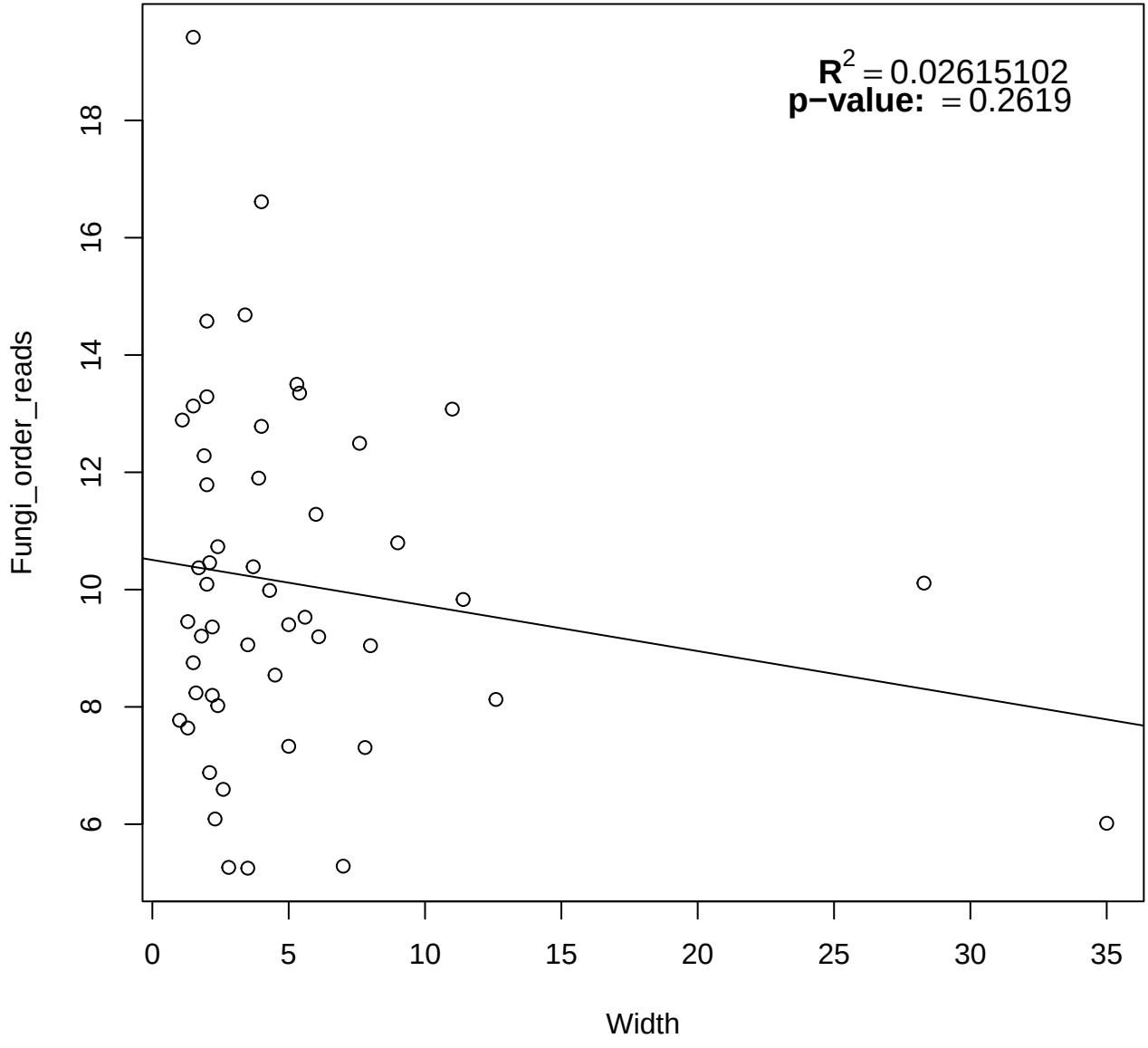

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
SEL1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MOU1
SEL1
0.5
Cook's distance

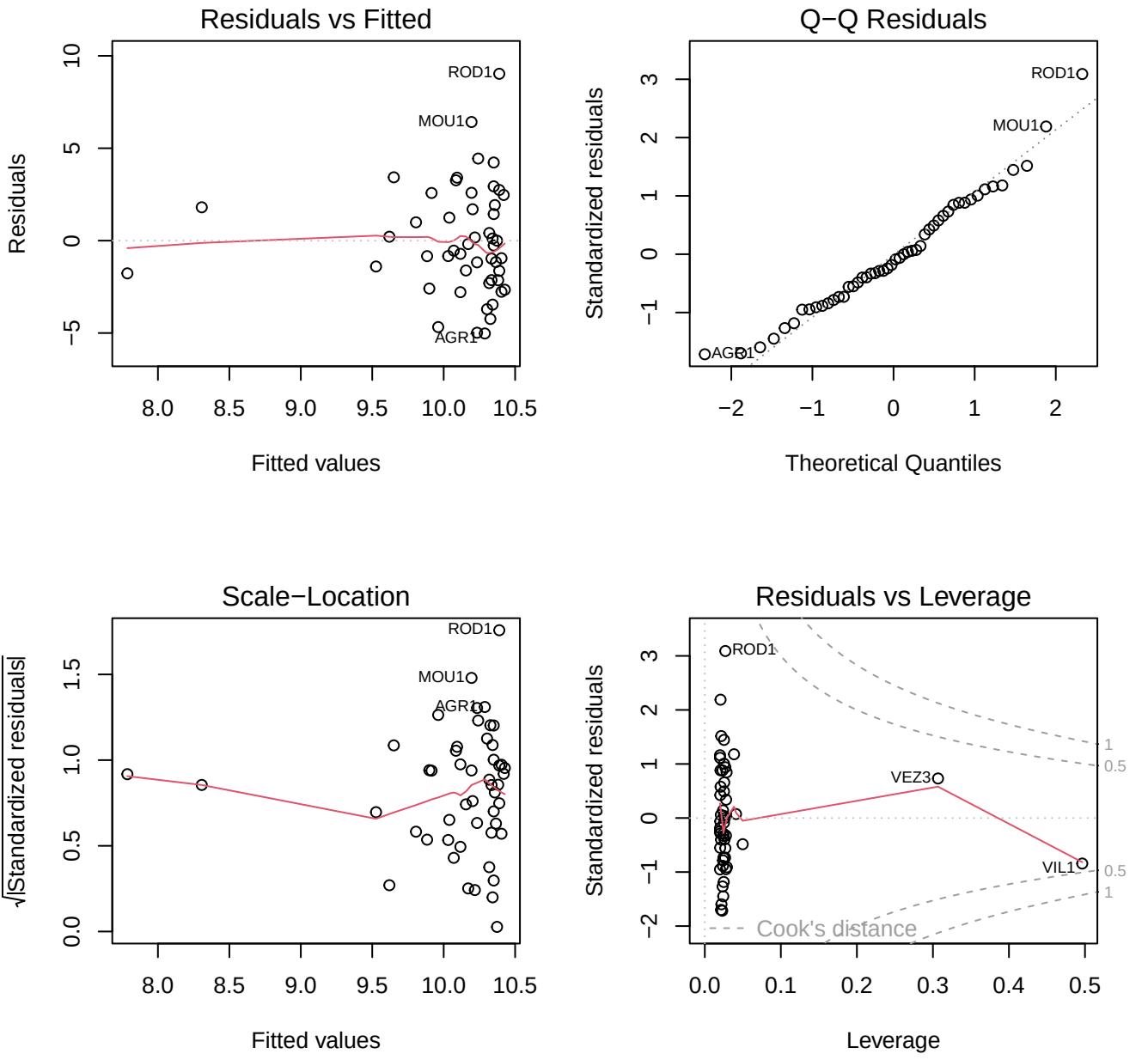

$R^2 = 0.009474647$
p−value: = 0.5013
Fungi_order_reads
mean.Depth
6
8
10
12
14
16
18
1.0
1.5
2.0
2.5
3.0
3.5
4.0

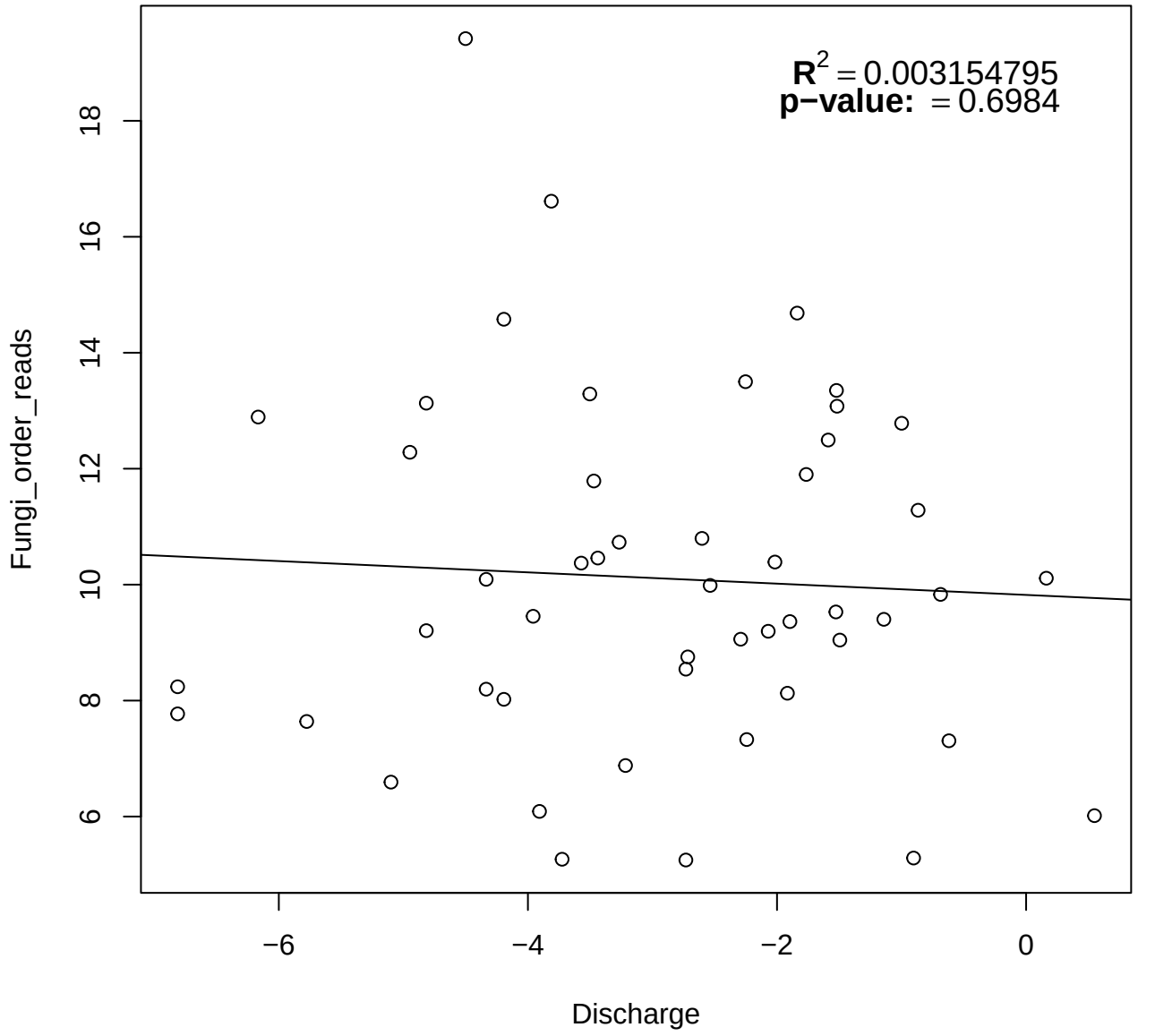

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
AGR1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MOU1
TAve1
Cook's distance
1
0.5
0.5

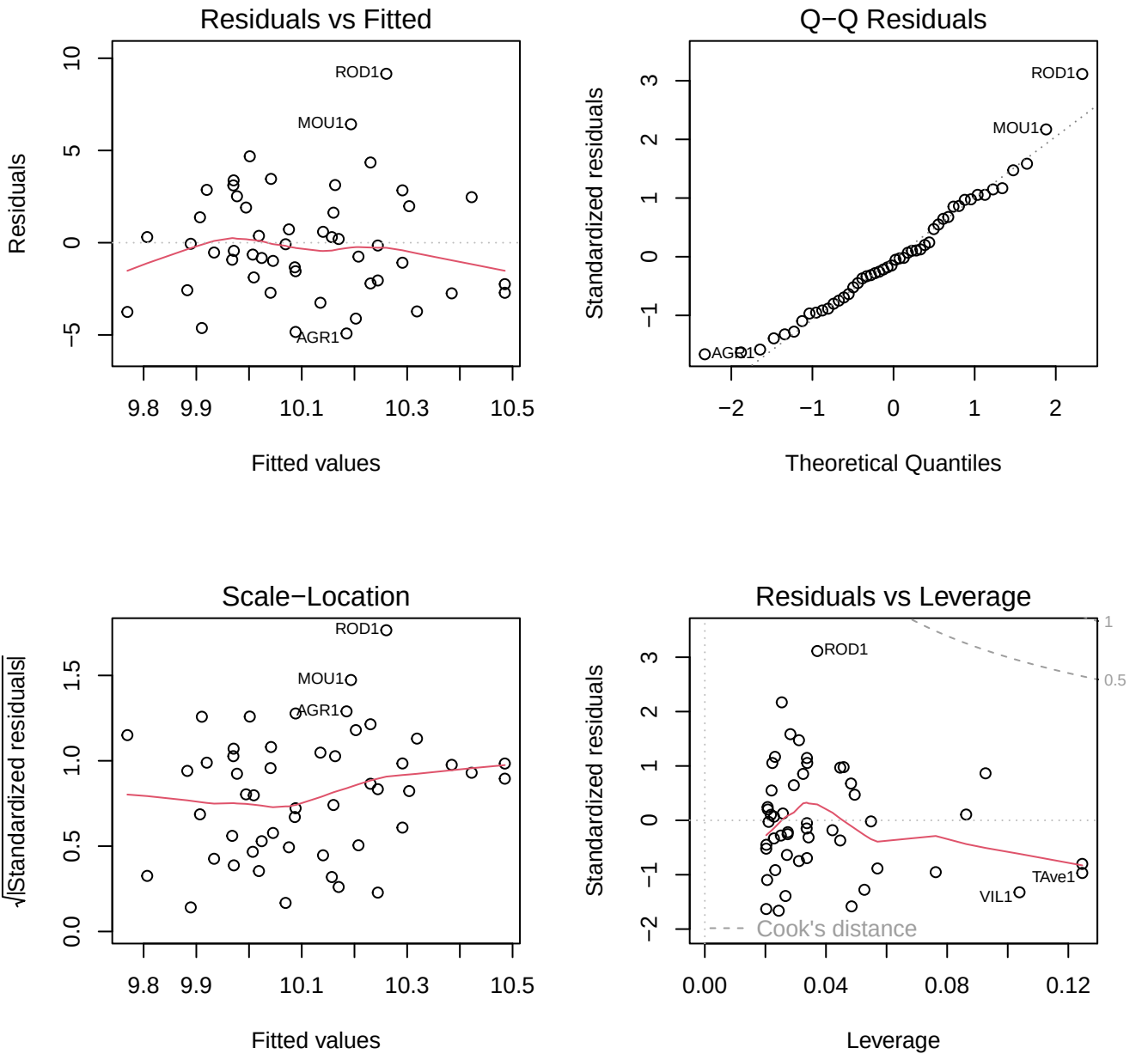

$R^2 = 0.01036345$
p−value: = 0.4818
Fungi_order_reads
mean.Velocity
6
8
10
12
14
16
18
0.1
0.2
0.3
0.4
0.5

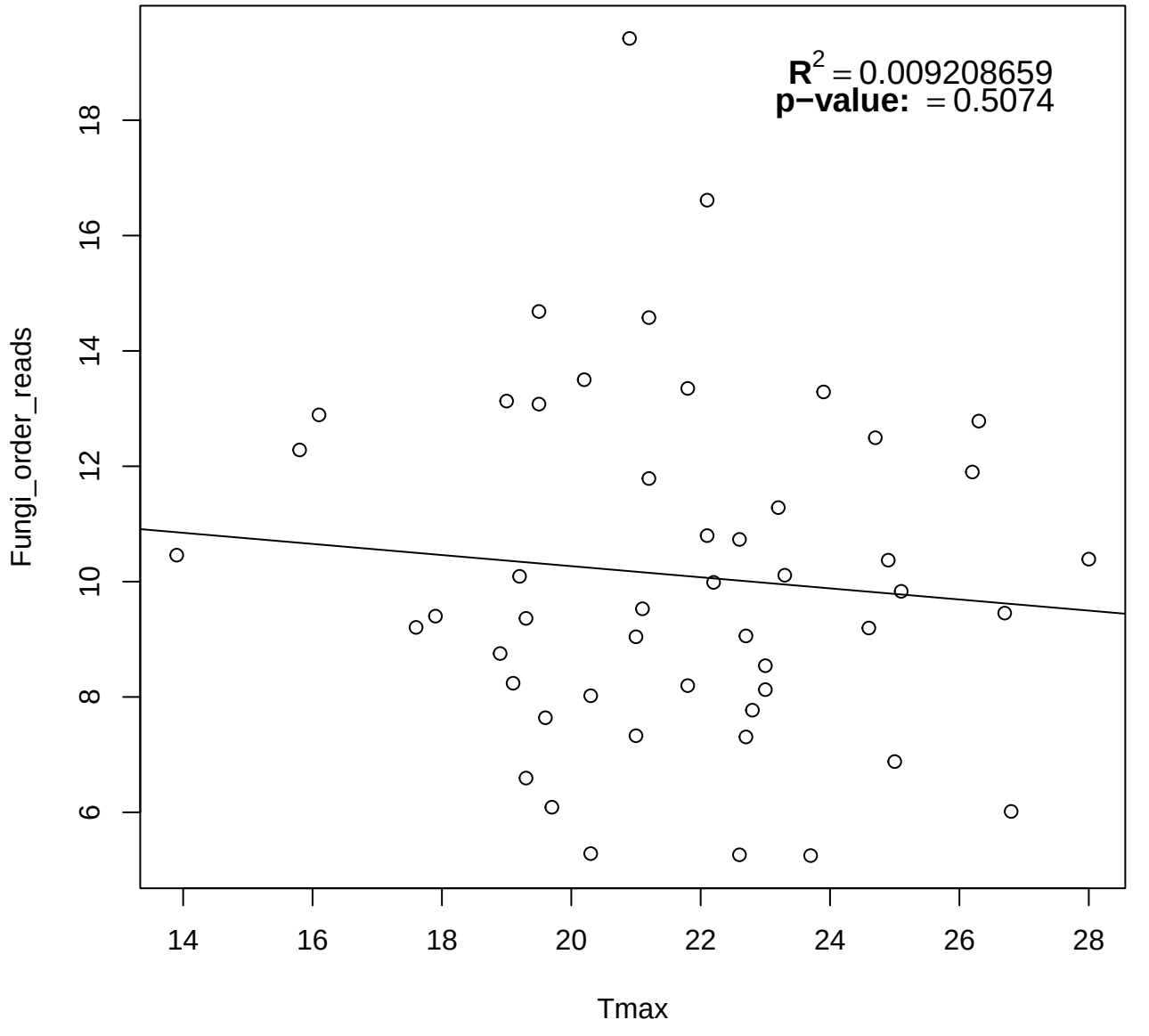

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
CBR1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
LAM1
CBR1
Cook's distance

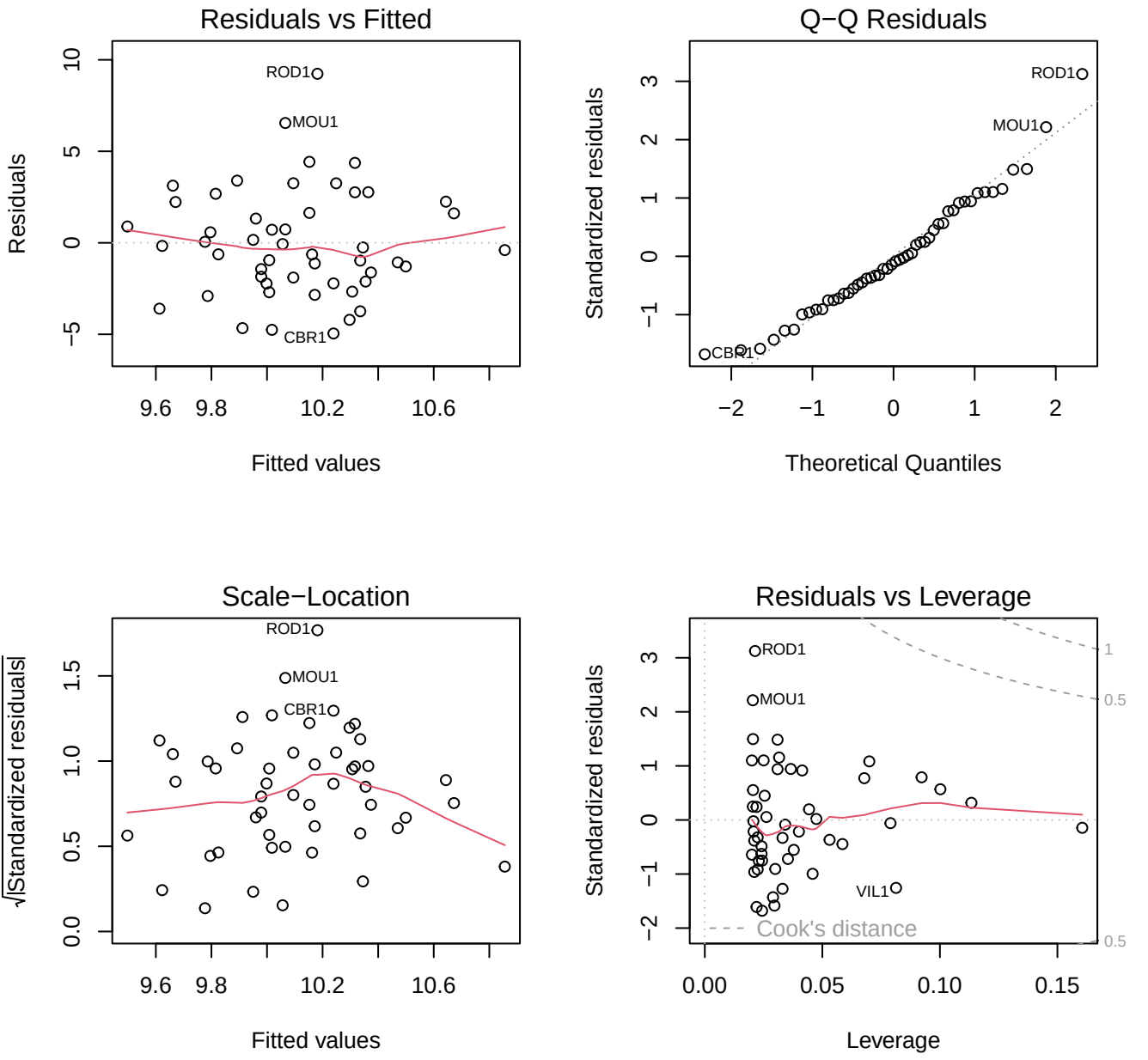

$R^2 = 0.02615102$
p−value: = 0.2619
Fungi_order_reads
Width
6
8
10
12
14
16
18
0
5
10
15
20
25
30
35

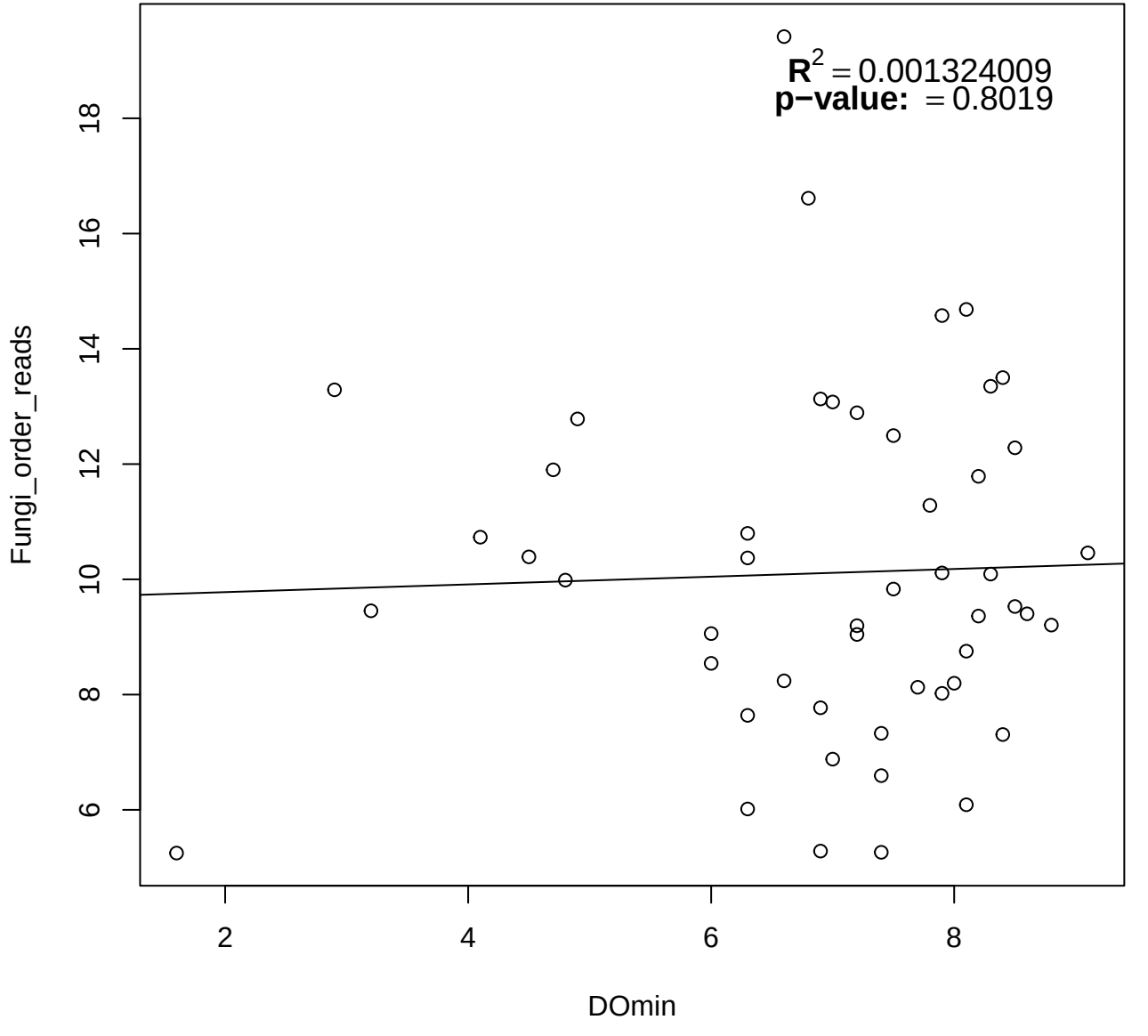

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
AGR1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
VEZ3
VIL1
Cook's distance
1
0.5
0.5
1

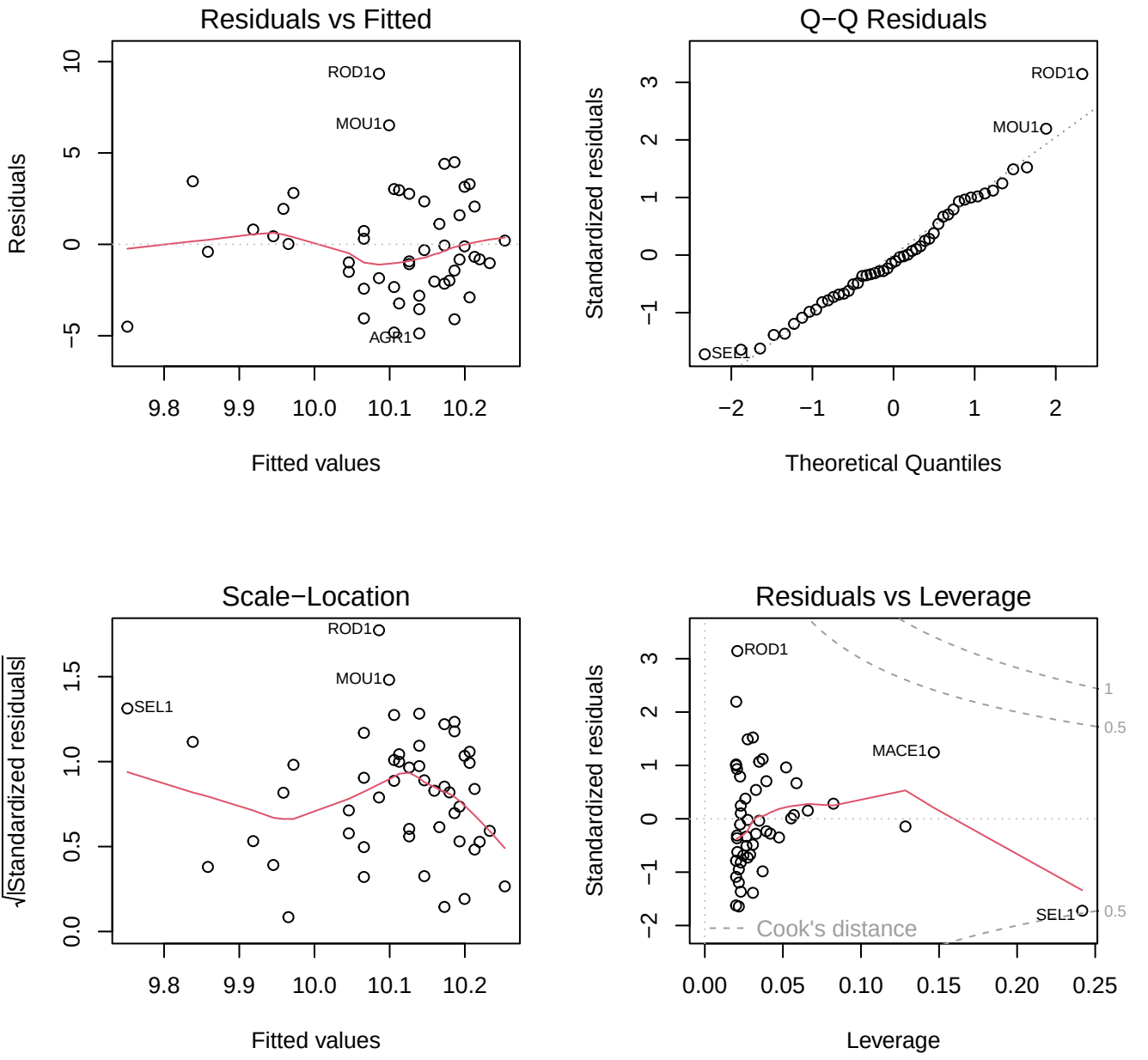

$R^2 = 0.003154795$
p−value: = 0.6984
Fungi_order_reads
Discharge
18
16
14
12
10
8
6
−6
−4
−2
0

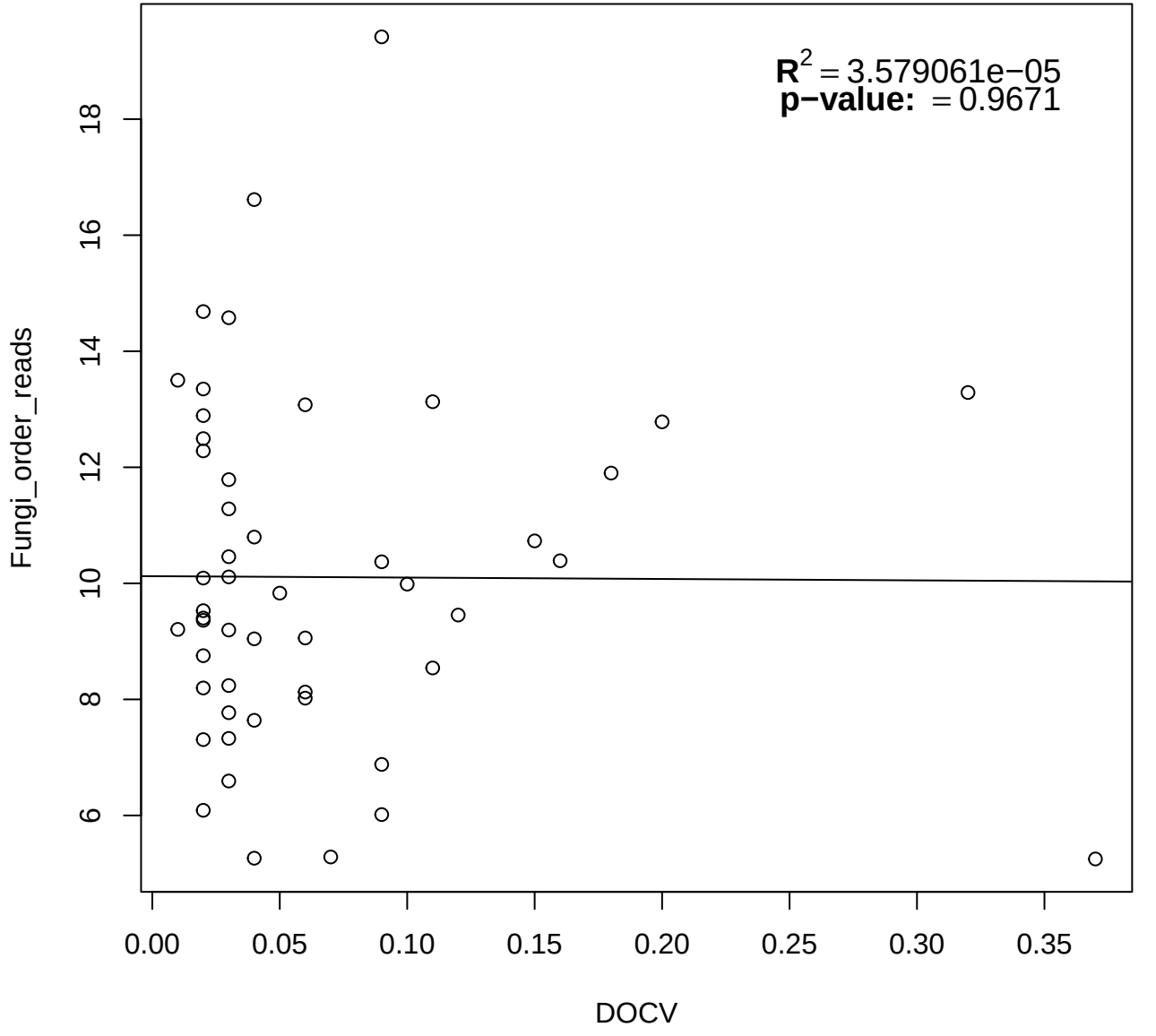

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
AGR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
AGR1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
TAve1
VIL1
Cook's distance
1
0.5

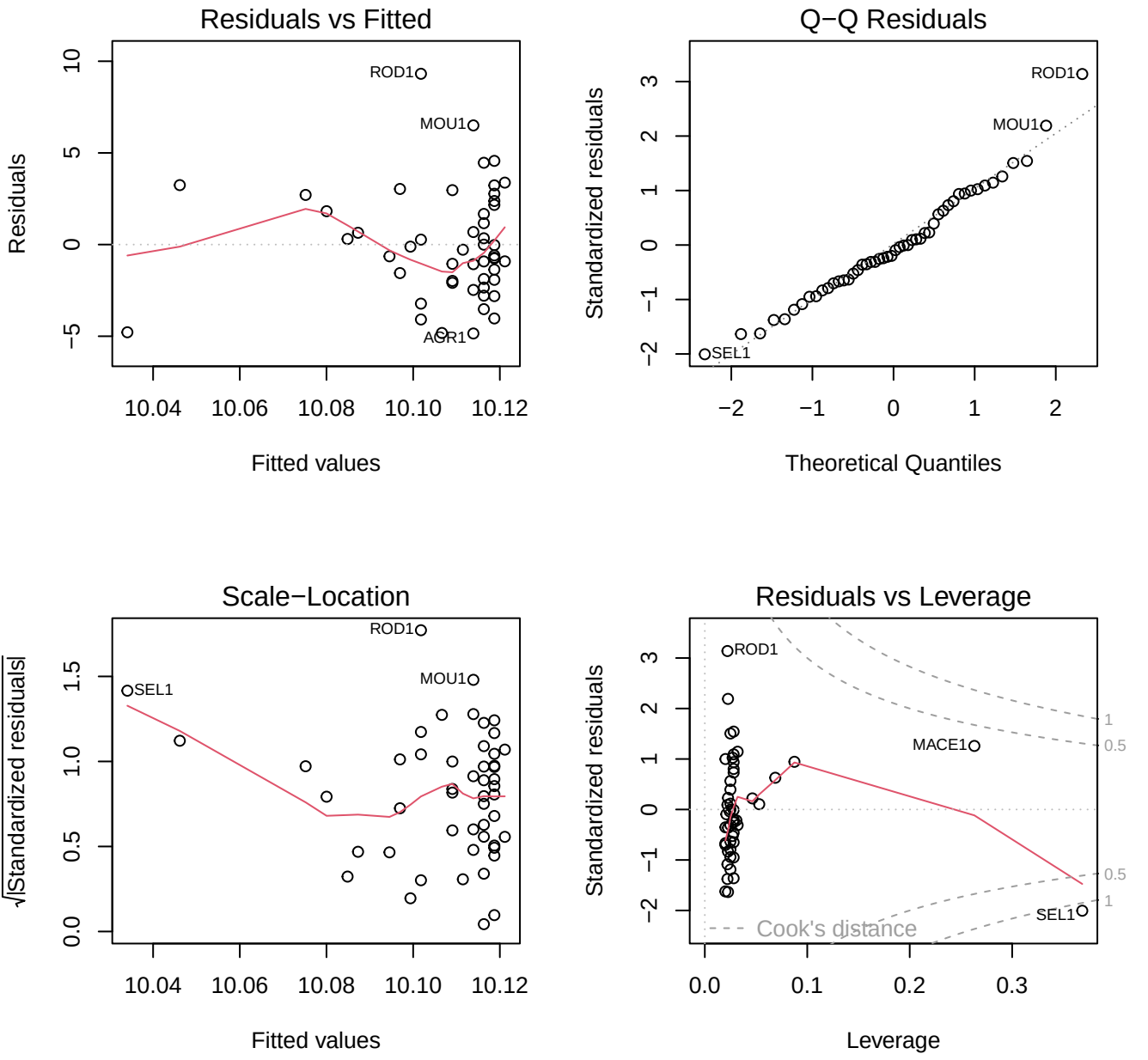

$R^2 = 0.009208659$
p−value: = 0.5074
Fungi_order_reads
Tmax
6
8
10
12
14
16
18
14
16
18
20
22
24
26
28

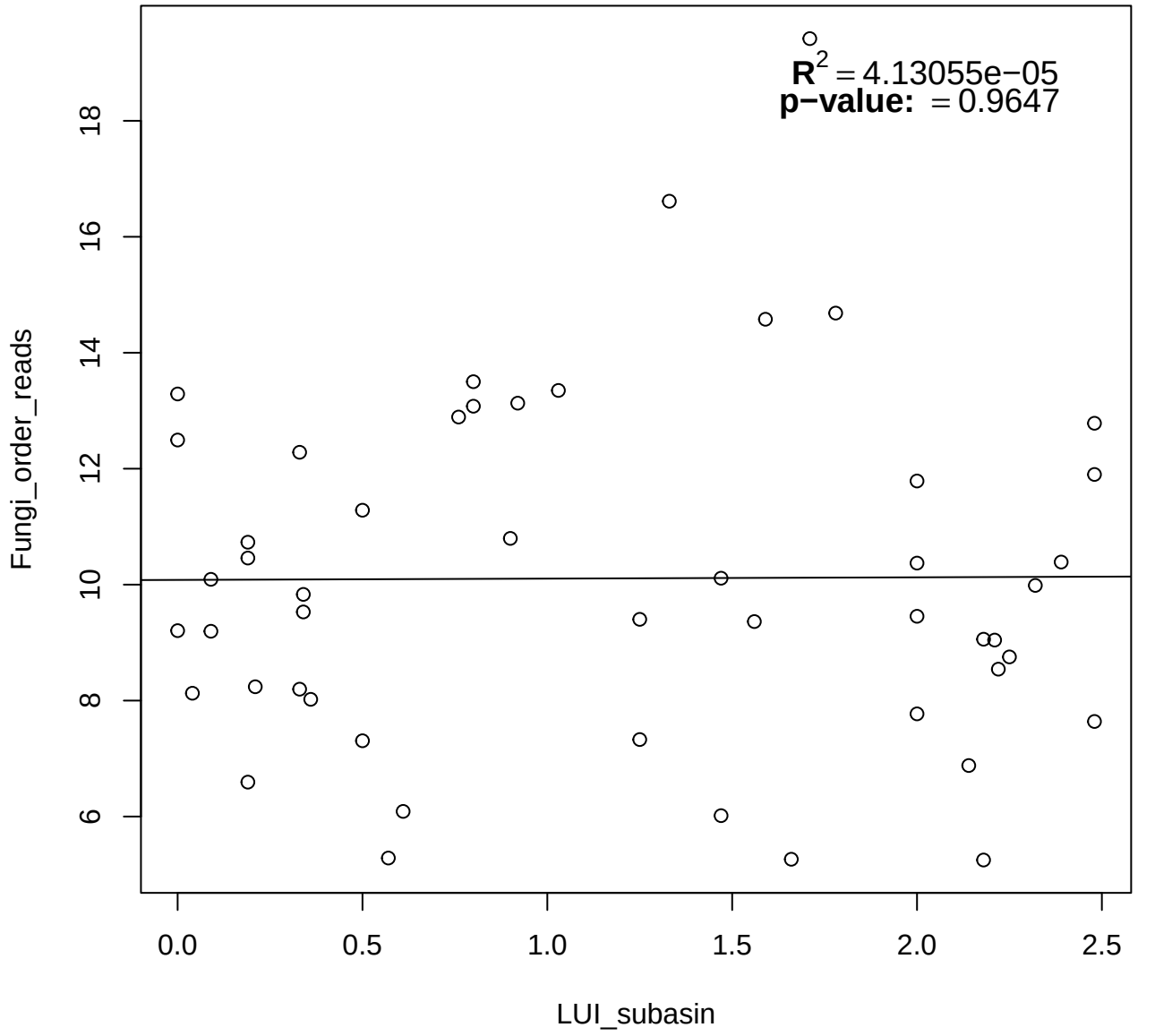

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
CBR1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
CBR1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MOU1
VIL1
Cook's distance

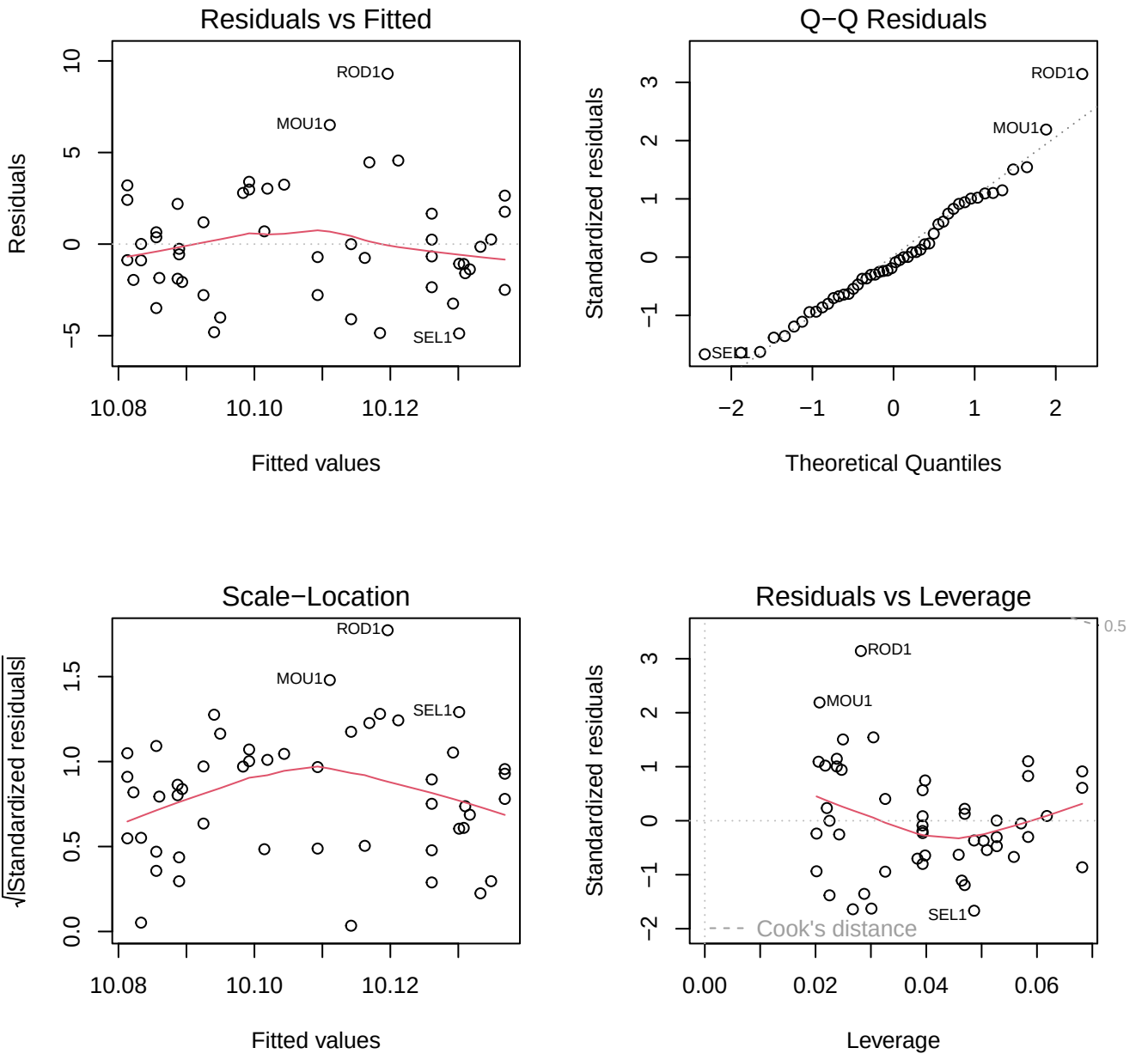

$R^2 = 0.001324009$
p−value: = 0.8019
Fungi_order_reads
DOmin
6
8
10
12
14
16
18
2
4
6
8

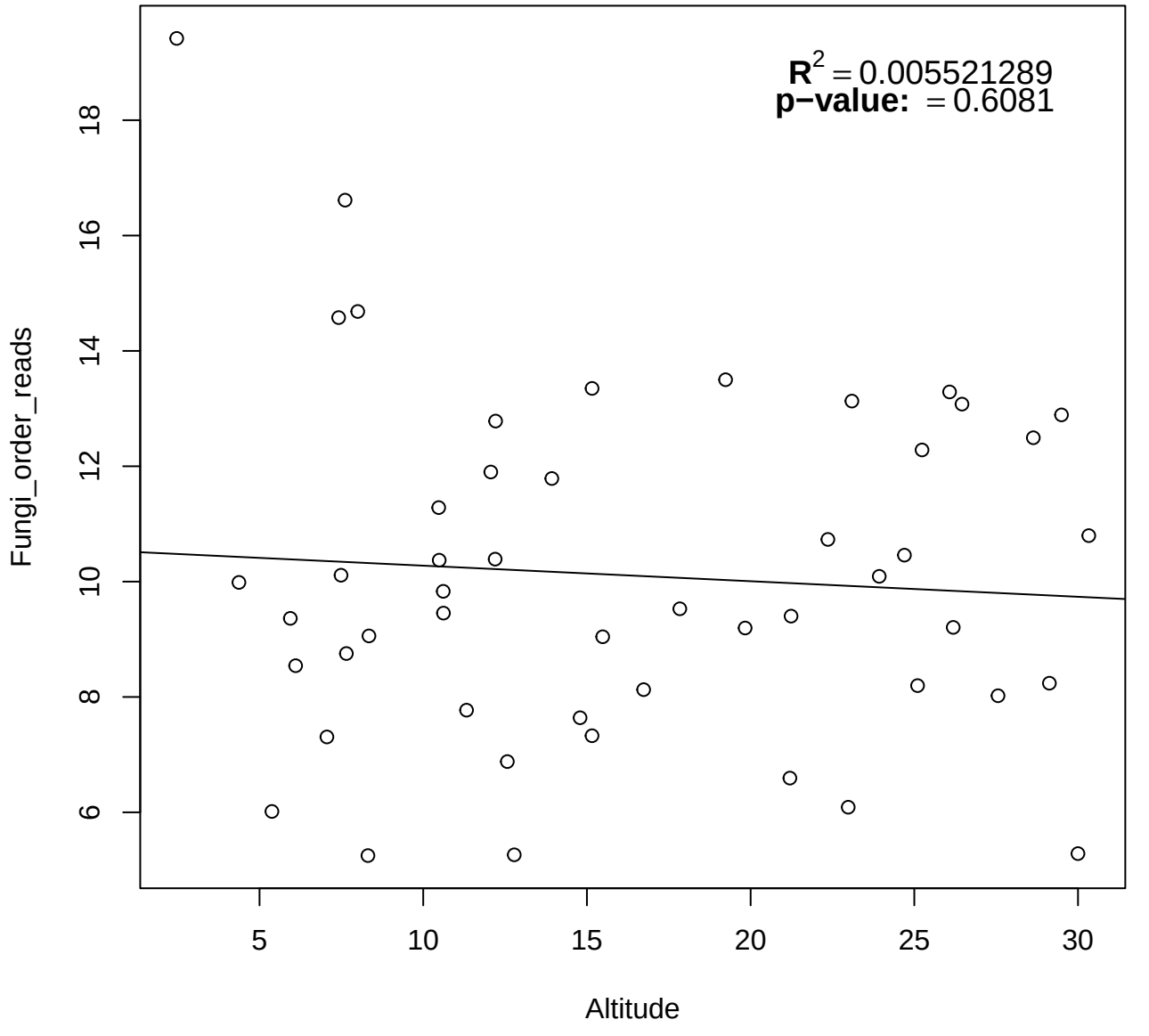

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
SEL1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MACE1
SEL1
Cook's distance
1
0.5
0.5

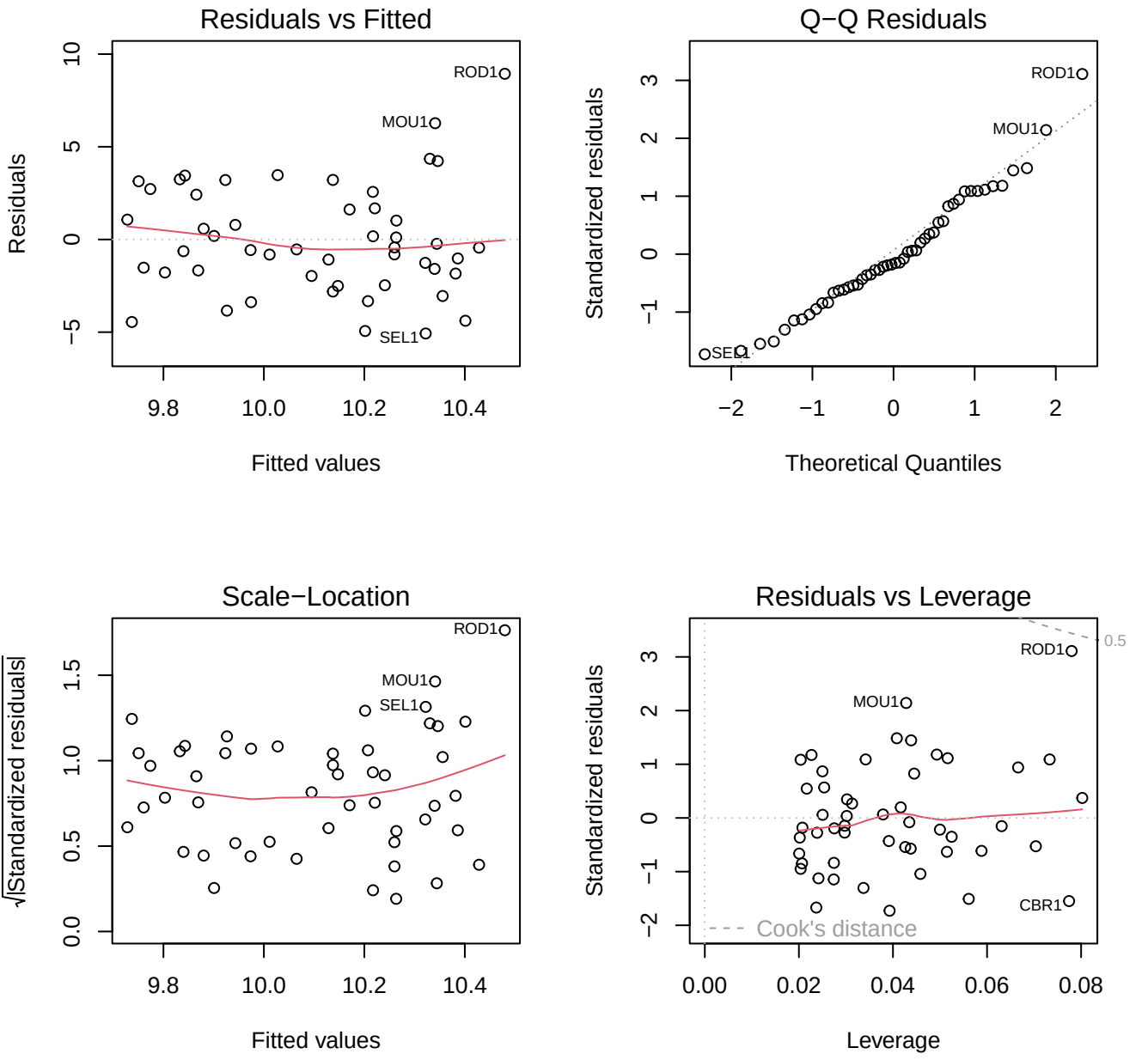

$R^2 = 3.579061e-05$
p−value: = 0.9671
Fungi_order_reads
DOCV
6
8
10
12
14
16
18
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35

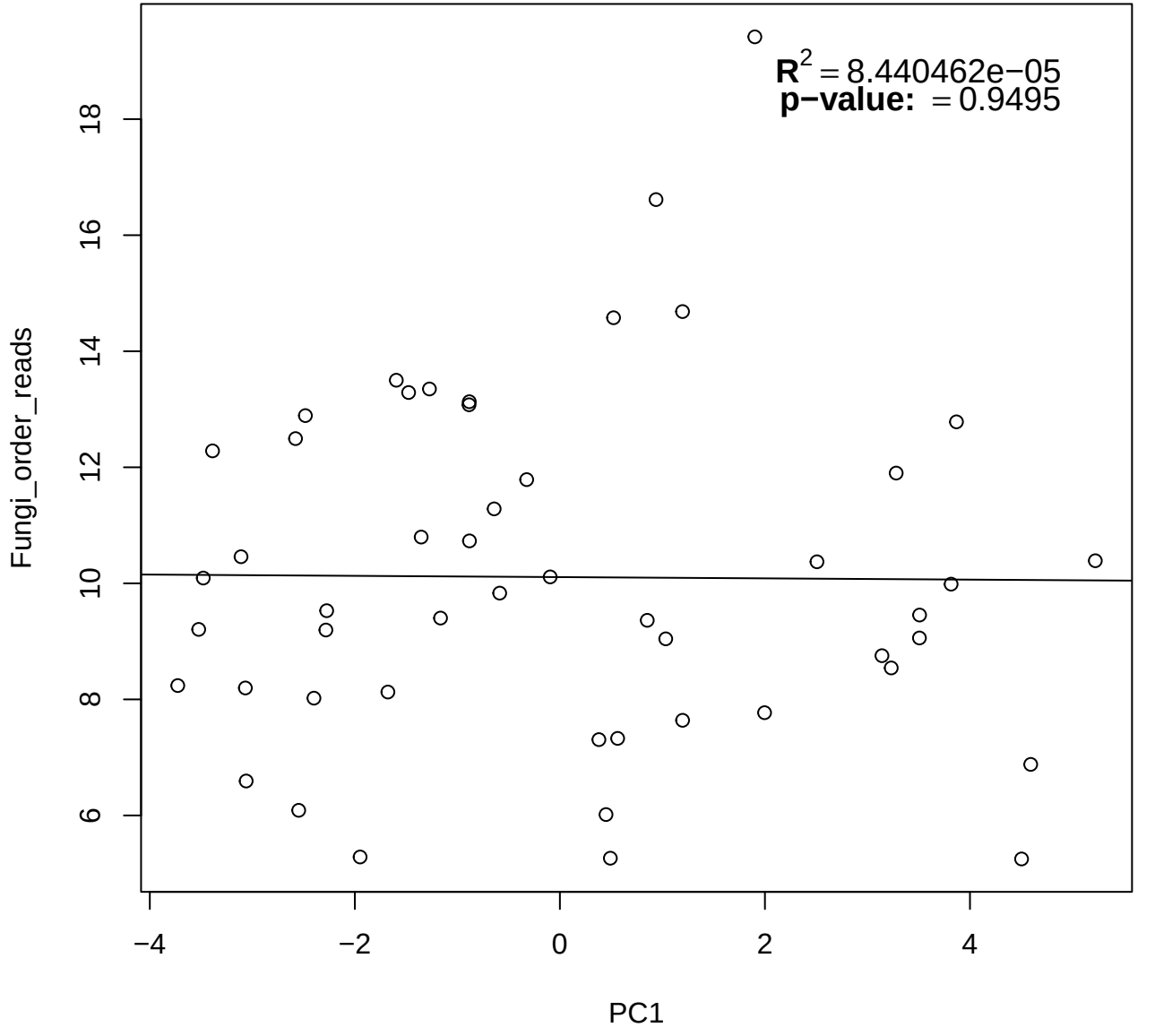

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
AGR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
SEL1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MACE1
SEL1
Cook's distance

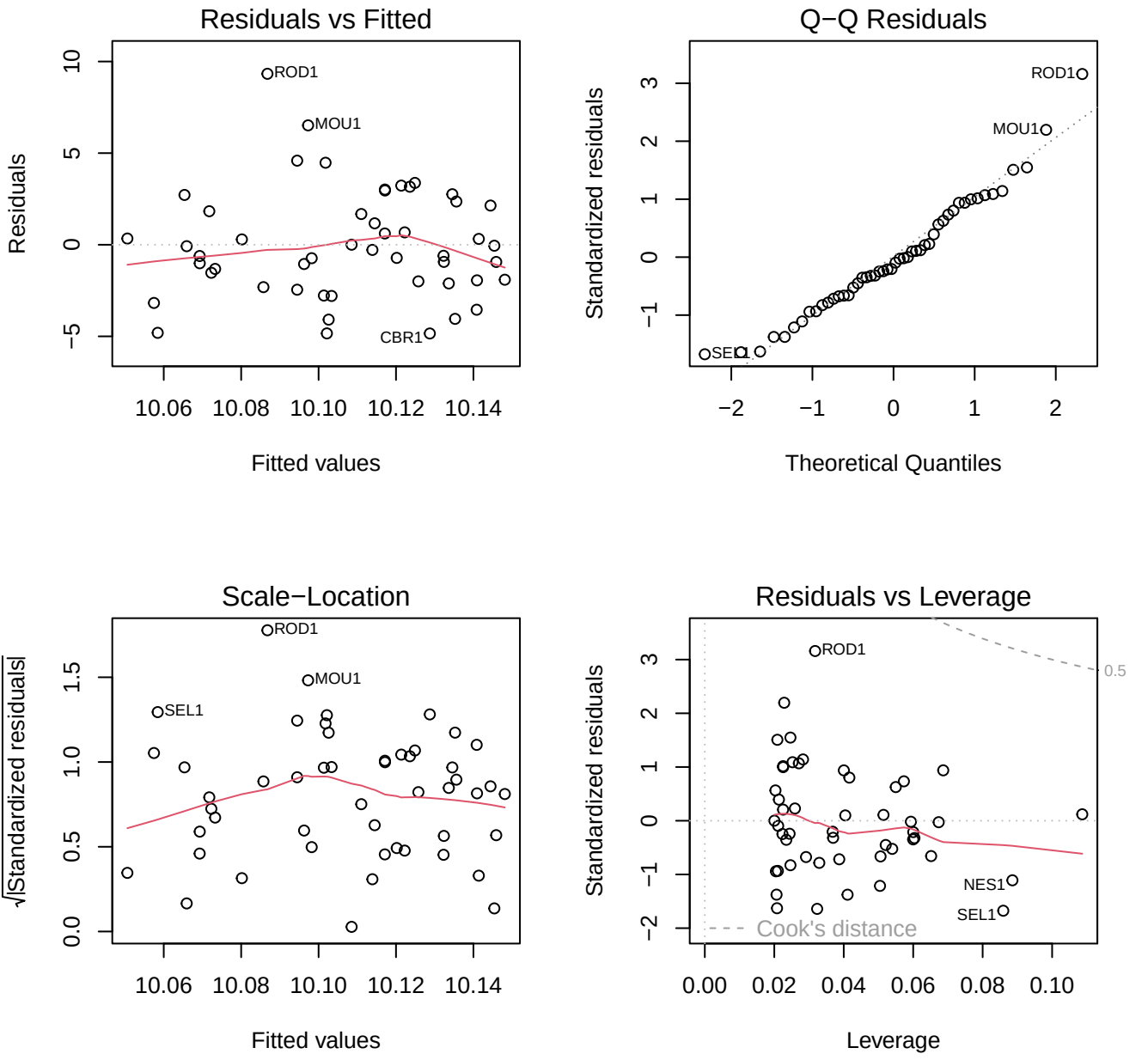

$R^2 = 4.13055e-05$
p−value: = 0.9647
Fungi_order_reads
LUI_subasin
6
8
10
12
14
16
18
0.0
0.5
1.0
1.5
2.0
2.5

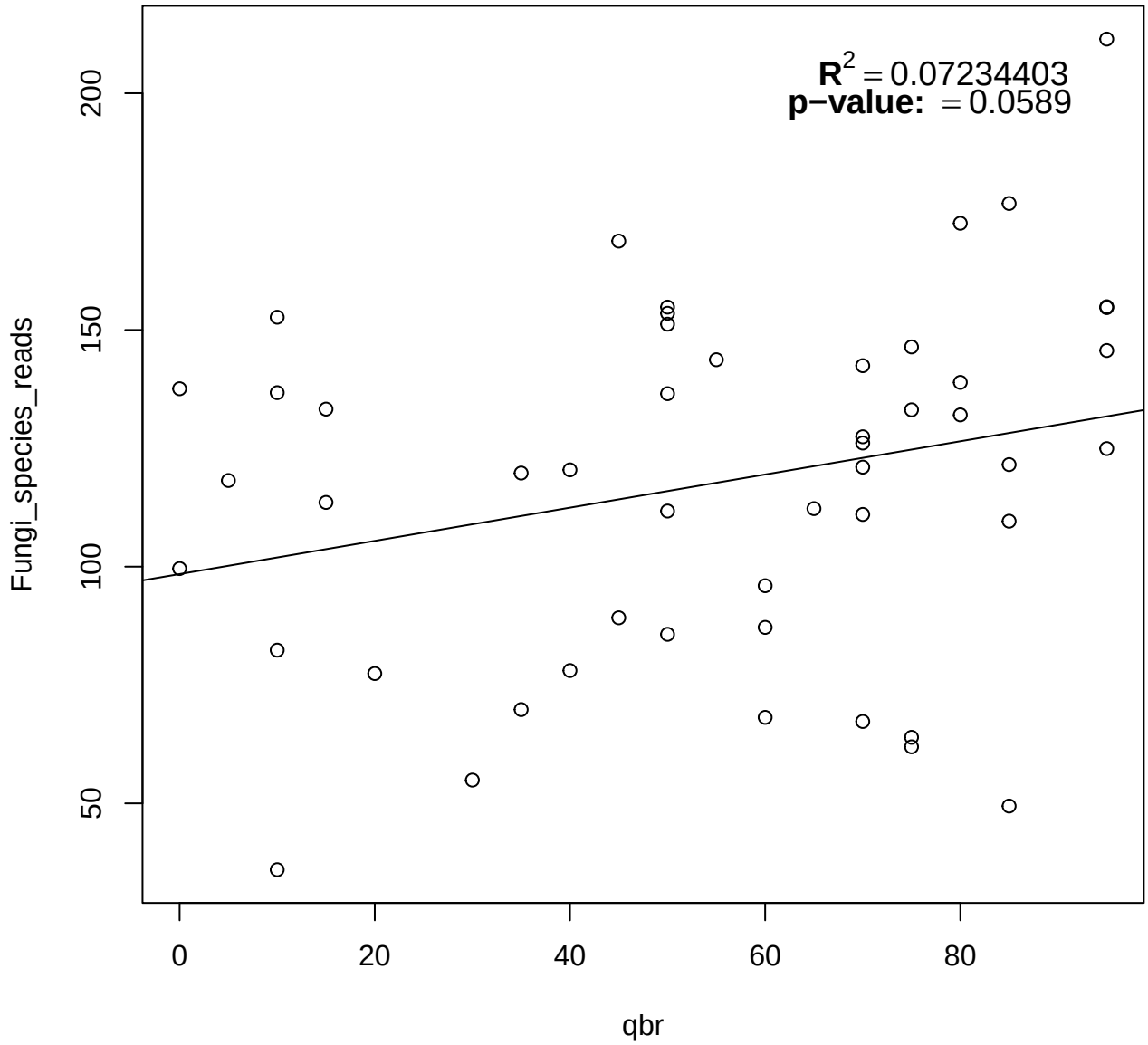

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
SEL1
10.08
10.10
10.12
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
SEL1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MOU1
SEL1
Cook's distance
0.5

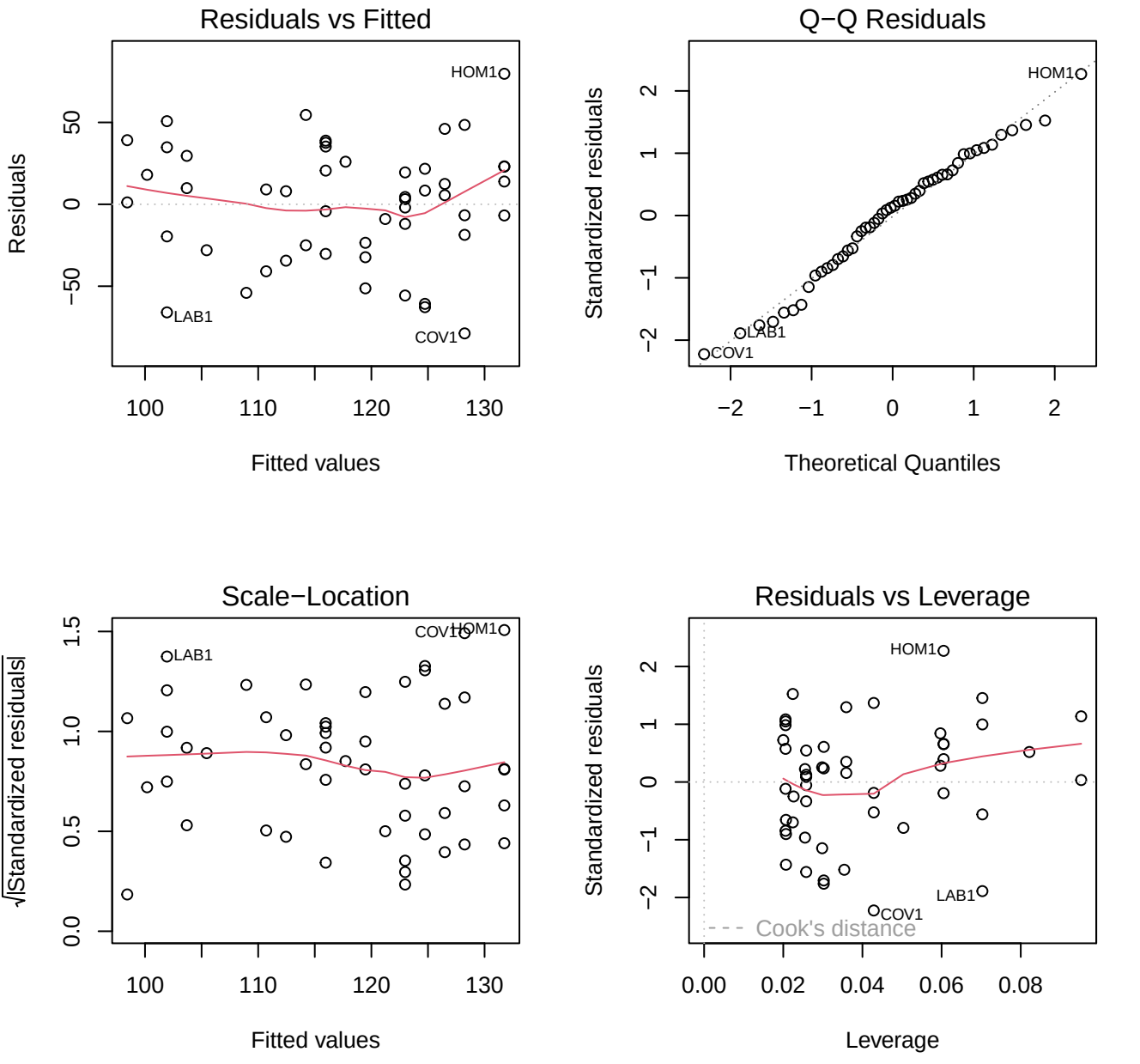

$R^2 = 0.005521289$
p−value: = 0.6081
Fungi_order_reads
Altitude
6
8
10
12
14
16
18
5
10
15
20
25
30

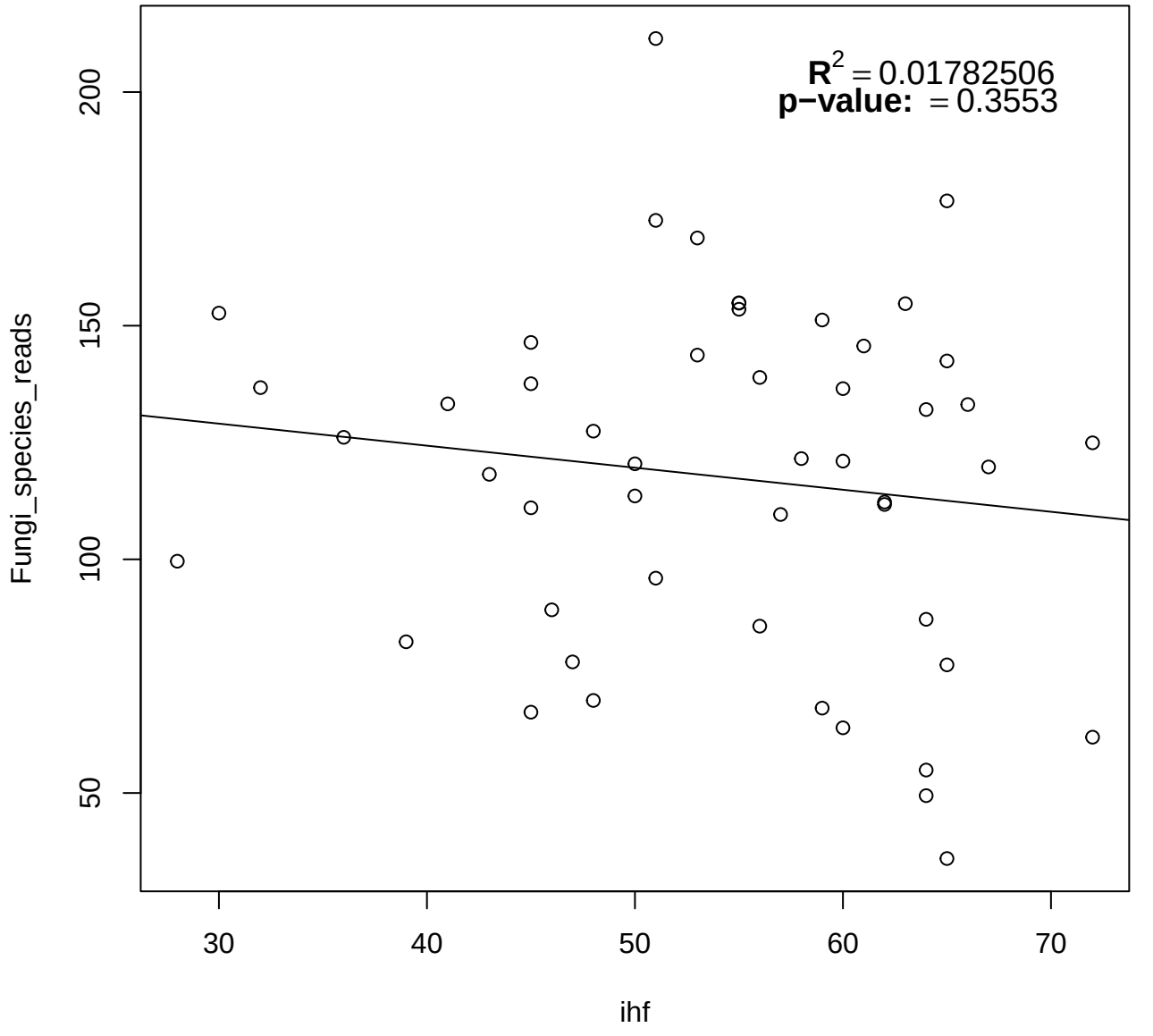

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
SEL1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
SEL1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
MOU1
CBR1
0.5
Cook's distance

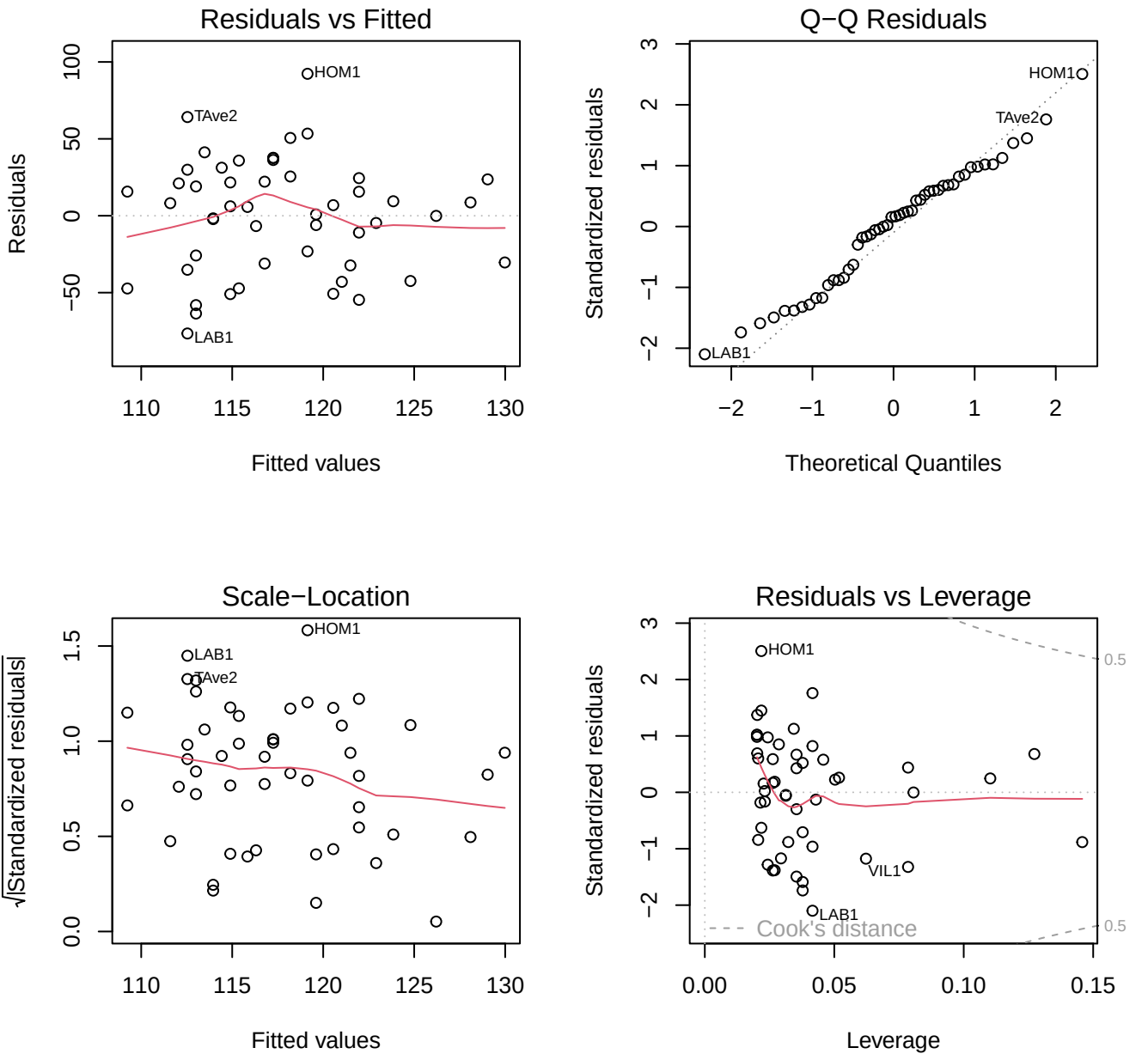

$R^2 = 8.440462e-05$
p−value: = 0.9495
Fungi_order_reads
PC1
18
16
14
12
10
8
6
−4
−2
0
2
4

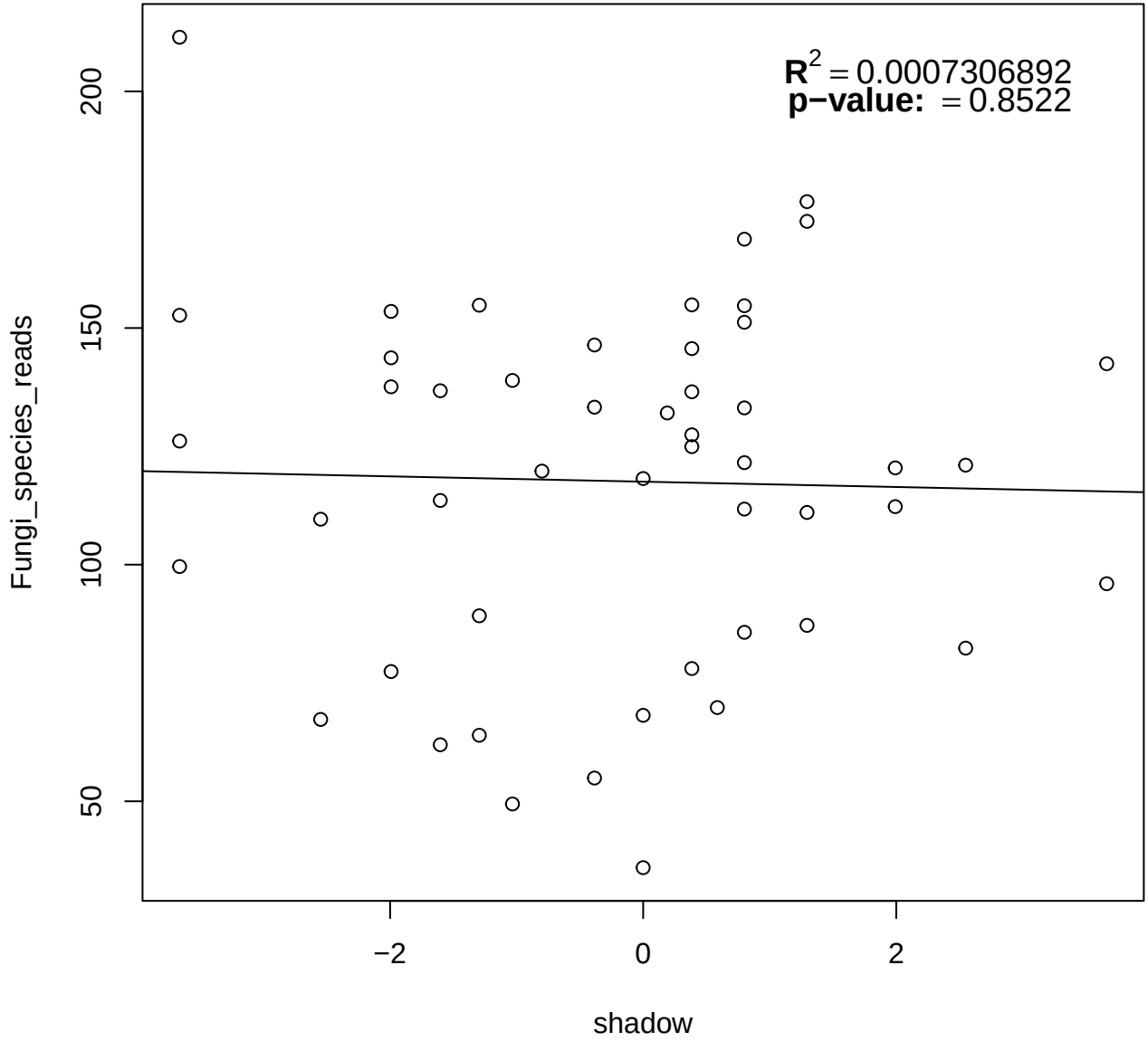

Residuals vs Fitted
Residuals
Fitted values
ROD1
MOU1
CBR1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
MOU1
SEL1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
MOU1
SEL1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
NES1
SEL1
0.5
Cook's distance

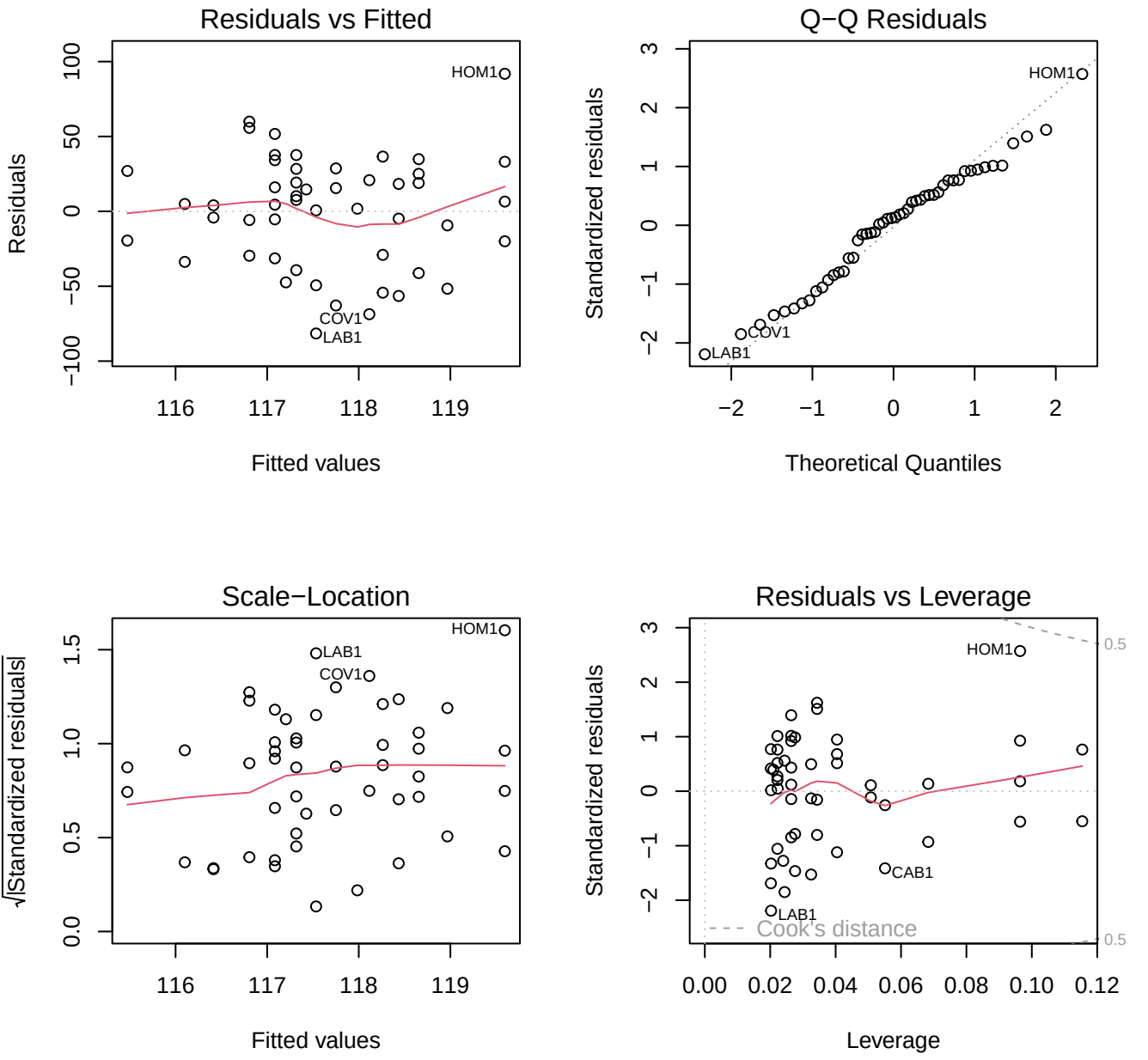

$R^2 = 0.07234403$
p−value: = 0.0589
Fungi_species_reads
qbr
0
20
40
60
80
50
100
150
200

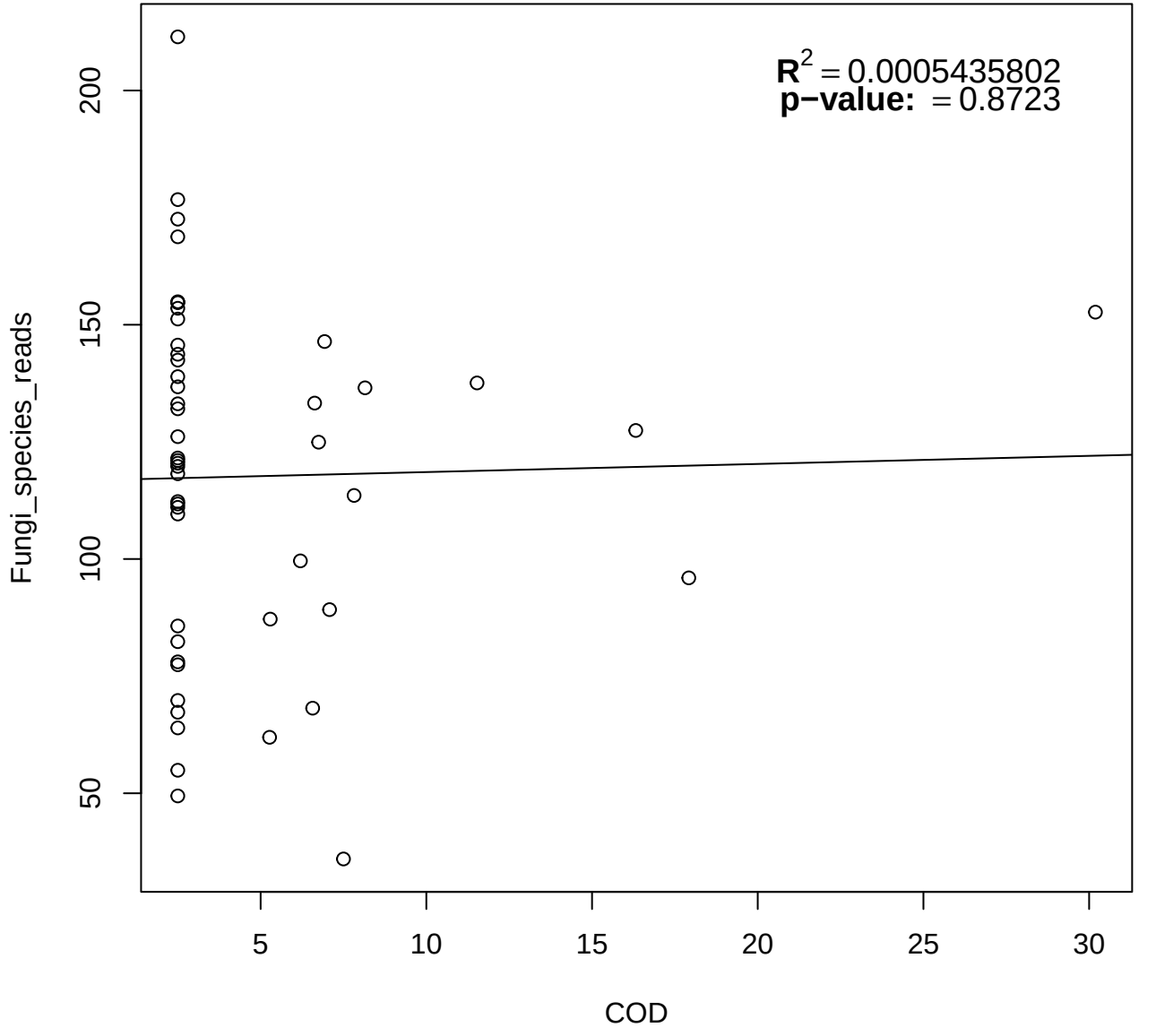

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
COV1
HOM1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
LAB1
COV1
Cook's distance

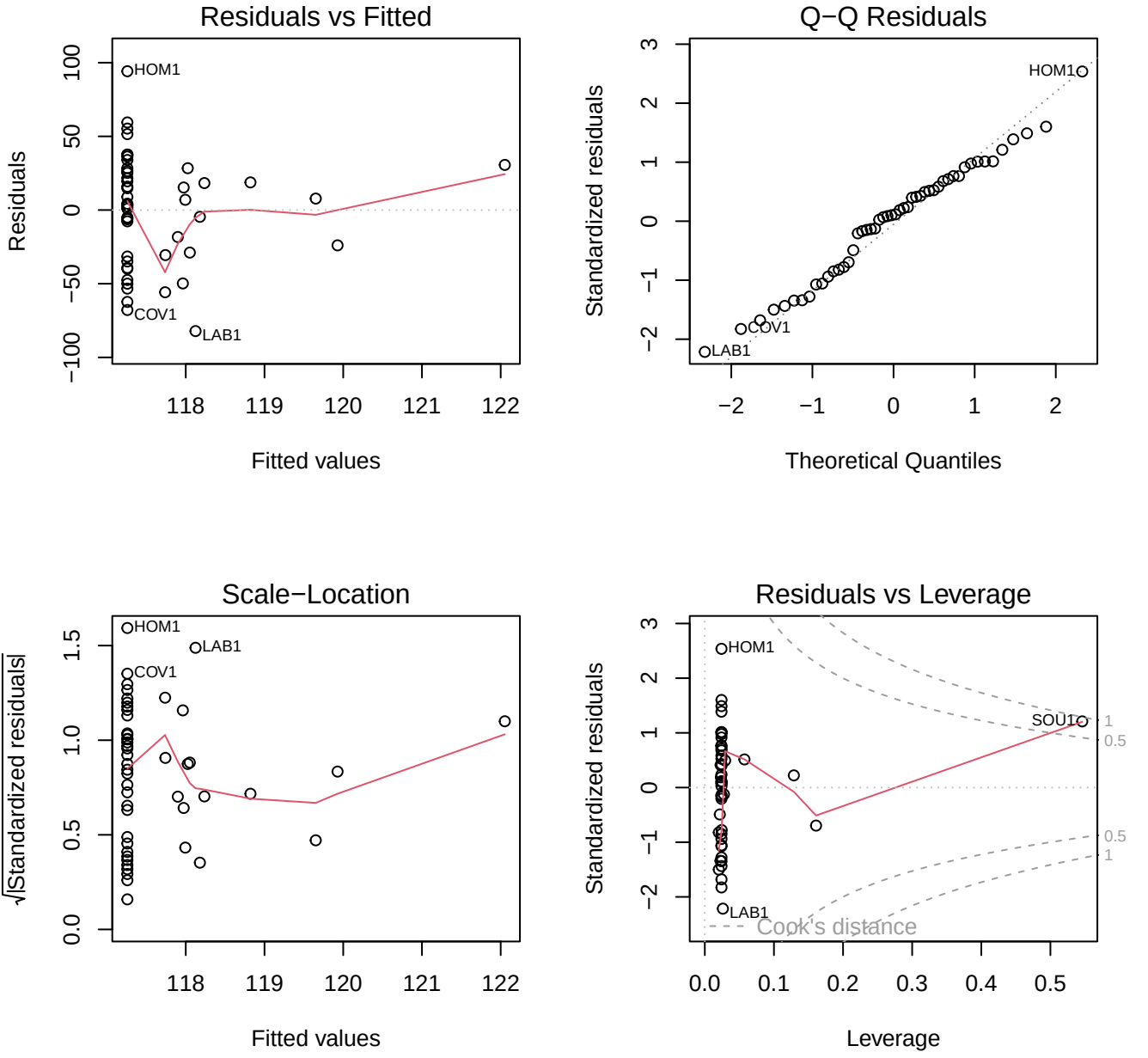

$R^2 = 0.01782506$
p−value: = 0.3553
Fungi_species_reads
ihf
200
150
100
50
30
40
50
60
70

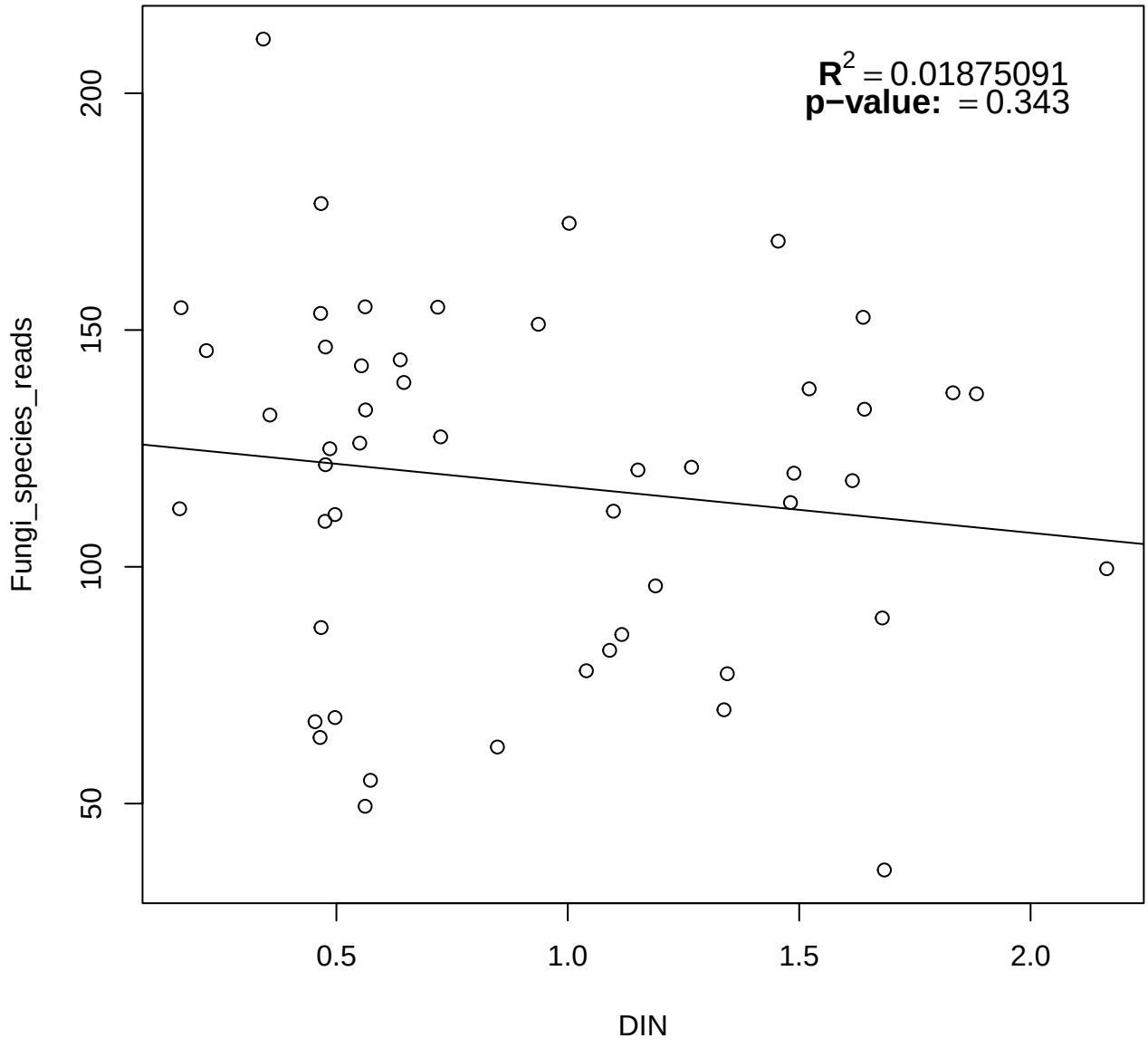

Residuals vs Fitted
Residuals
Fitted values
HOM1
TAve2
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
TAve2
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
TAve2
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
VIL1
LAB1
Cook's distance
0.5
0.5

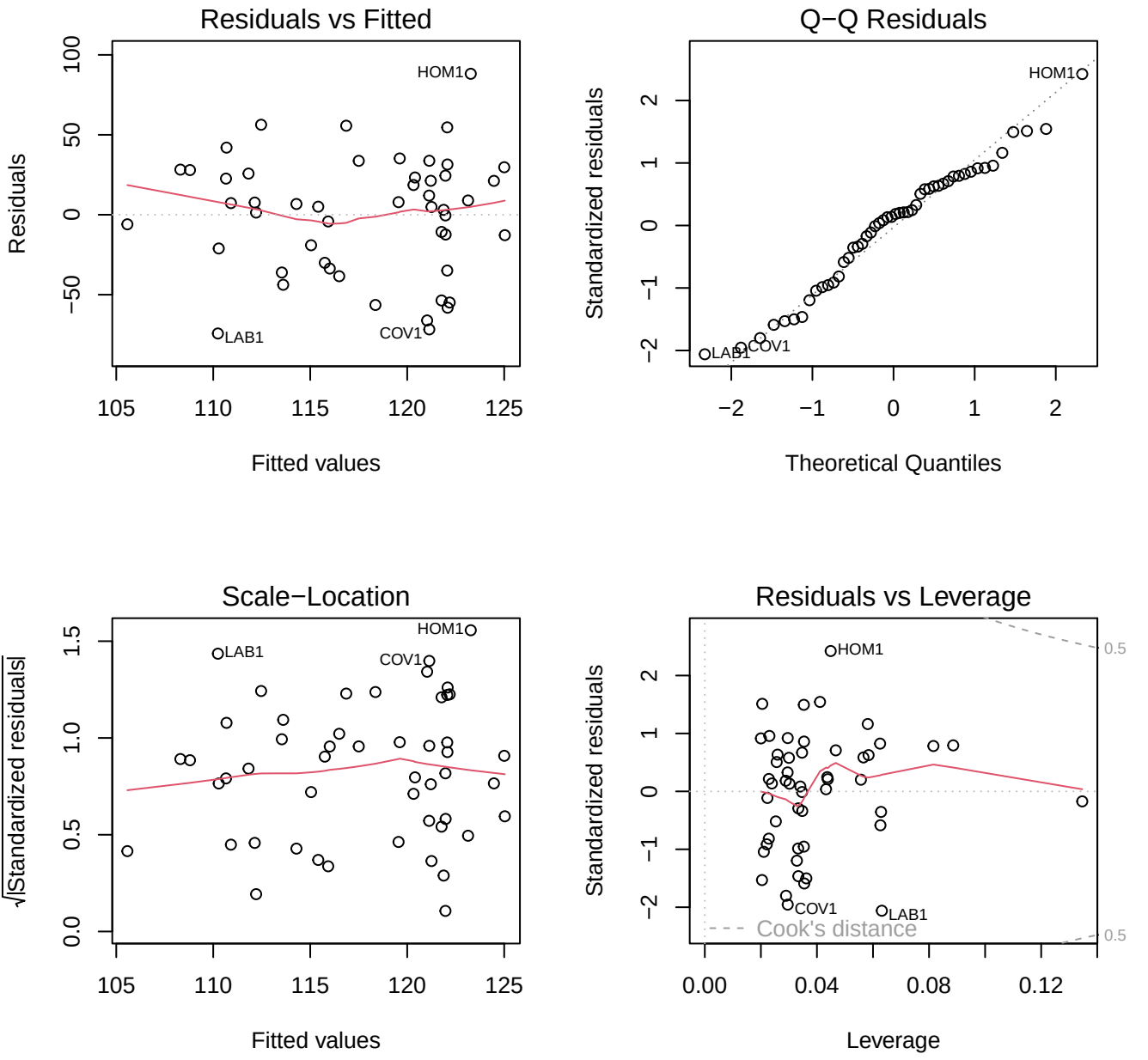

$R^2 = 0.0007306892$
p−value: $= 0.8522$
Fungi_species_reads
200
150
100
50
−2
0
2
shadow

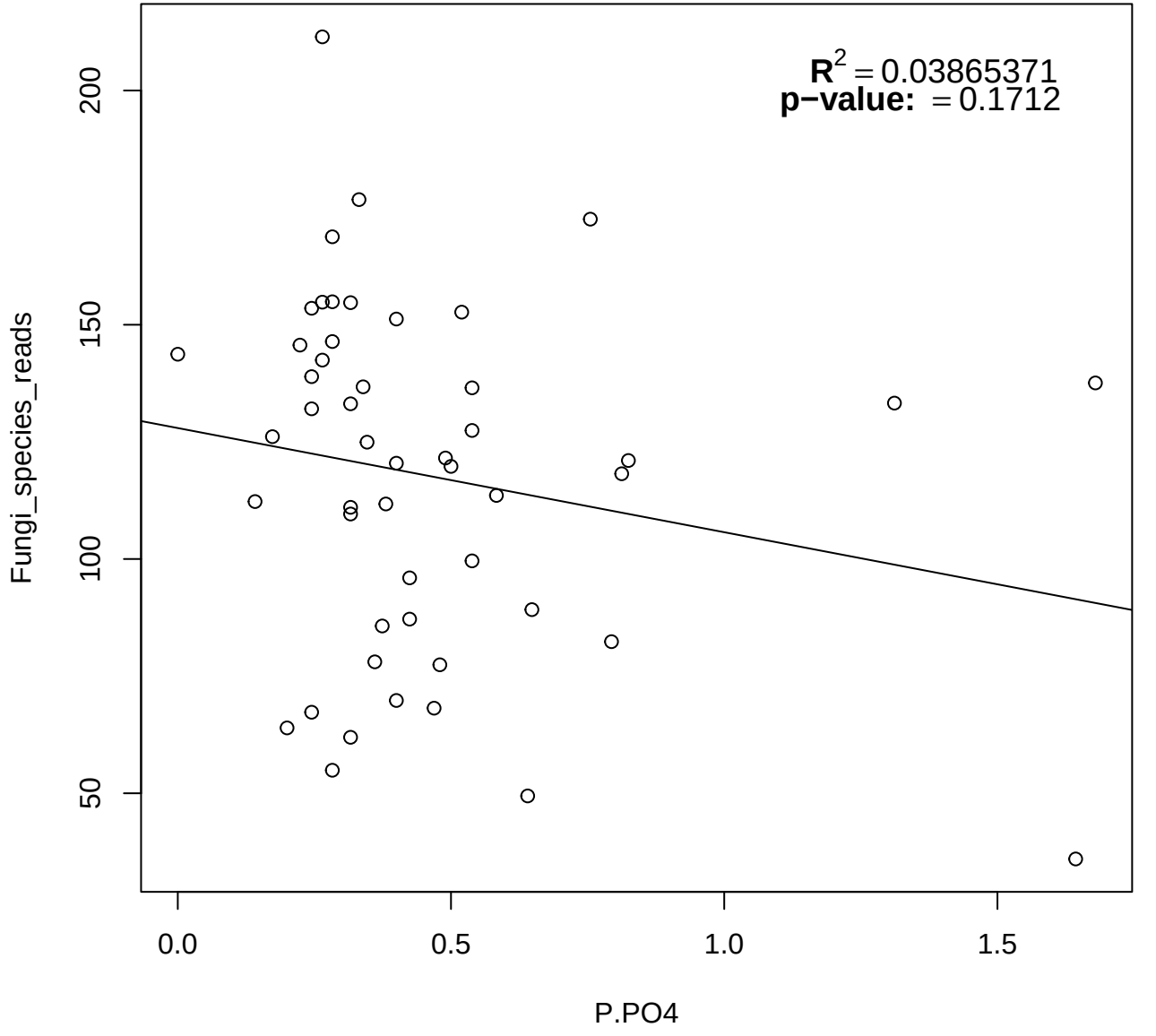

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
CAB1
LAB1
Cook's distance
0.5
0.5

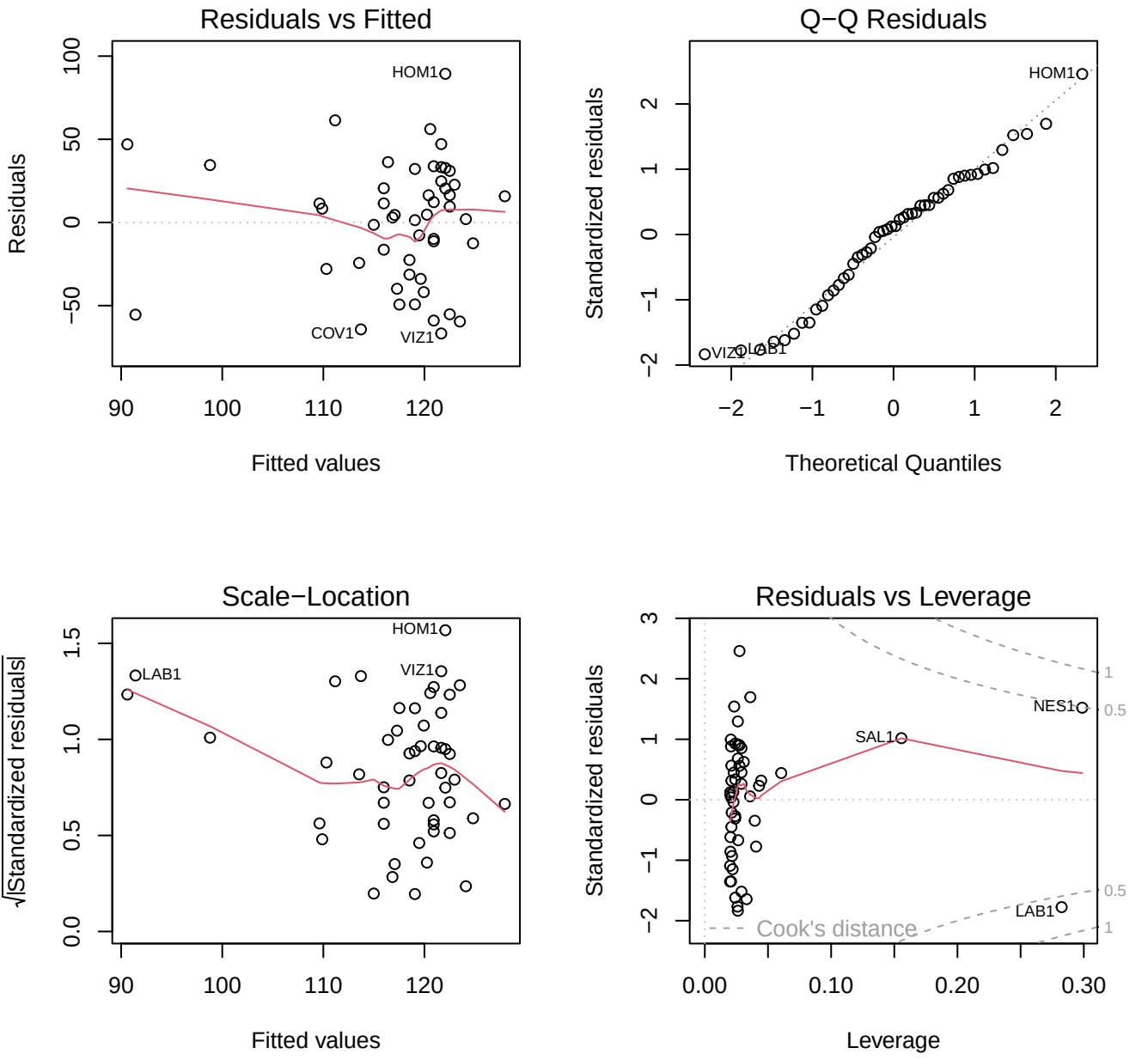

$R^2 = 0.0005435802$
p−value: = 0.8723
Fungi_species_reads
COD
50
100
150
200
5
10
15
20
25
30

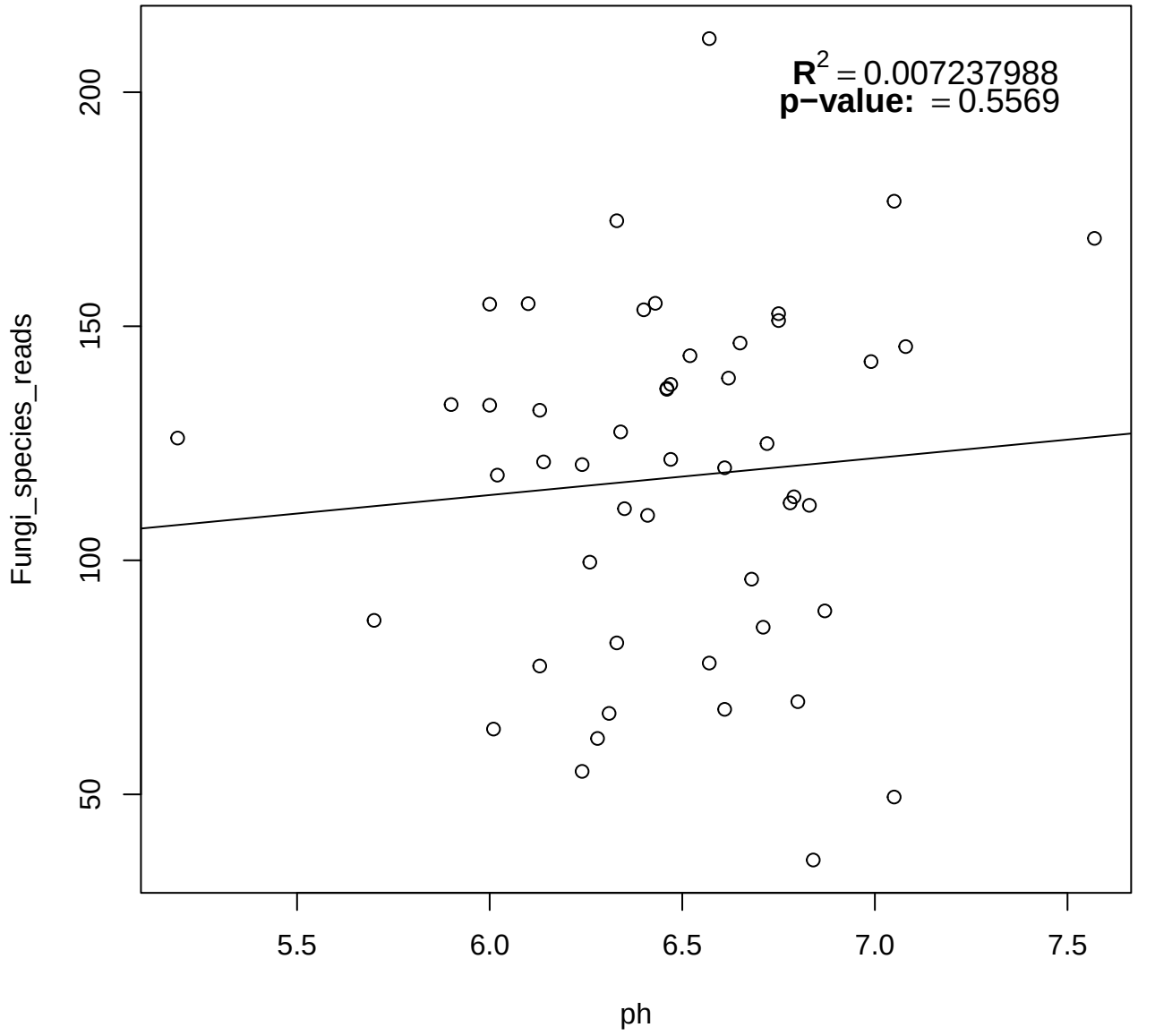

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
SOU1
LAB1
Cook's distance

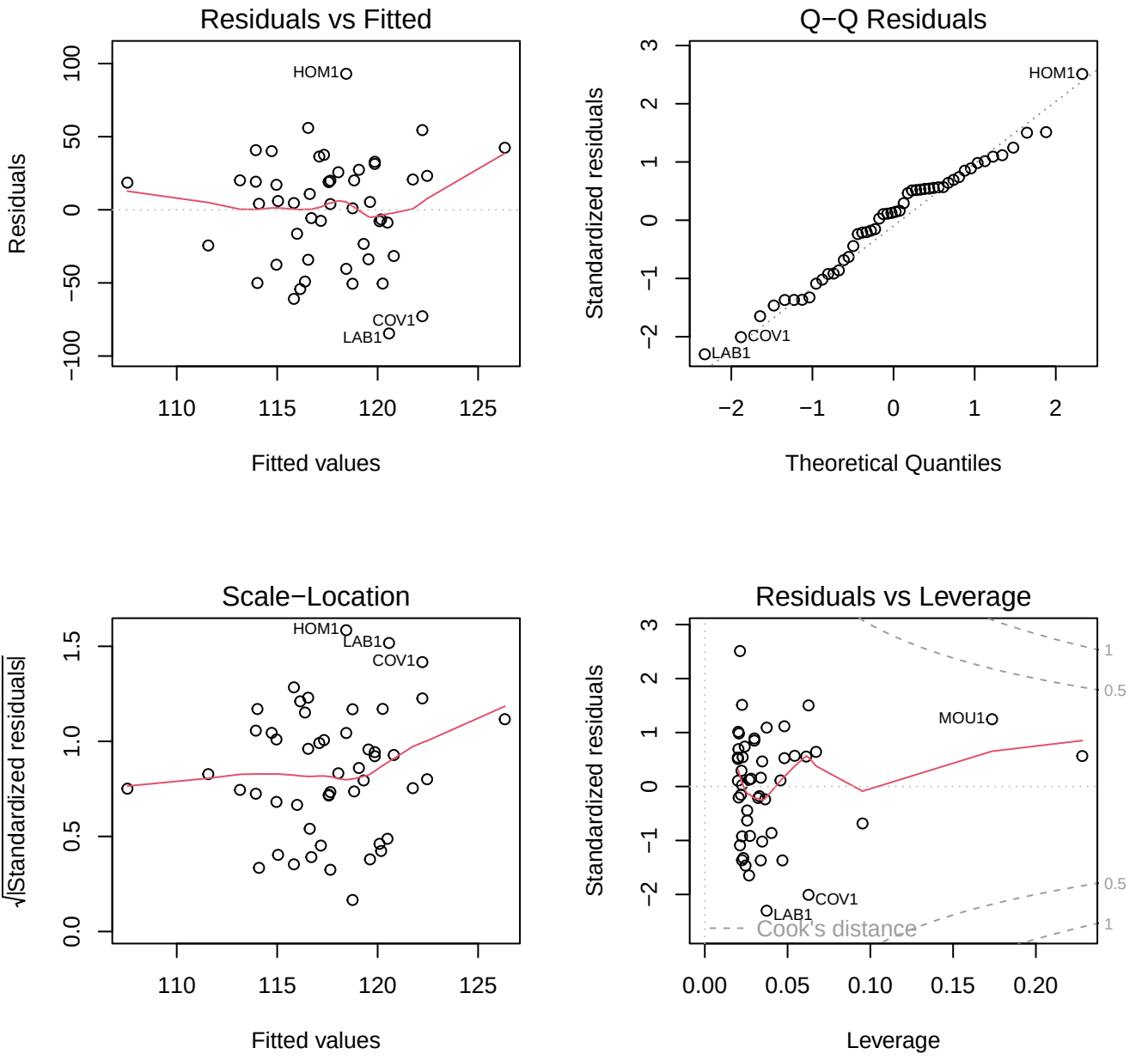

$R^2 = 0.01875091$
p−value: = 0.343
Fungi_species_reads
200
150
100
50
0.5
1.0
1.5
2.0
DIN

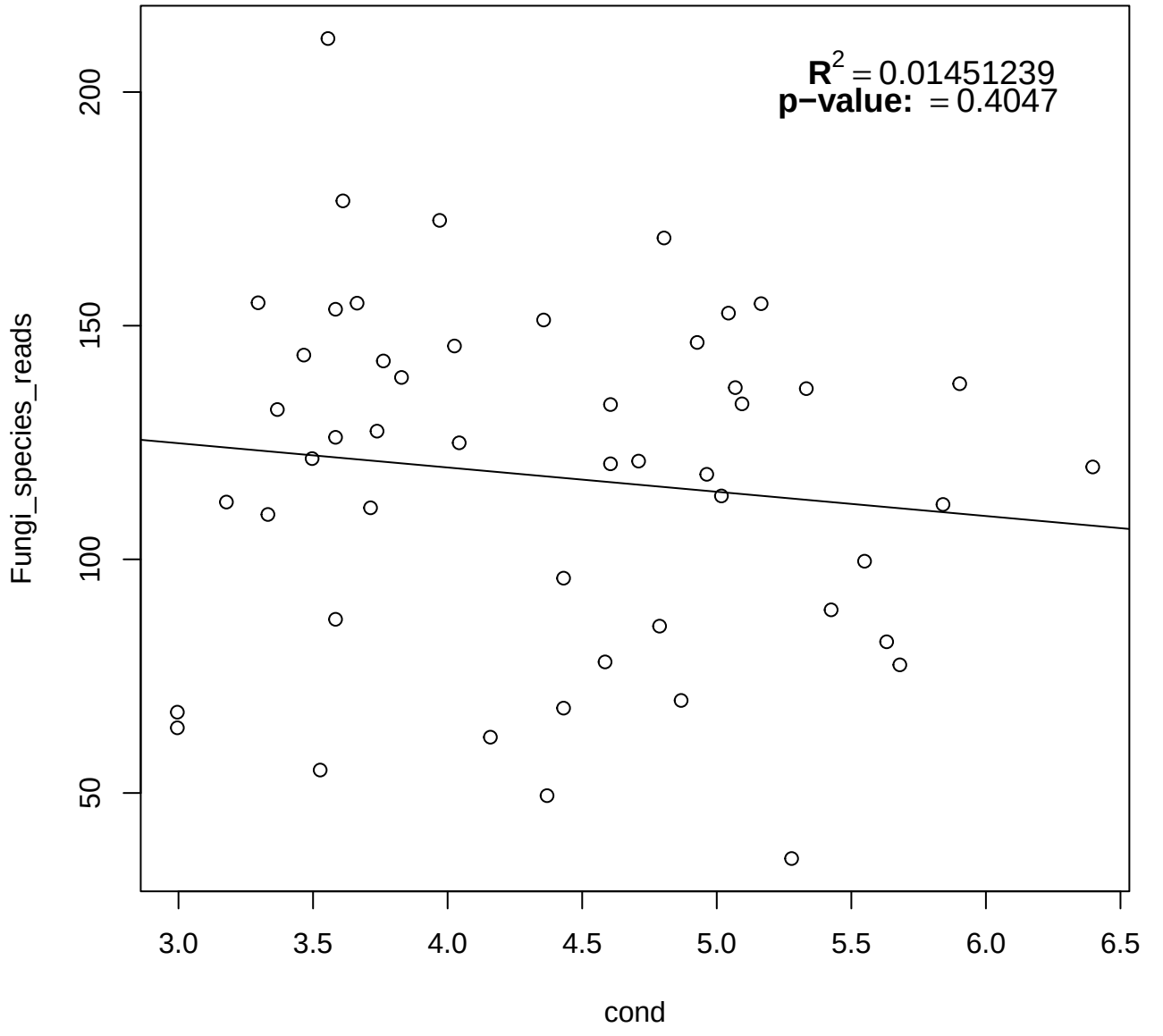

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
COV1
LAB1
Cook's distance
0.5
0.5

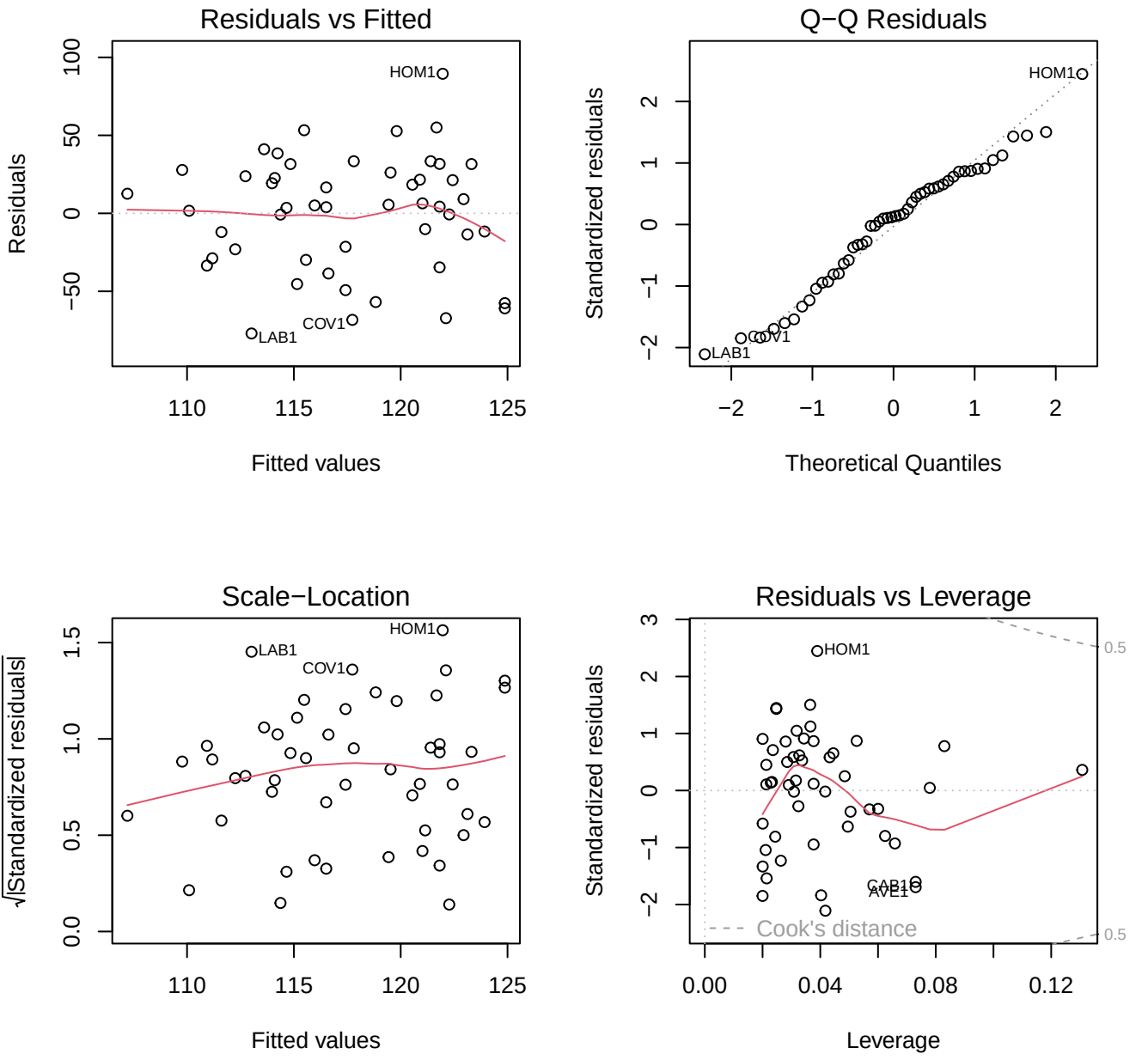

$R^2 = 0.03865371$
p−value: = 0.1712
Fungi_species_reads
P.PO4
0.0
0.5
1.0
1.5
50
100
150
200

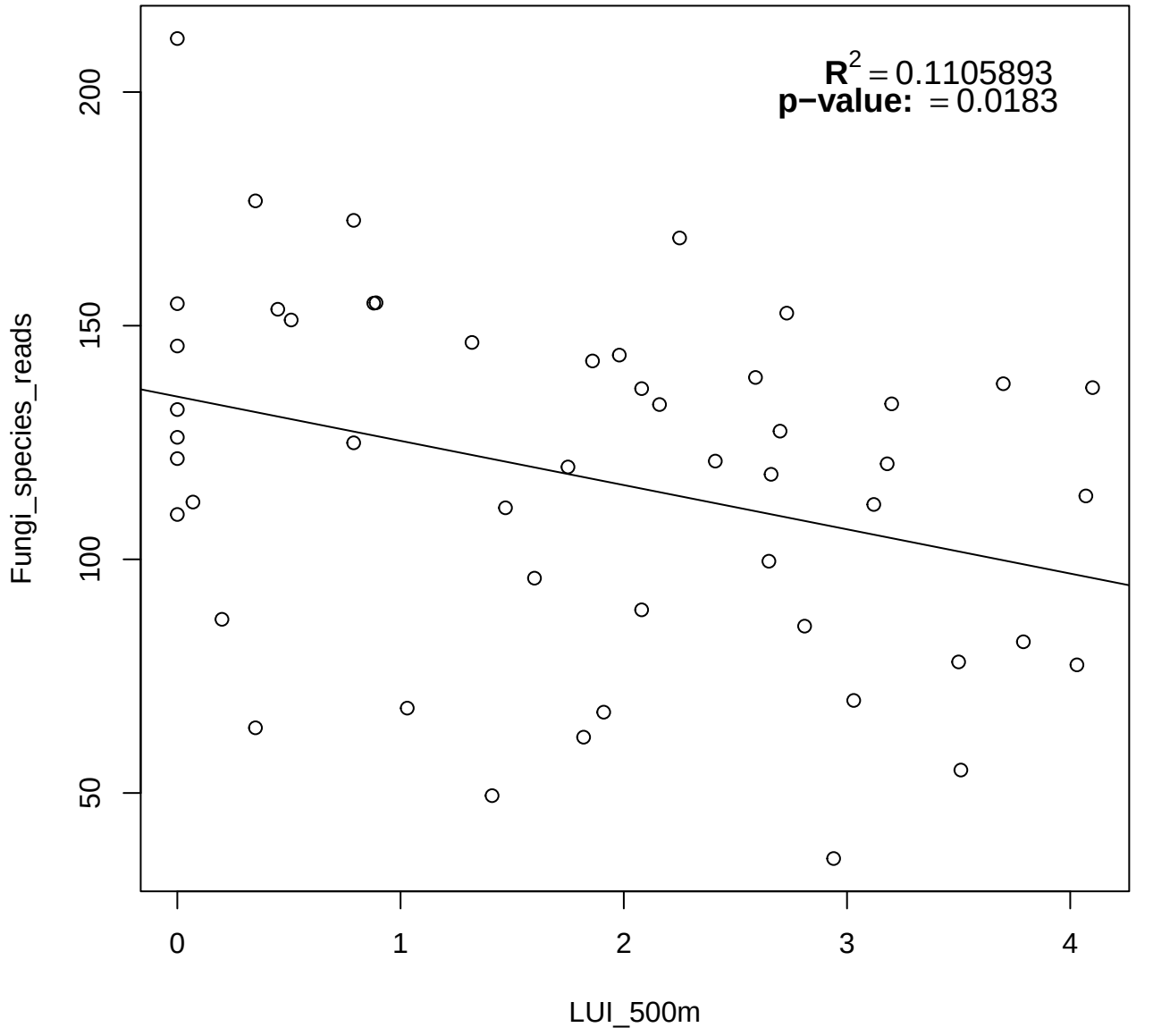

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
VIZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
VIZ1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
NES1
SAL1
LAB1
Cook's distance

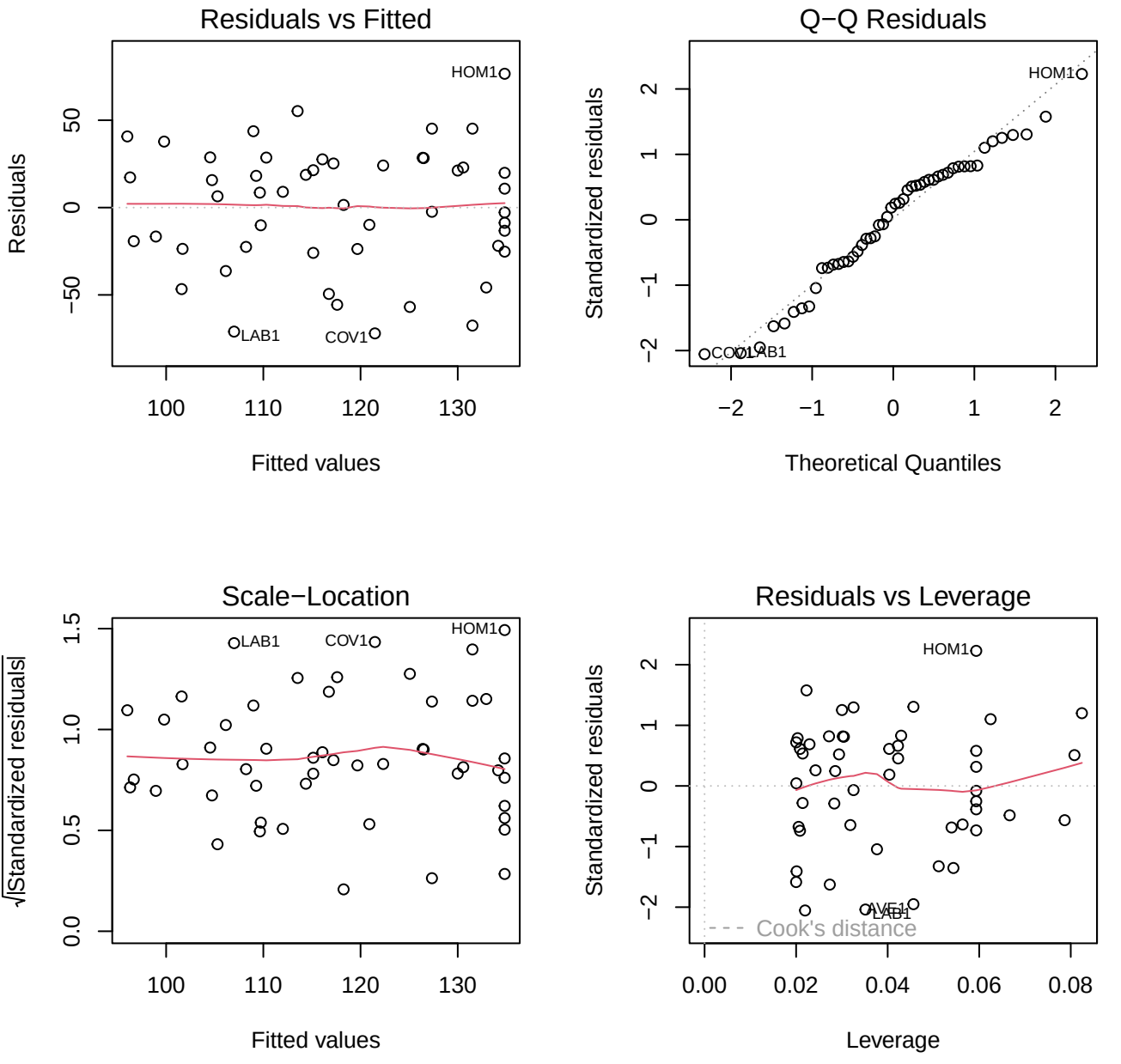

$R^2 = 0.007237988$
p−value: = 0.5569
Fungi_species_reads
ph
50
100
150
200
5.5
6.0
6.5
7.0
7.5

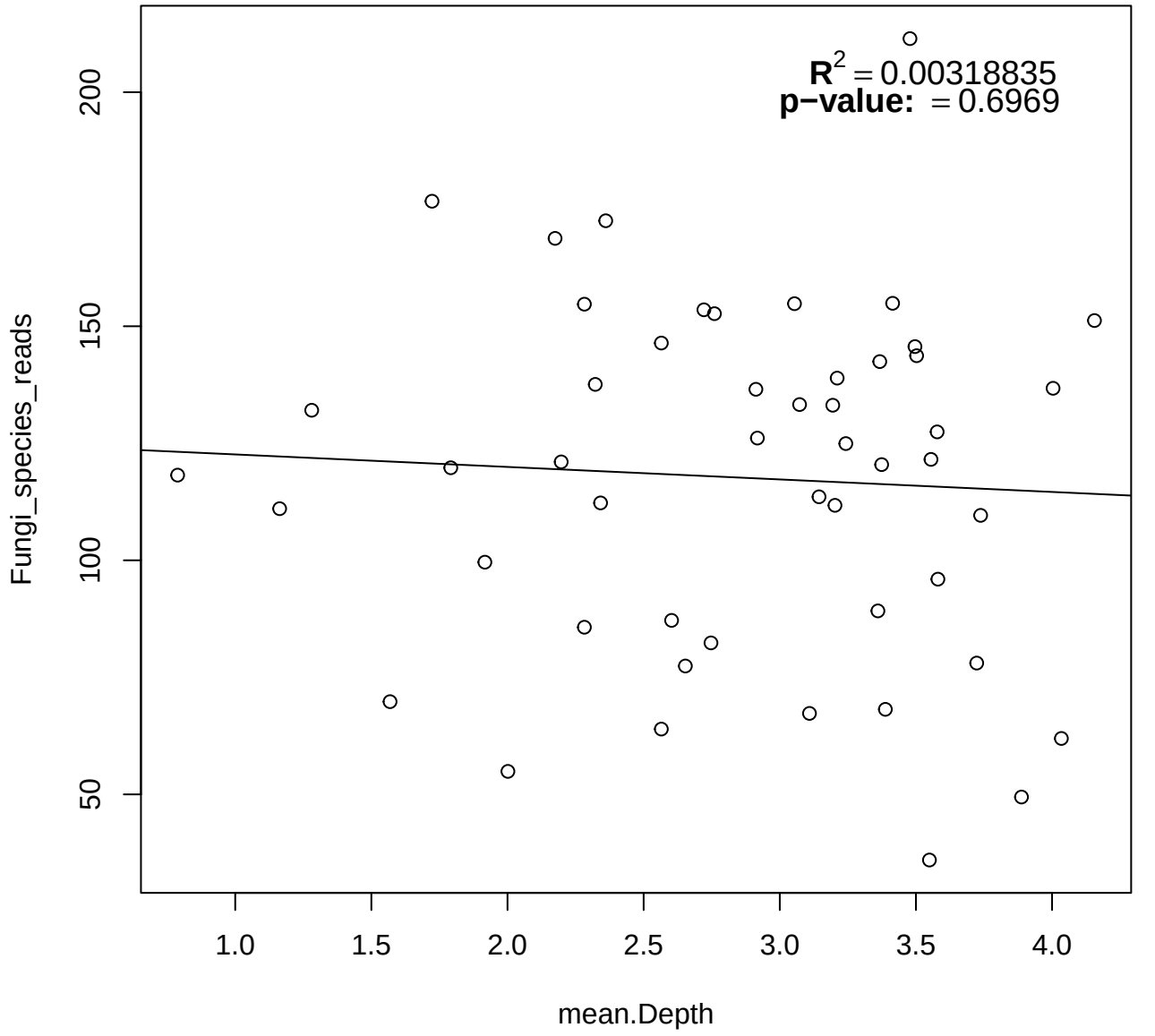

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
MOU1
COV1
LAB1
Cook's distance

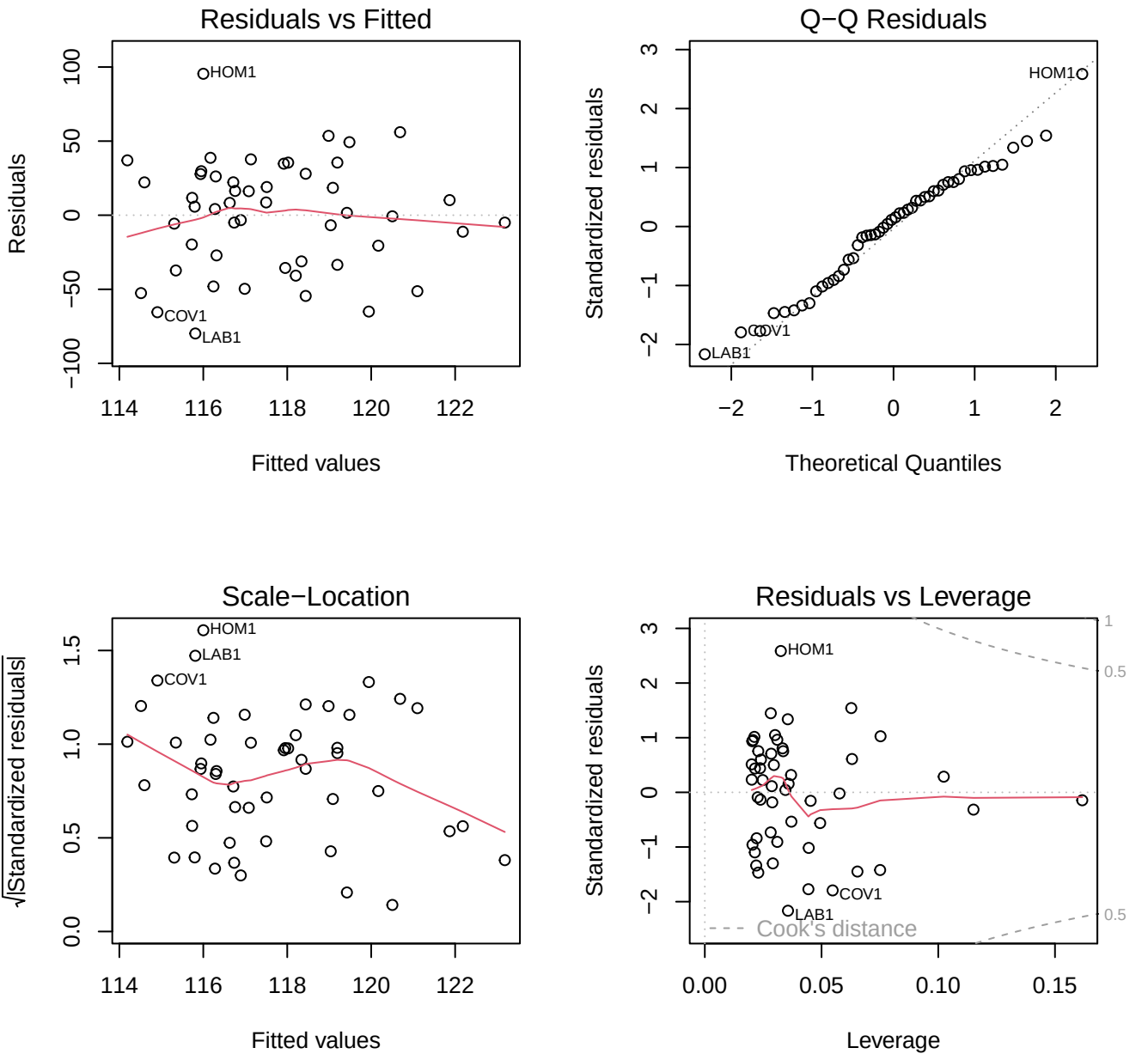

$R^2 = 0.01451239$
p−value: = 0.4047
Fungi_species_reads
200
150
100
50
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
cond

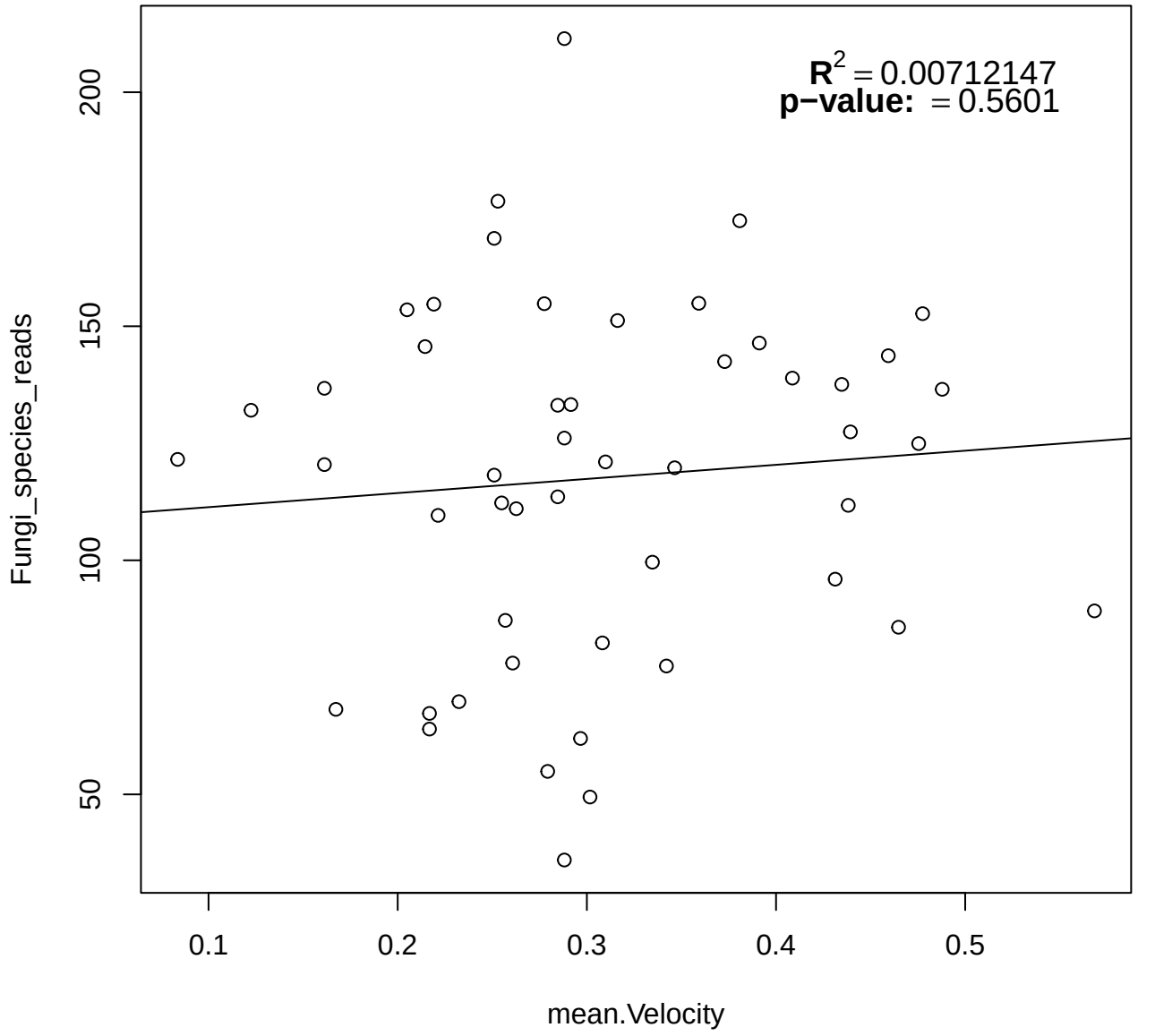

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
Cook's distance
0.5
0.5

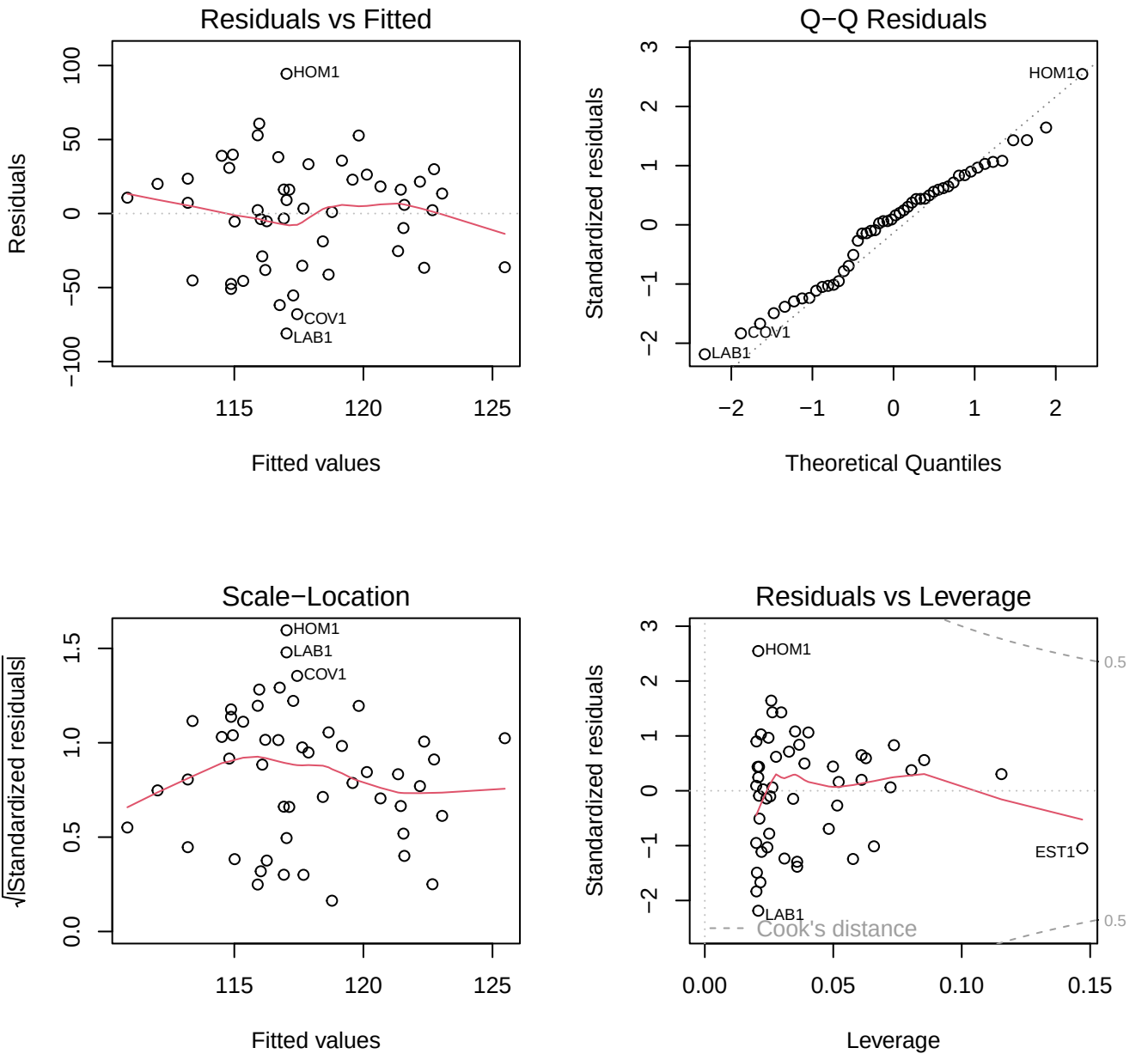

$R^2 = 0.1105893$
p−value: = 0.0183
Fungi_species_reads
LUI_500m
200
150
100
50
0
1
2
3
4

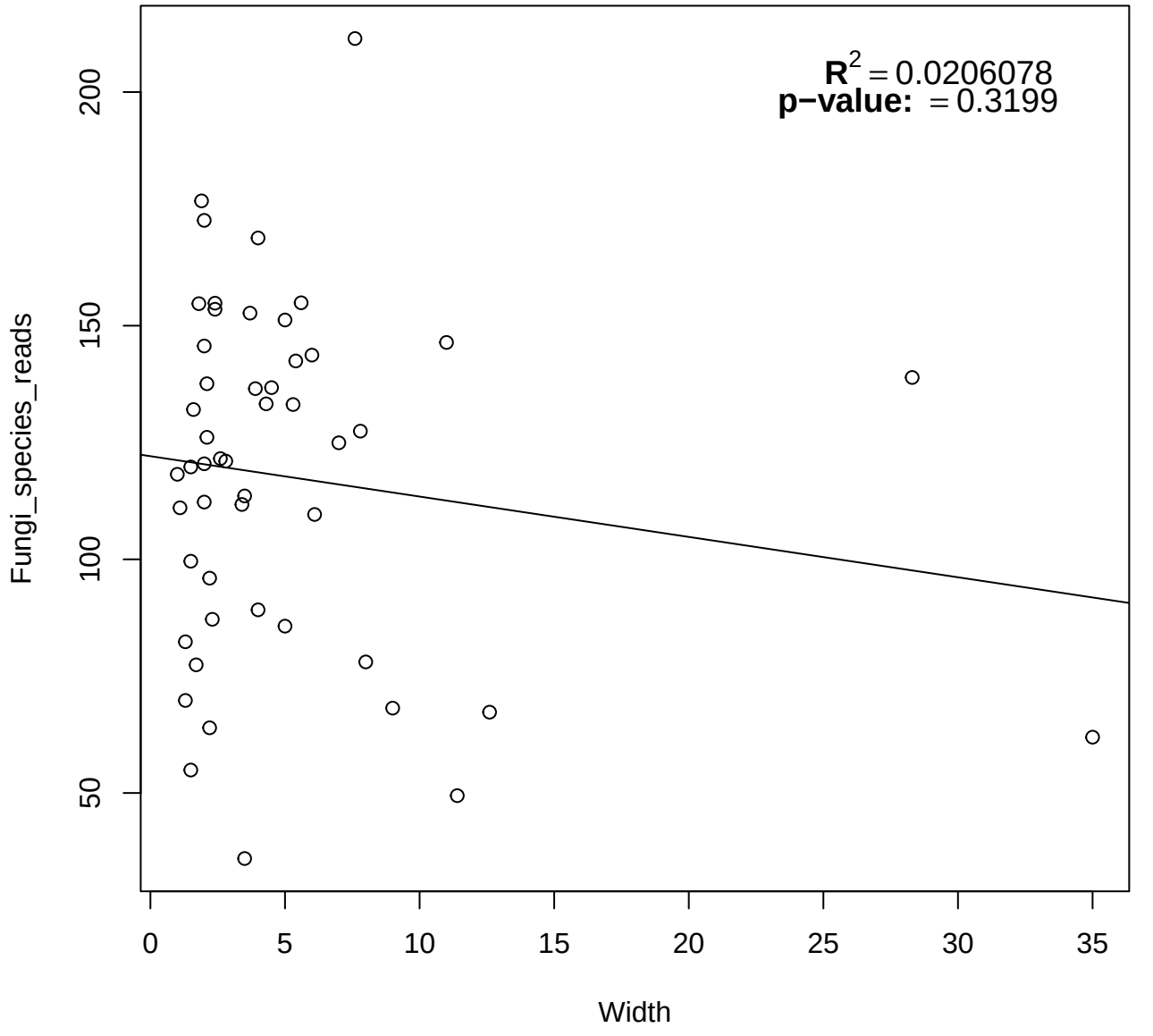

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
LAB1
Cook's distance

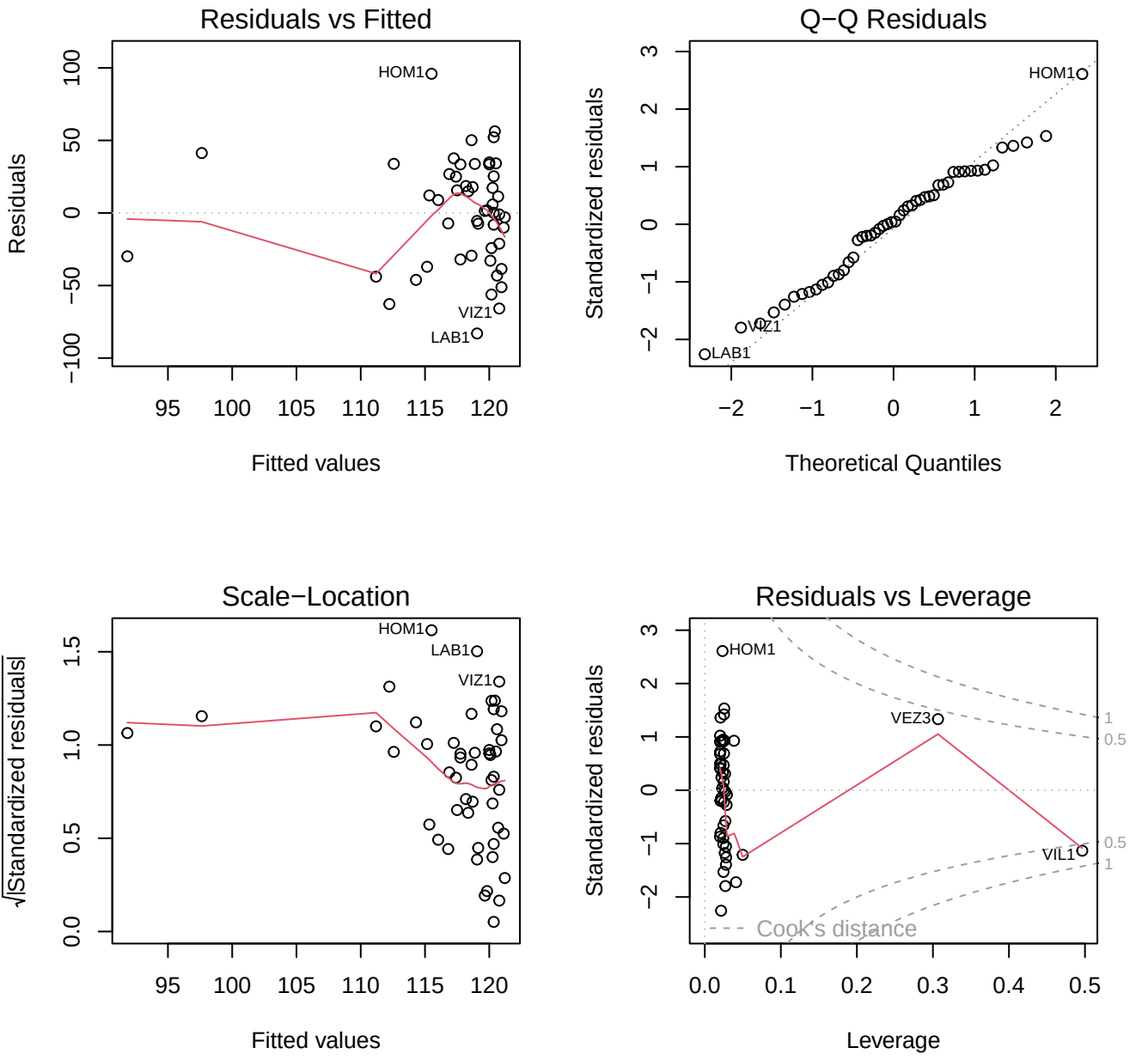

$R^2 = 0.00318835$
p−value: = 0.6969
Fungi_species_reads
200
150
100
50
1.0
1.5
2.0
2.5
3.0
3.5
4.0
mean.Depth

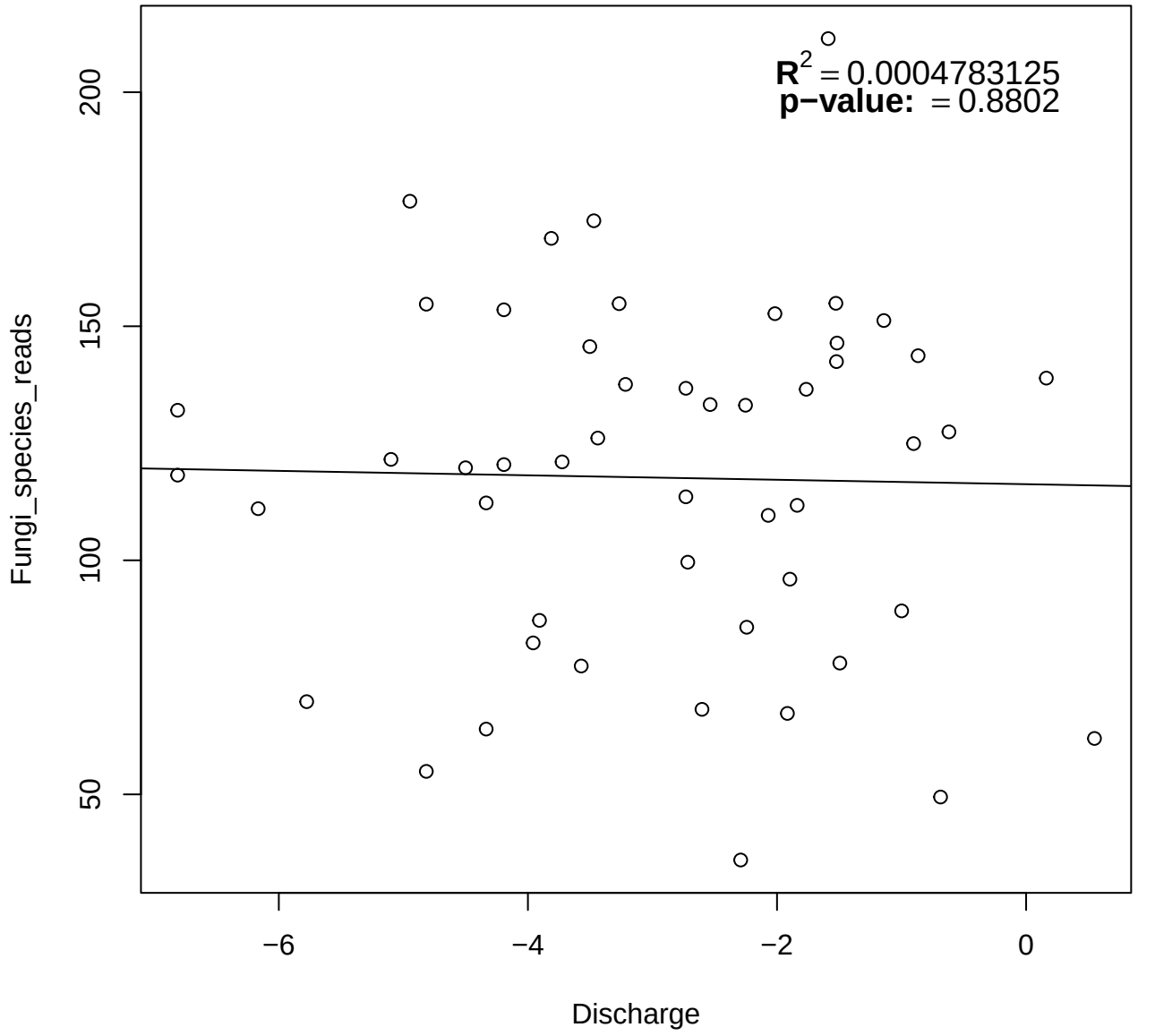

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
COV1
LAB1
Cook's distance
1
0.5
0.5

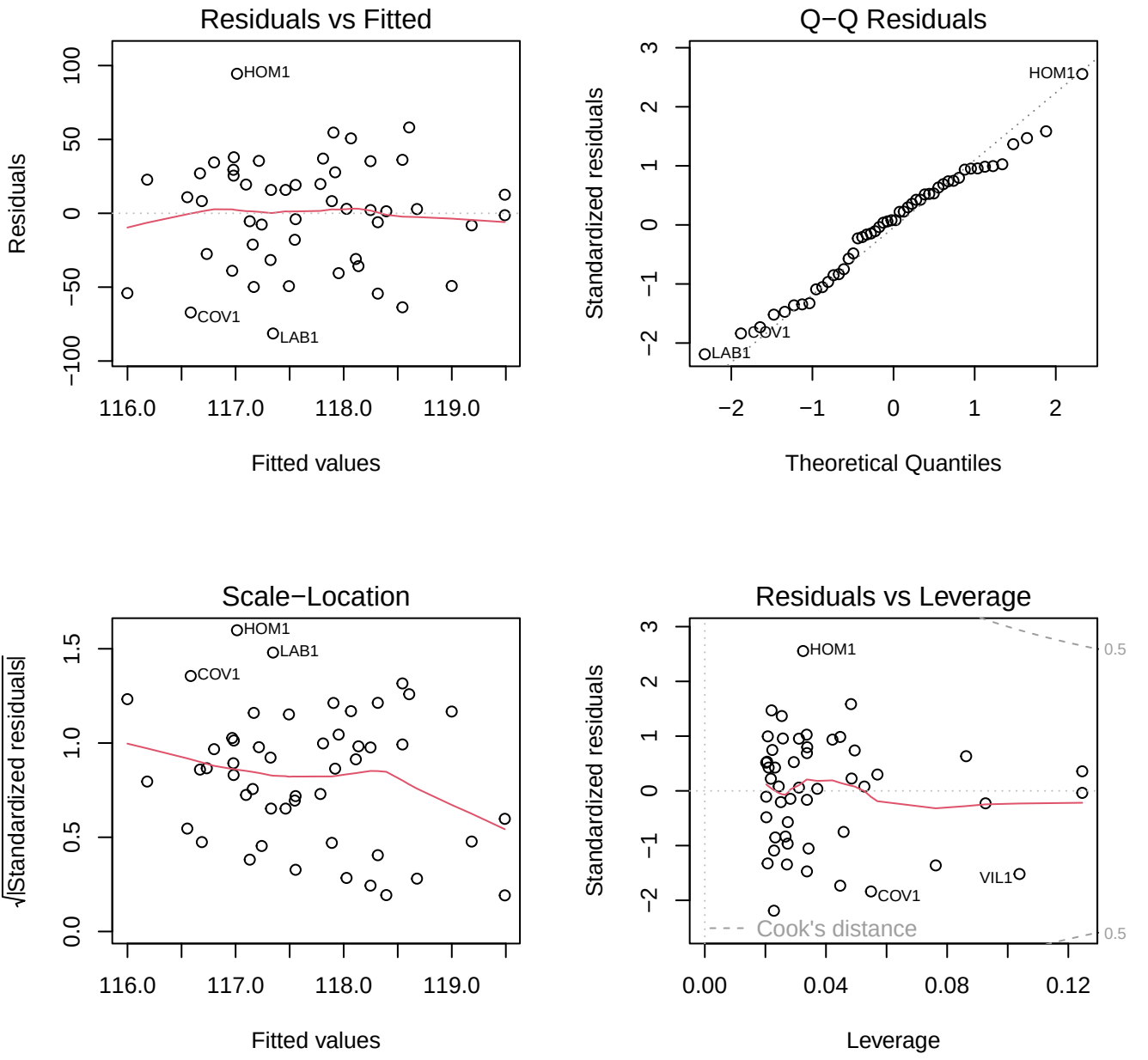

$R^2 = 0.00712147$
p−value: = 0.5601
Fungi_species_reads
200
150
100
50
0.1
0.2
0.3
0.4
0.5
mean.Velocity

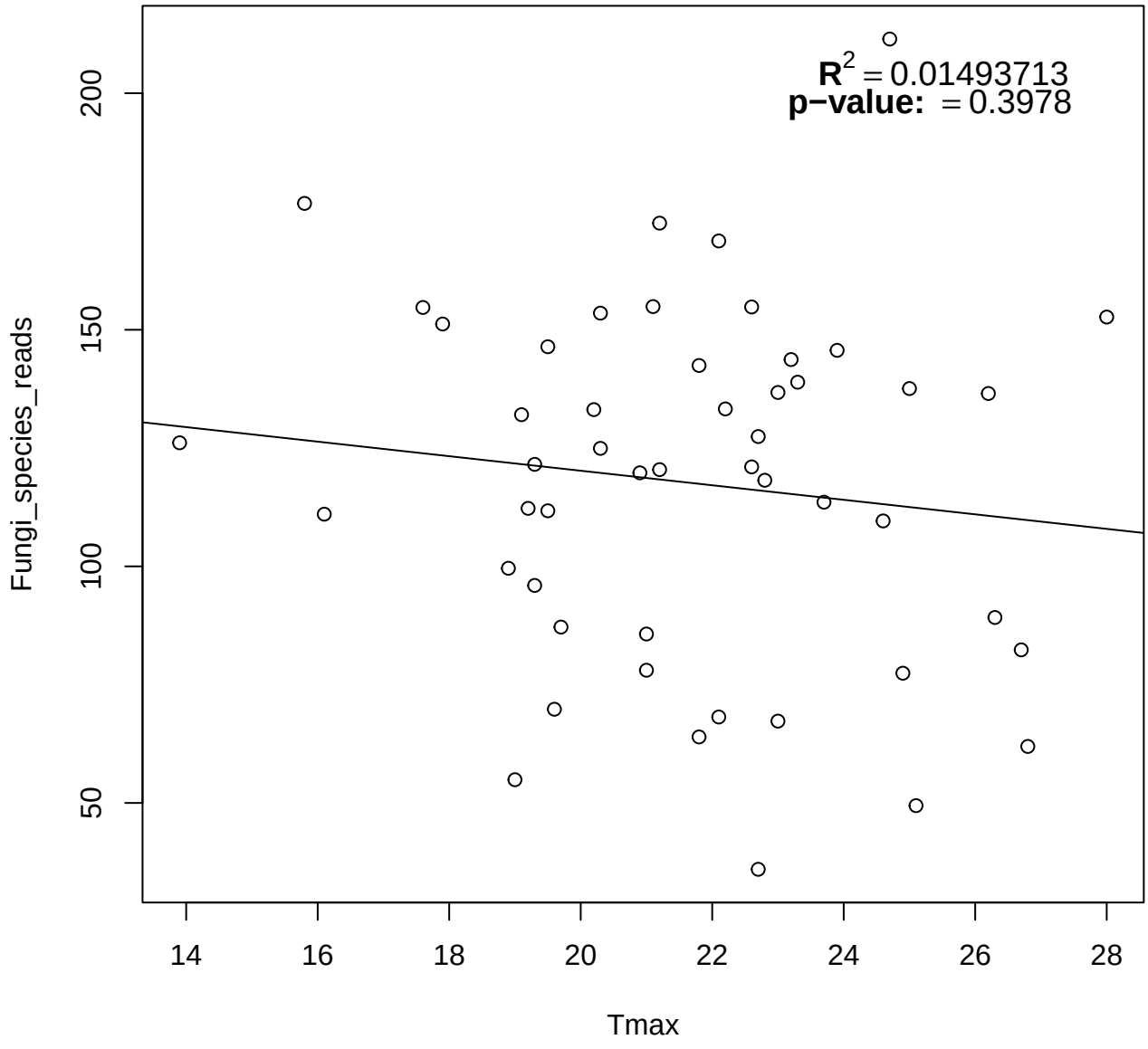

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
EST1
LAB1
Cook's distance
0.5
0.5

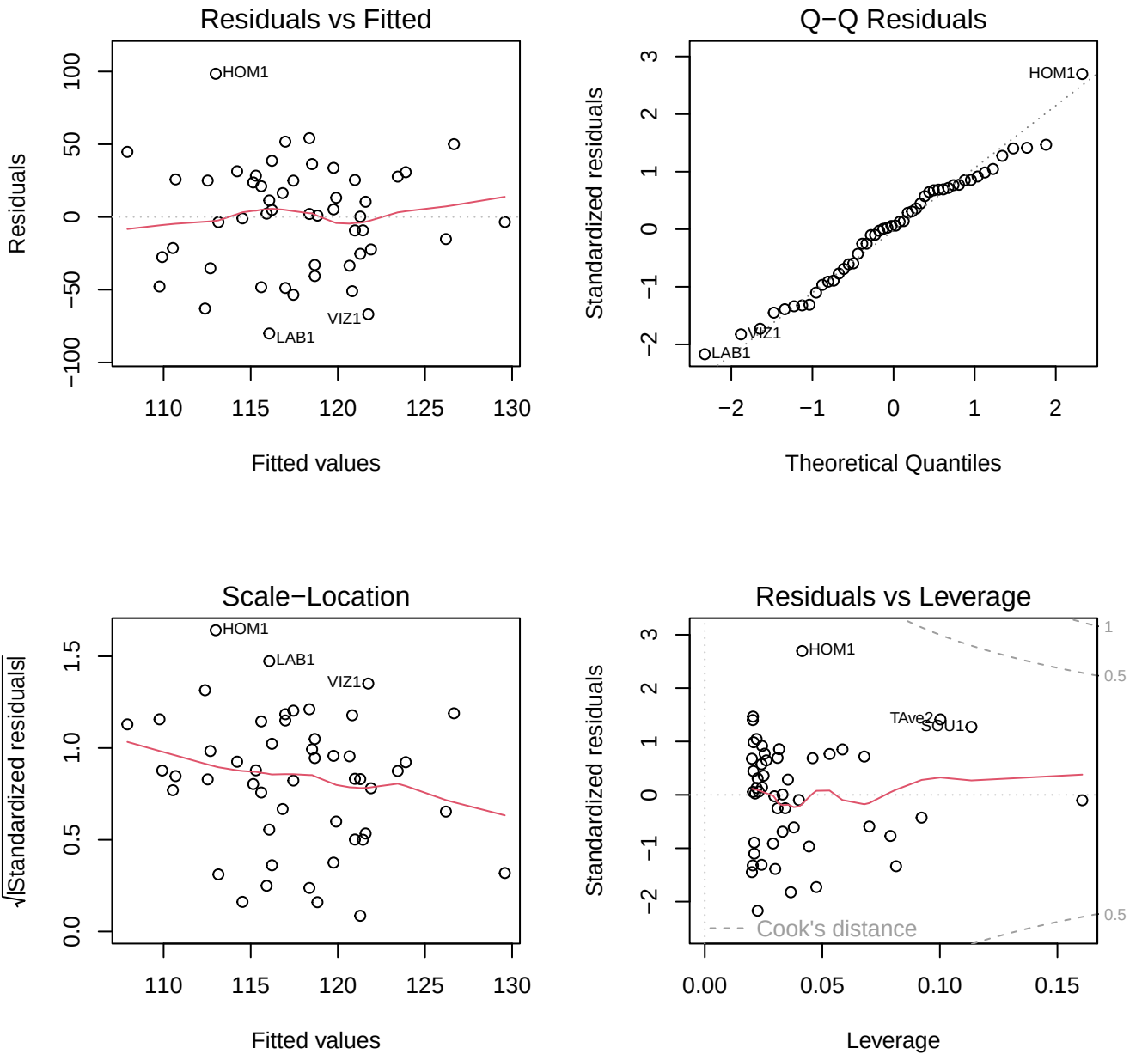

$R^2 = 0.0206078$
p−value: = 0.3199
Fungi_species_reads
Width
0
5
10
15
20
25
30
35
50
100
150
200

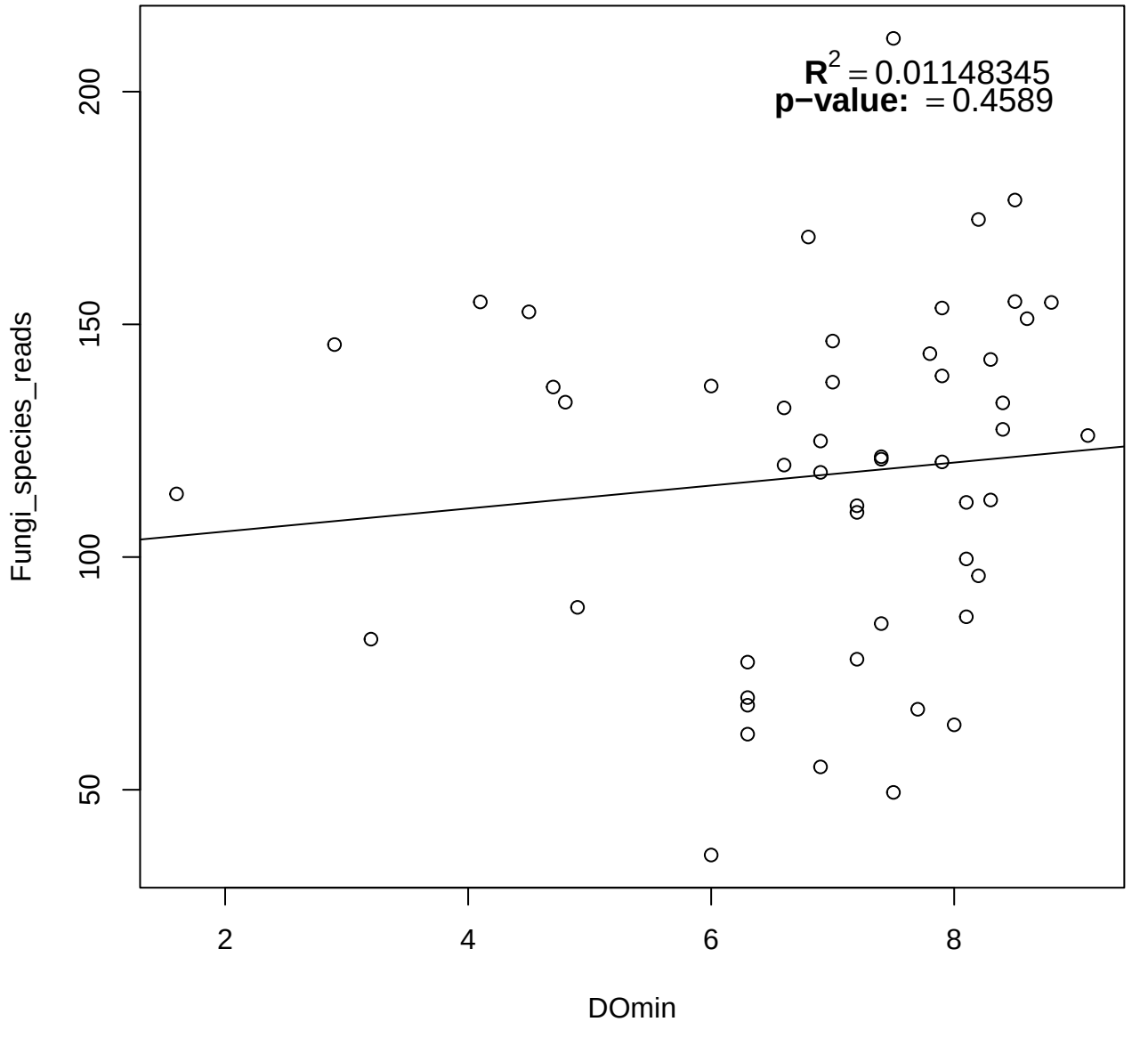

Residuals vs Fitted
Residuals
Fitted values
HOM1
VIZ1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
VIZ1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
VEZ3
VIL1
Cook's distance

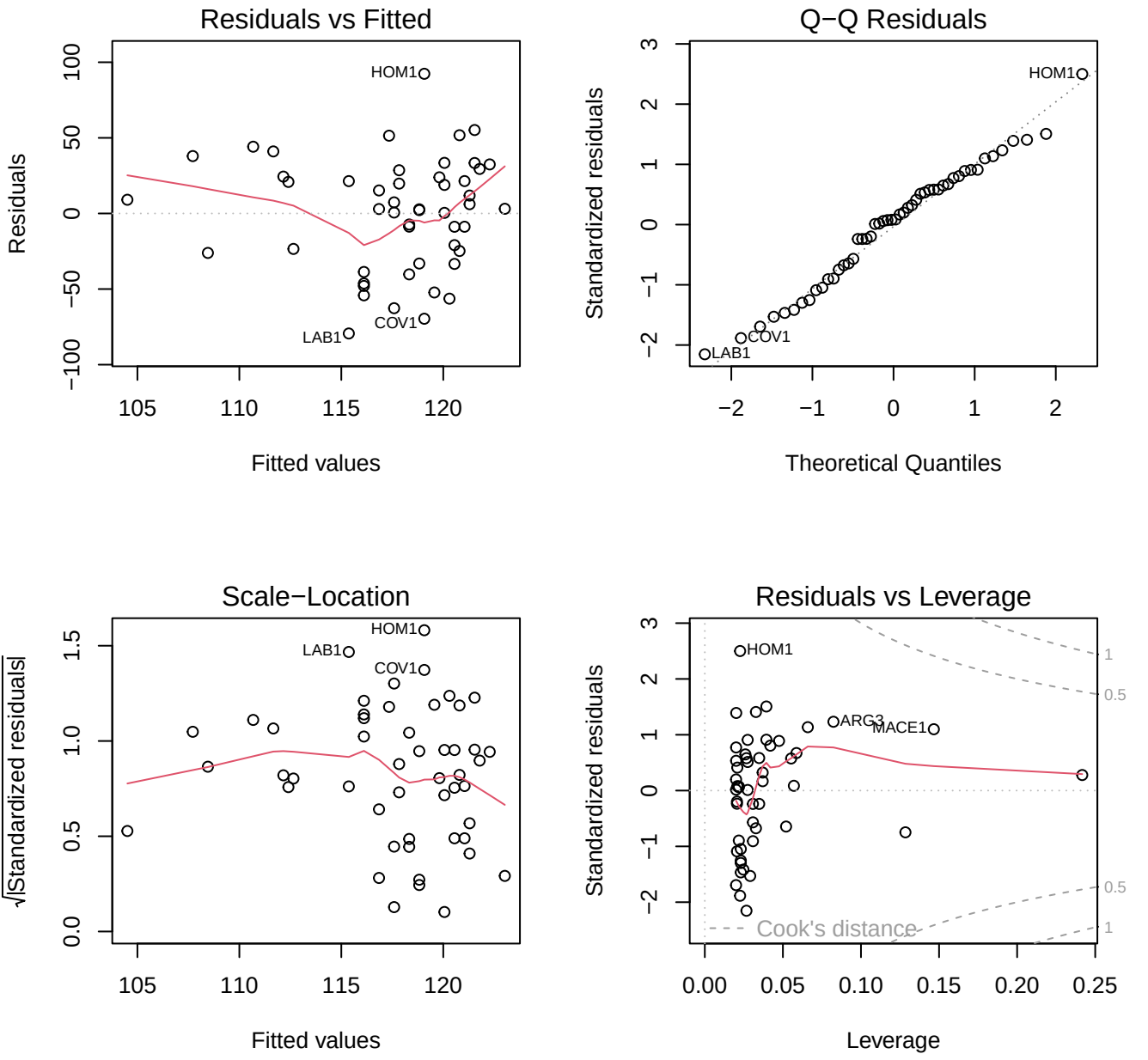

$R^2 = 0.0004783125$
p−value: = 0.8802
Fungi_species_reads
200
150
100
50
−6
−4
−2
0
Discharge

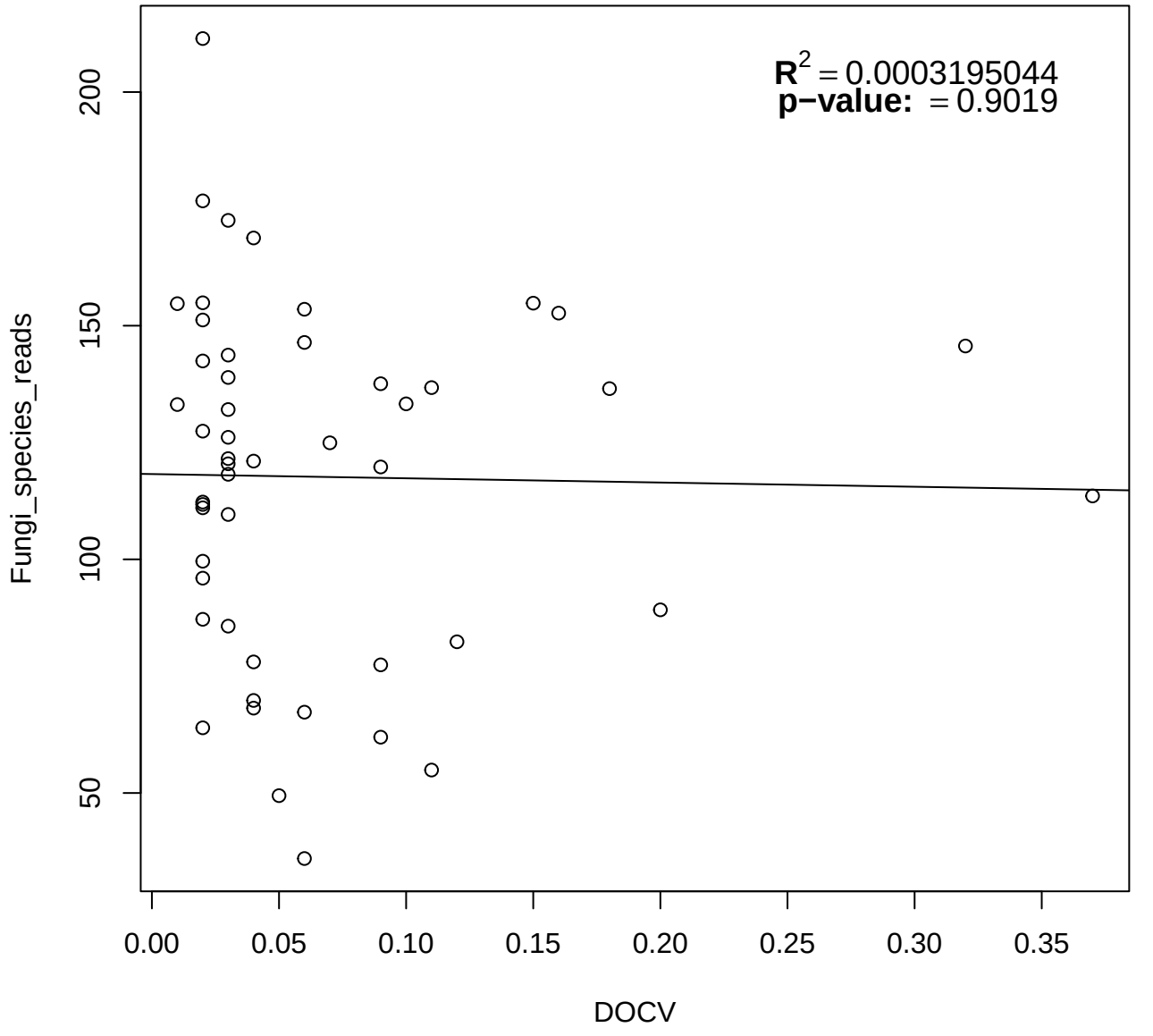

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
COV1
VIL1
Cook's distance
0.5
0.5

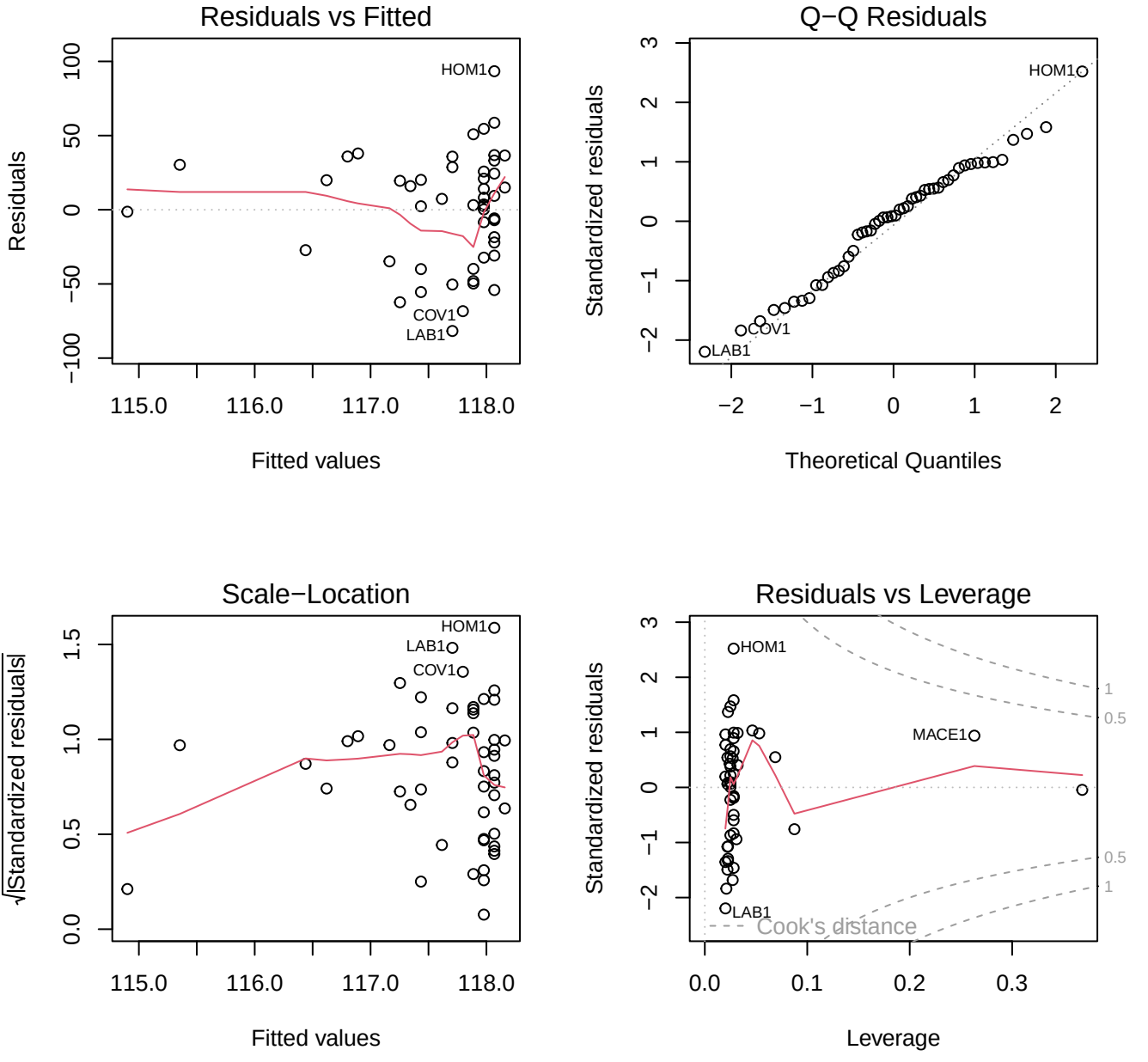

$R^2 = 0.01493713$
p−value: = 0.3978
Fungi_species_reads
Tmax
50
100
150
200
14
16
18
20
22
24
26
28

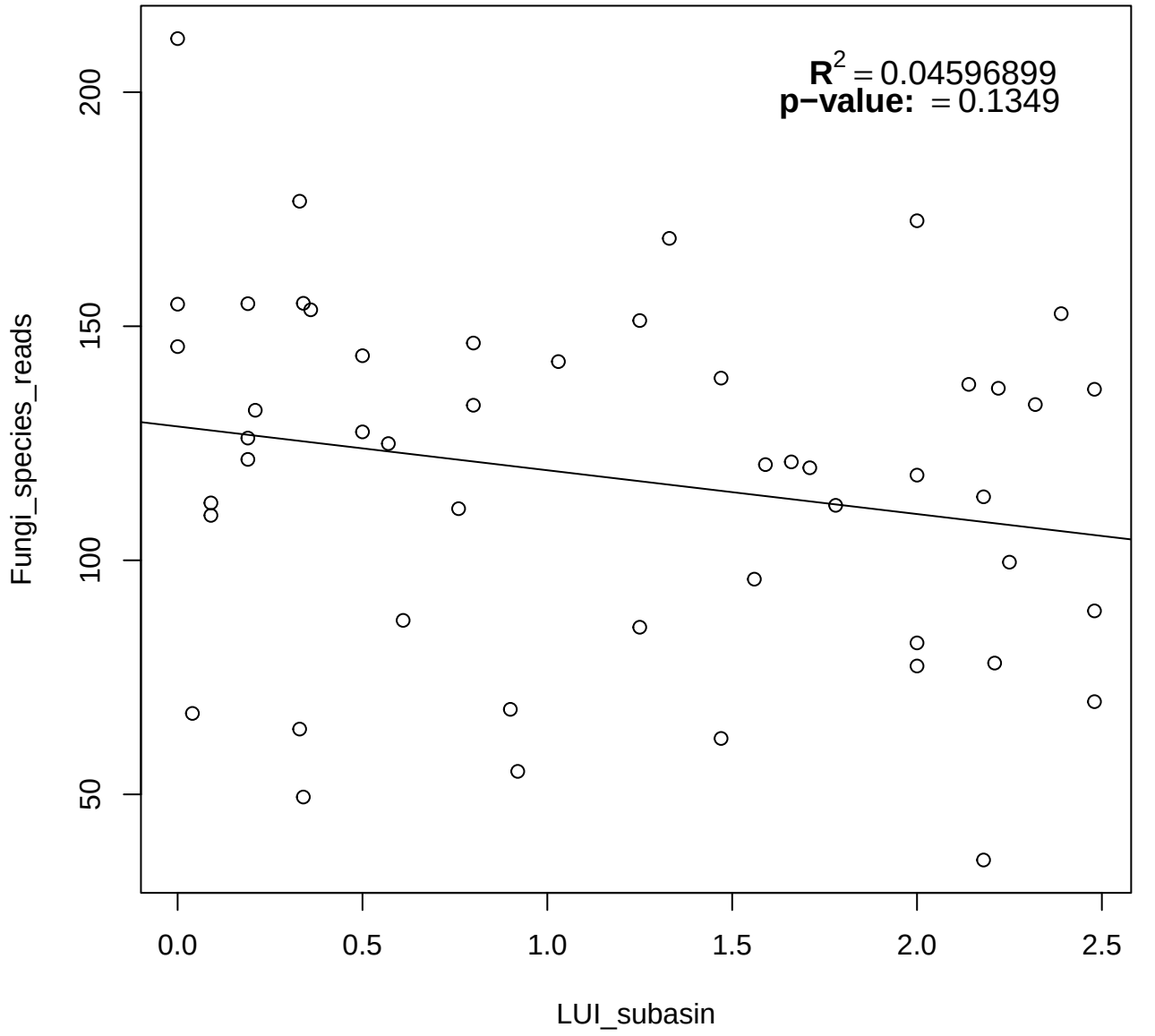

Residuals vs Fitted
Residuals
Fitted values
HOM1
VIZ1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
VIZ1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
TAve2
SOU1
Cook's distance

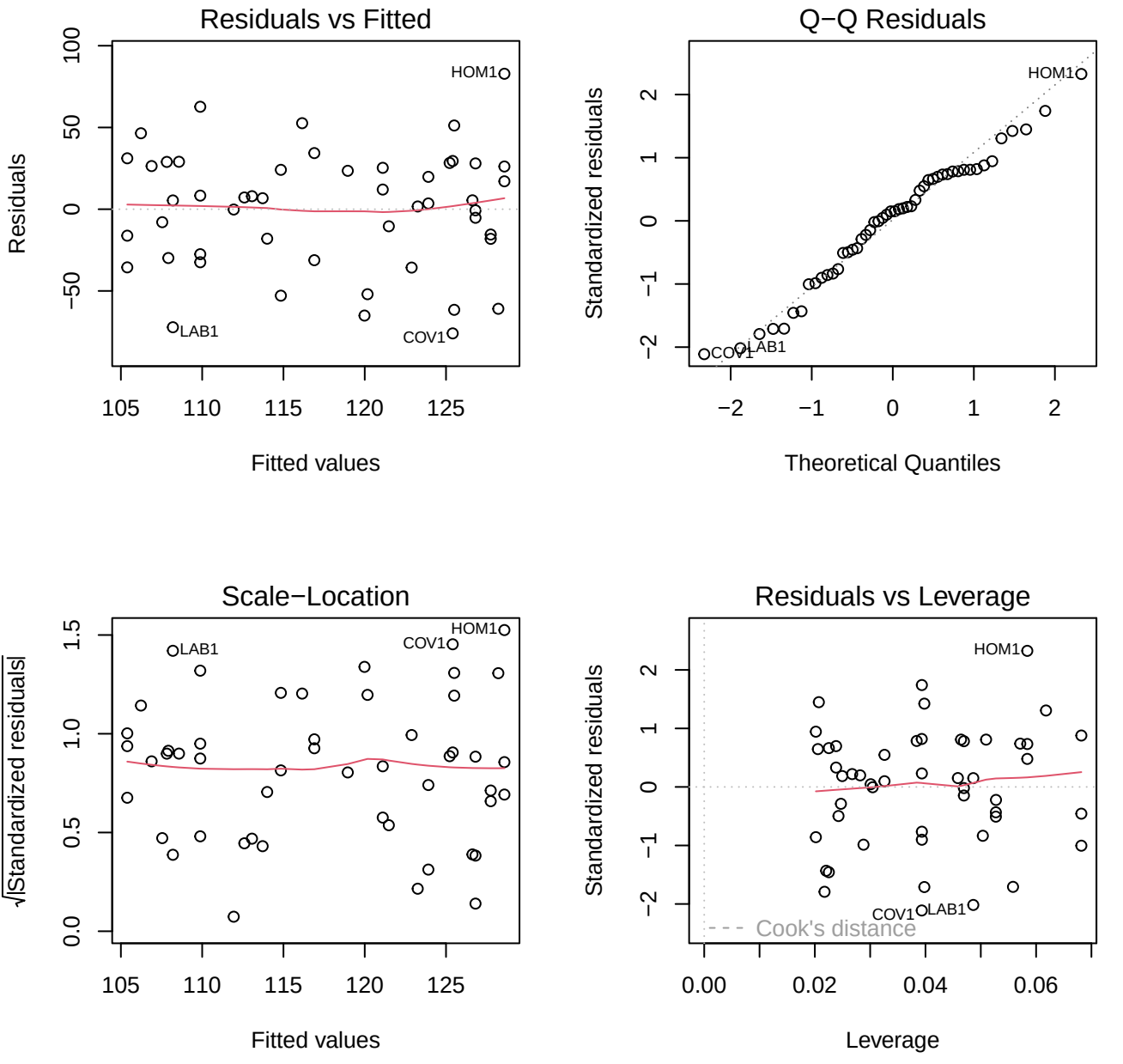

$R^2 = 0.01148345$
p−value: = 0.4589
Fungi_species_reads
DOmin
200
150
100
50
2
4
6
8

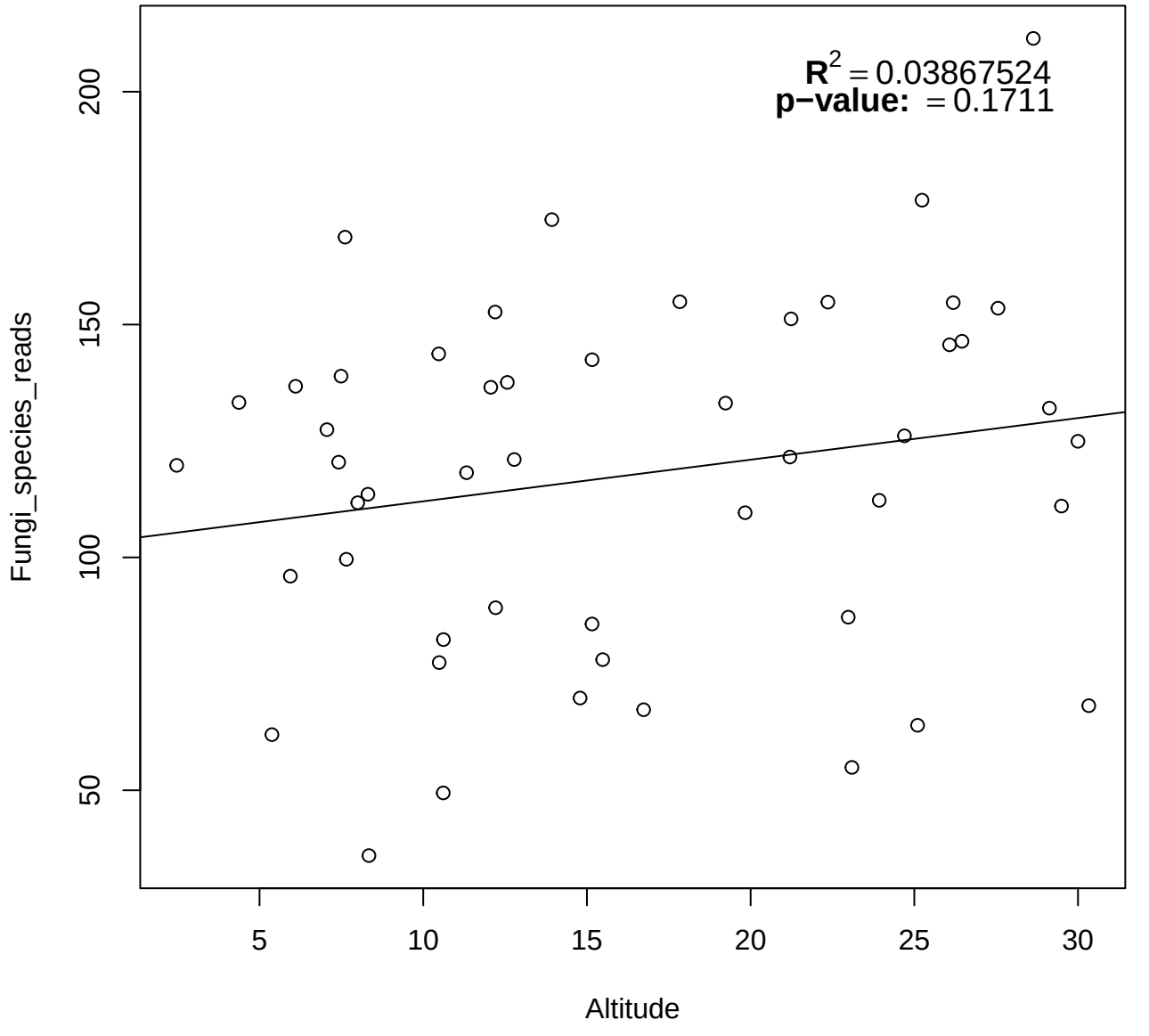

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
ARG3
MACE1
Cook's distance

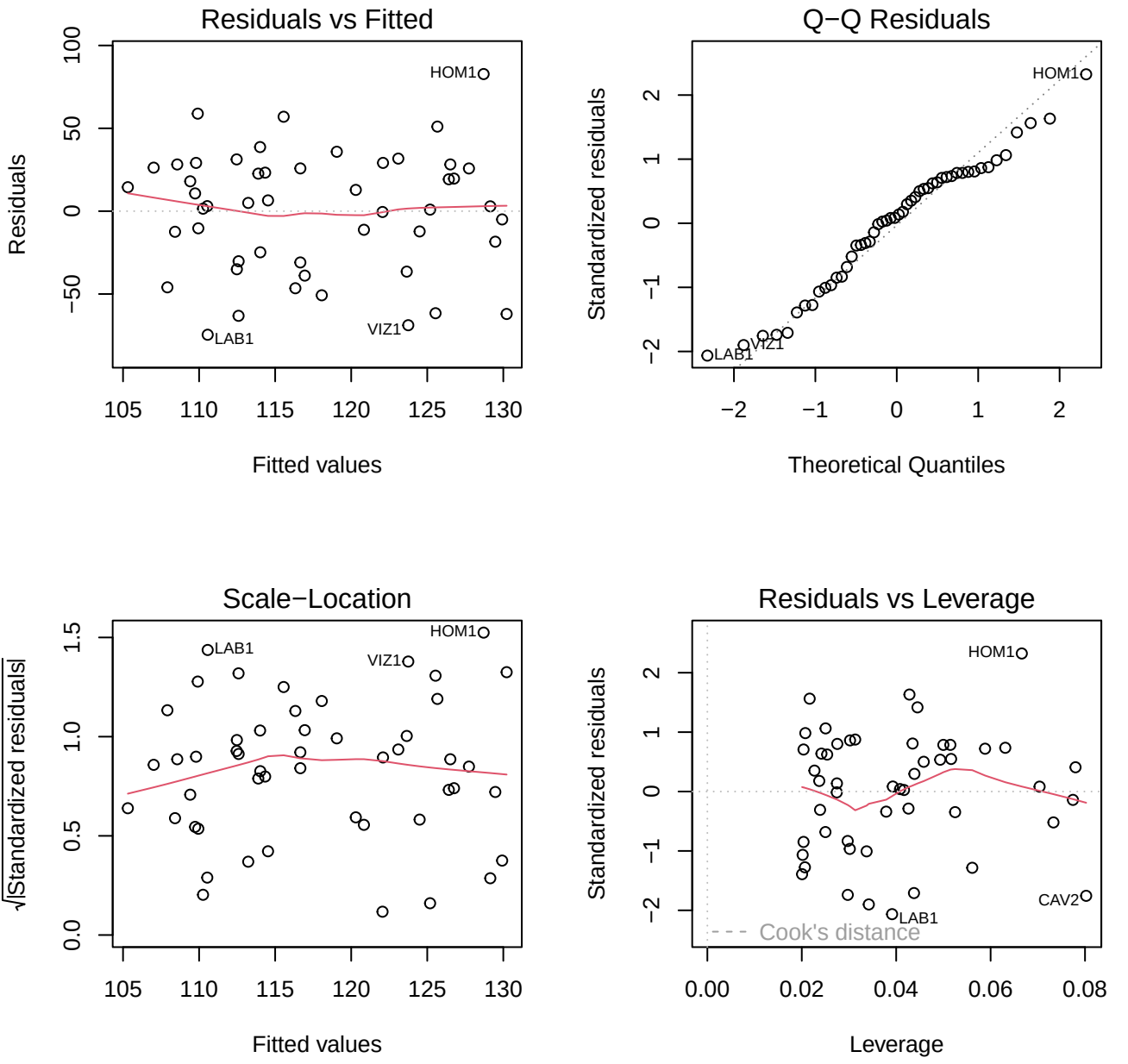

$R^2 = 0.0003195044$
p−value: = 0.9019
Fungi_species_reads
DOCV
50
100
150
200
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35

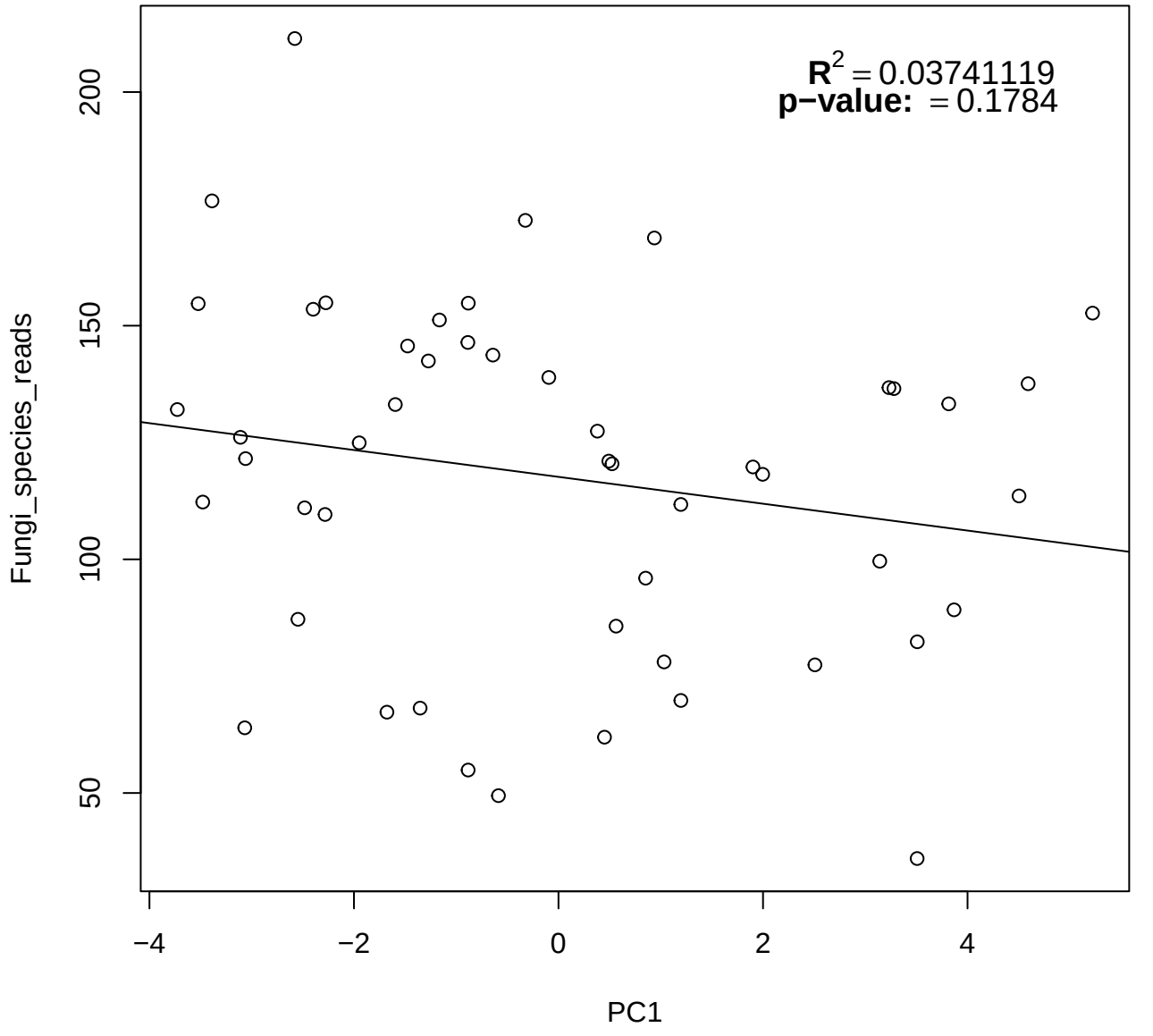

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
MACE1
LAB1
Cook's distance

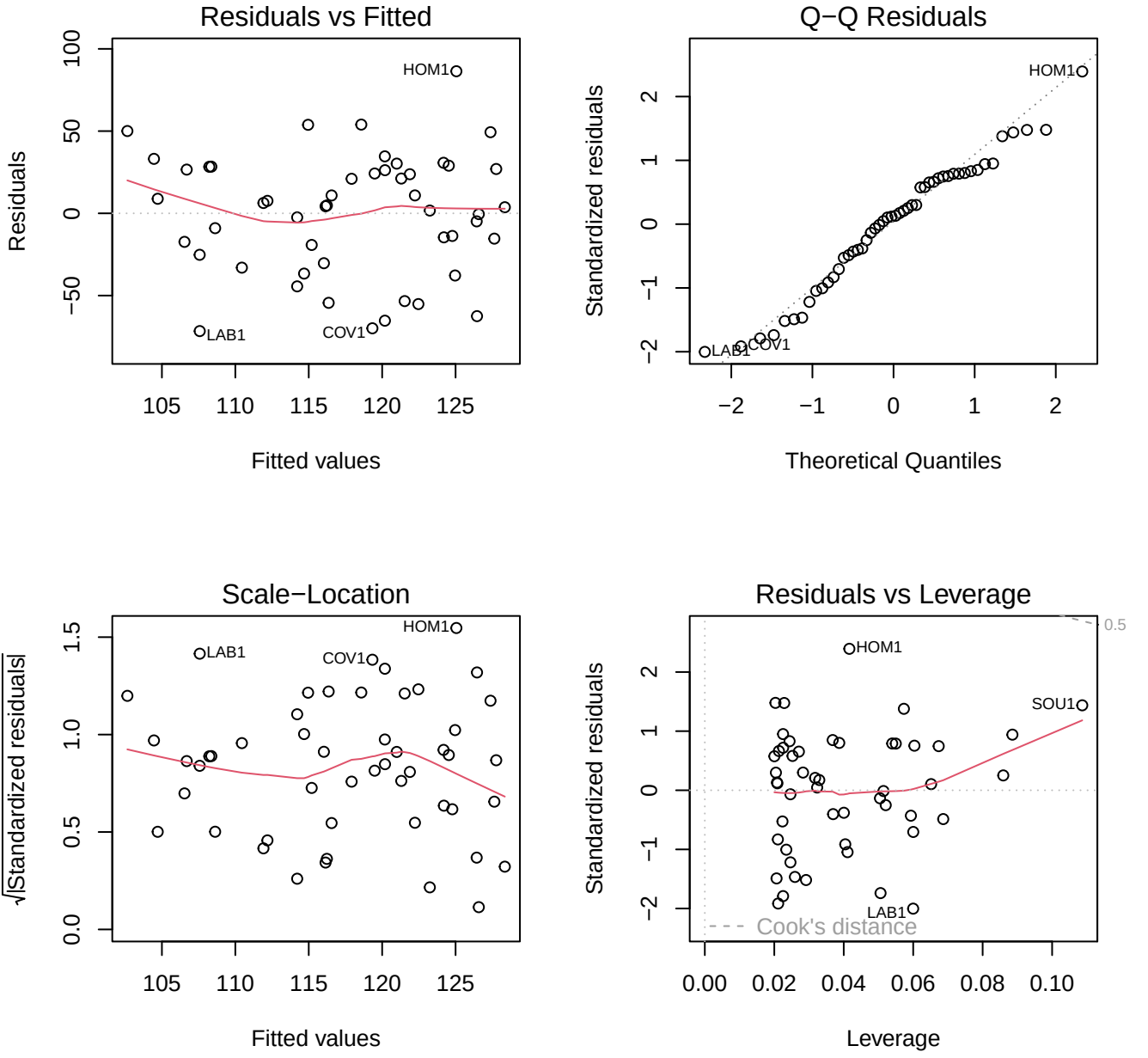

$R^2 = 0.04596899$
p−value: = 0.1349
Fungi_species_reads
LUI_subasin
50
100
150
200
0.0
0.5
1.0
1.5
2.0
2.5

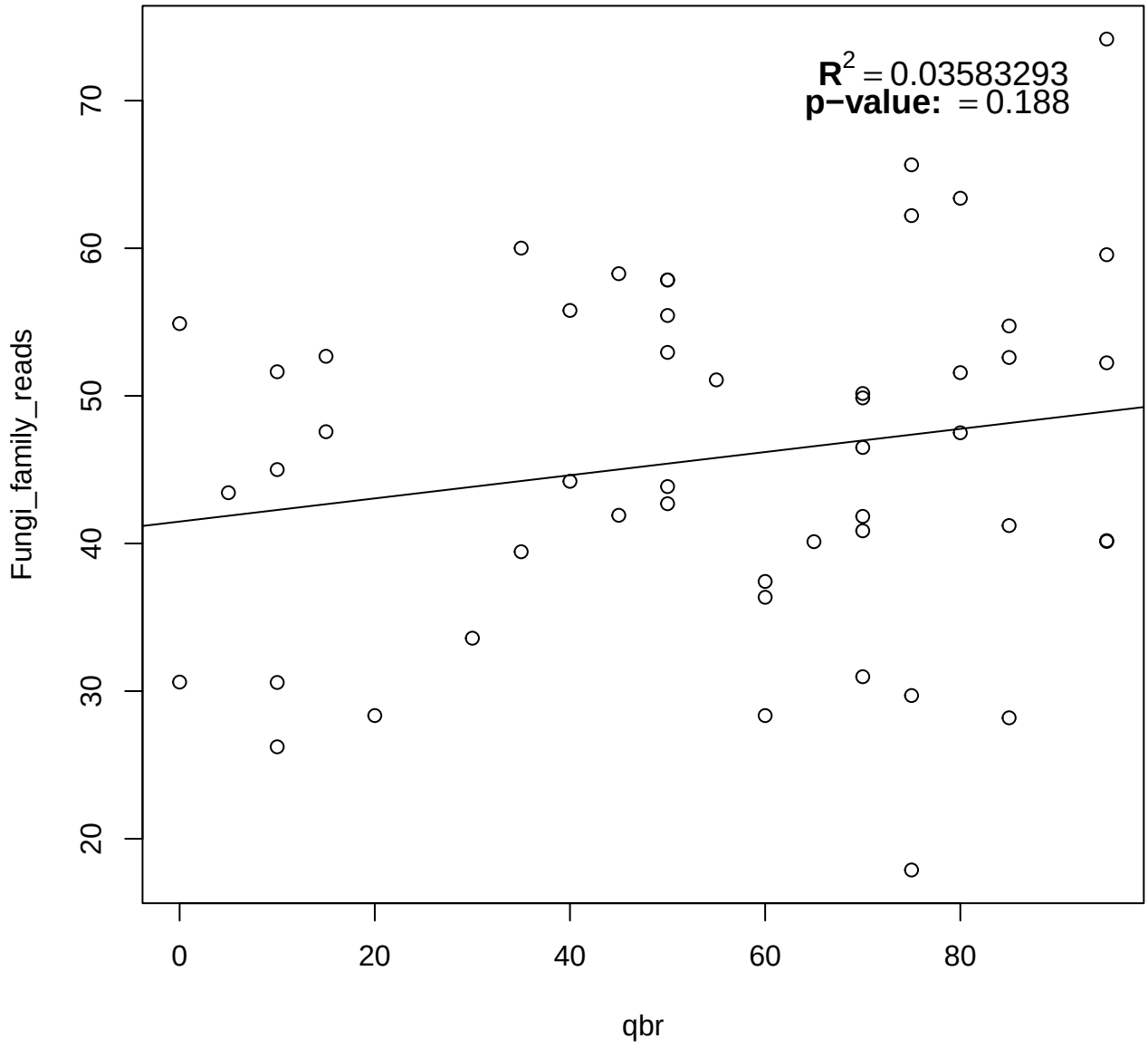

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
COV1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
COV1
LAB1
Cook's distance

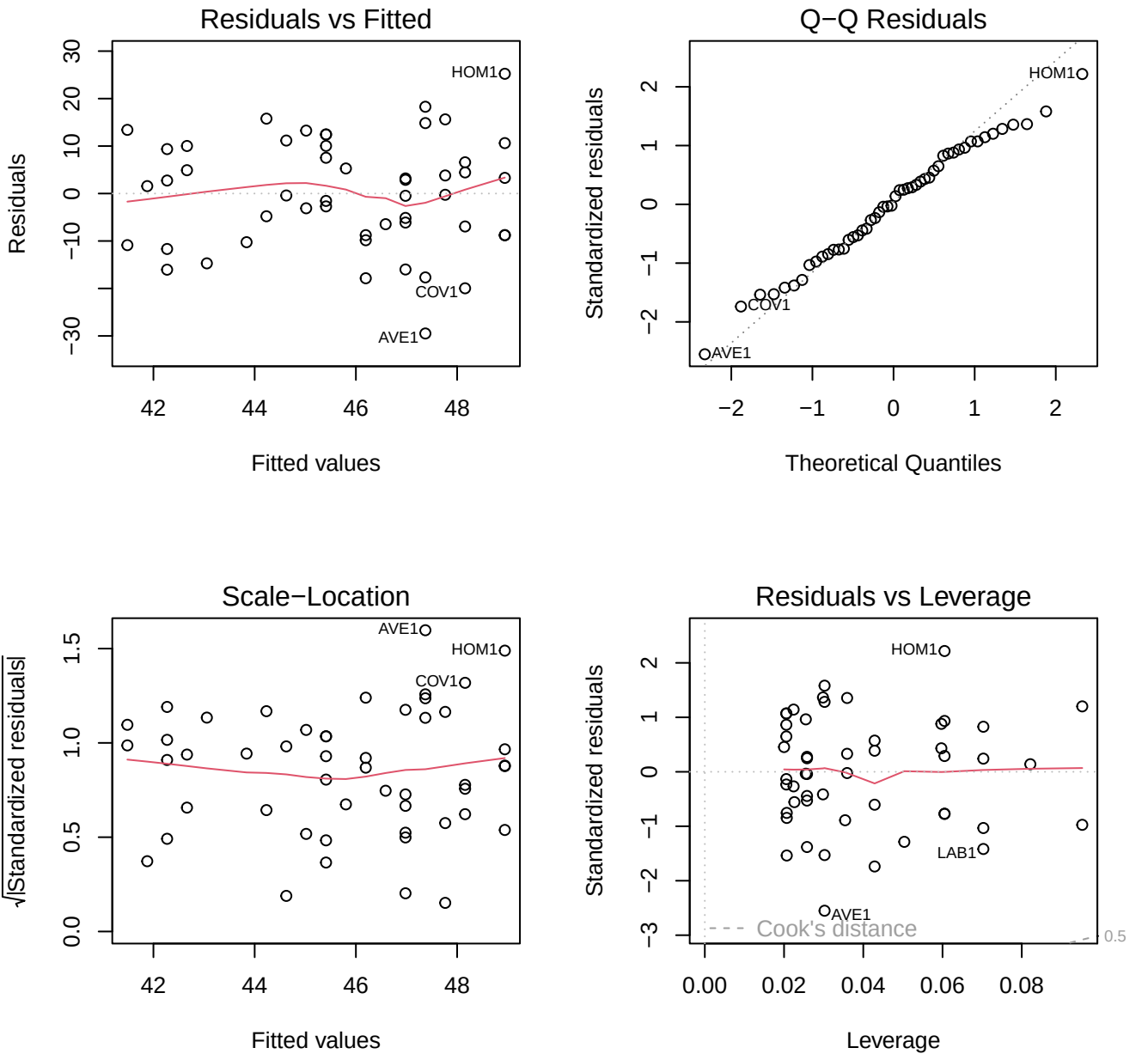

$R^2 = 0.03867524$
p−value: = 0.1711
Fungi_species_reads
Altitude
50
100
150
200
5
10
15
20
25
30

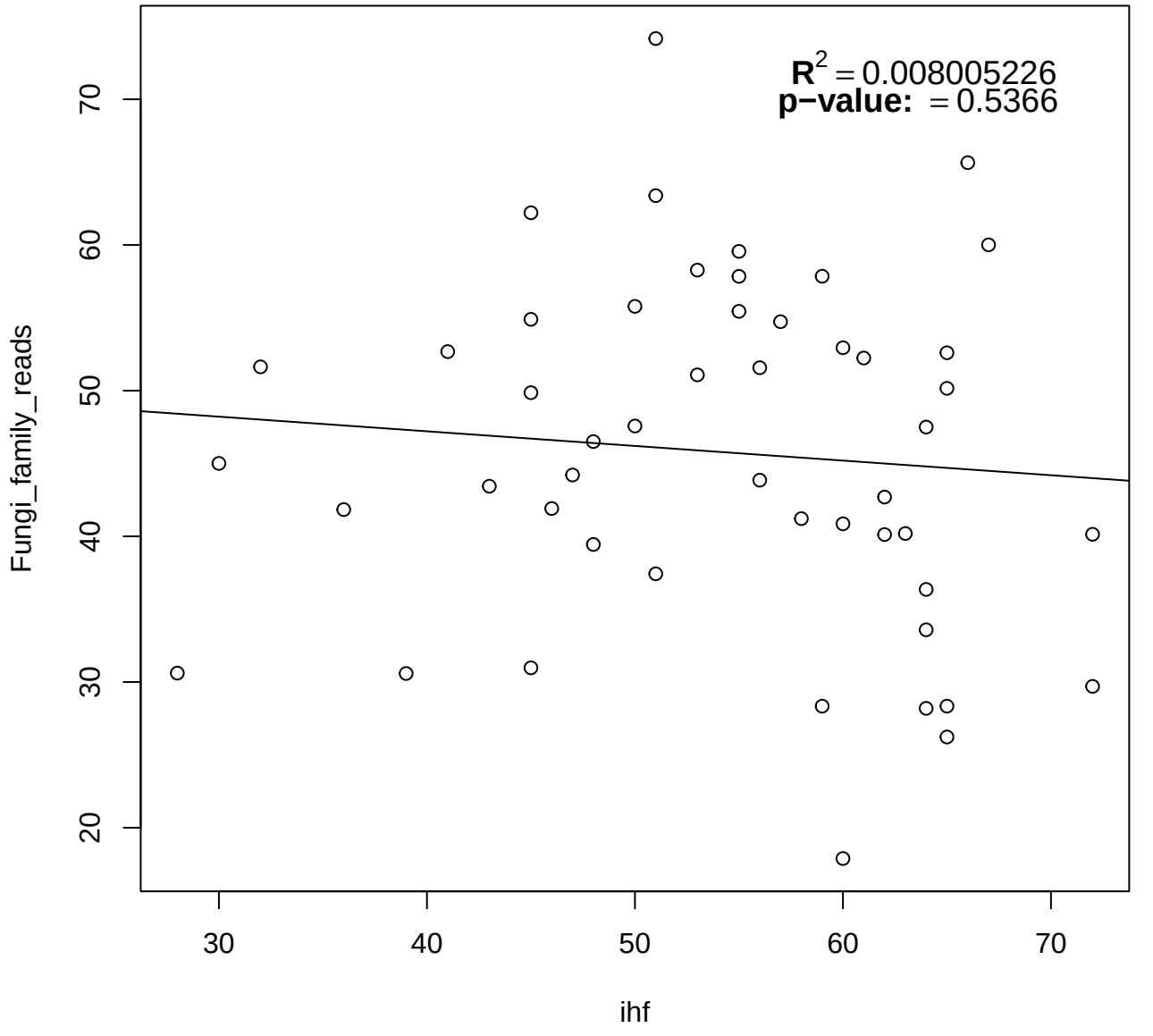

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
VIZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
LAB1
CAV2
Cook's distance

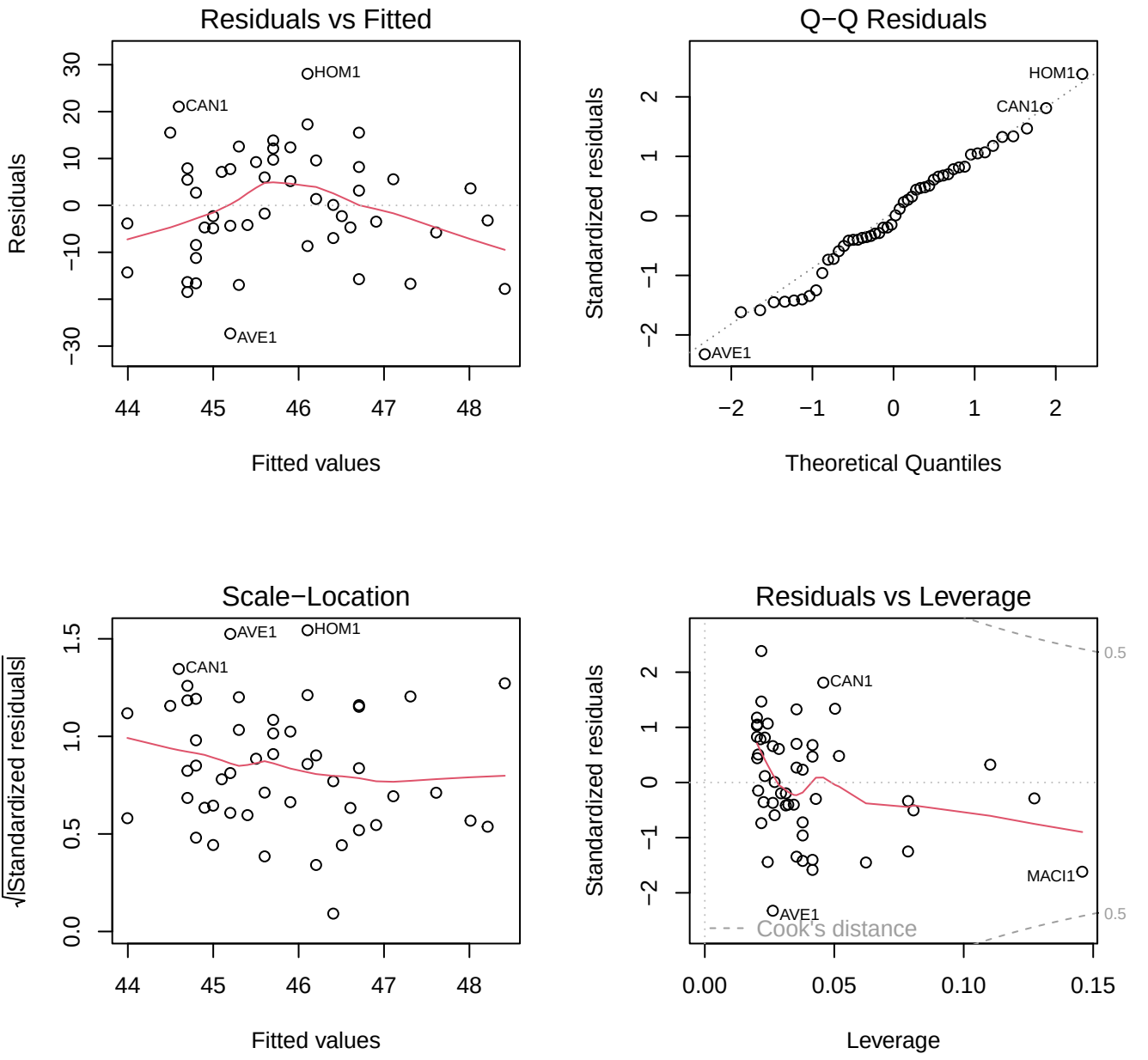

$R^2 = 0.03741119$
p−value: = 0.1784
Fungi_species_reads
200
150
100
50
−4
−2
0
2
4
PC1

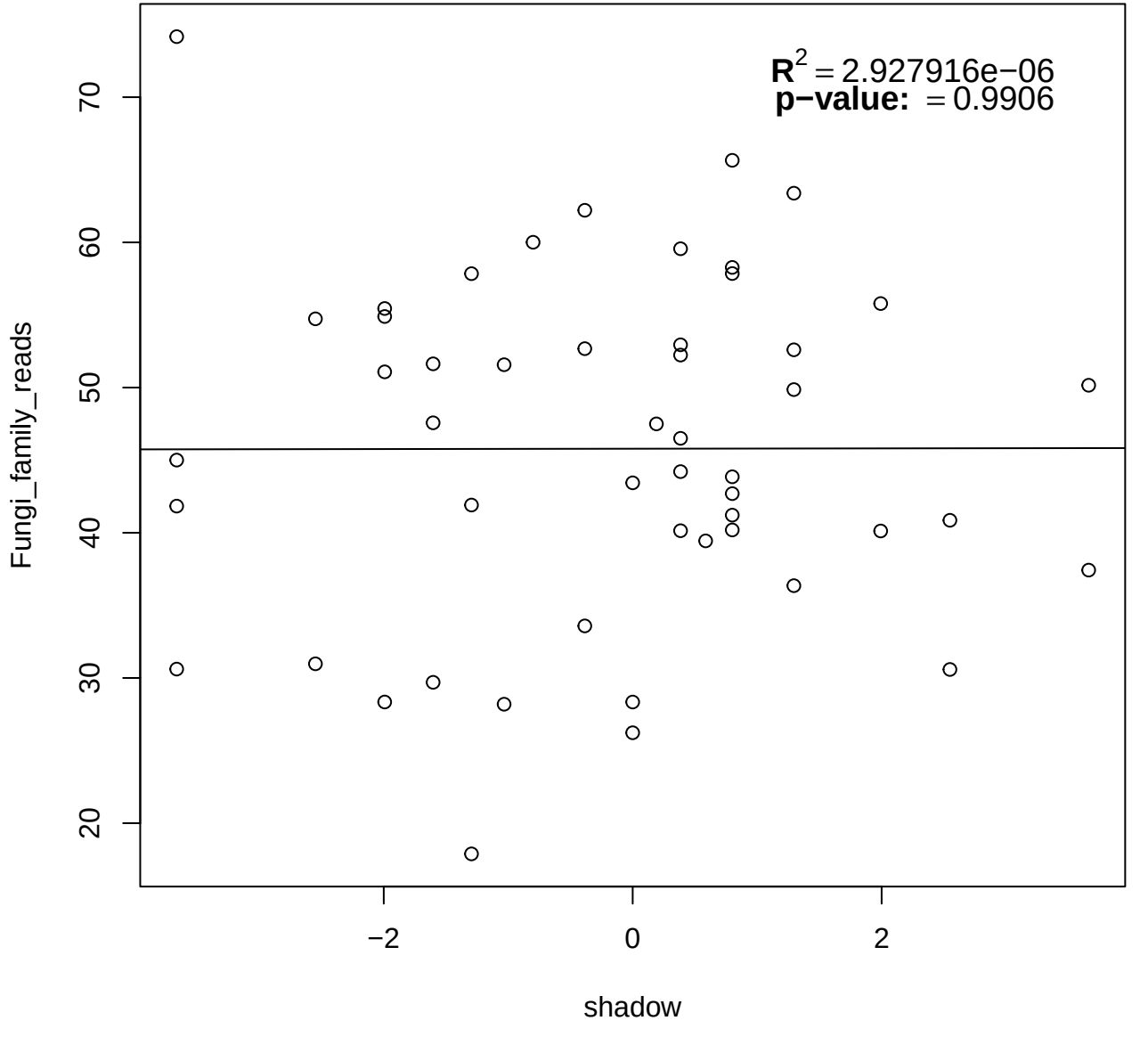

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
SOU1
LAB1
Cook's distance
0.5

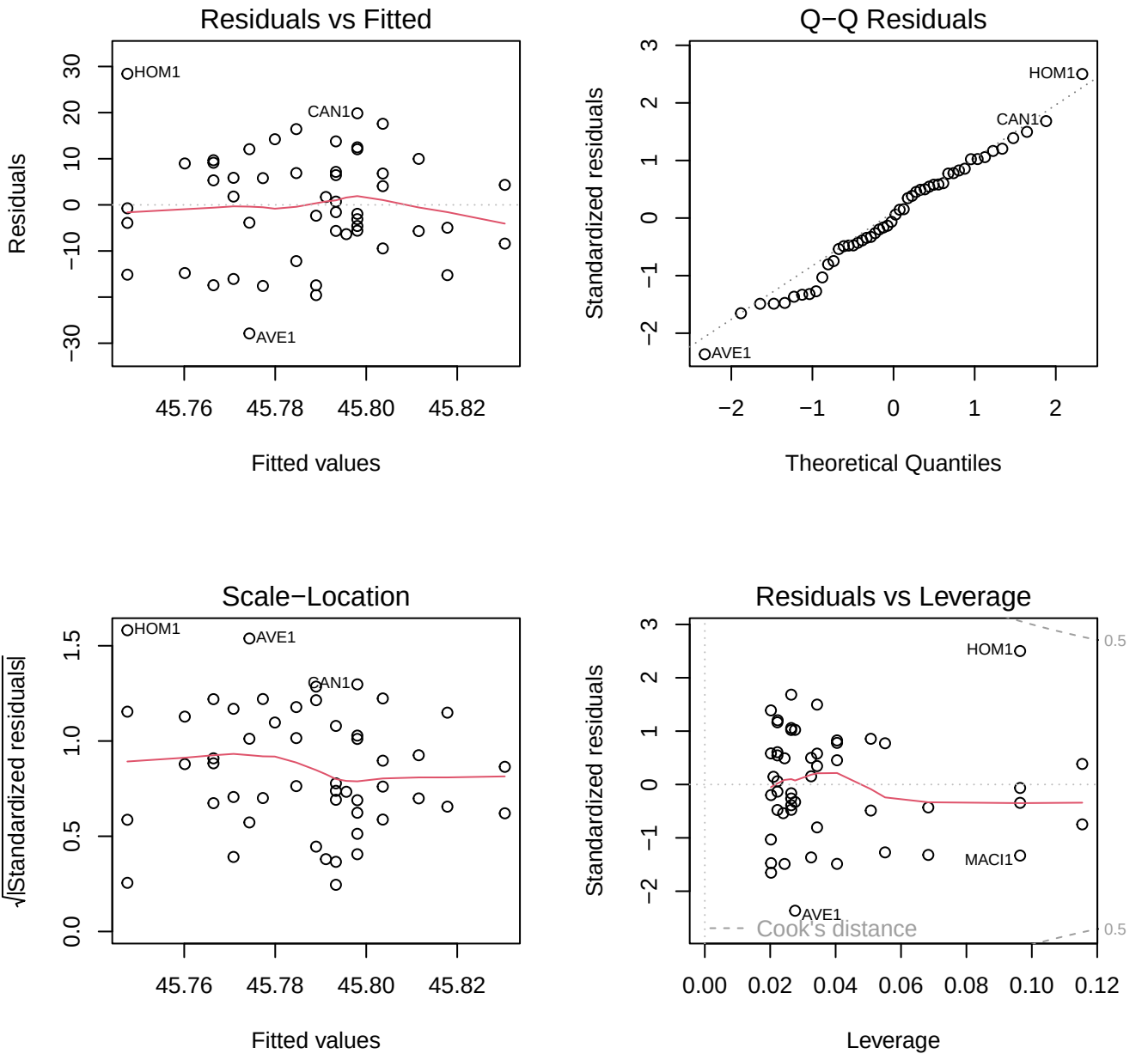

$R^2 = 0.03583293$
p−value: = 0.188
Fungi_family_reads
qbr
20
30
40
50
60
70
0
20
40
60
80

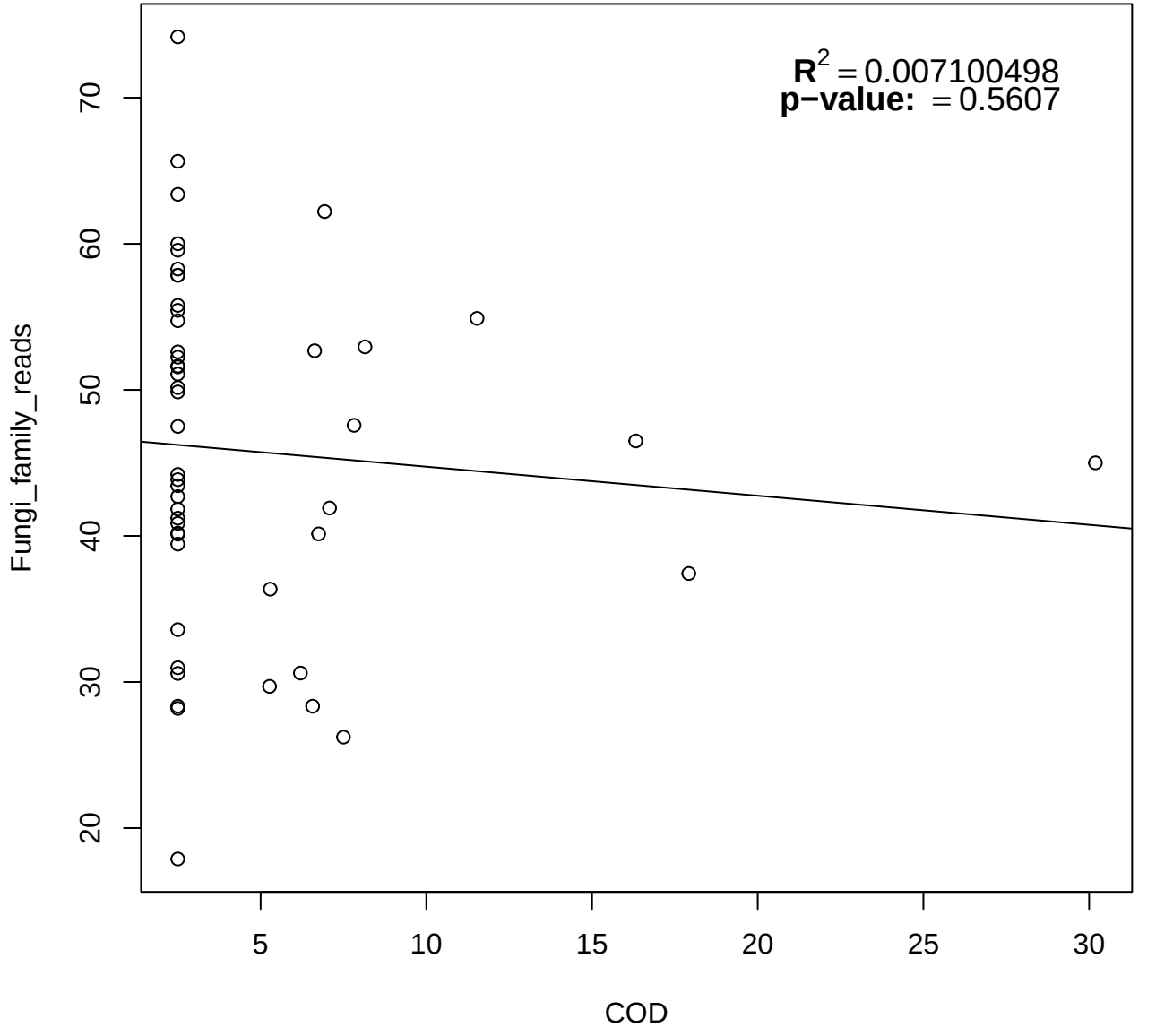

Residuals vs Fitted
Residuals
Fitted values
HOM1
COV1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
COV1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
LAB1
AVE1
Cook's distance
0.5

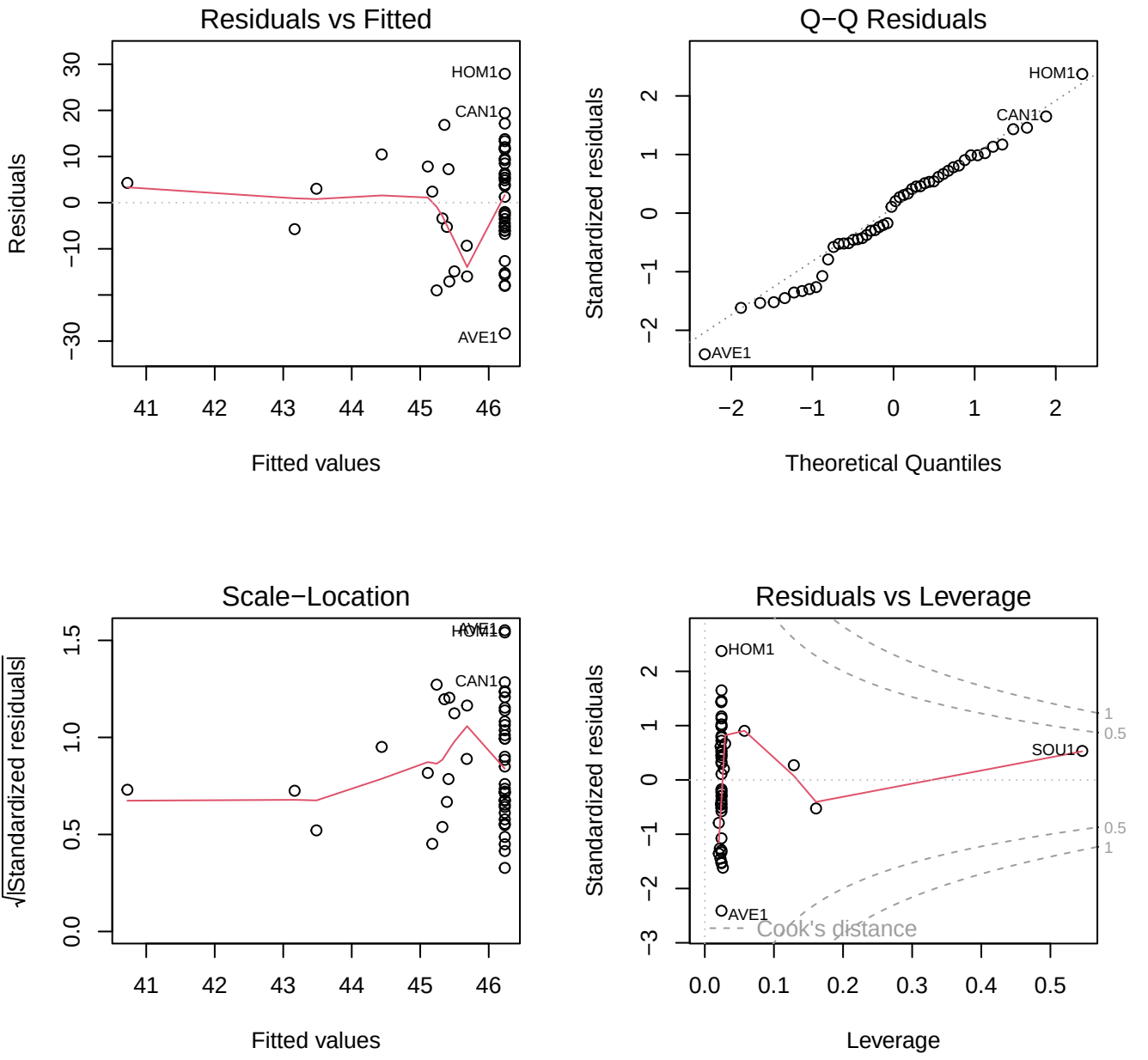

$R^2 = 0.008005226$
p−value: = 0.5366
Fungi_family_reads
ihf
20
30
40
50
60
70
30
40
50
60
70

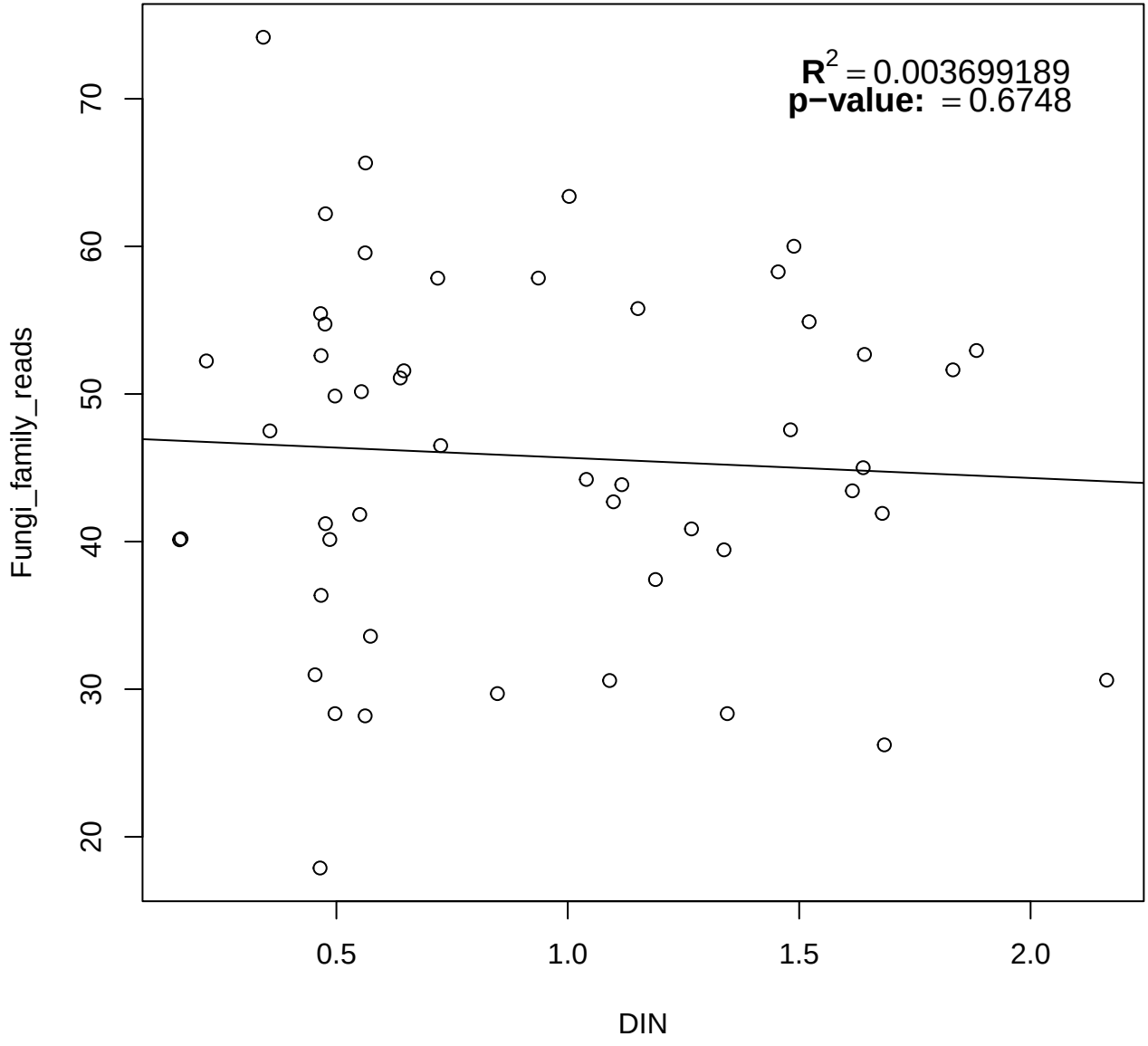

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
CAN1
MACI1
AVE1
Cook's distance
0.5
0.5

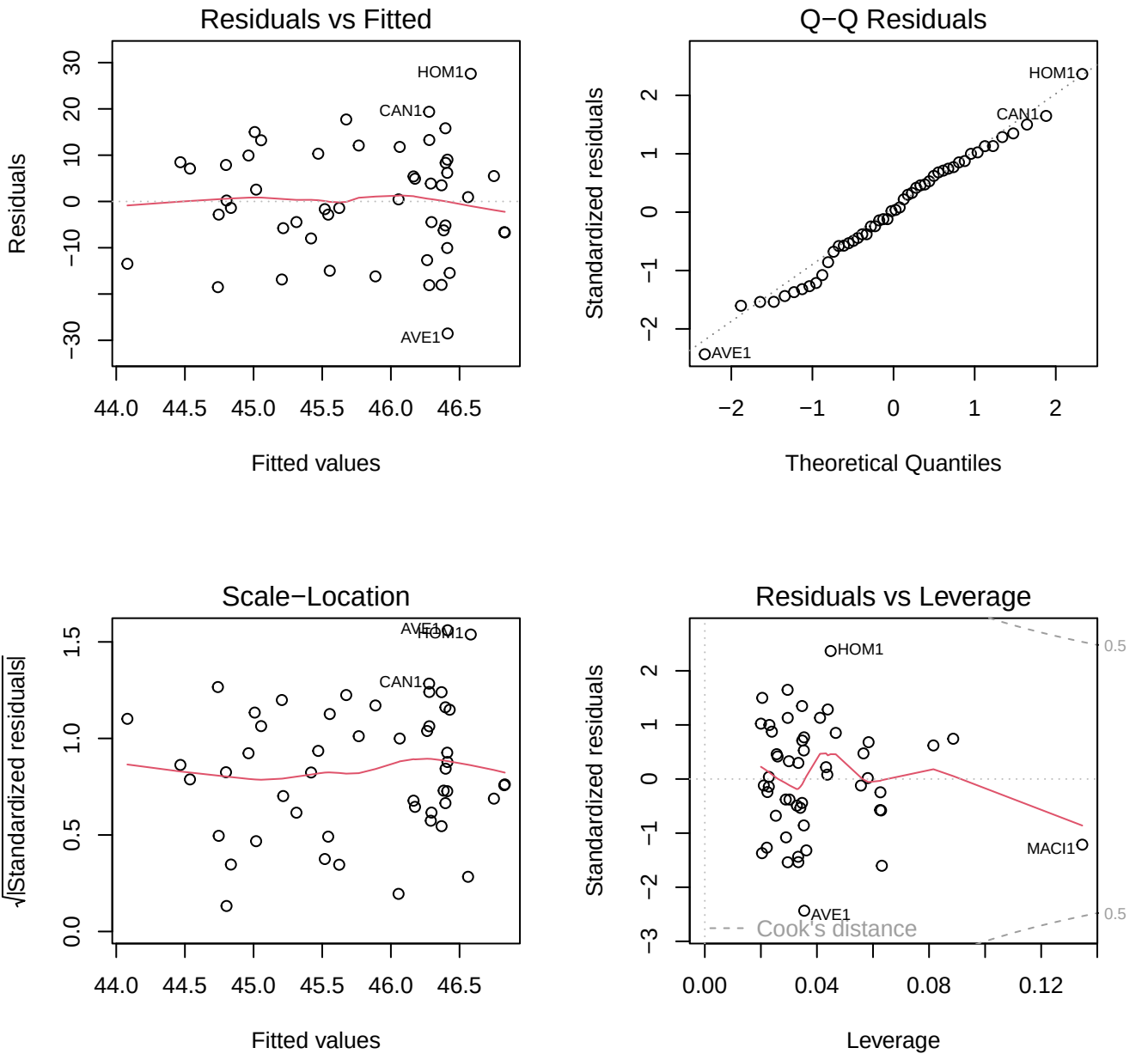

$R^2 = 2.927916e-06$
p−value: = 0.9906
Fungi_family_reads
shadow
20
30
40
50
60
70
−2
0
2

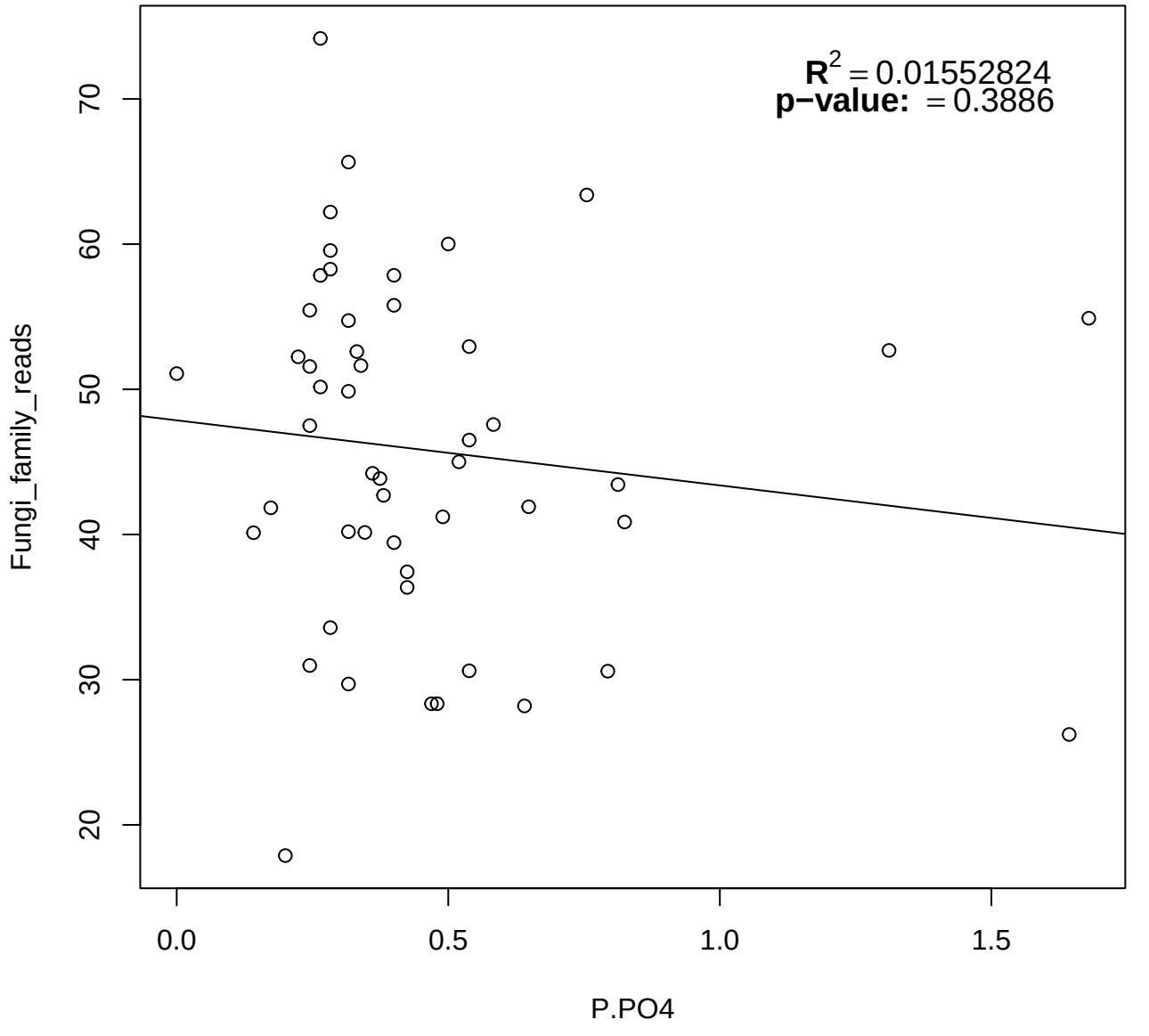

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
MACI1
AVE1
Cook's distance

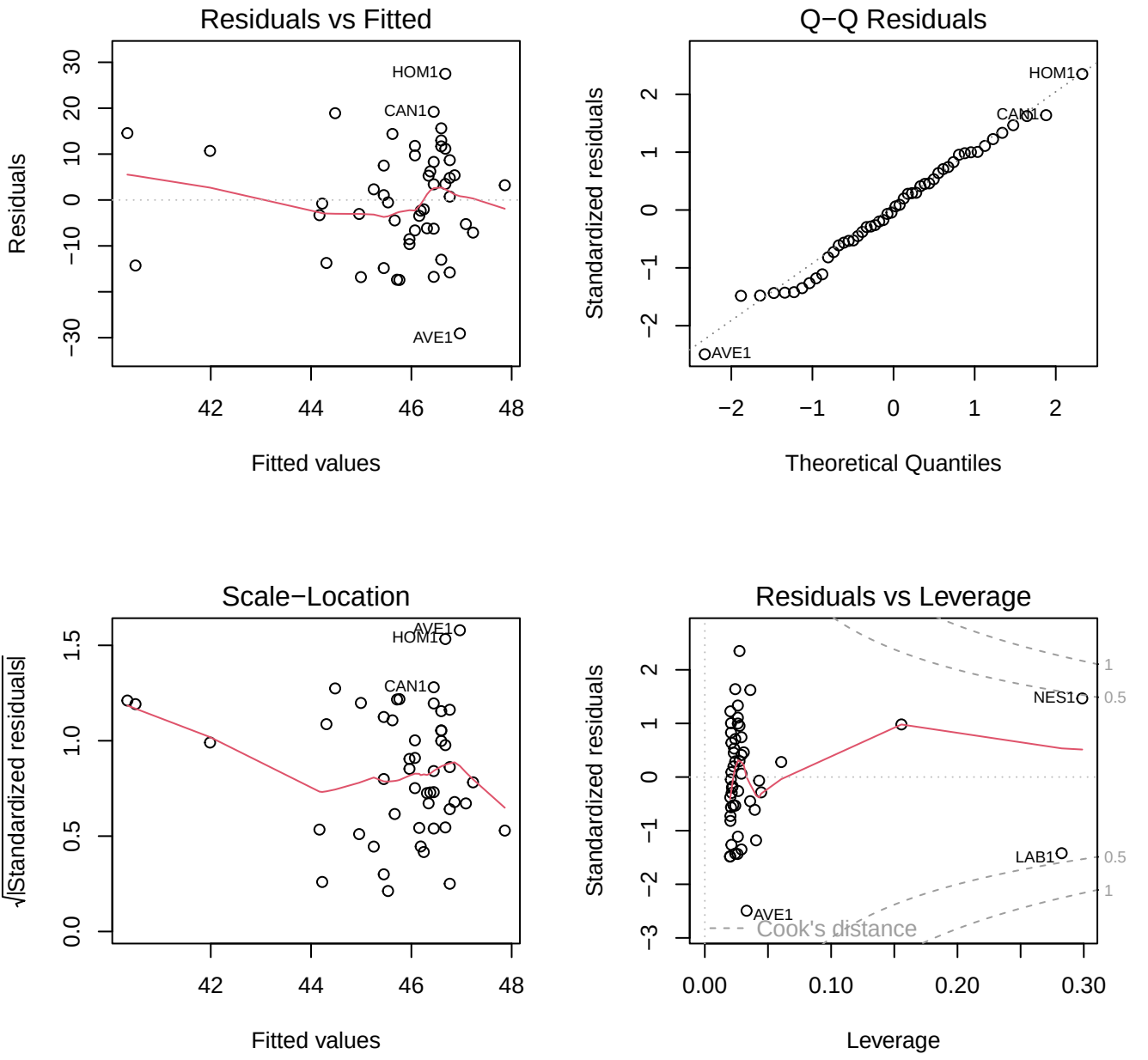

$R^2 = 0.007100498$
p−value: = 0.5607
Fungi_family_reads
COD
20
30
40
50
60
70
5
10
15
20
25
30

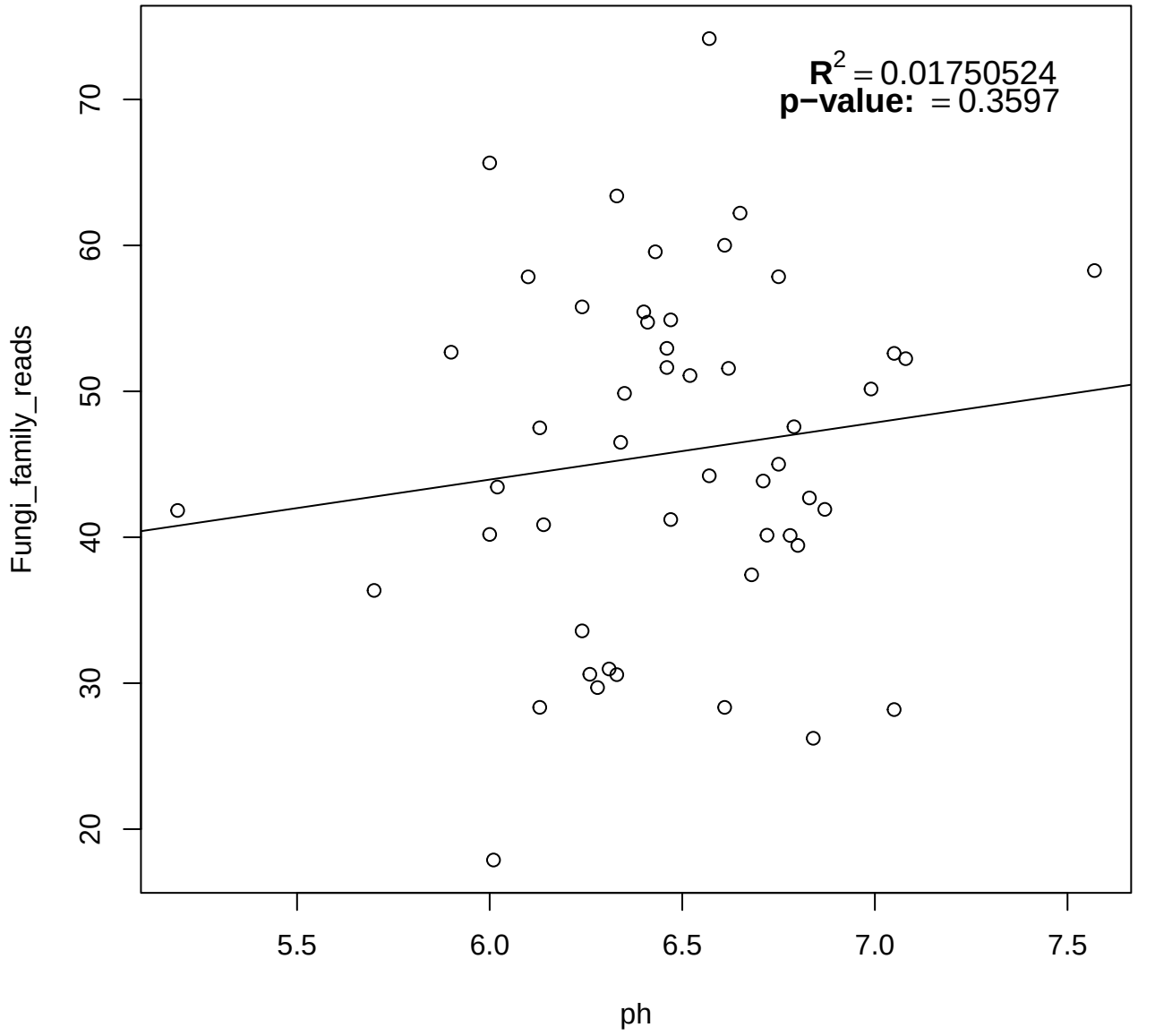

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
CAN1
AVE1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
SOU1
AVE1
Cook's distance
1
0.5
0.5
1

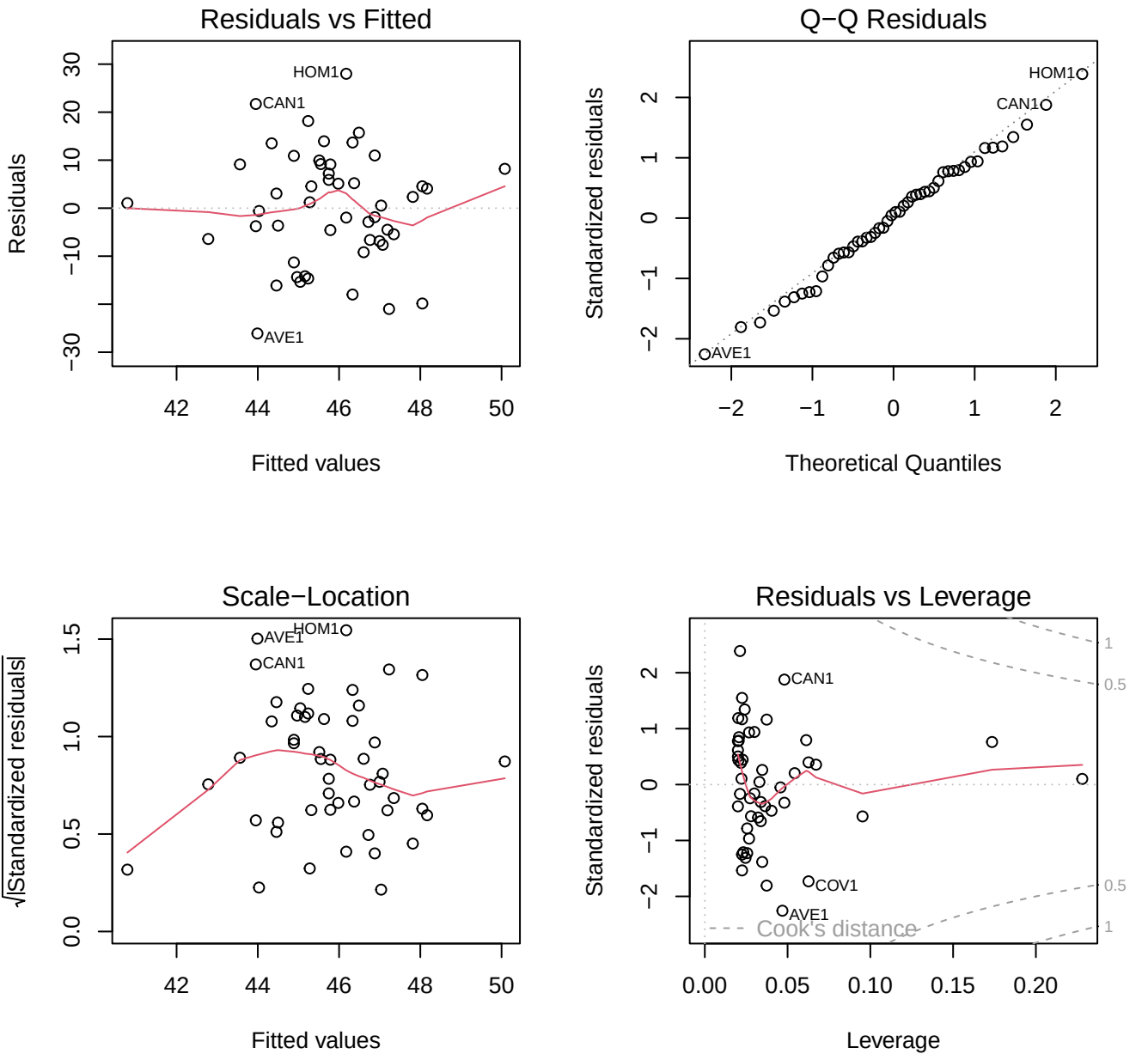

$R^2 = 0.003699189$
p−value: = 0.6748
Fungi_family_reads
20
30
40
50
60
70
0.5
1.0
1.5
2.0
DIN

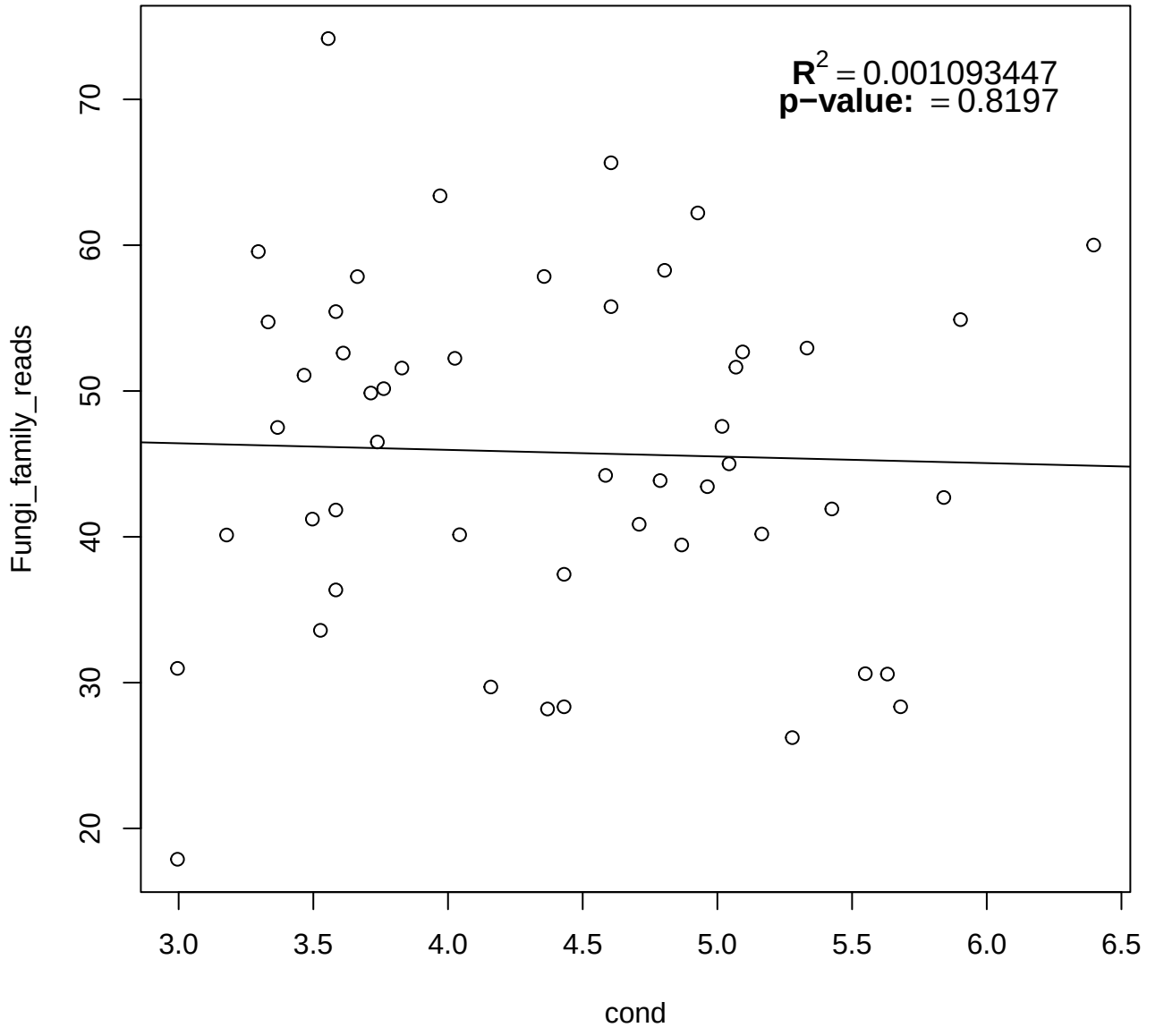

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
MACI1
AVE1
Cook's distance
0.5
0.5

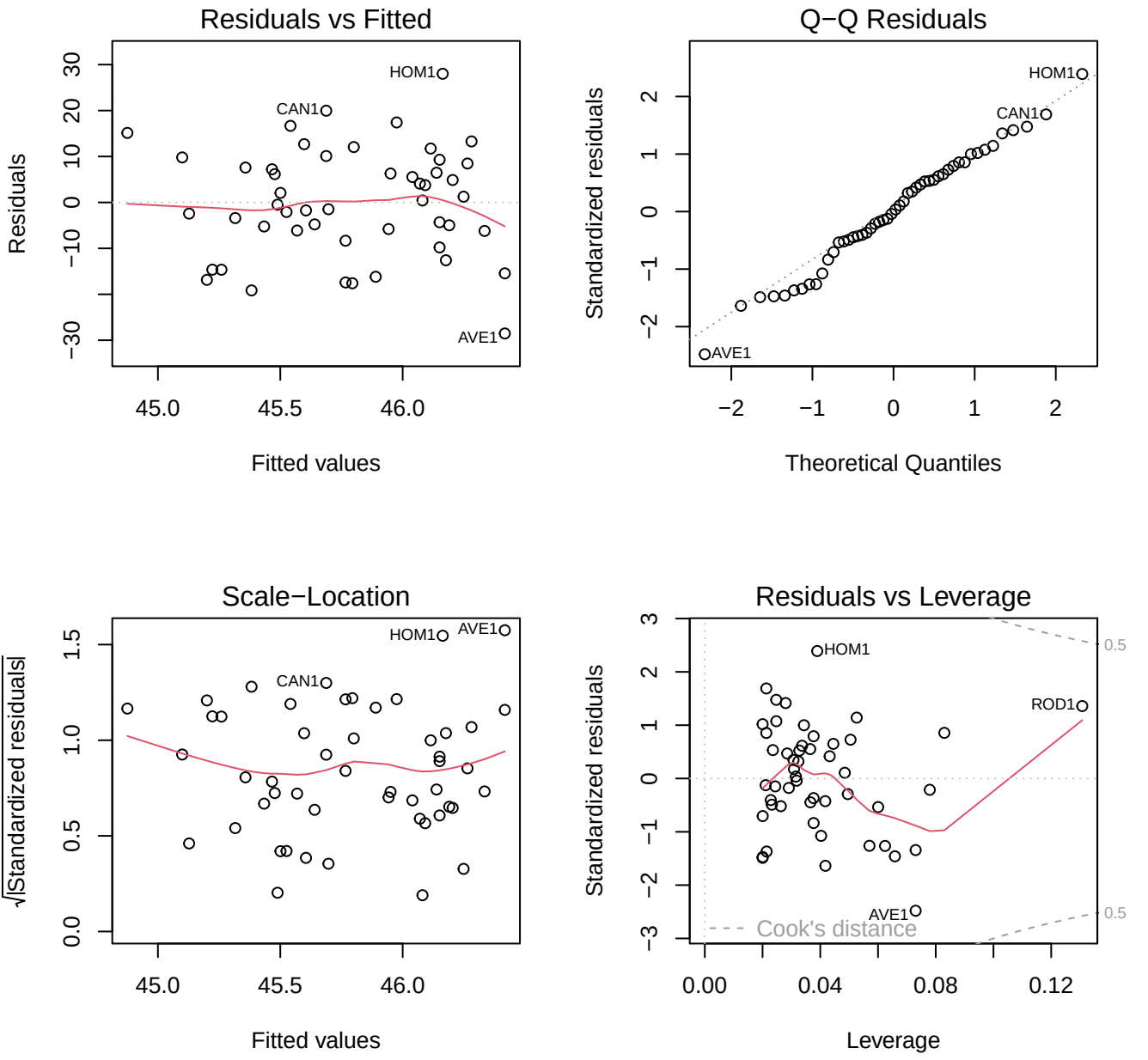

$R^2 = 0.01552824$
p−value: = 0.3886
Fungi_family_reads
P.PO4
20
30
40
50
60
70
0.0
0.5
1.0
1.5

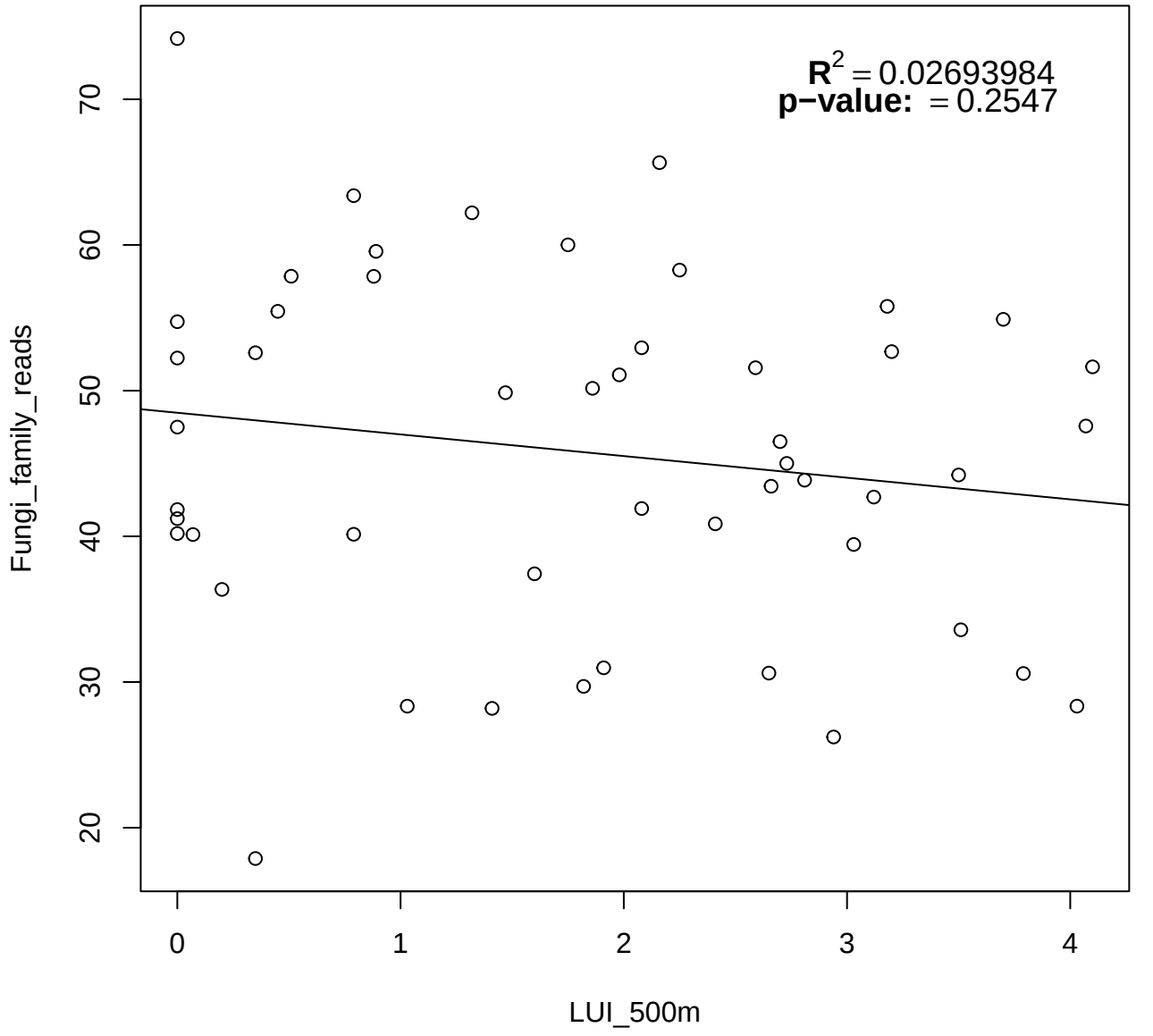

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
NES1
LAB1
AVE1
Cook's distance

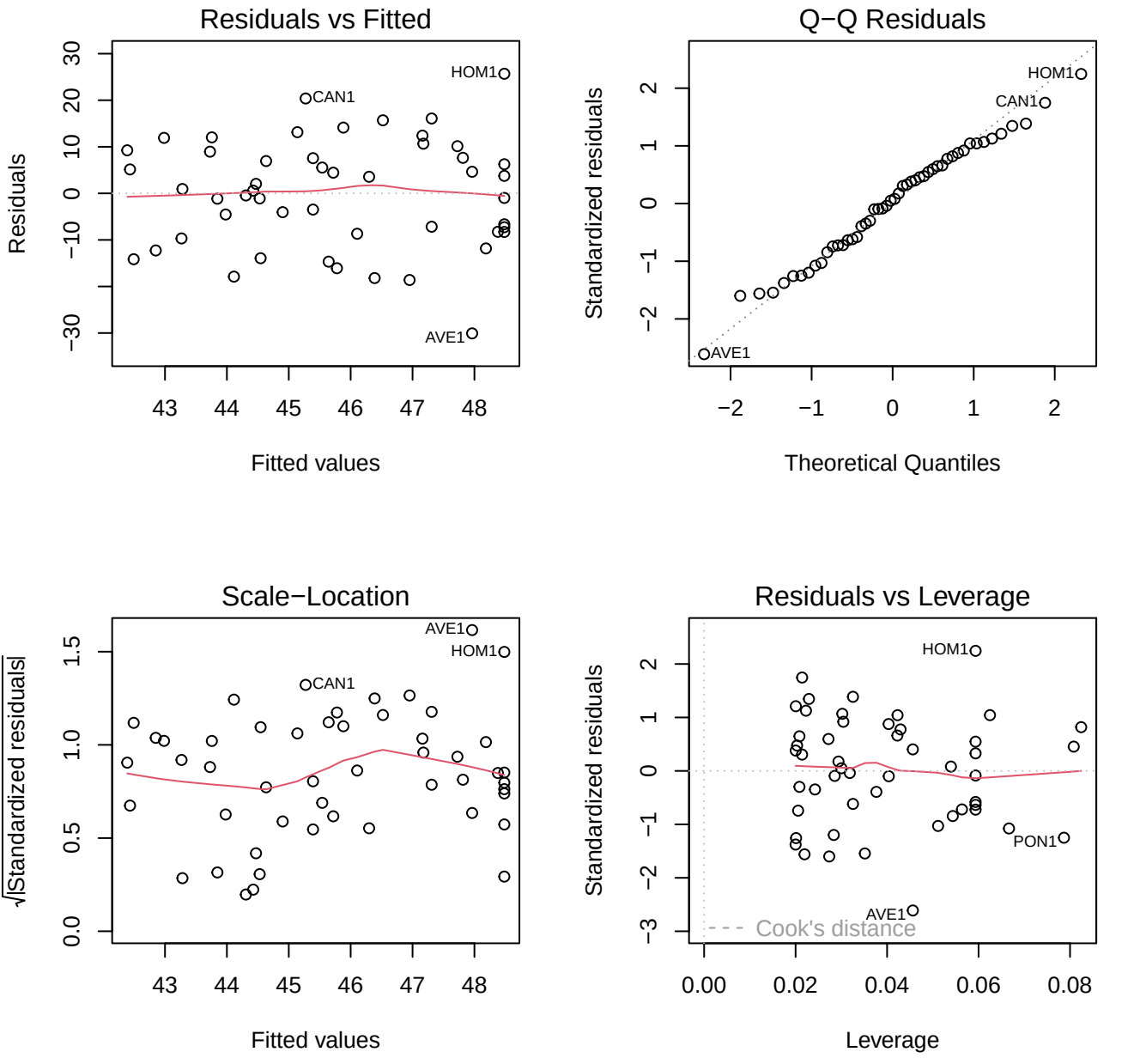

$R^2 = 0.01750524$
p−value: = 0.3597
Fungi_family_reads
ph
20
30
40
50
60
70
5.5
6.0
6.5
7.0
7.5

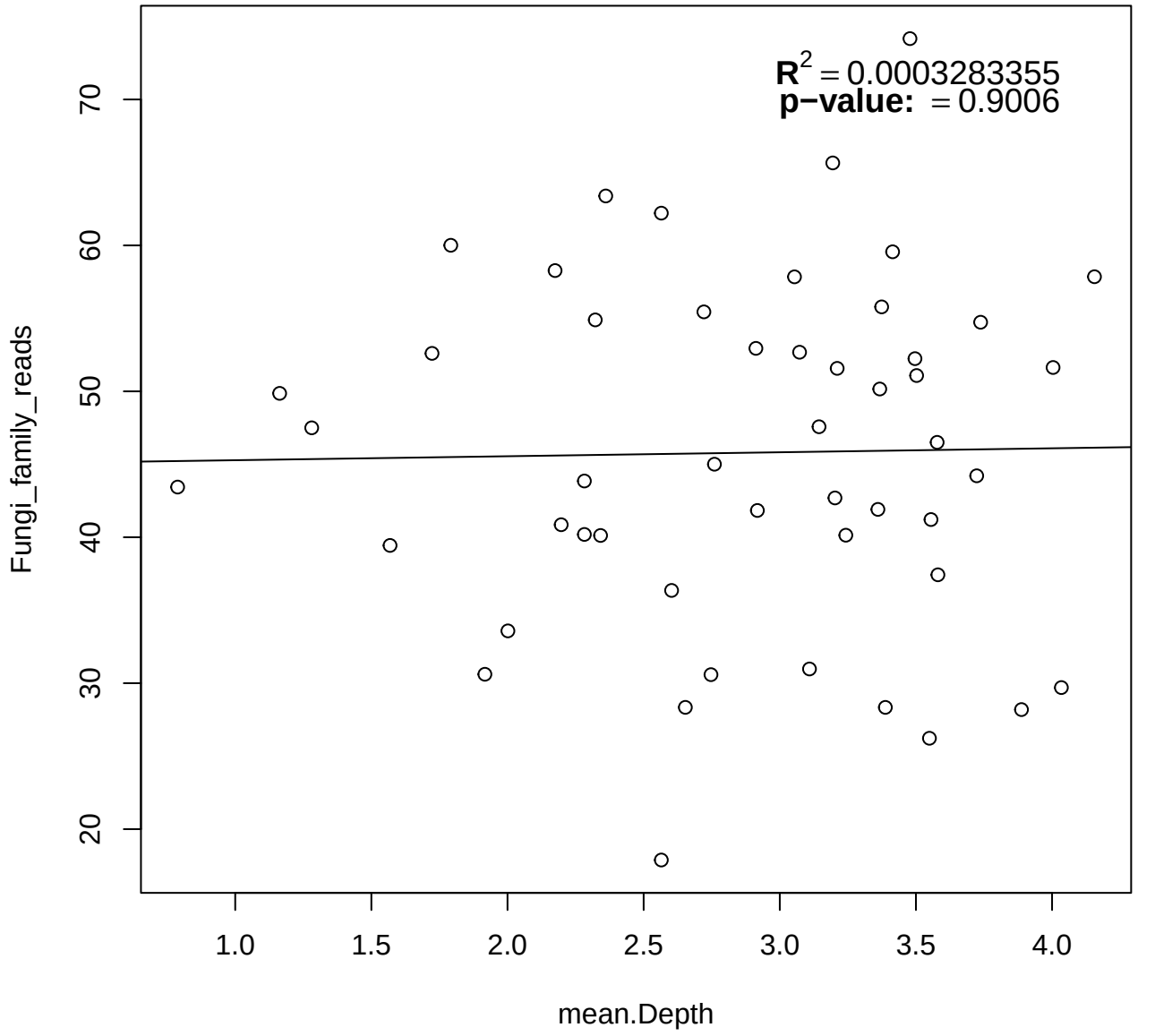

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
CAN1
COV1
AVE1
Cook's distance

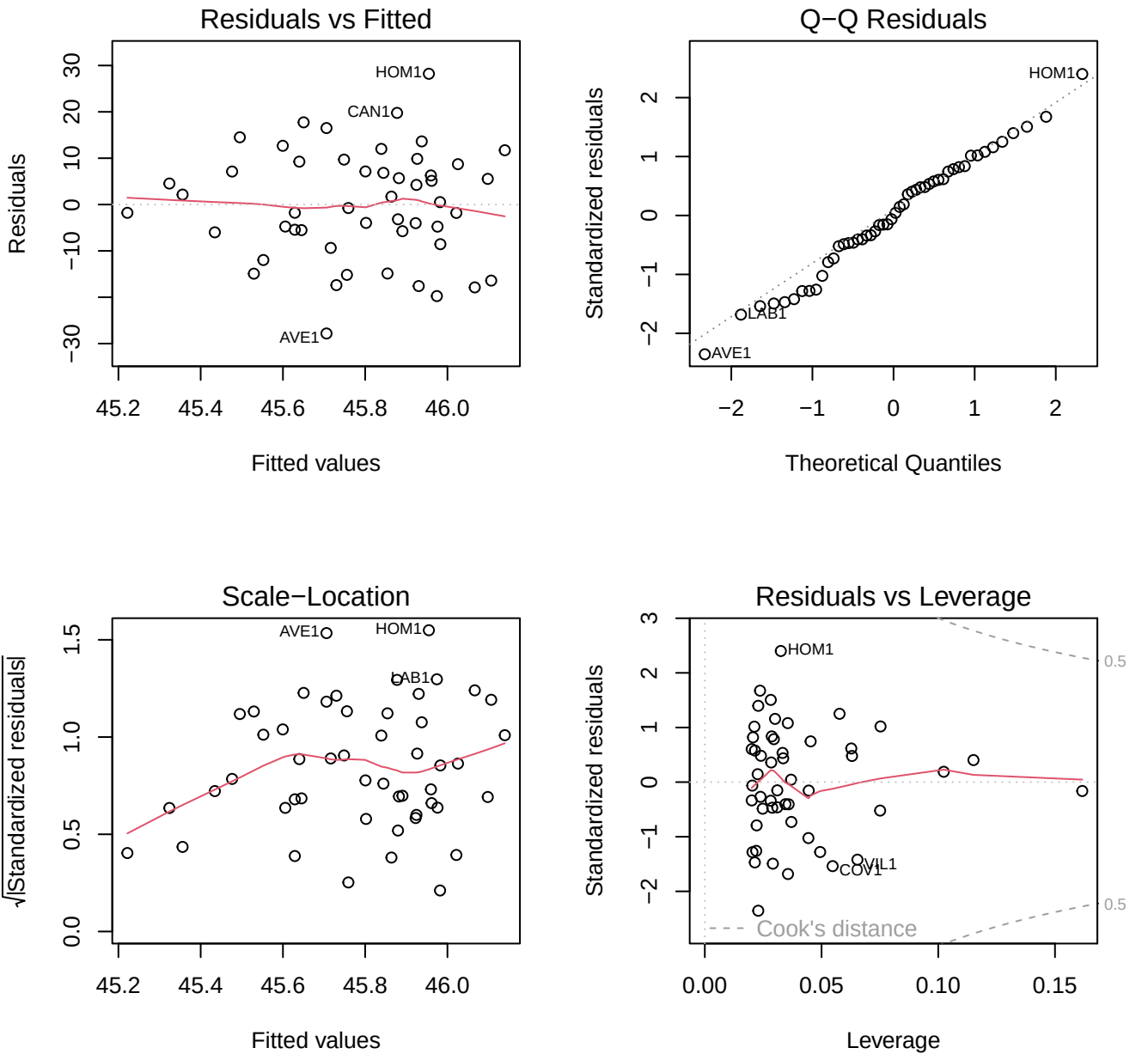

$R^2 = 0.001093447$
p−value: = 0.8197
Fungi_family_reads
cond
20
30
40
50
60
70
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5

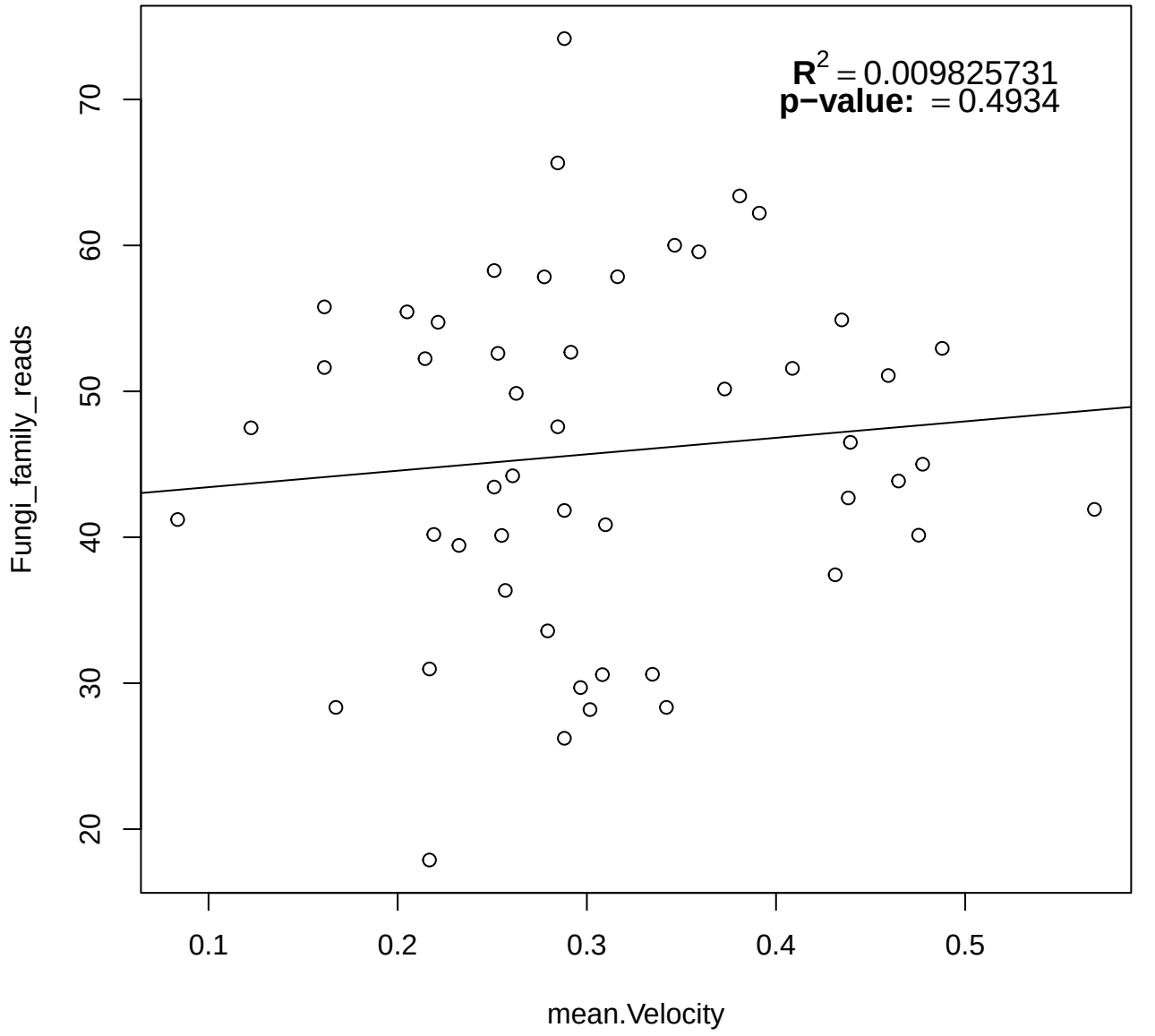

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
ROD1
AVE1
Cook's distance
0.5
0.5

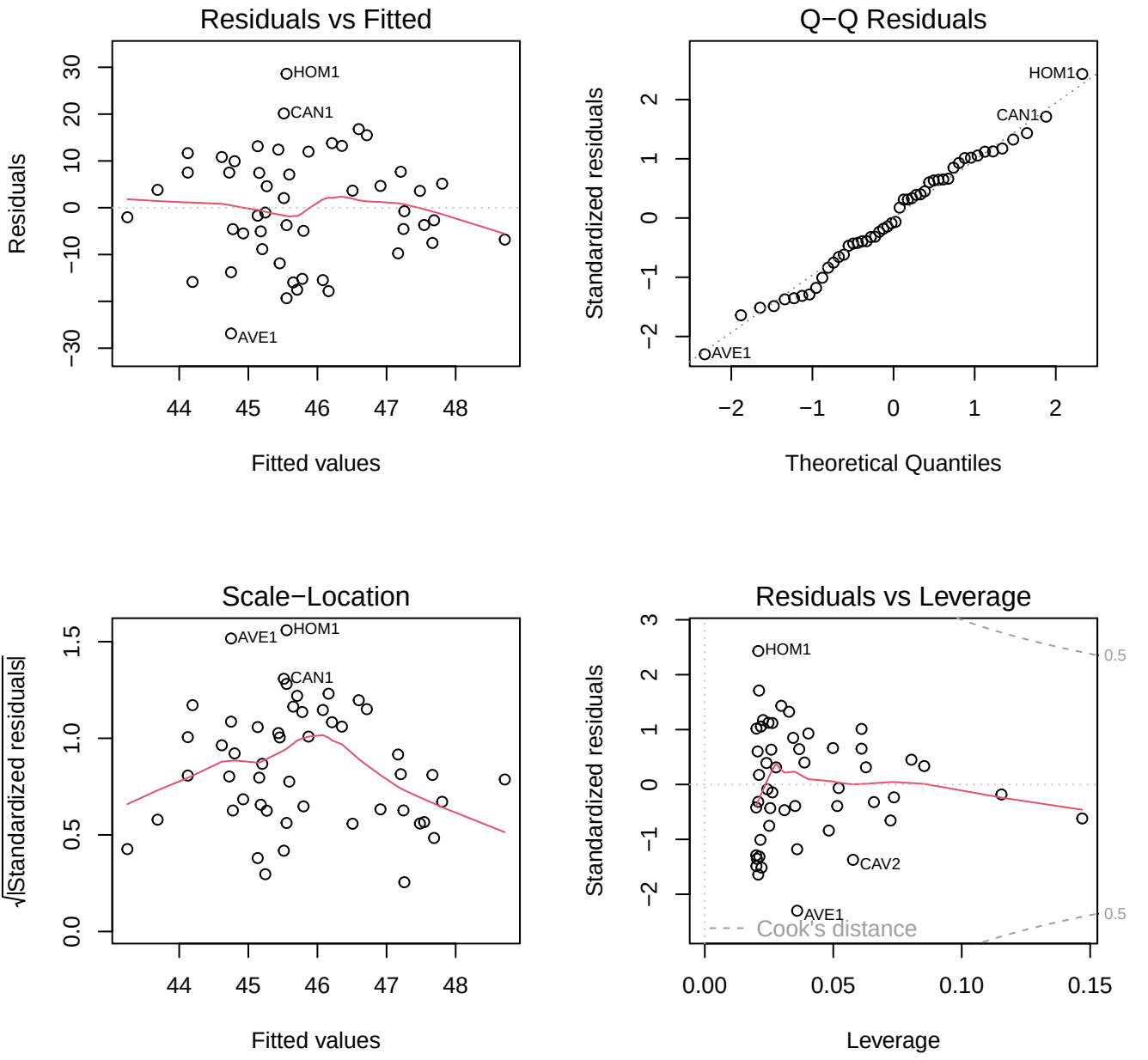

$R^2 = 0.02693984$
p−value: = 0.2547
Fungi_family_reads
LUI_500m
20
30
40
50
60
70
0
1
2
3
4

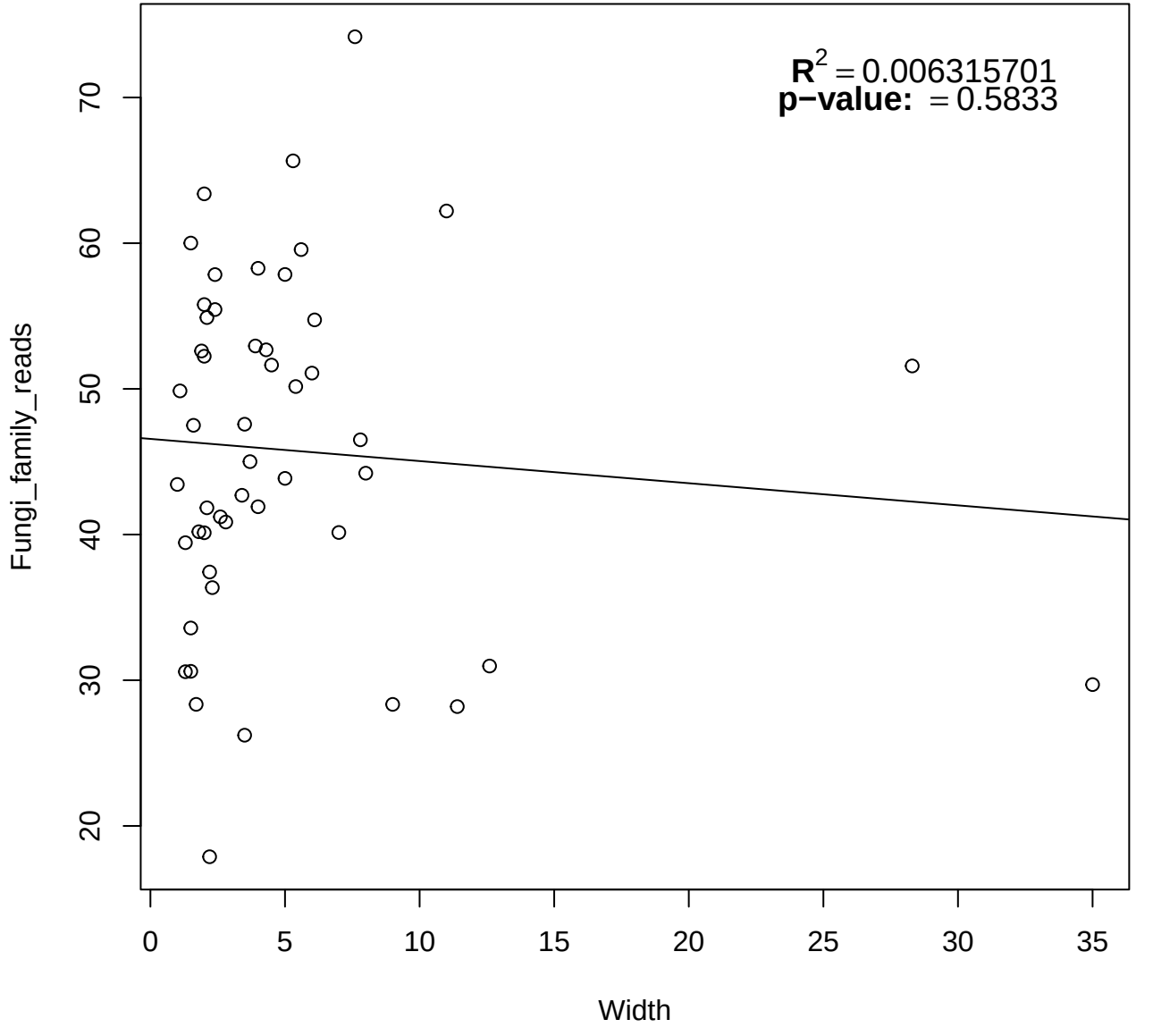

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
PON1
AVE1
Cook's distance

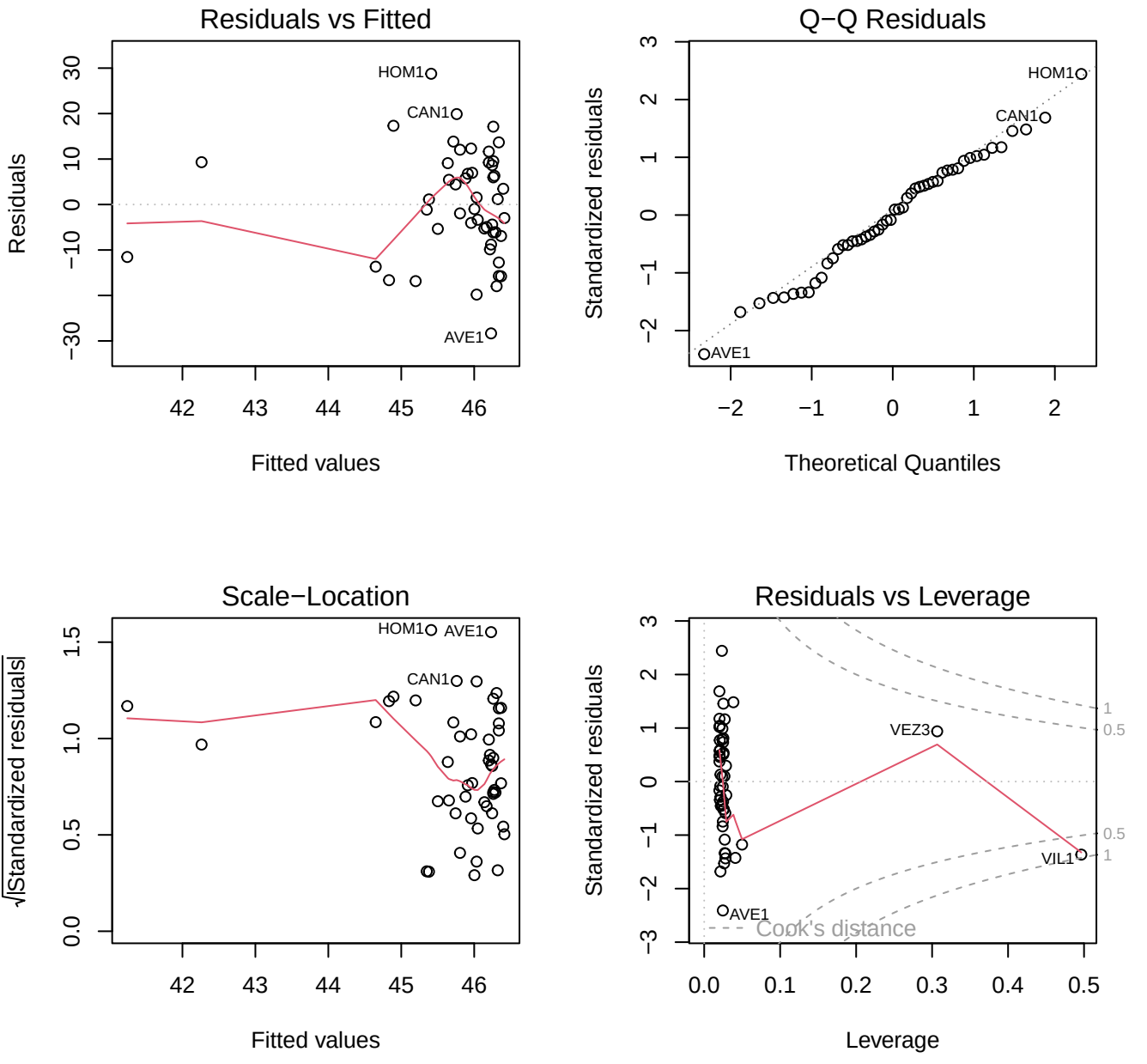

$R^2 = 0.0003283355$
p−value: = 0.9006
Fungi_family_reads
mean.Depth
20
30
40
50
60
70
1.0
1.5
2.0
2.5
3.0
3.5
4.0

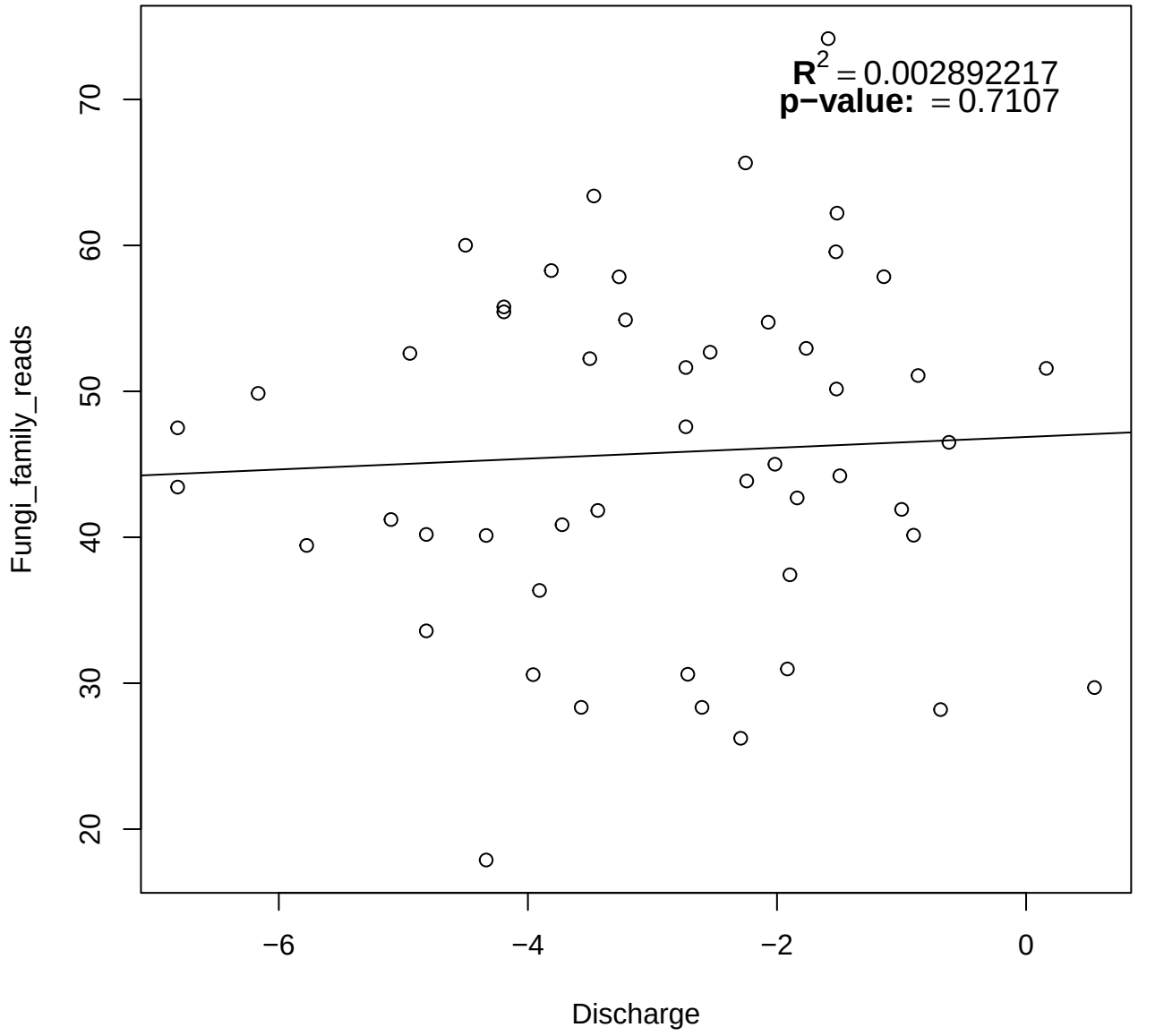

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
COV1
VIL1
Cook's distance
0.5
0.5

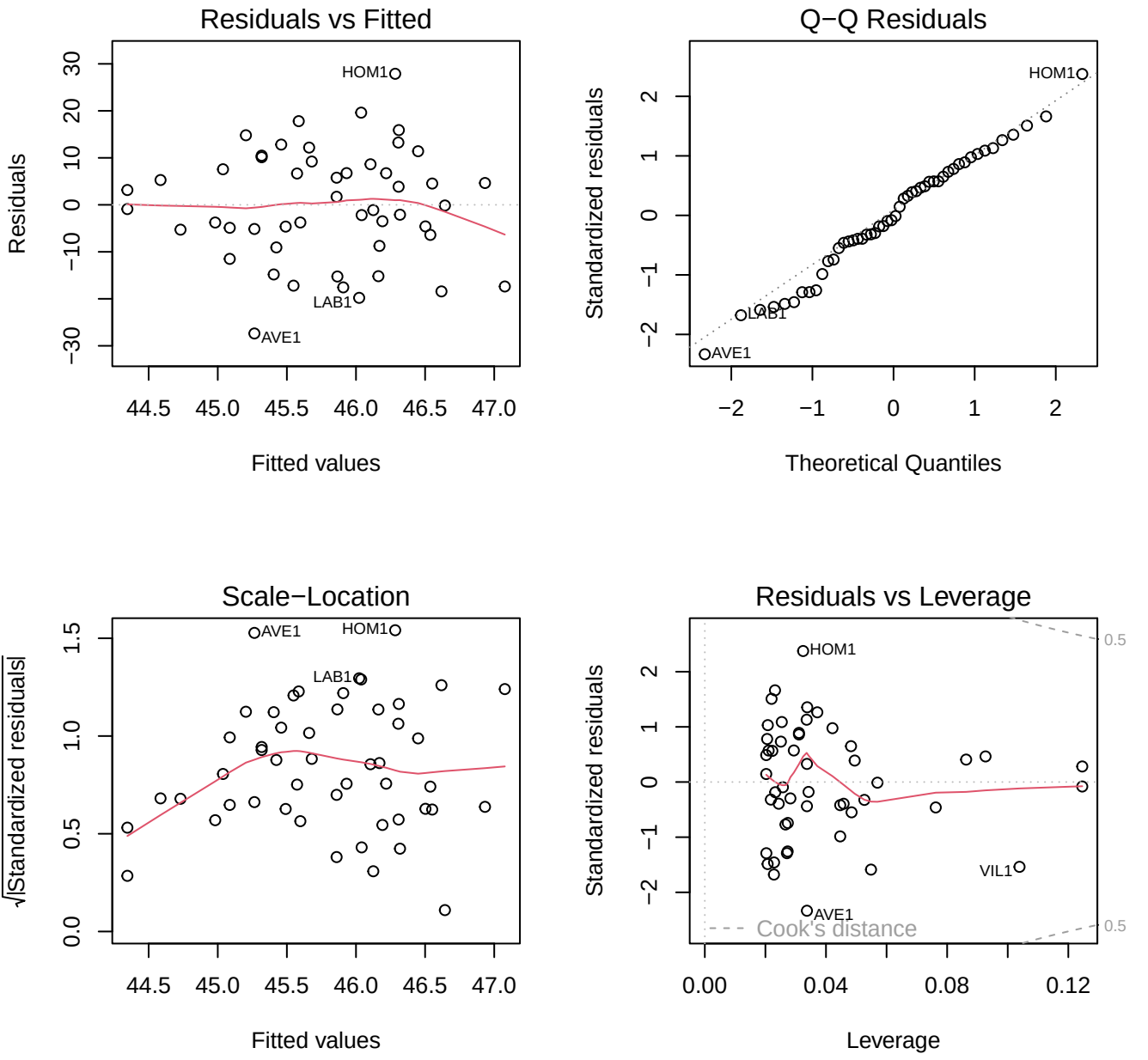

$R^2 = 0.009825731$
p−value: = 0.4934
Fungi_family_reads
mean.Velocity
20
30
40
50
60
70
0.1
0.2
0.3
0.4
0.5

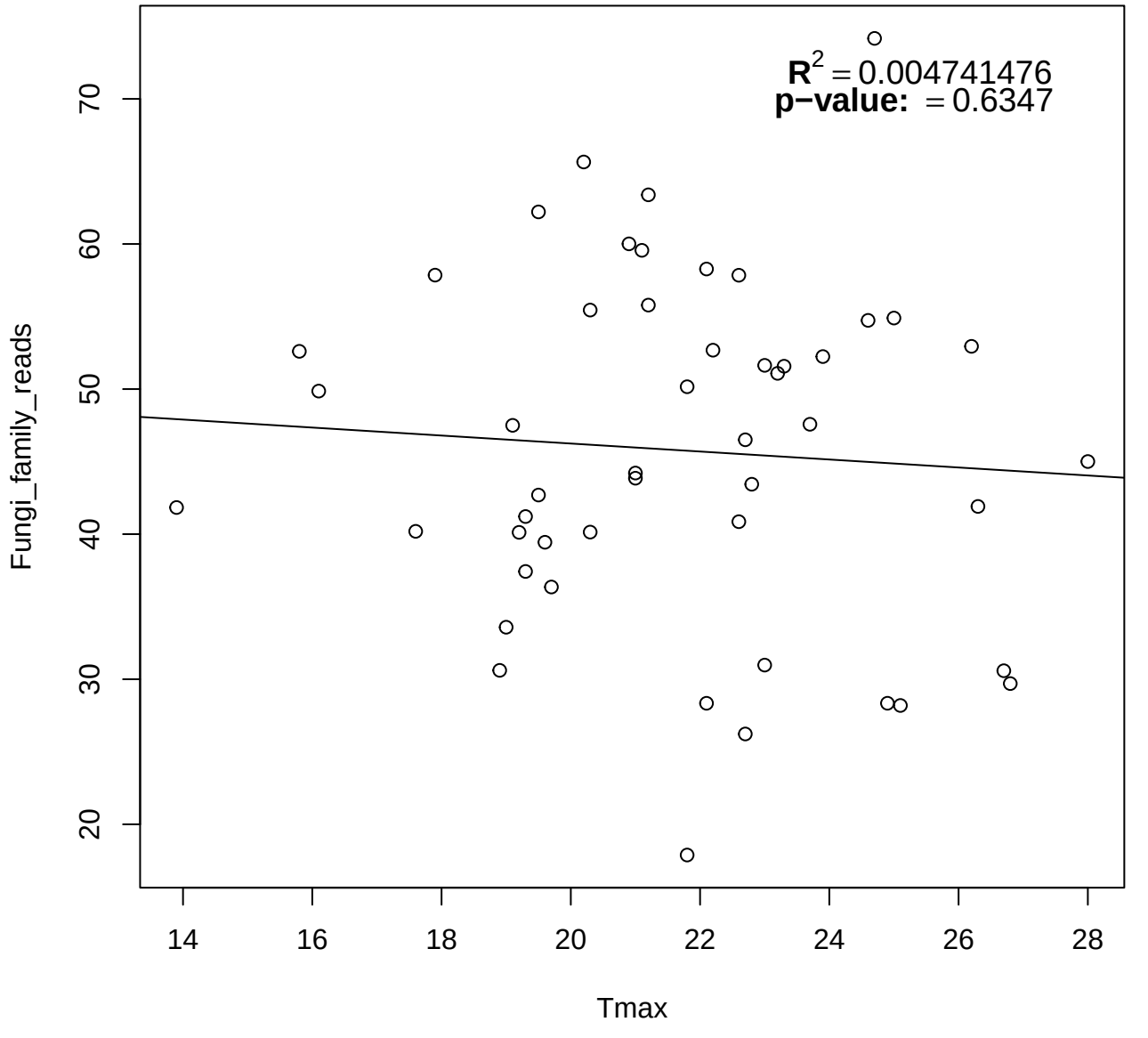

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
CAV2
AVE1
Cook's distance
0.5
0.5

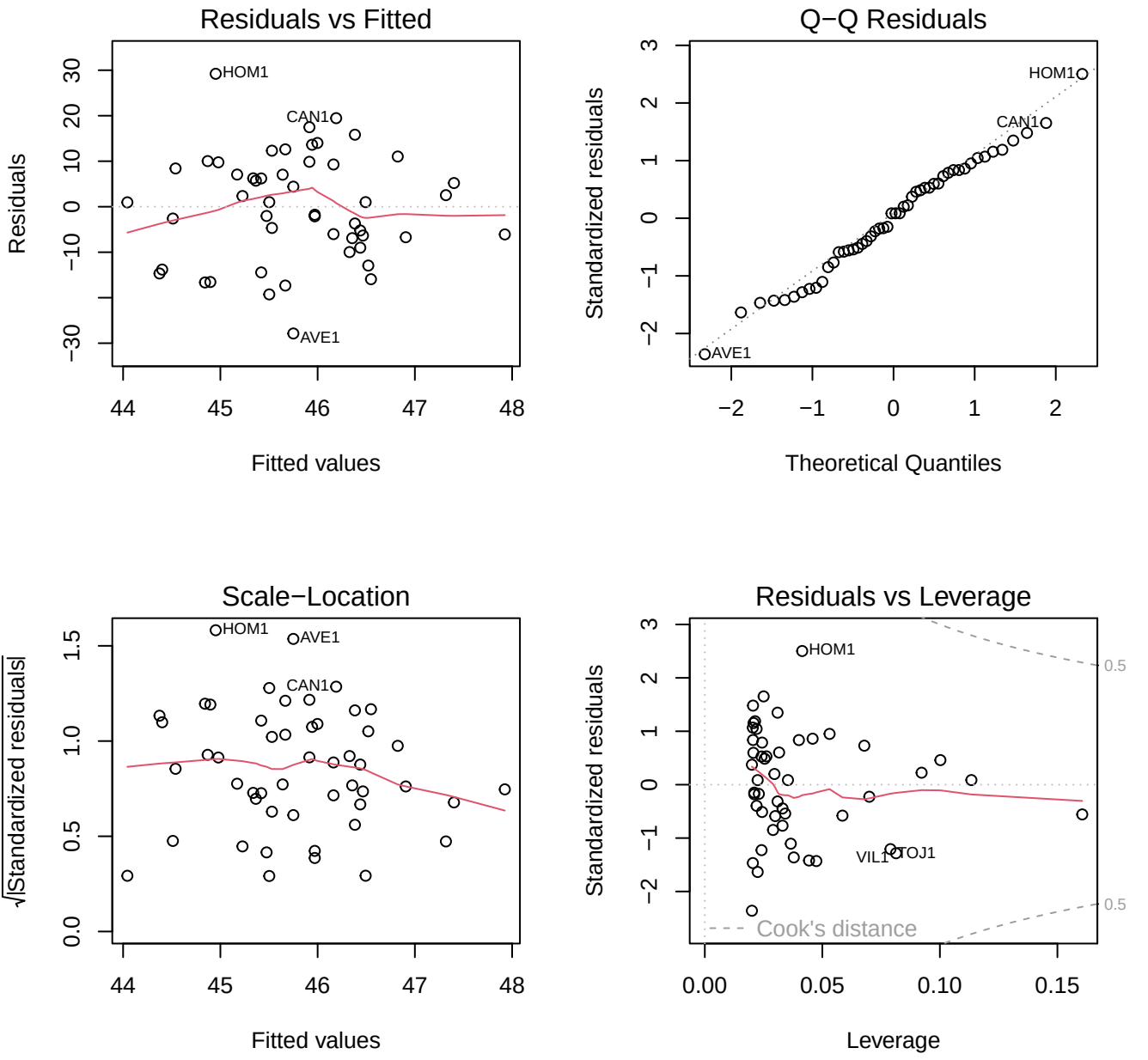

$R^2 = 0.006315701$
p−value: = 0.5833
Fungi_family_reads
Width
20
30
40
50
60
70
0
5
10
15
20
25
30
35

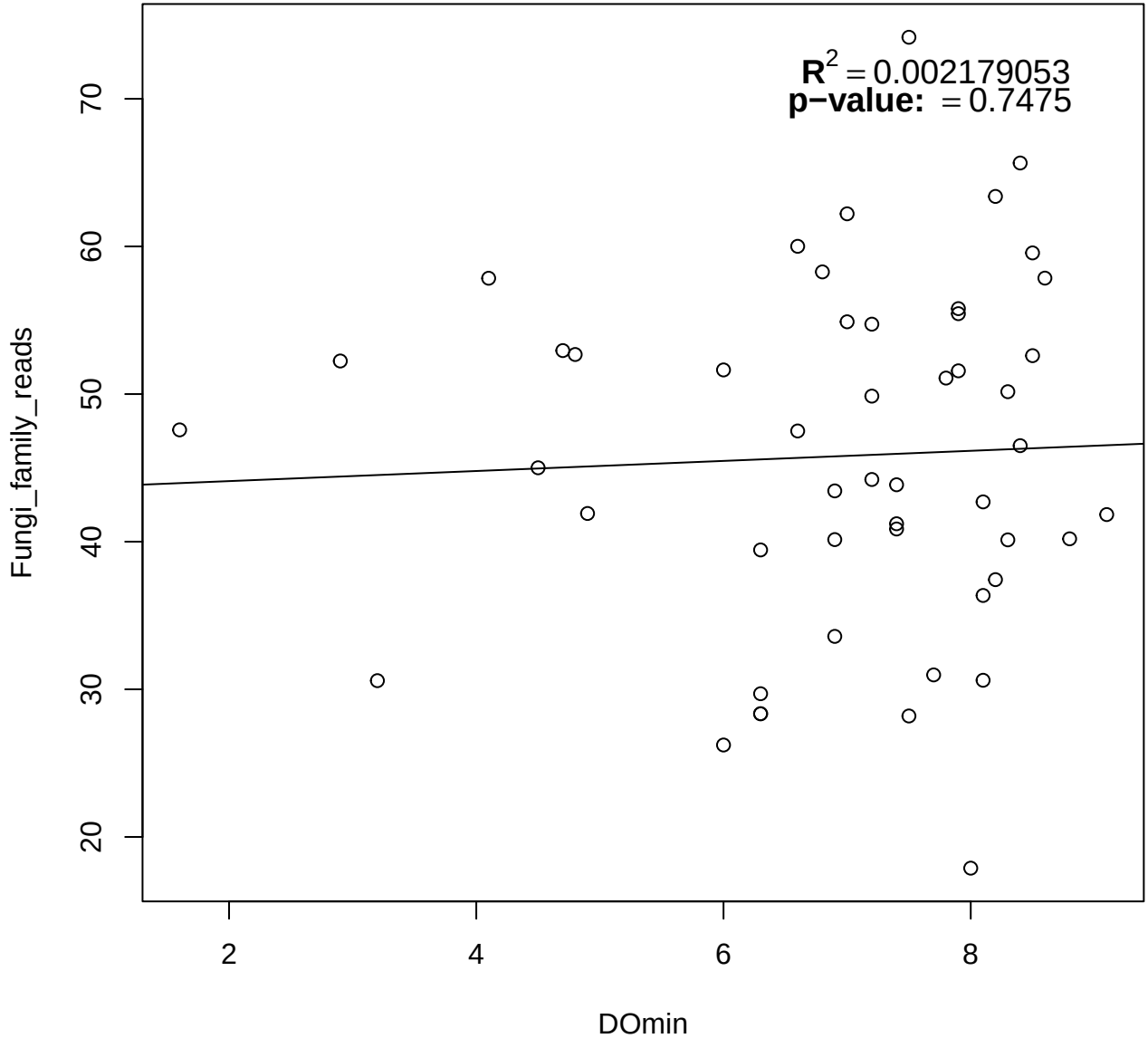

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
VEZ3
VIL1
AVE1
Cook's distance

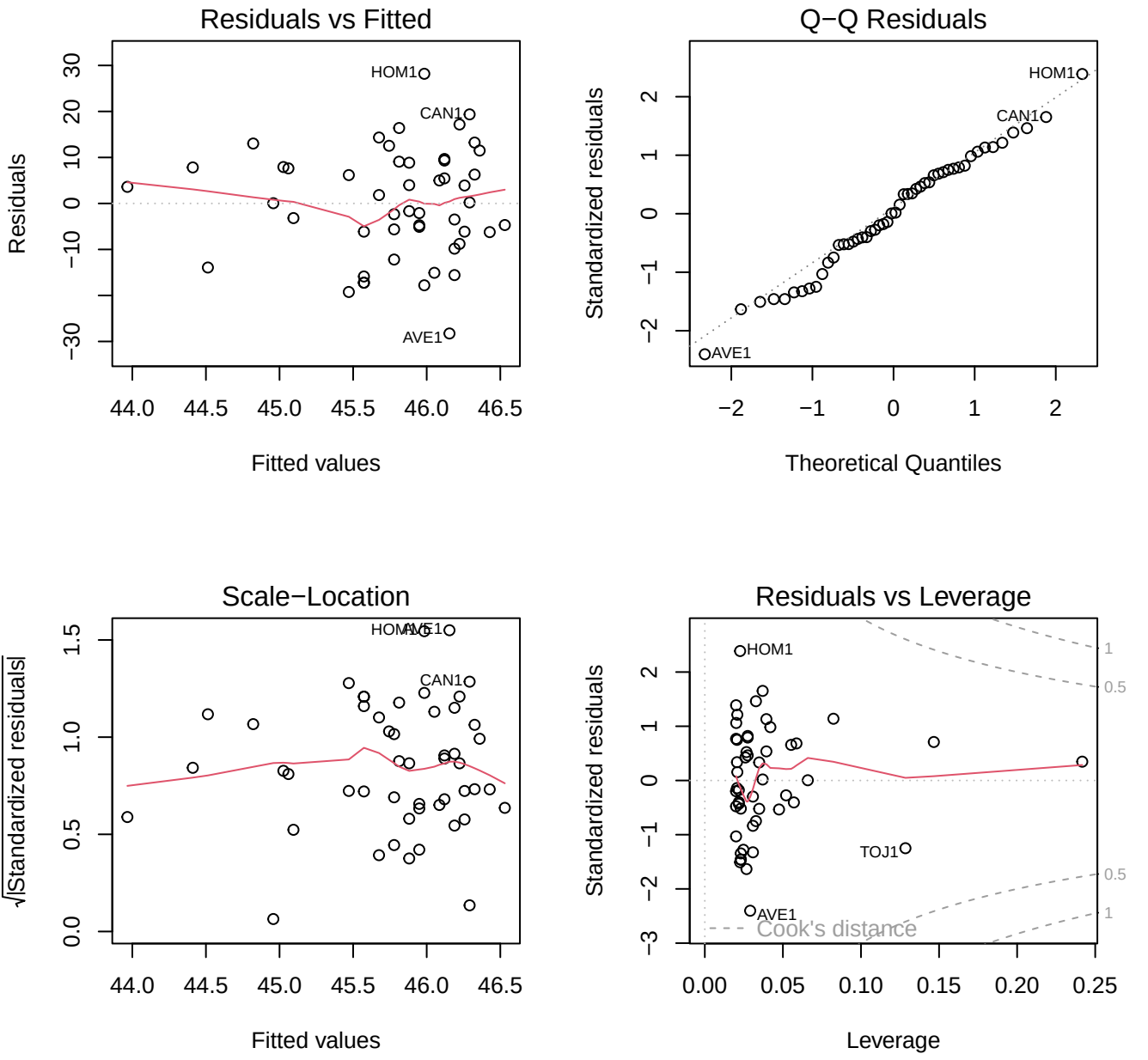

$R^2 = 0.002892217$
p−value: = 0.7107
Fungi_family_reads
Discharge
20
30
40
50
60
70
−6
−4
−2
0

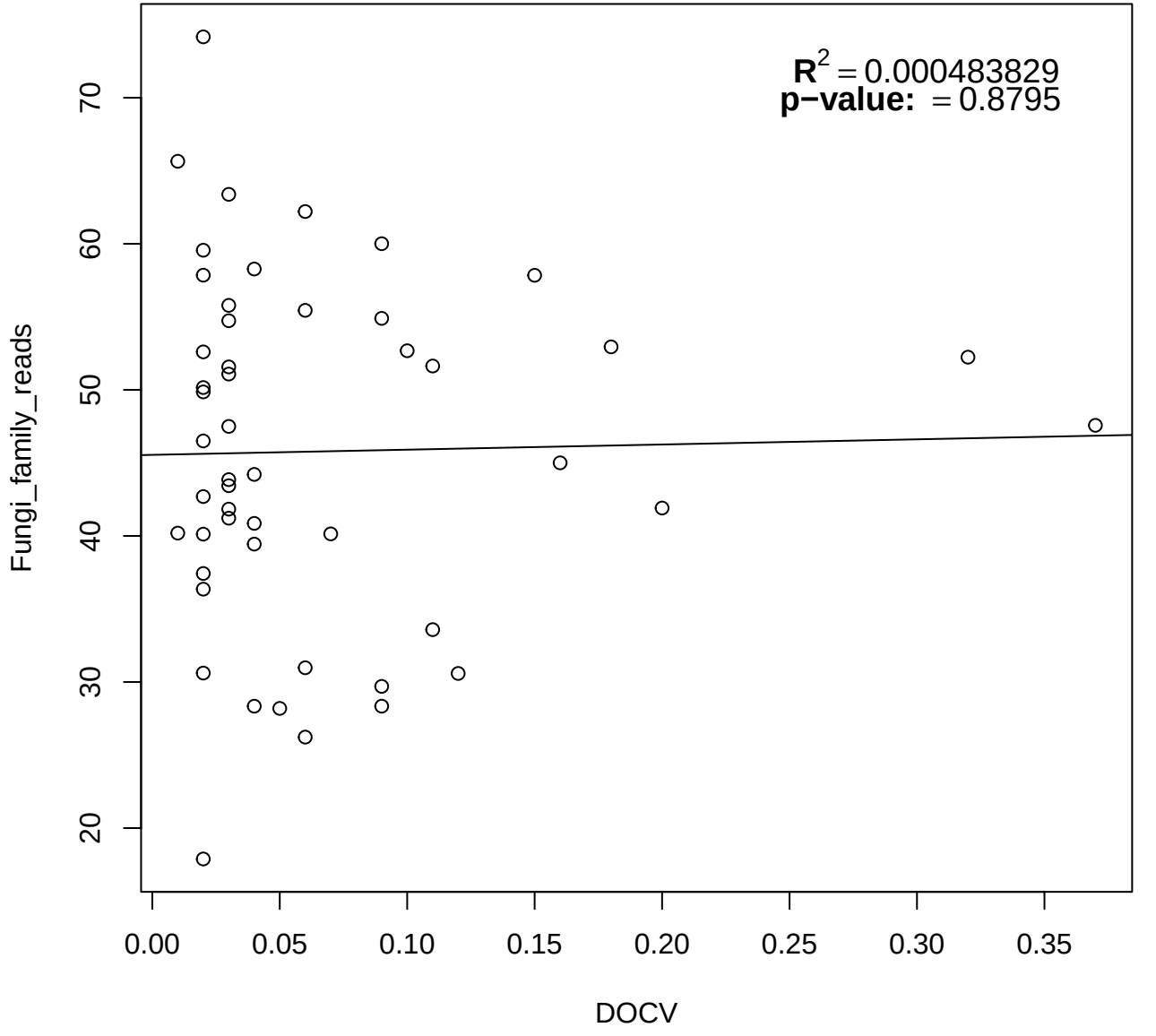

Residuals vs Fitted
Residuals
Fitted values
HOM1
LAB1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
LAB1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
VIL1
AVE1
Cook's distance
0.5
0.5

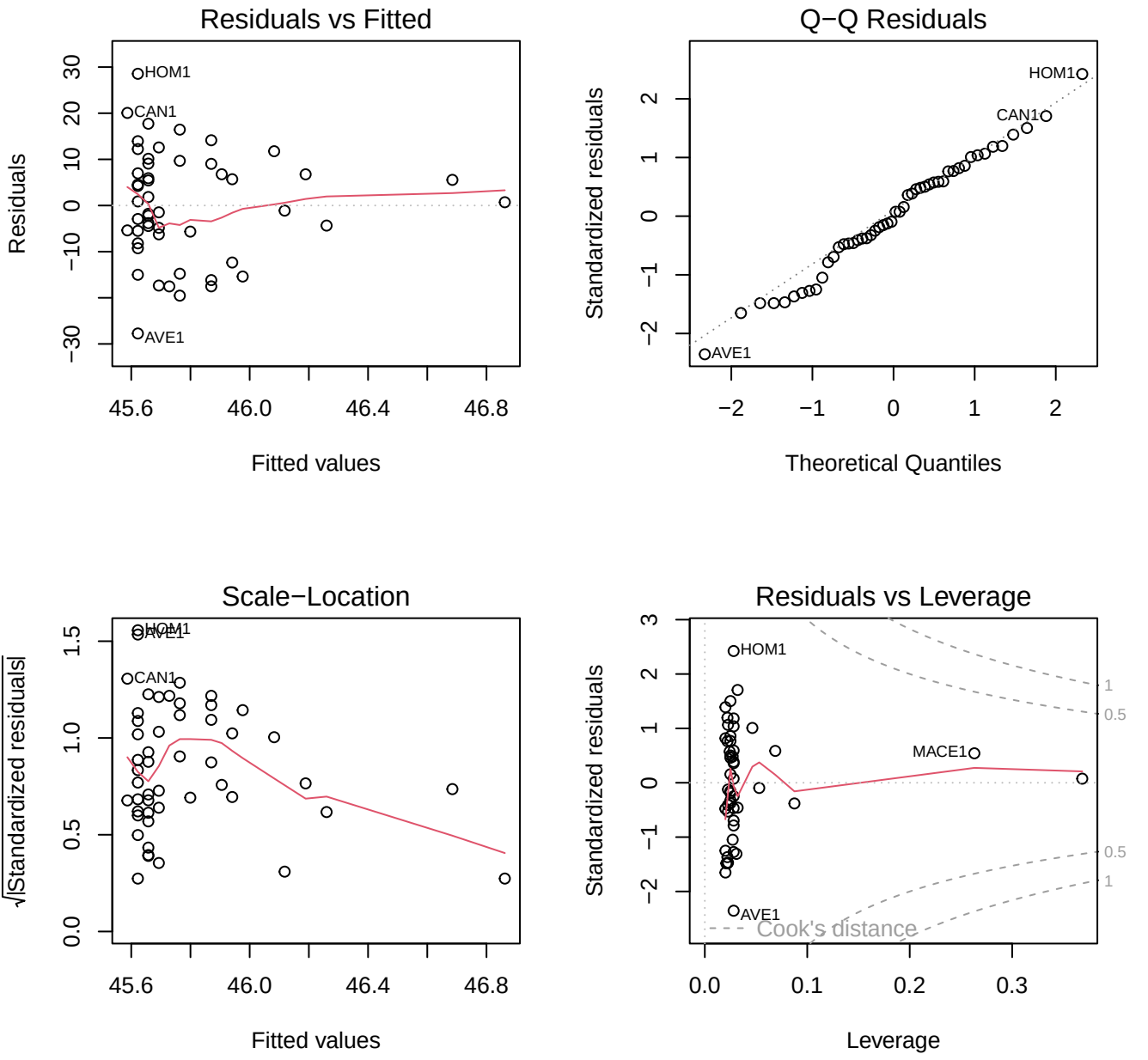

$R^2 = 0.004741476$
p−value: = 0.6347
Fungi_family_reads
Tmax
20
30
40
50
60
70
14
16
18
20
22
24
26
28

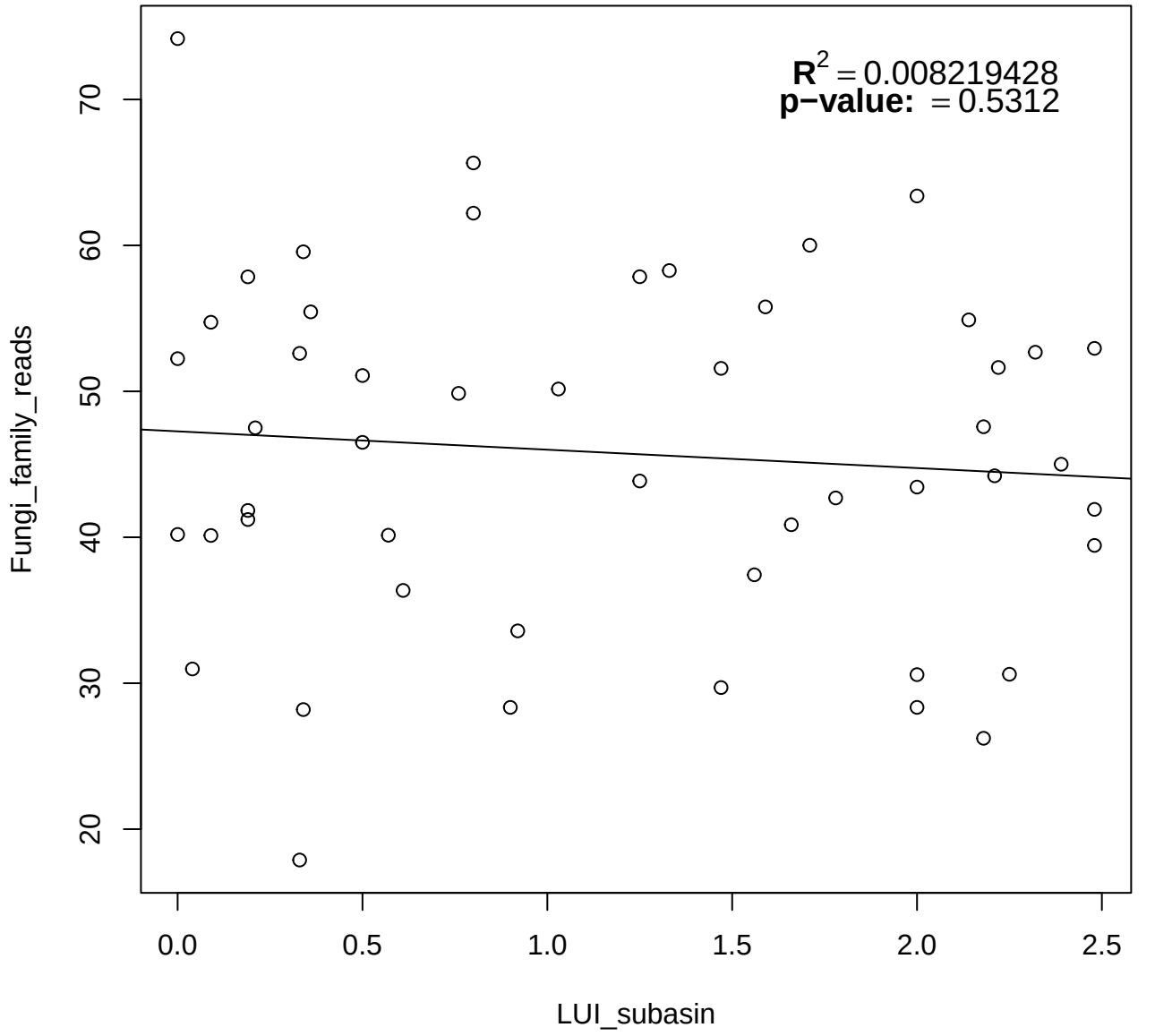

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
VIL1
TOJ1
Cook's distance
0.5
0.5

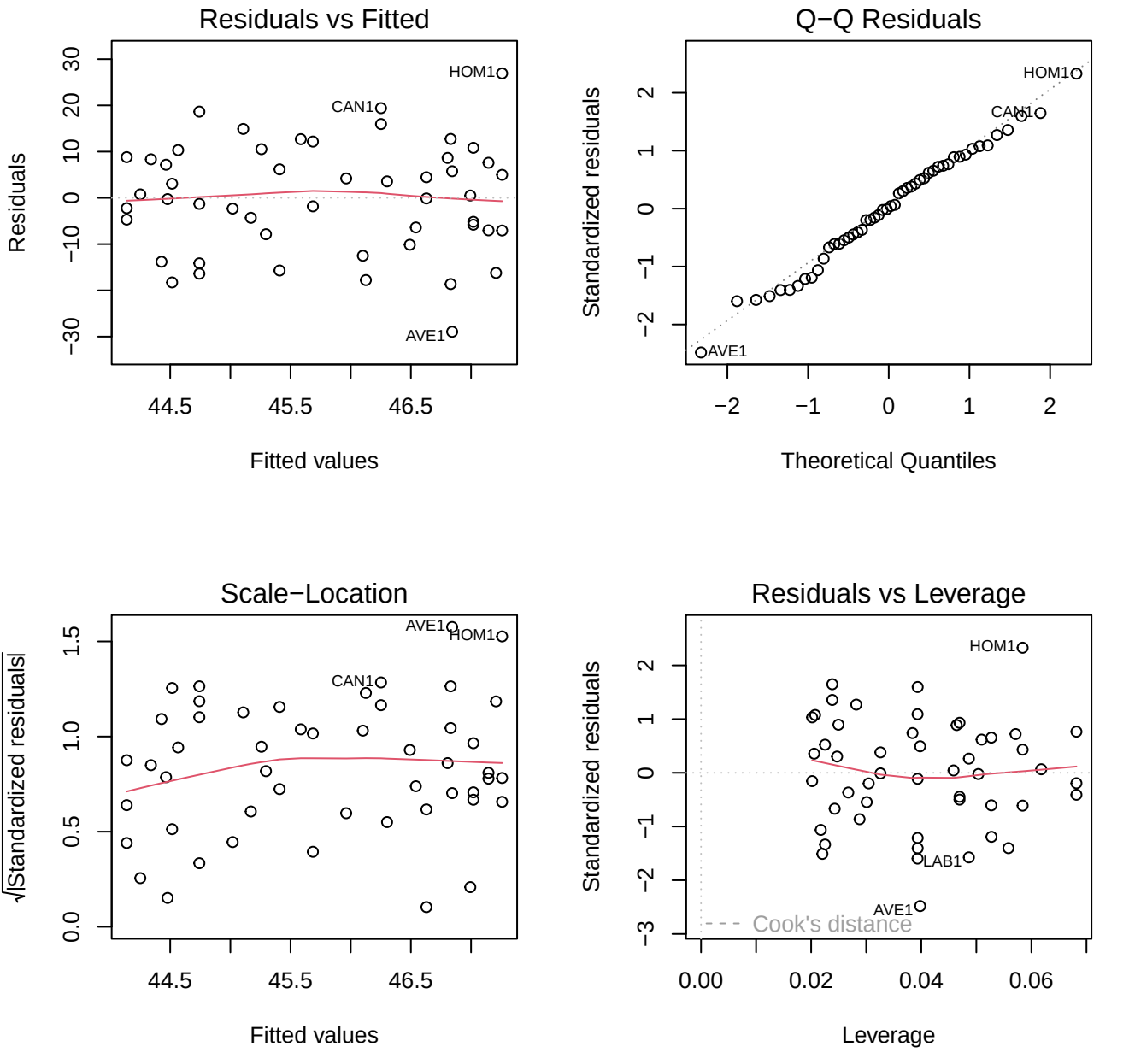

$R^2 = 0.002179053$
p−value: = 0.7475
Fungi_family_reads
DOmin
20
30
40
50
60
70
2
4
6
8

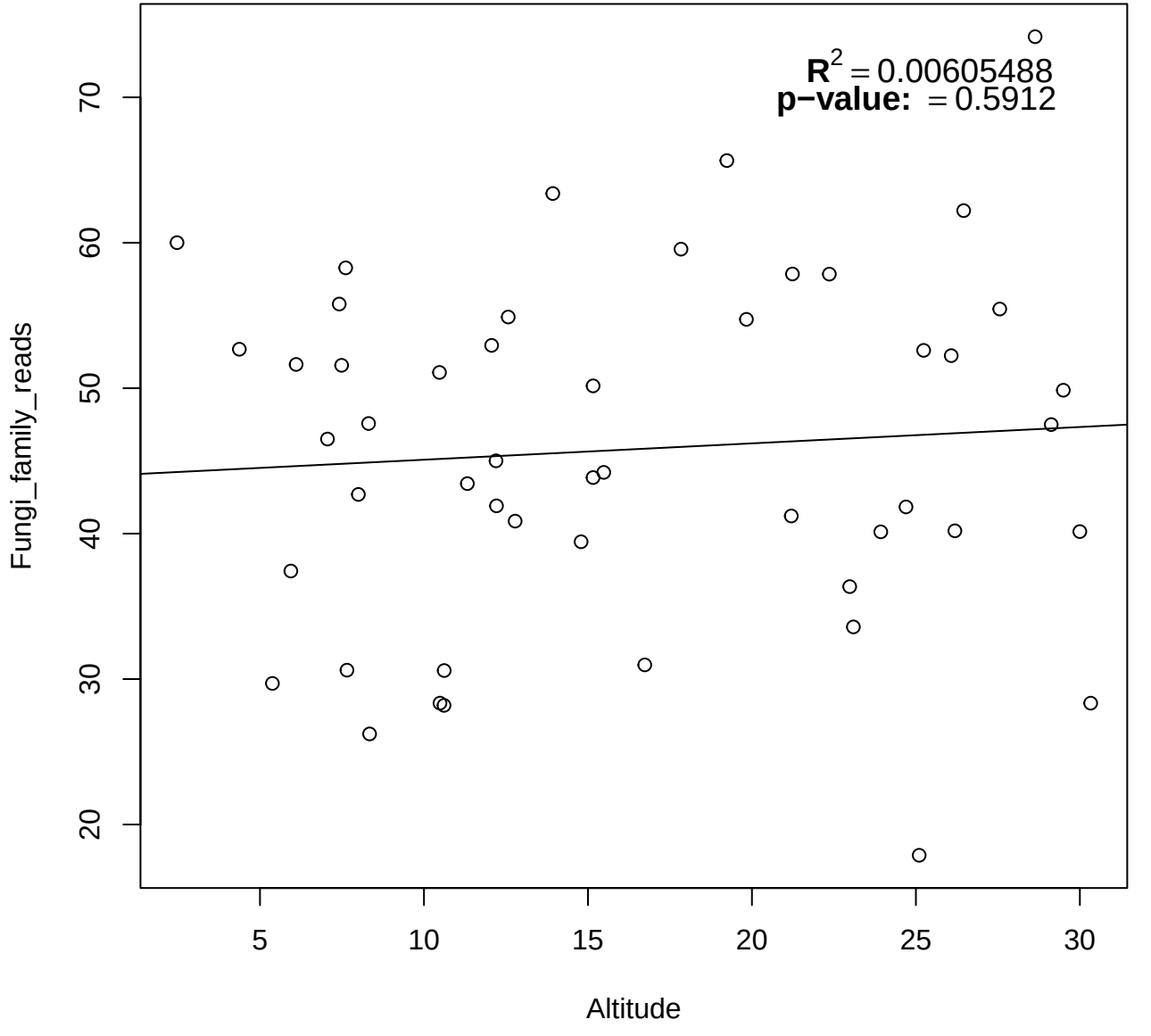

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
TOJ1
AVE1
Cook's distance

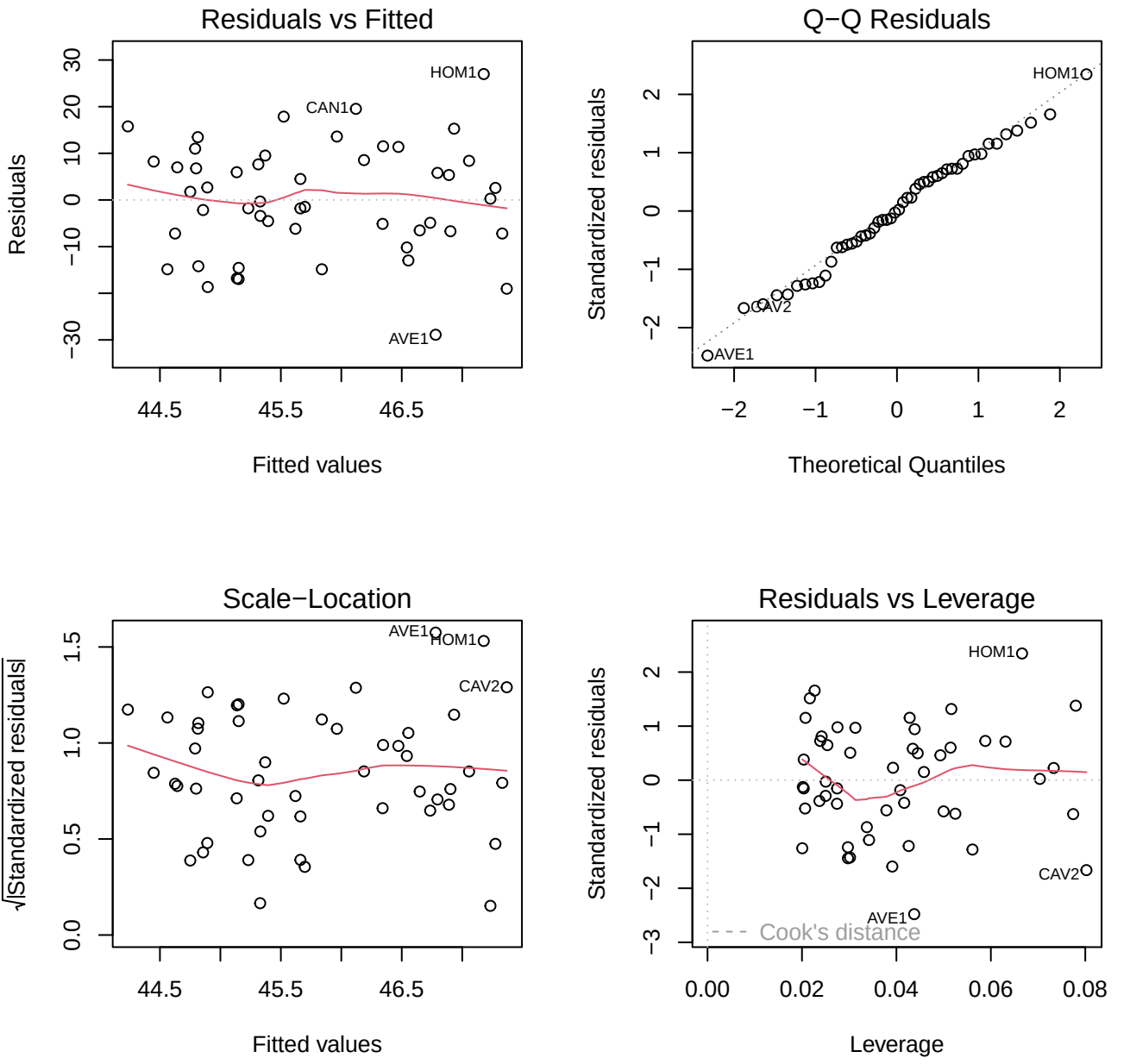

$R^2 = 0.000483829$
p−value: = 0.8795
Fungi_family_reads
DOCV
20
30
40
50
60
70
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35

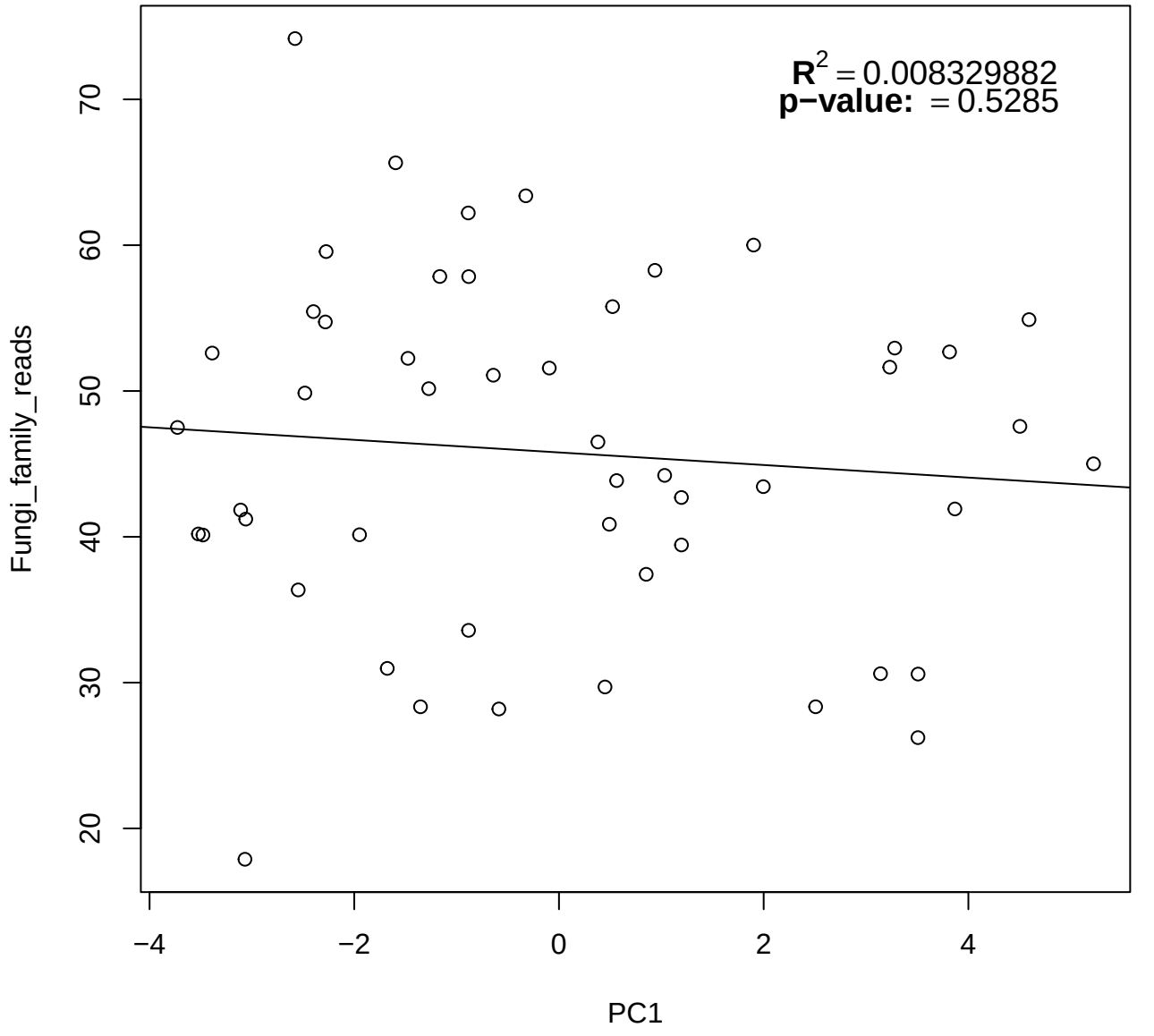

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
HOM1
AVE1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
MACE1
AVE1
Cook's distance

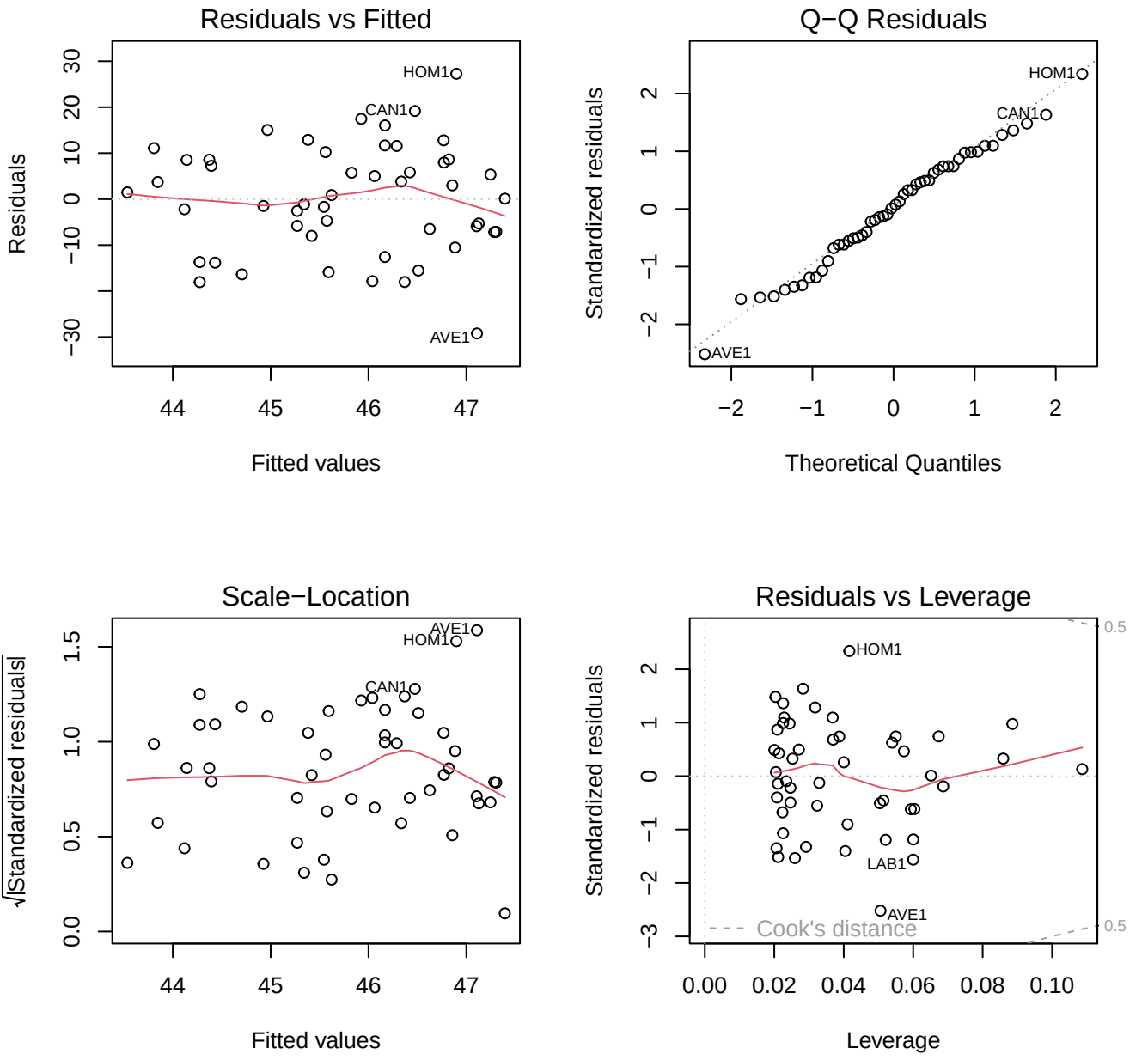

$R^2 = 0.008219428$
p−value: = 0.5312
Fungi_family_reads
LUI_subasin
20
30
40
50
60
70
0.0
0.5
1.0
1.5
2.0
2.5

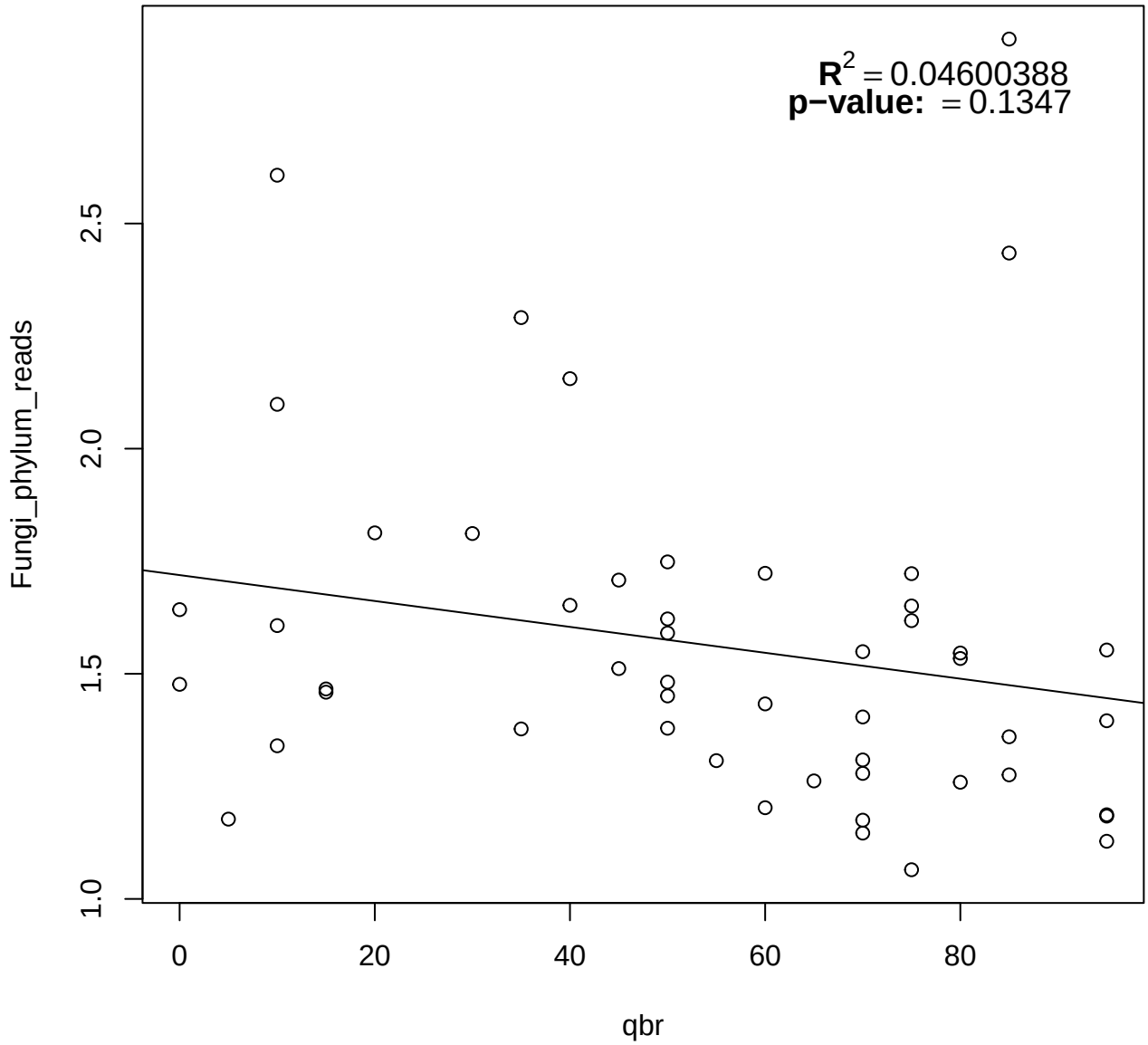

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
LAB1
AVE1
Cook's distance

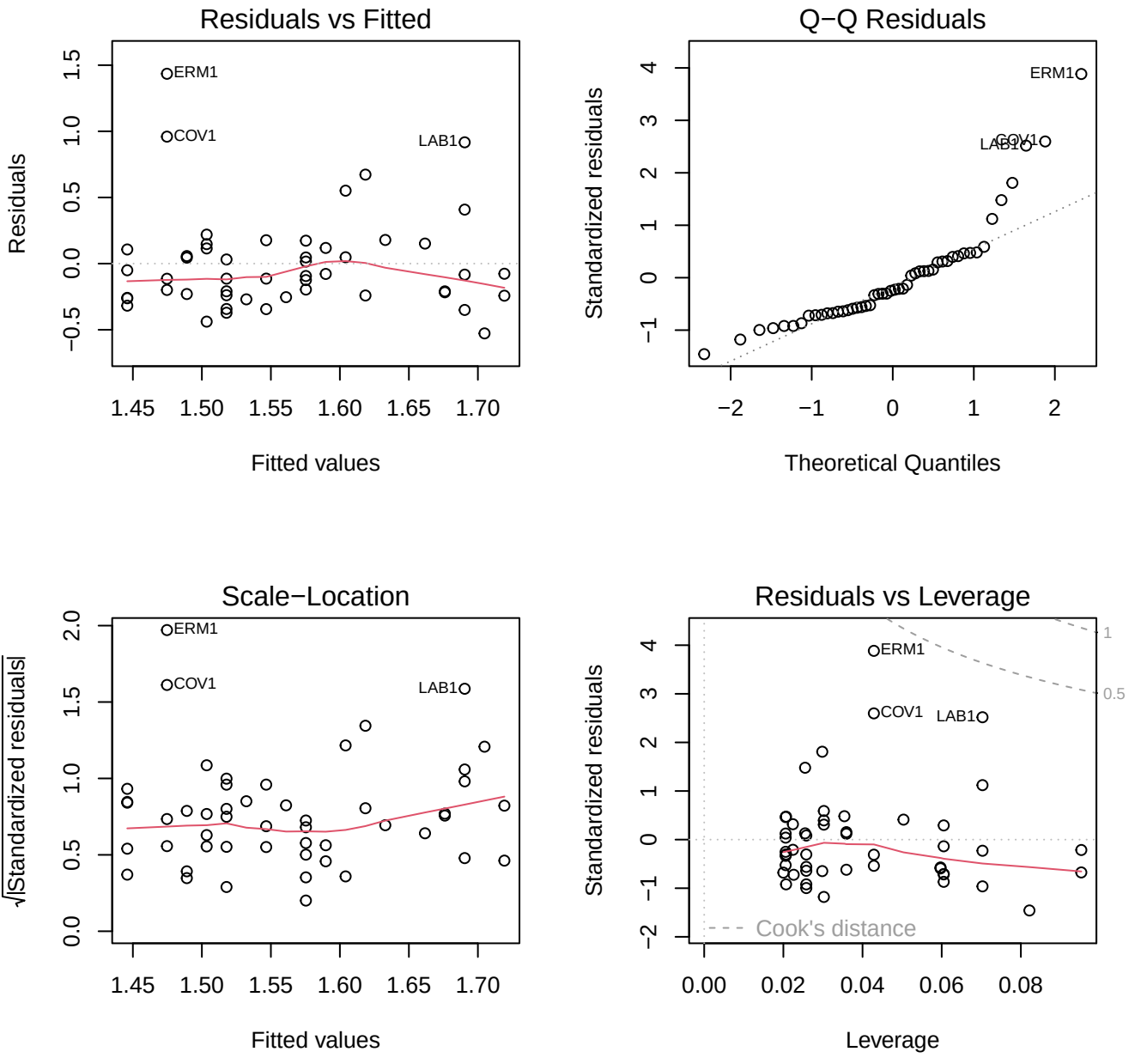

$R^2 = 0.00605488$
p−value: = 0.5912
Fungi_family_reads
Altitude
20
30
40
50
60
70
5
10
15
20
25
30

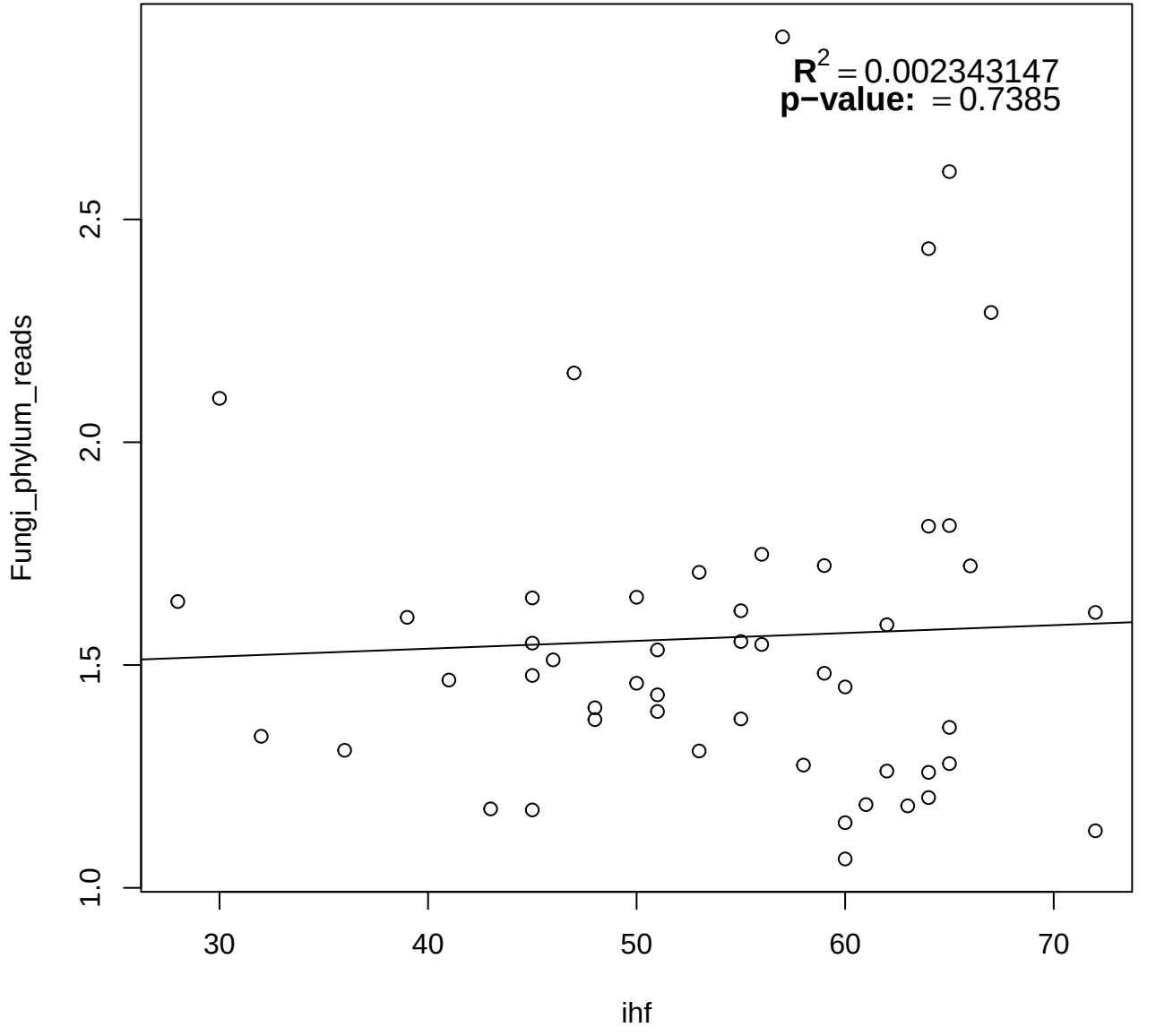

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAV2
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
CAV2
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
CAV2
AVE1
Cook's distance

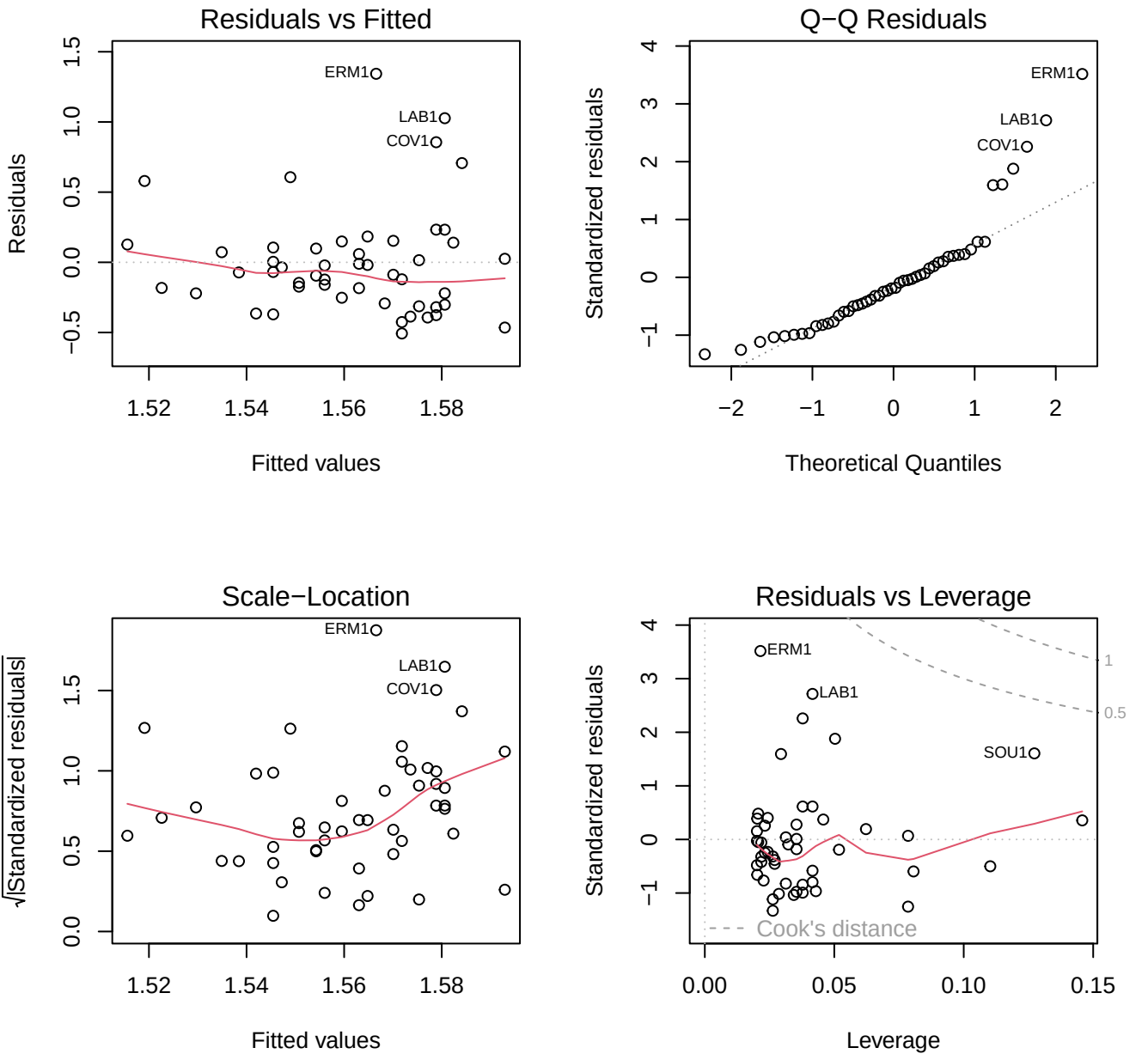

$R^2 = 0.008329882$
p−value: = 0.5285
Fungi_family_reads
PC1
70
60
50
40
30
20
−4
−2
0
2
4

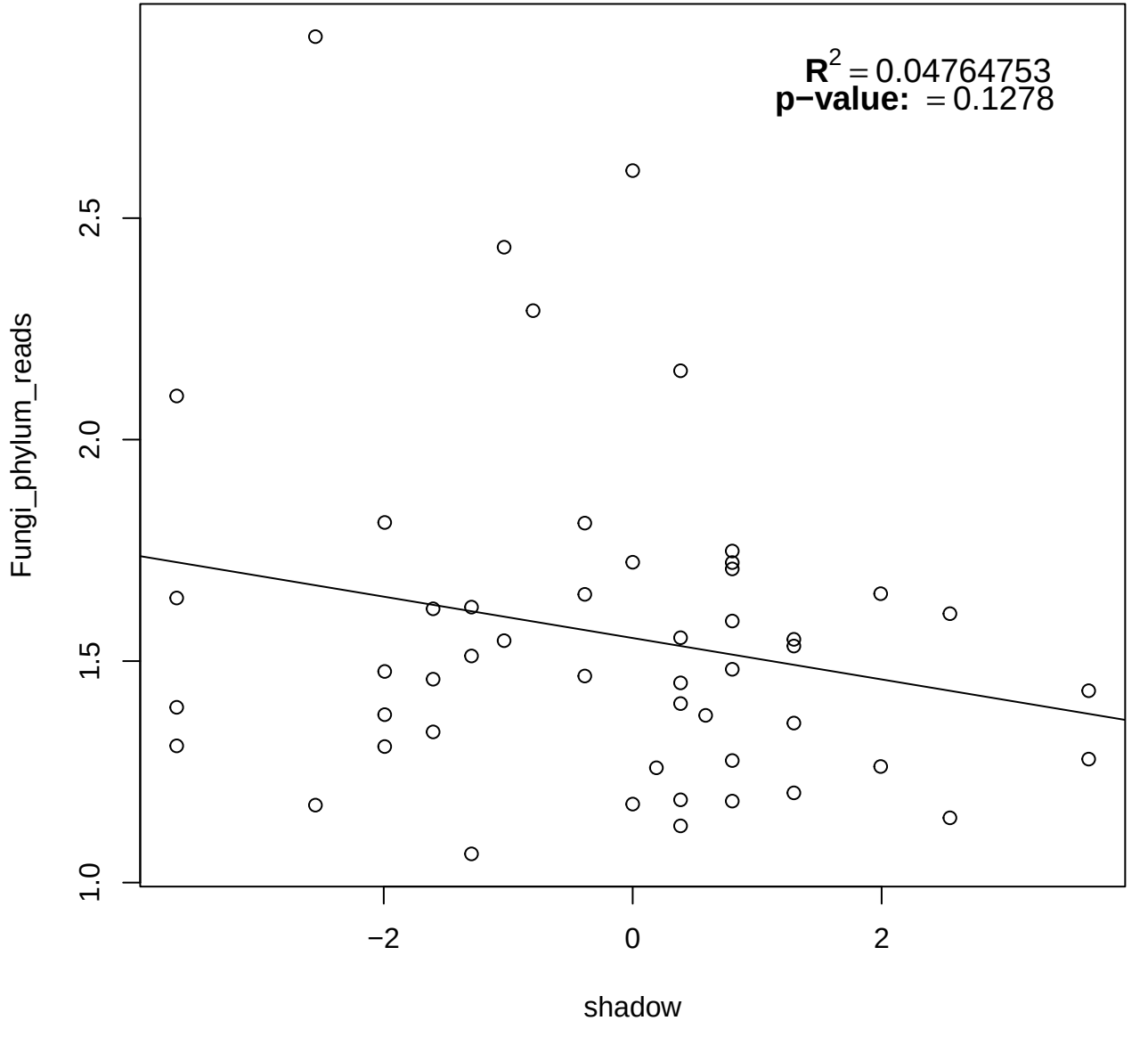

Residuals vs Fitted
Residuals
Fitted values
HOM1
CAN1
AVE1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
HOM1
CAN1
AVE1
Scale−Location
√|Standardized residuals|
Fitted values
AVE1
HOM1
CAN1
Residuals vs Leverage
Standardized residuals
Leverage
HOM1
LAB1
AVE1
Cook's distance
0.5
0.5

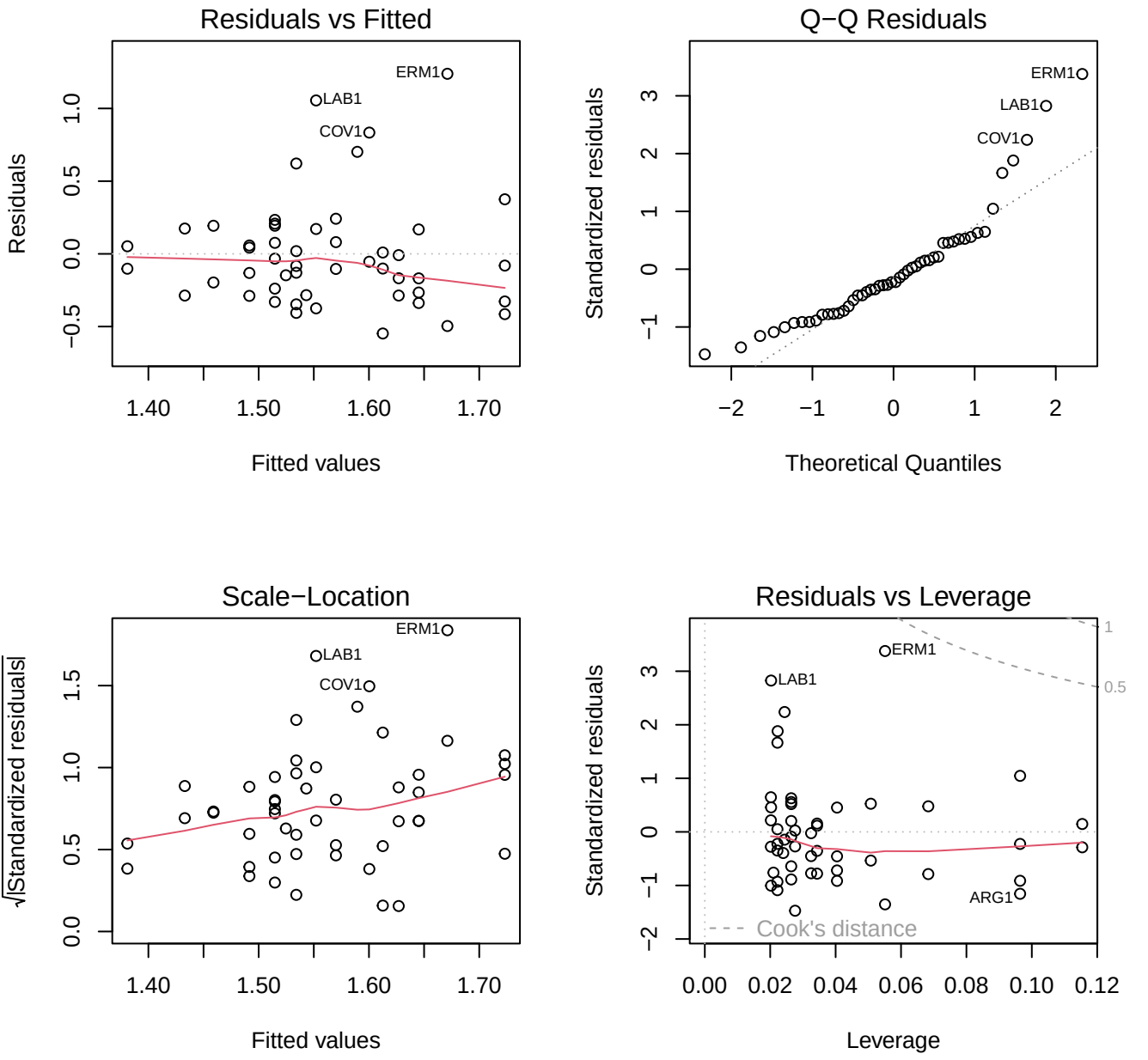

$R^2 = 0.04600388$
p−value: = 0.1347
Fungi_phylum_reads
1.0
1.5
2.0
2.5
0
20
40
60
80
qbr

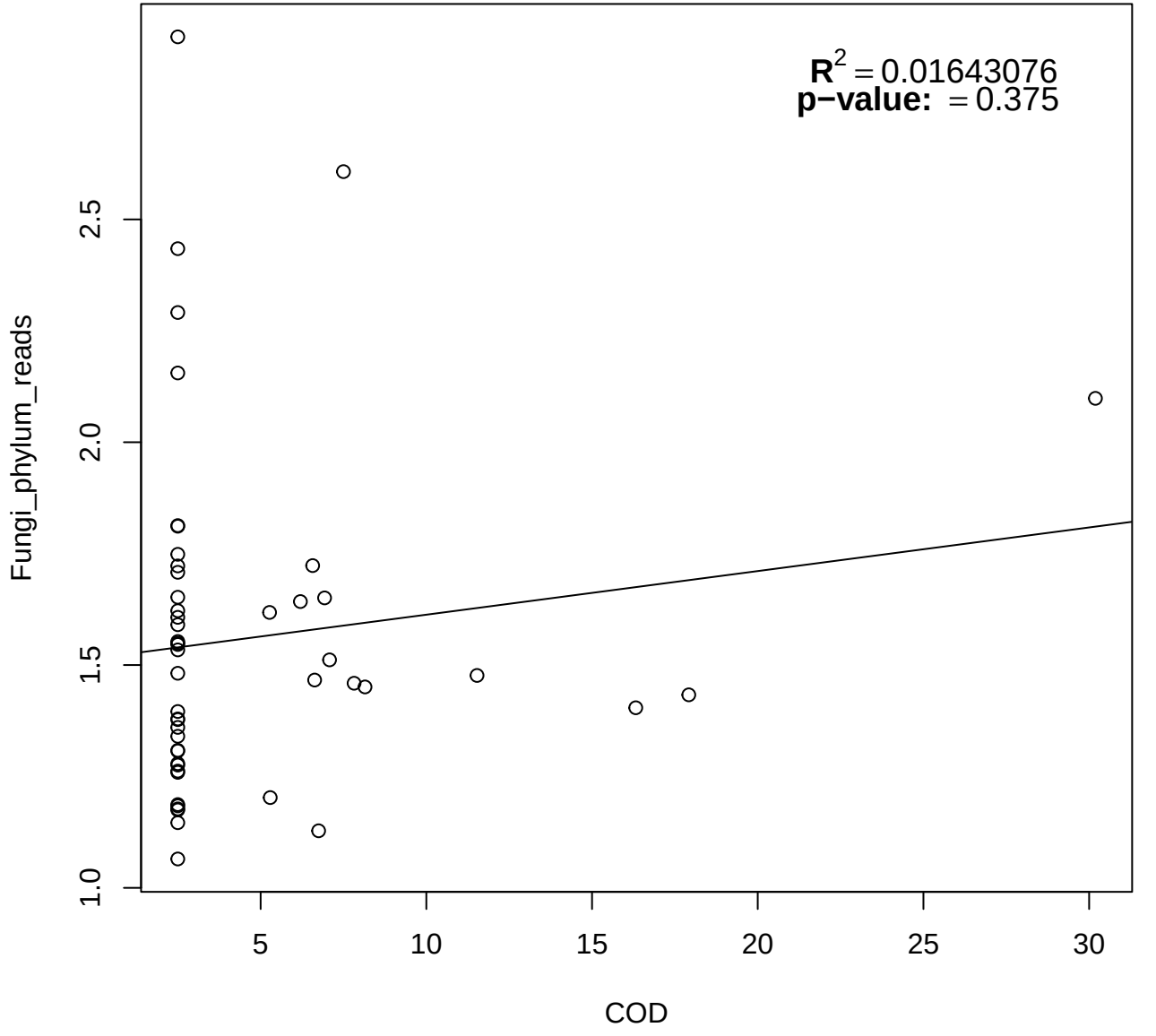

Residuals vs Fitted
Residuals
Fitted values
ERM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
COV1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
COV1
LAB1
Cook's distance
1
0.5

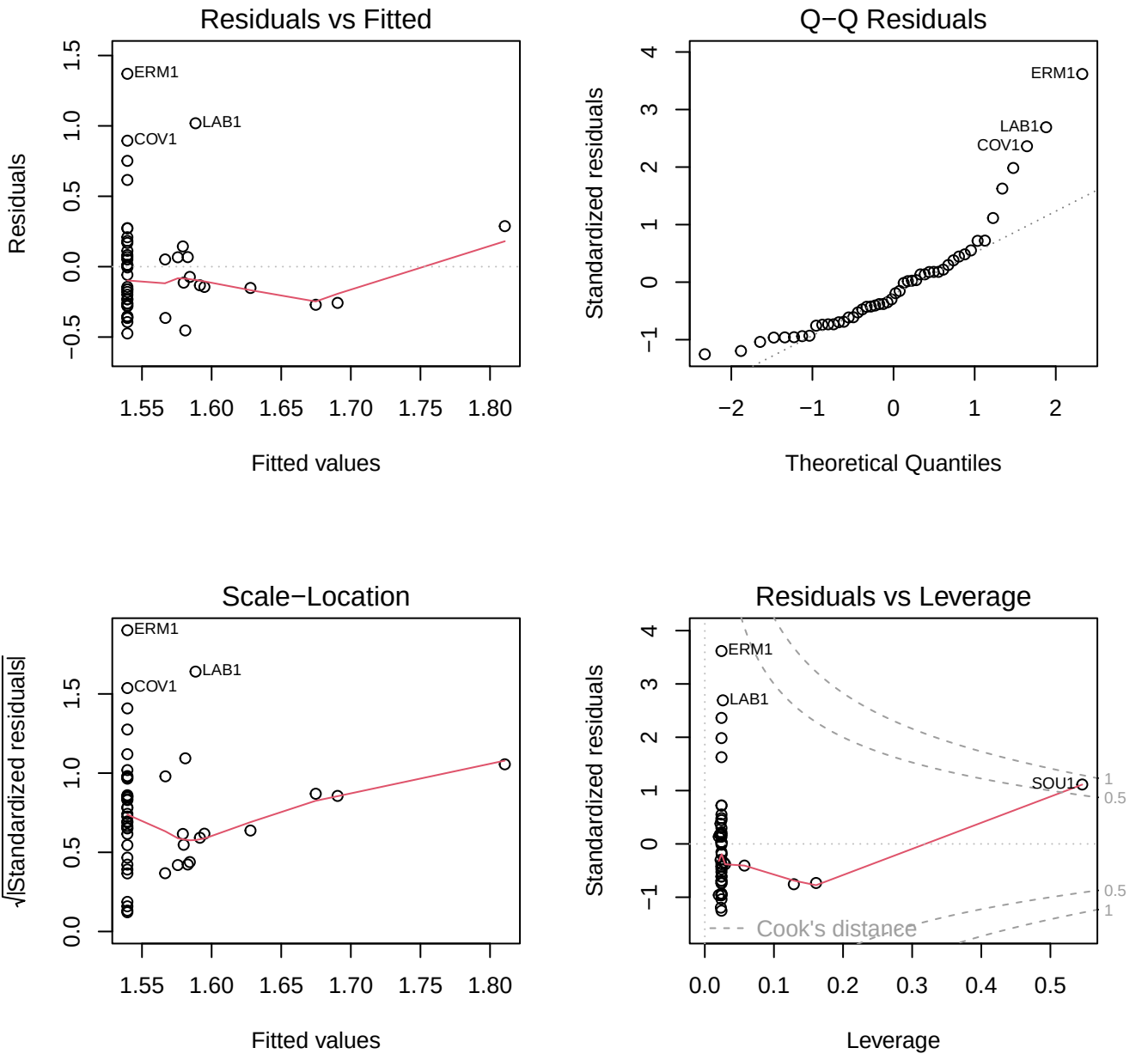

$R^2 = 0.002343147$
p−value: = 0.7385
Fungi_phylum_reads
1.0
1.5
2.0
2.5
30
40
50
60
70
ihf

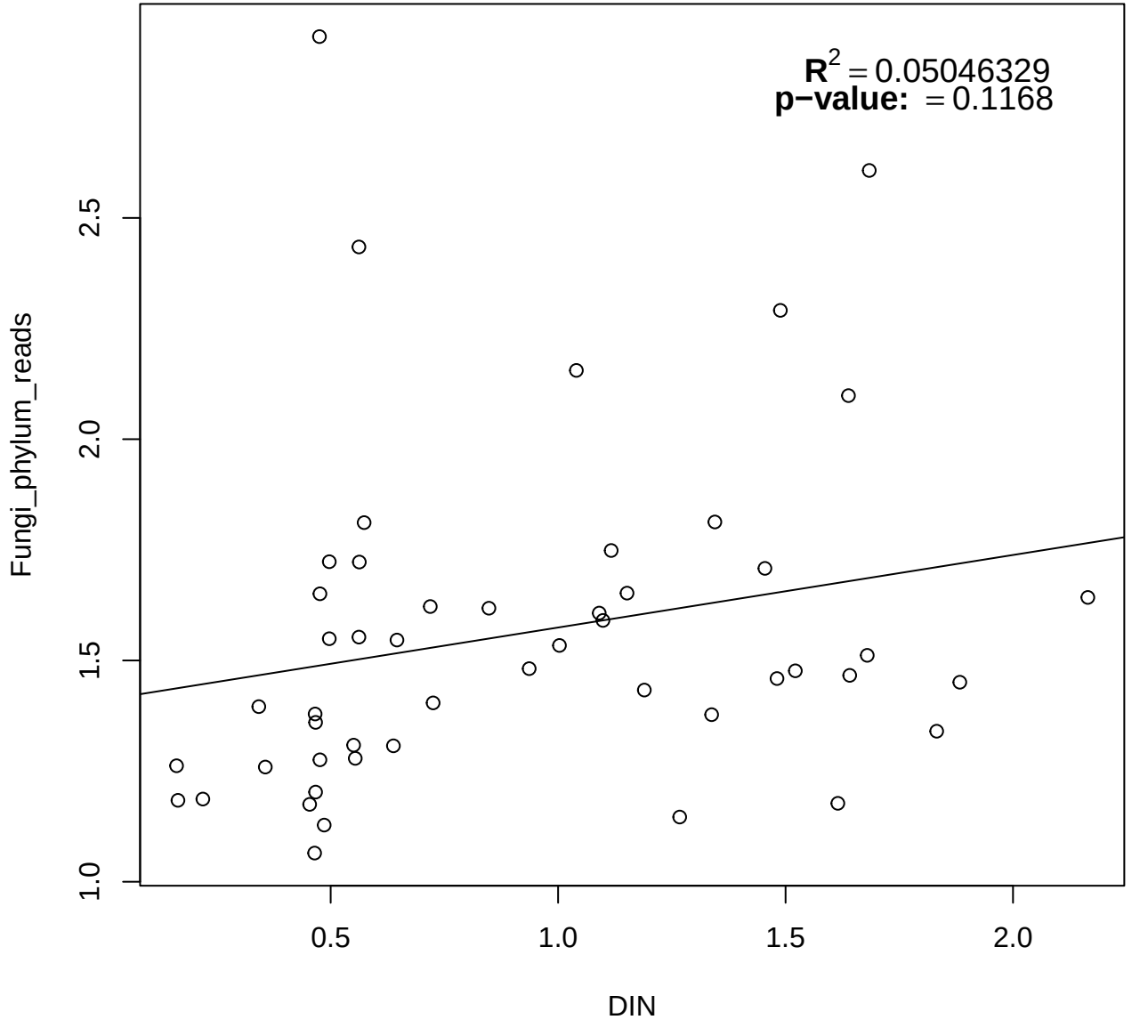

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
SOU1
Cook's distance
1
0.5

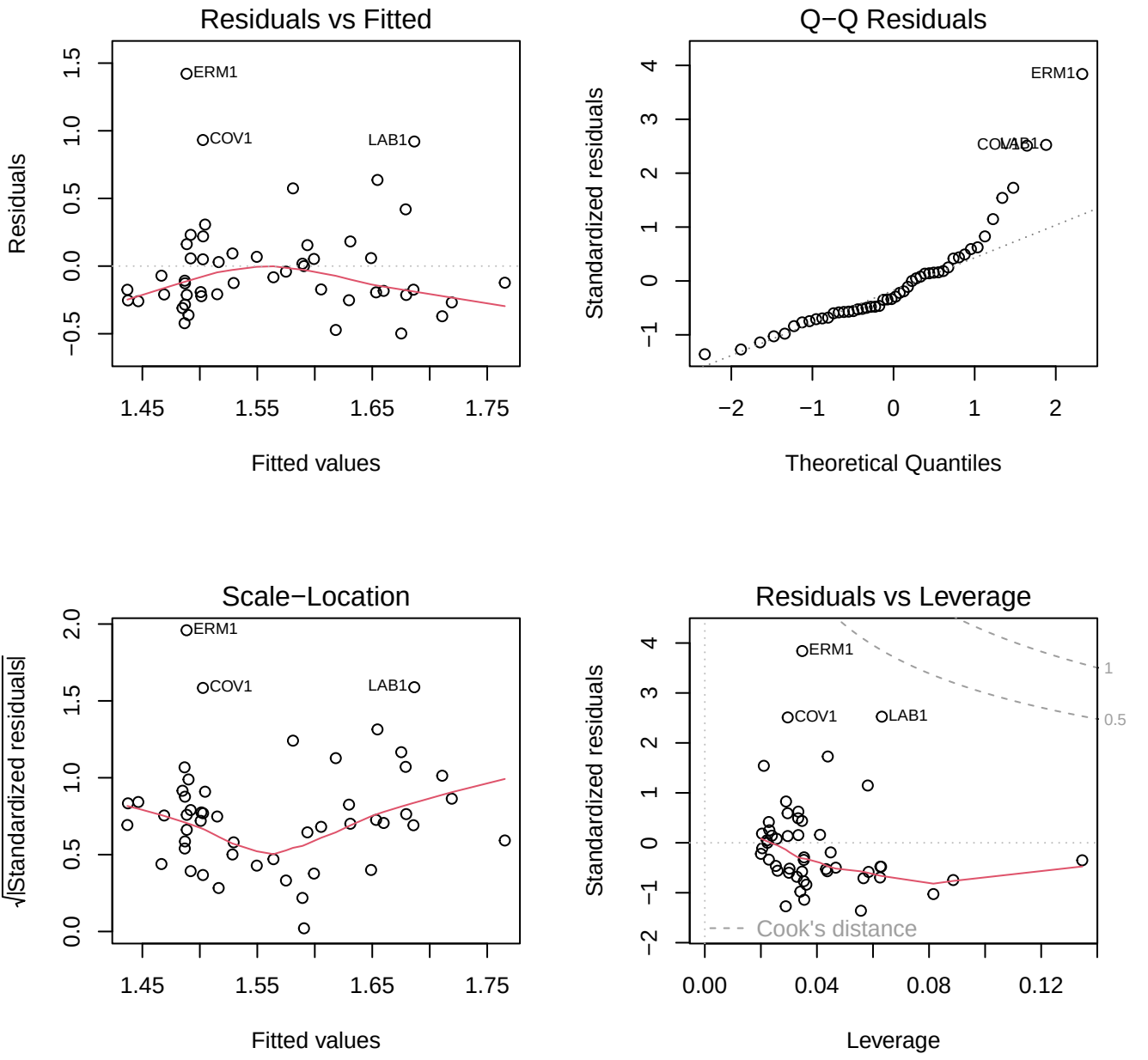

$R^2 = 0.04764753$
p−value: = 0.1278
Fungi_phylum_reads
1.0
1.5
2.0
2.5
−2
0
2
shadow

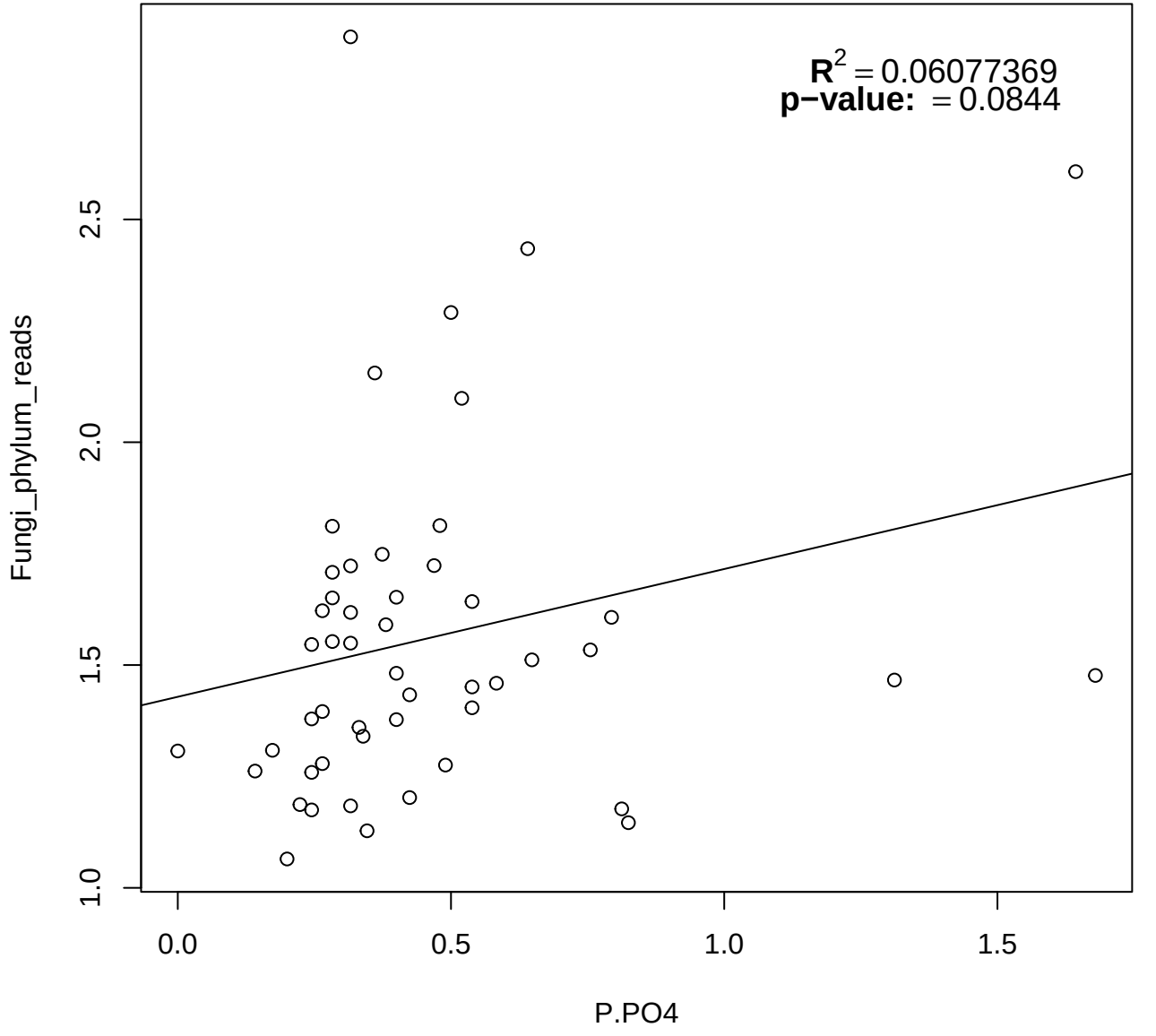

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
ARG1
Cook's distance
1
0.5

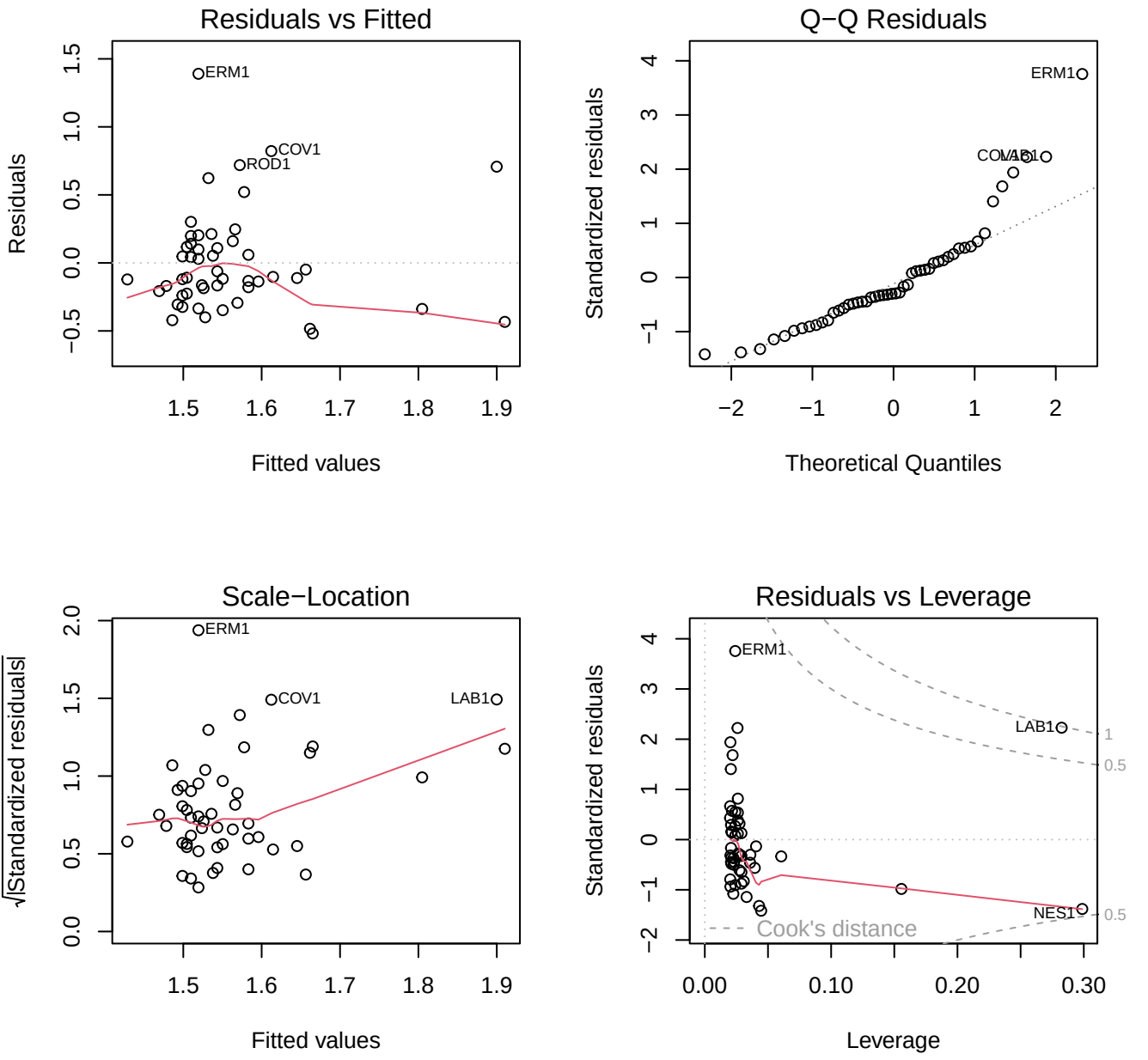

$R^2 = 0.01643076$
p−value: = 0.375
Fungi_phylum_reads
1.0
1.5
2.0
2.5
5
10
15
20
25
30
COD

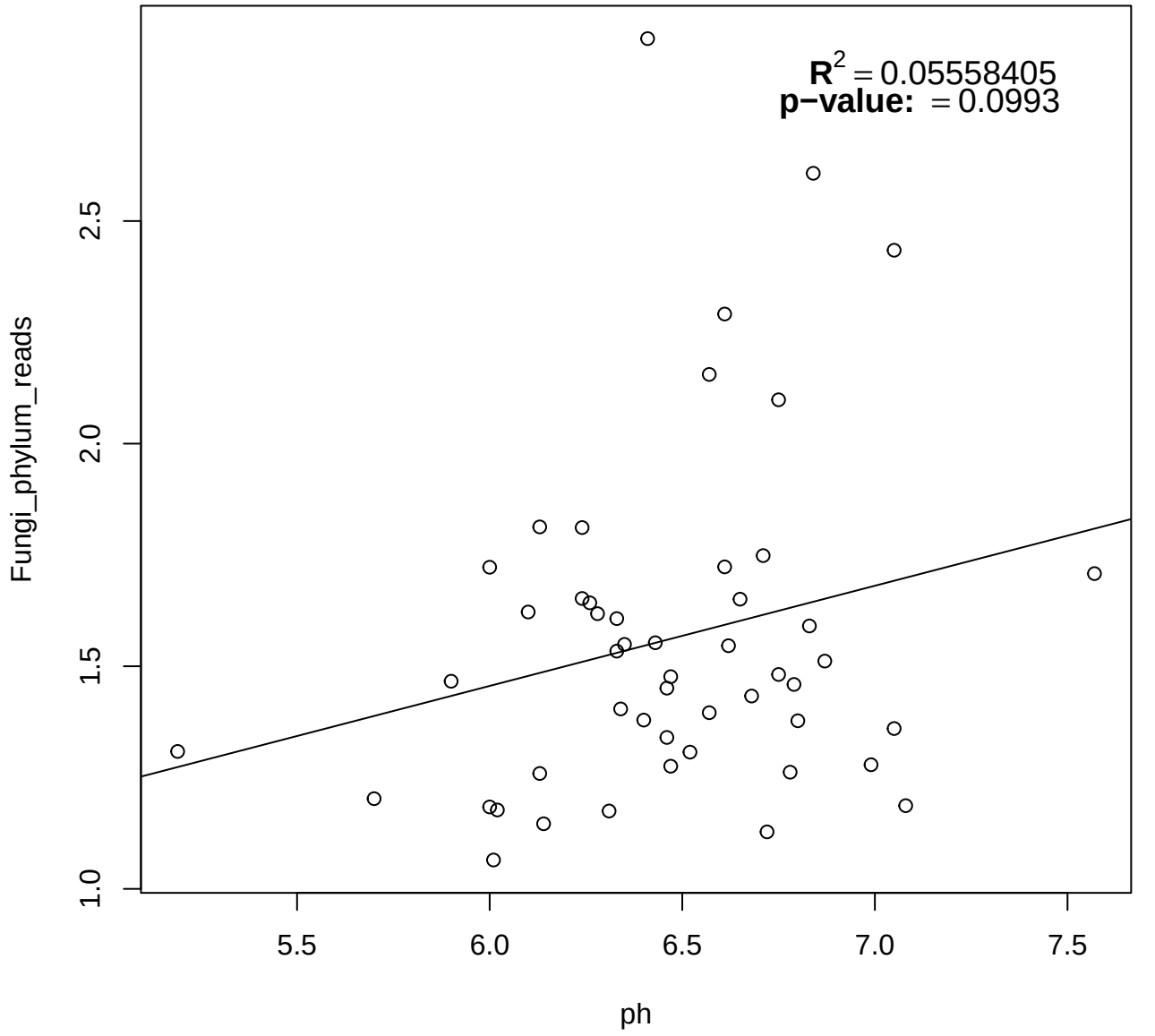

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
SOU1
Cook's distance

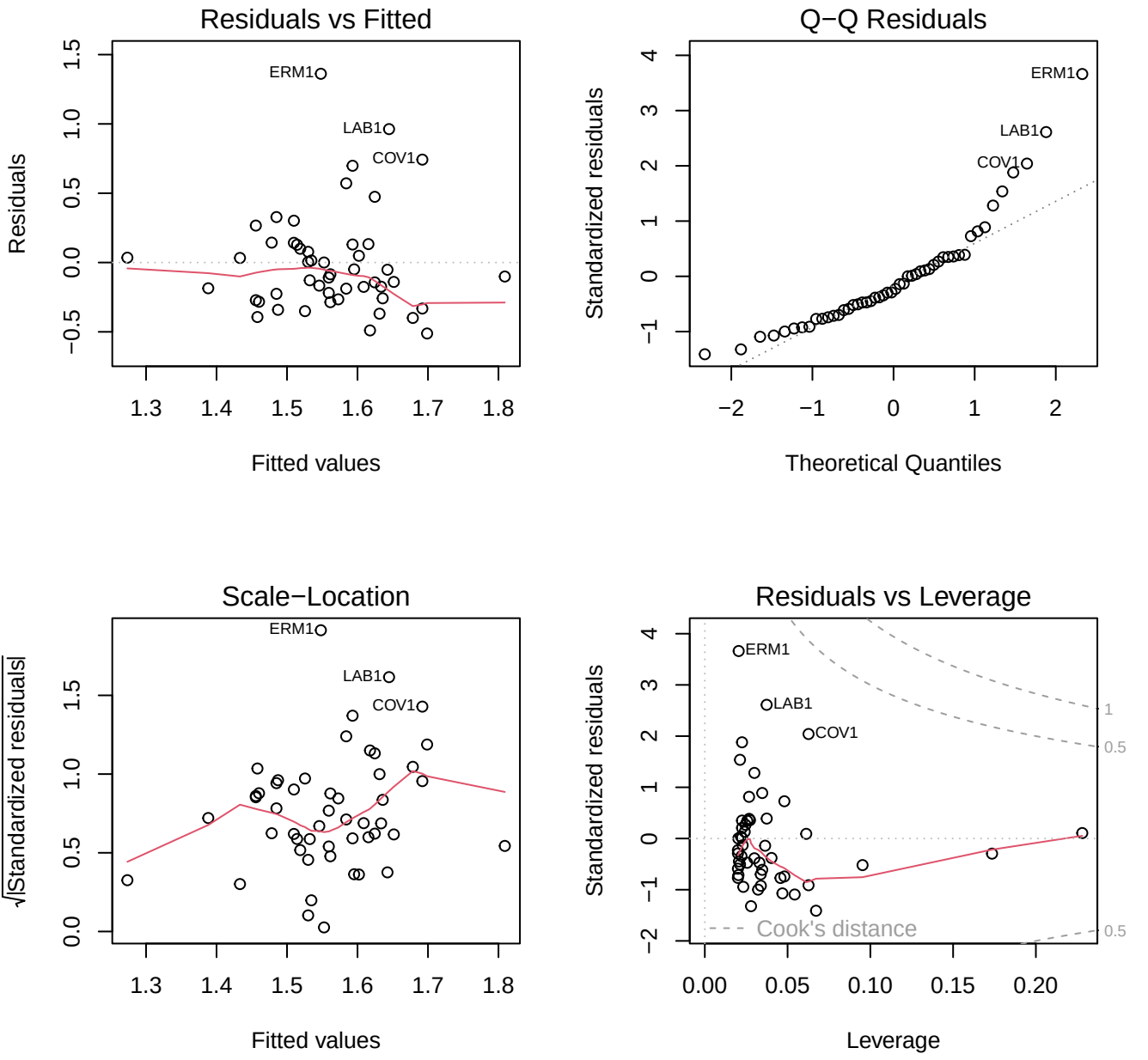

$R^2 = 0.05046329$
p−value: = 0.1168
Fungi_phylum_reads
1.0
1.5
2.0
2.5
0.5
1.0
1.5
2.0
DIN

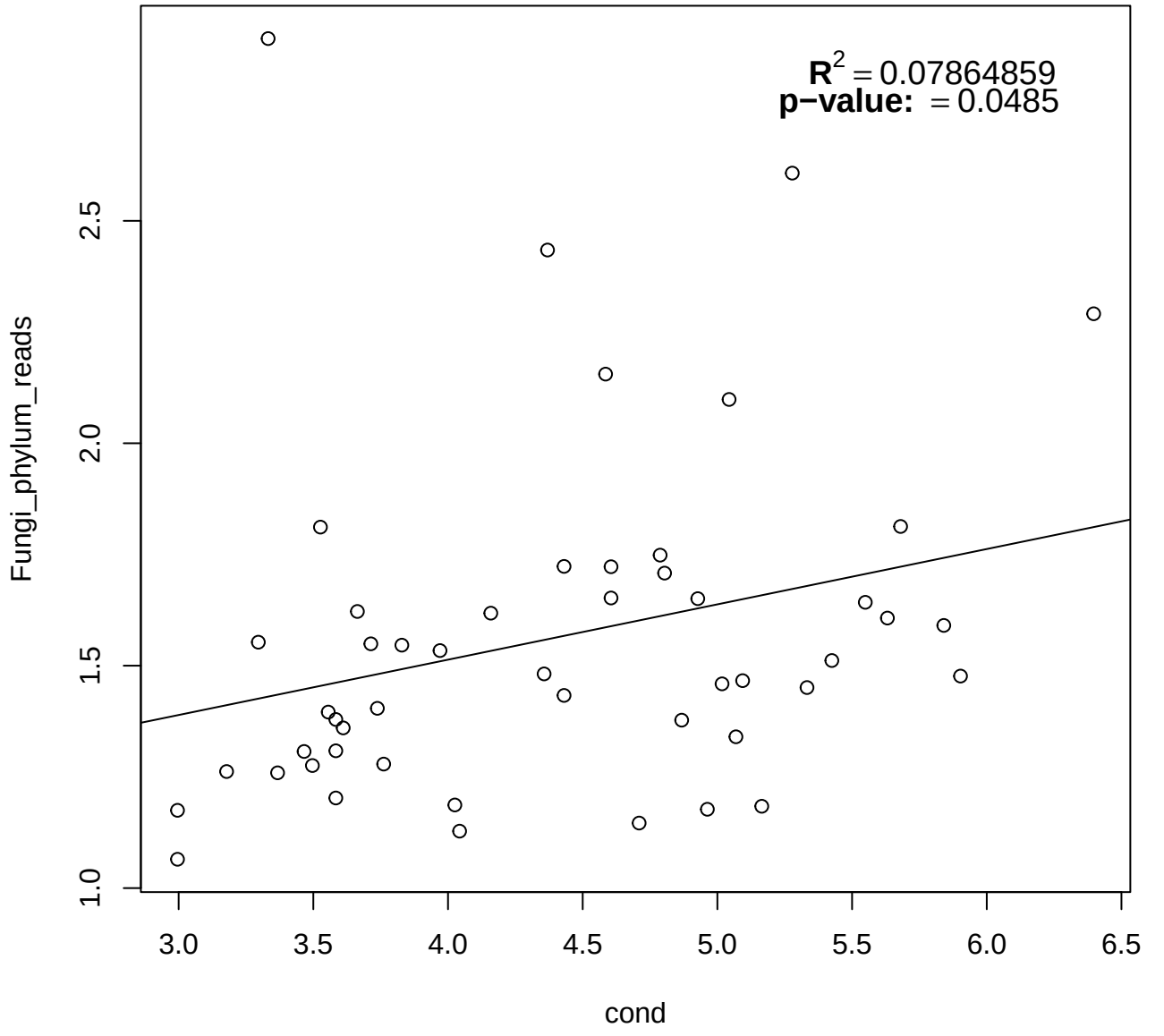

Residuals vs Fitted
Residuals
Fitted values
ERM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
COV1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
COV1
LAB1
1
0.5
Cook's distance

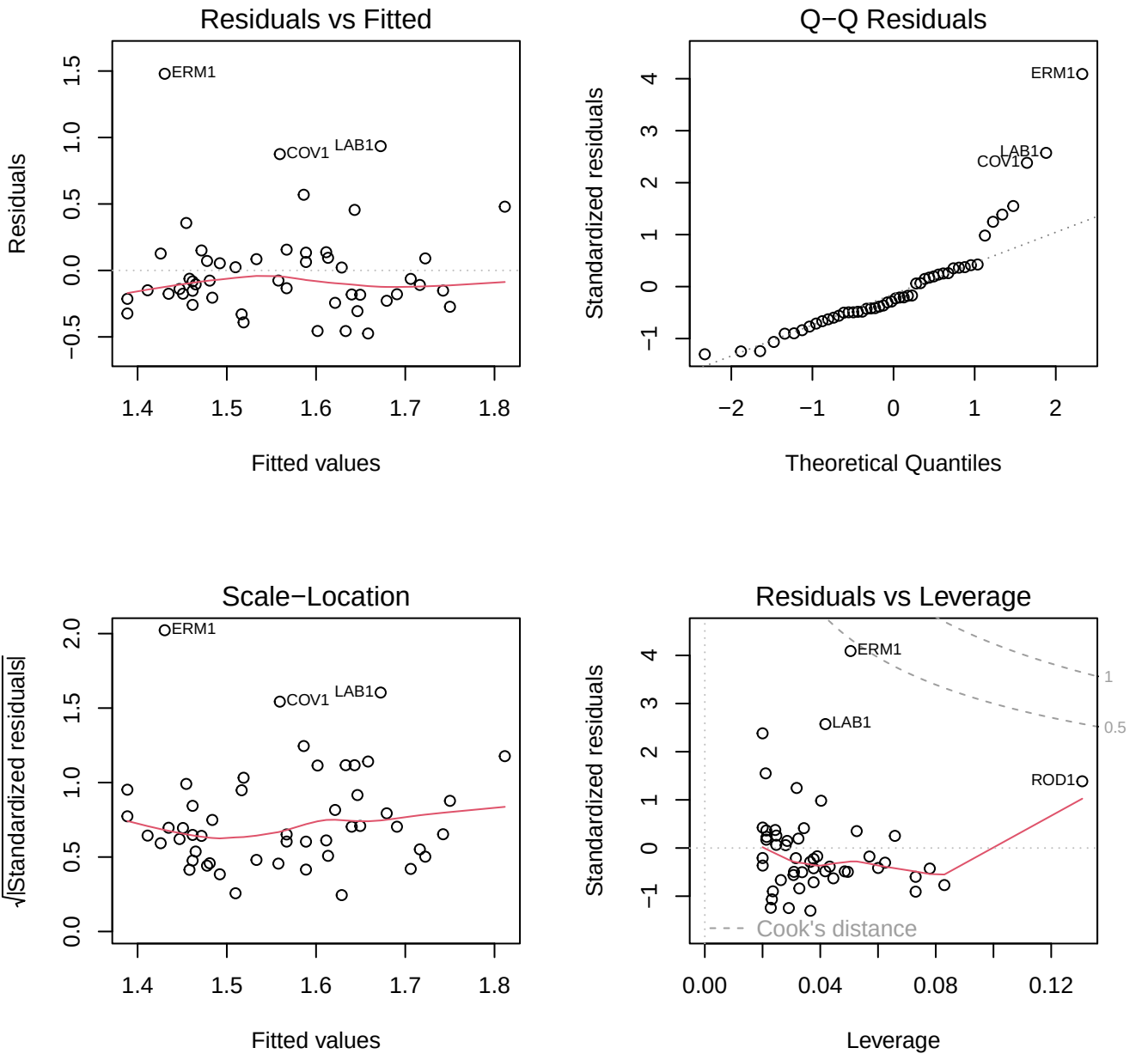

$R^2 = 0.06077369$
p−value: = 0.0844
Fungi_phylum_reads
P.PO4
1.0
1.5
2.0
2.5
0.0
0.5
1.0
1.5

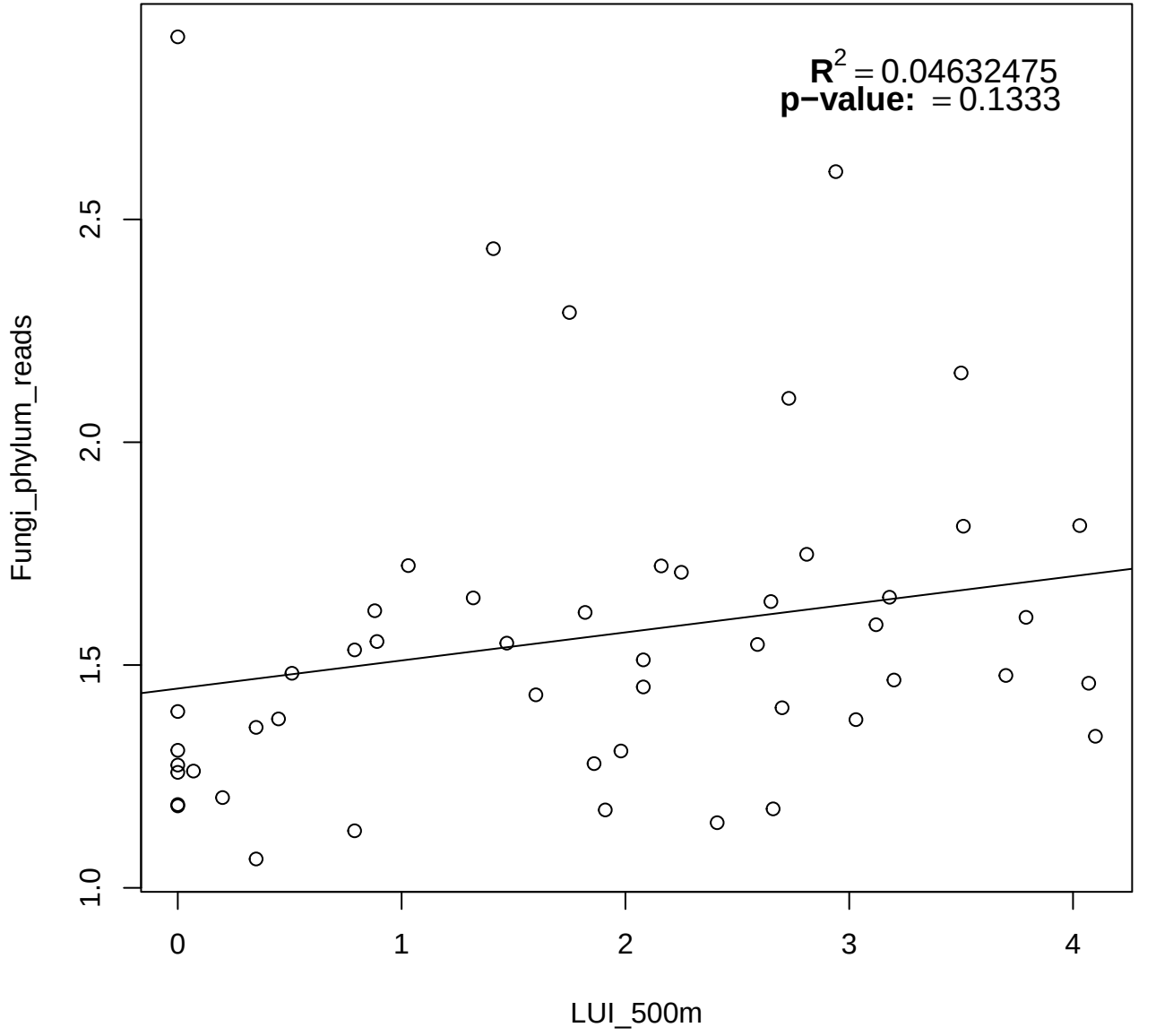

Residuals vs Fitted
Residuals
Fitted values
ERM1
COV1
ROD1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
COV1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
NES1
Cook's distance

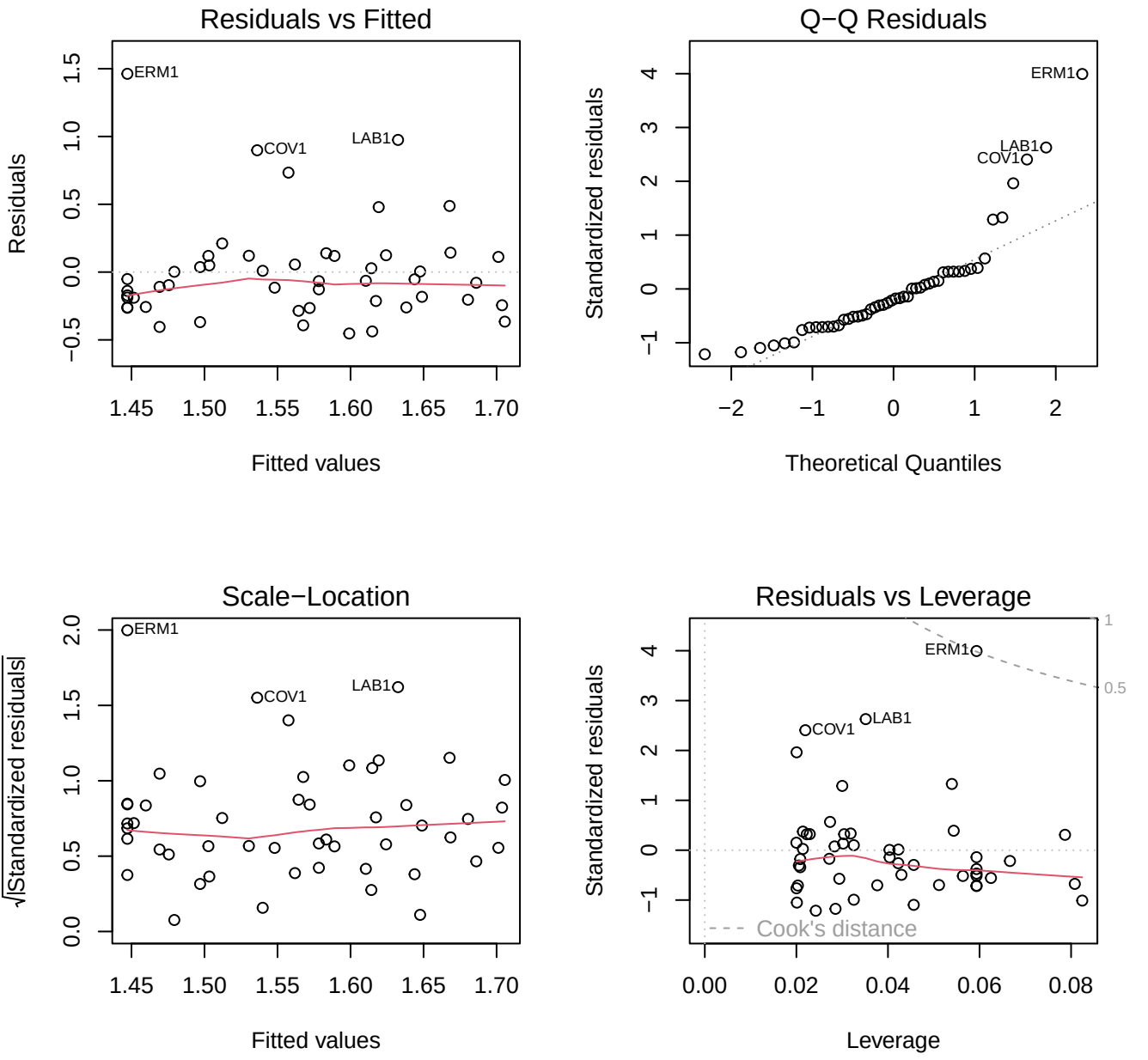

$R^2 = 0.05558405$
p−value: = 0.0993
Fungi_phylum_reads
1.0
1.5
2.0
2.5
5.5
6.0
6.5
7.0
7.5
ph

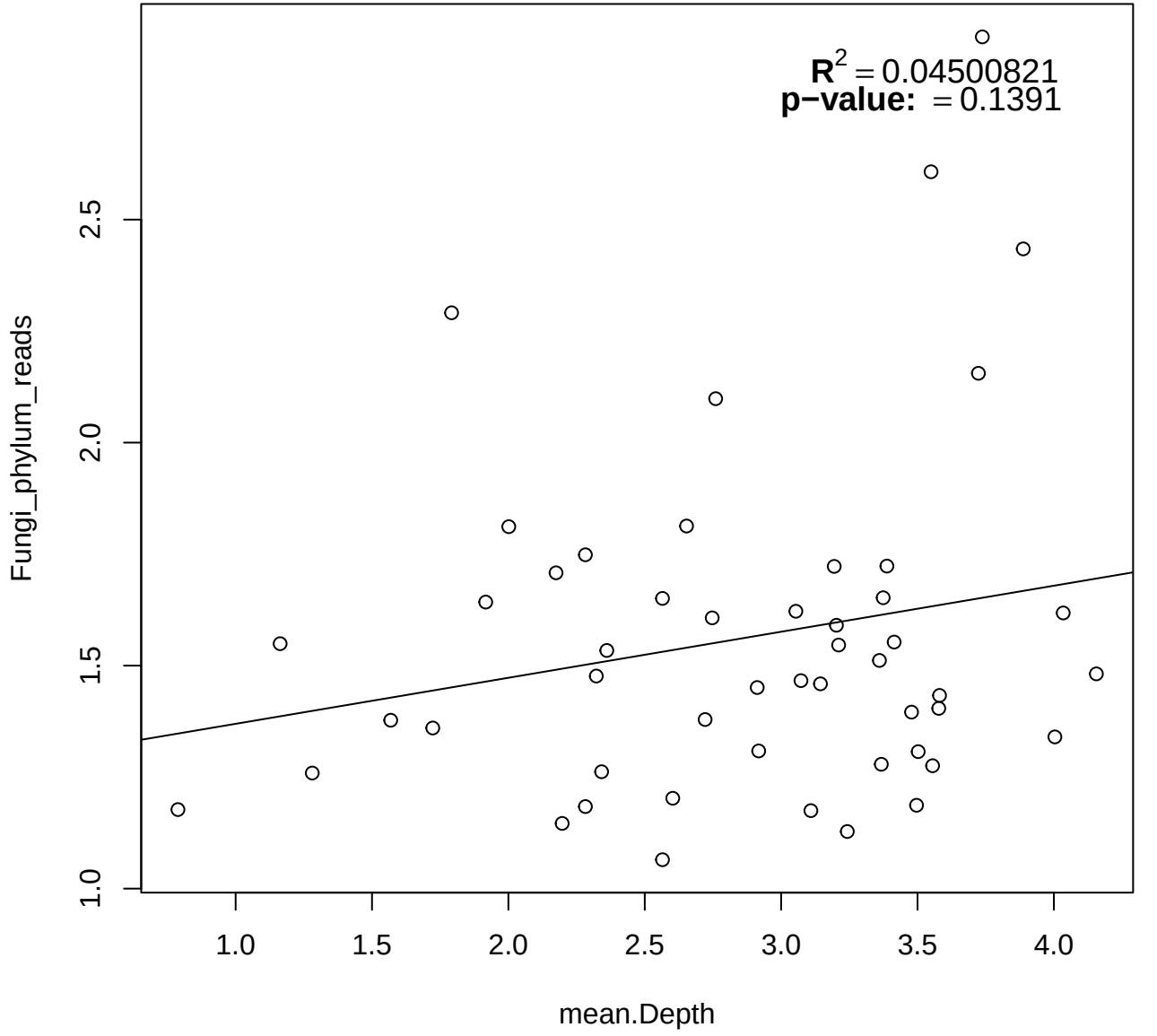

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
COV1
Cook's distance
1
0.5
0.5

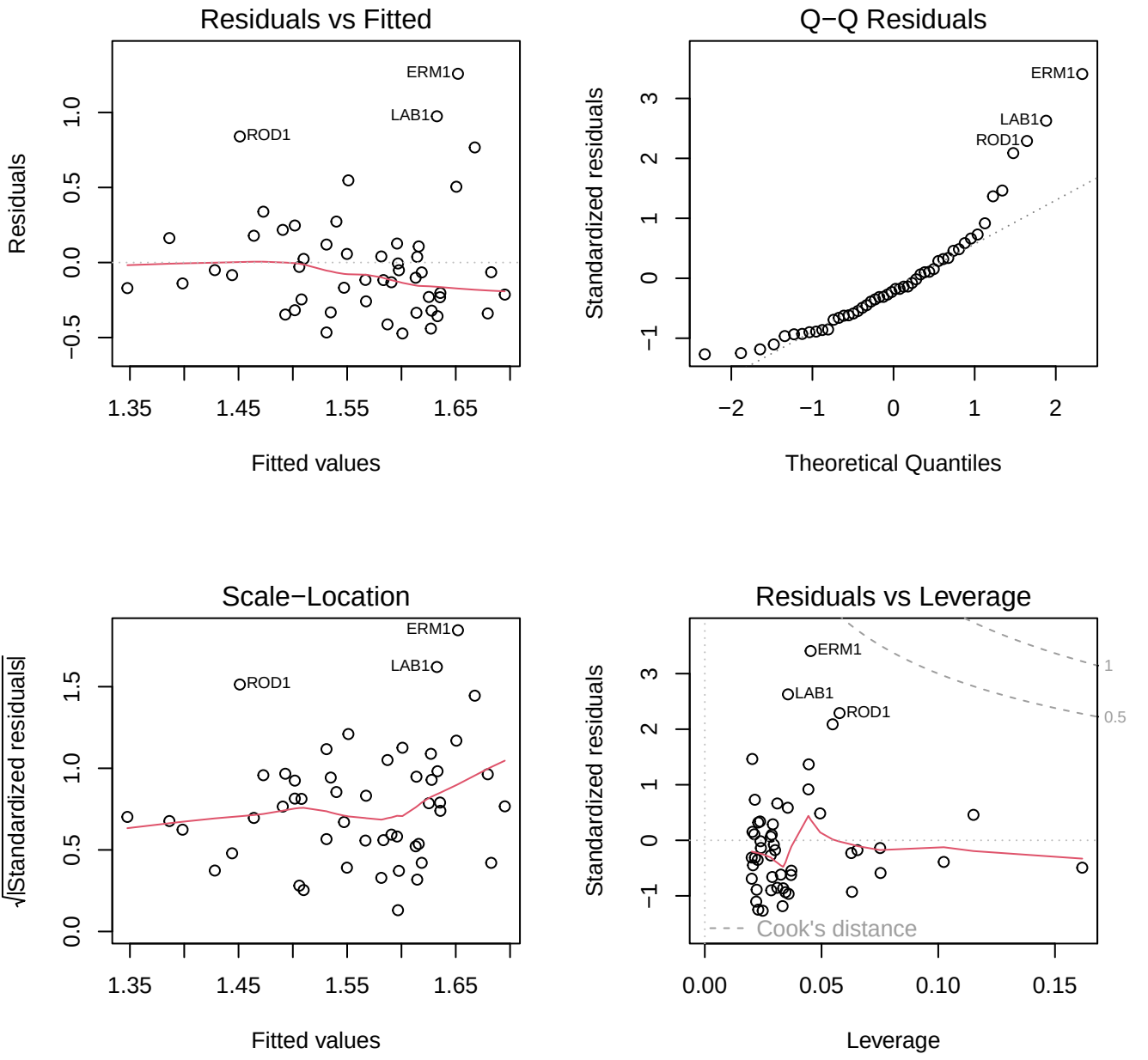

$R^2 = 0.07864859$
p−value: = 0.0485
Fungi_phylum_reads
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
cond

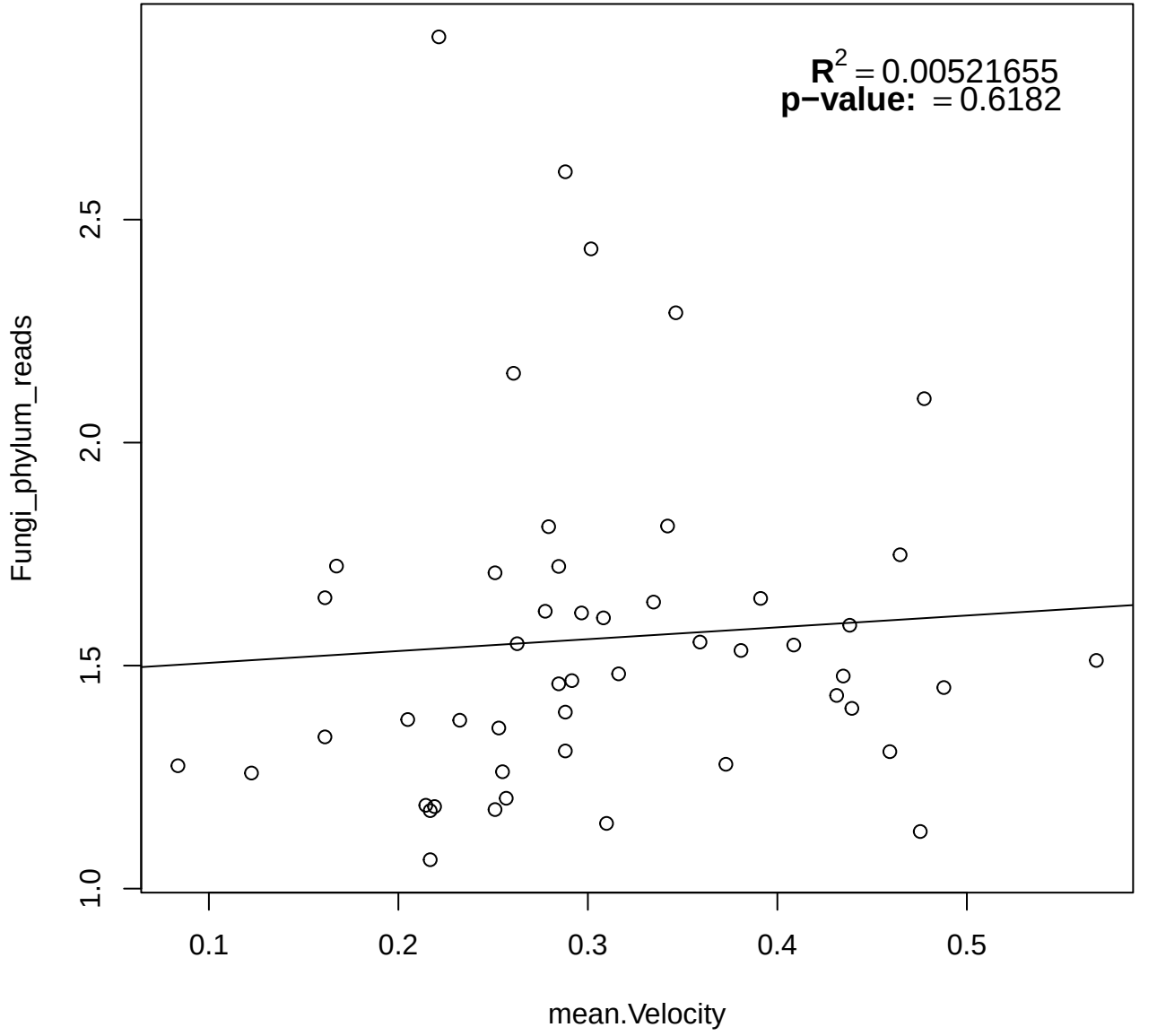

Residuals vs Fitted
Residuals
Fitted values
ERM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
COV1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
ROD1
1
0.5
Cook's distance

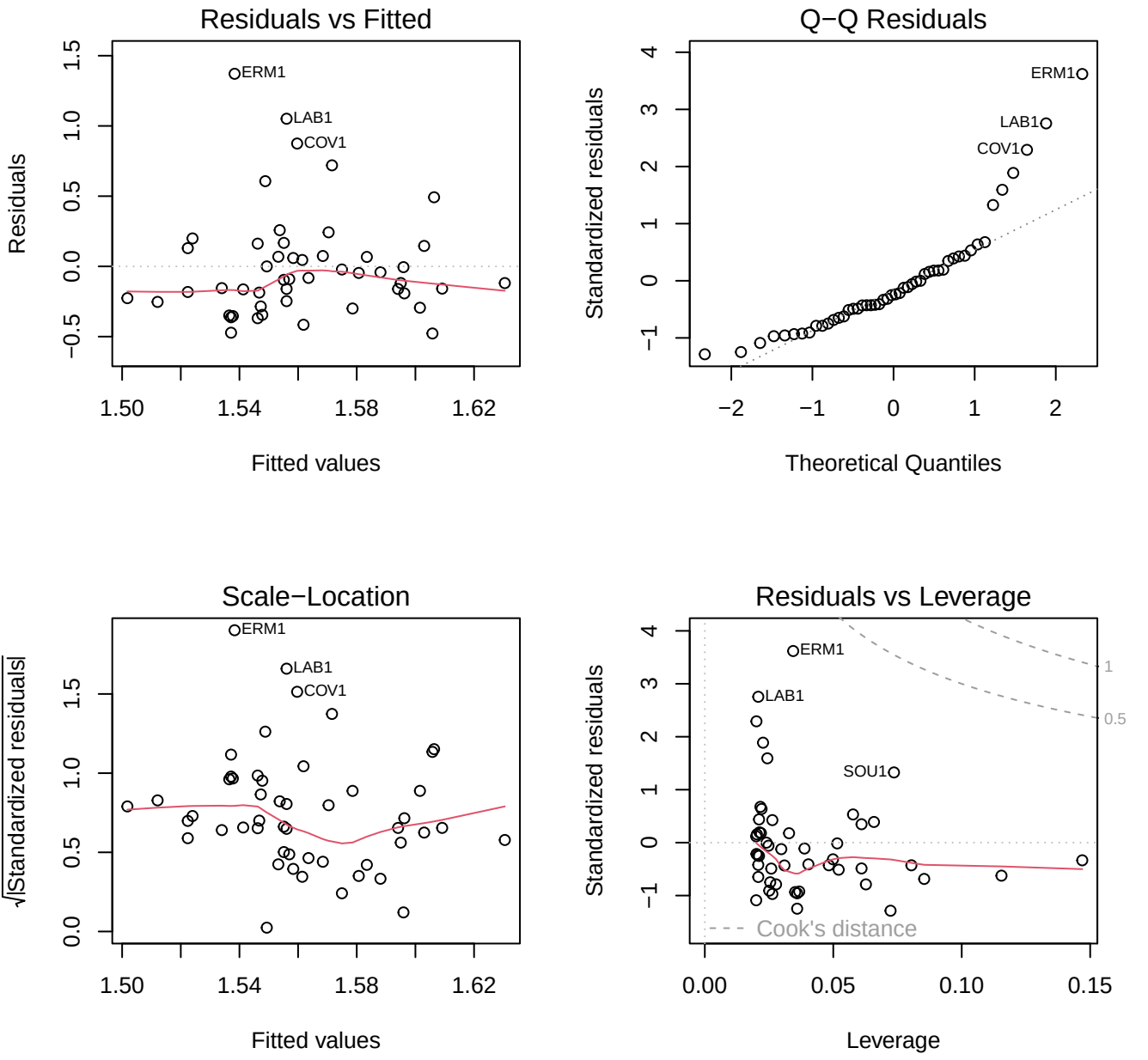

$R^2 = 0.04632475$
p−value: = 0.1333
Fungi_phylum_reads
1.0
1.5
2.0
2.5
0
1
2
3
4
LUI_500m

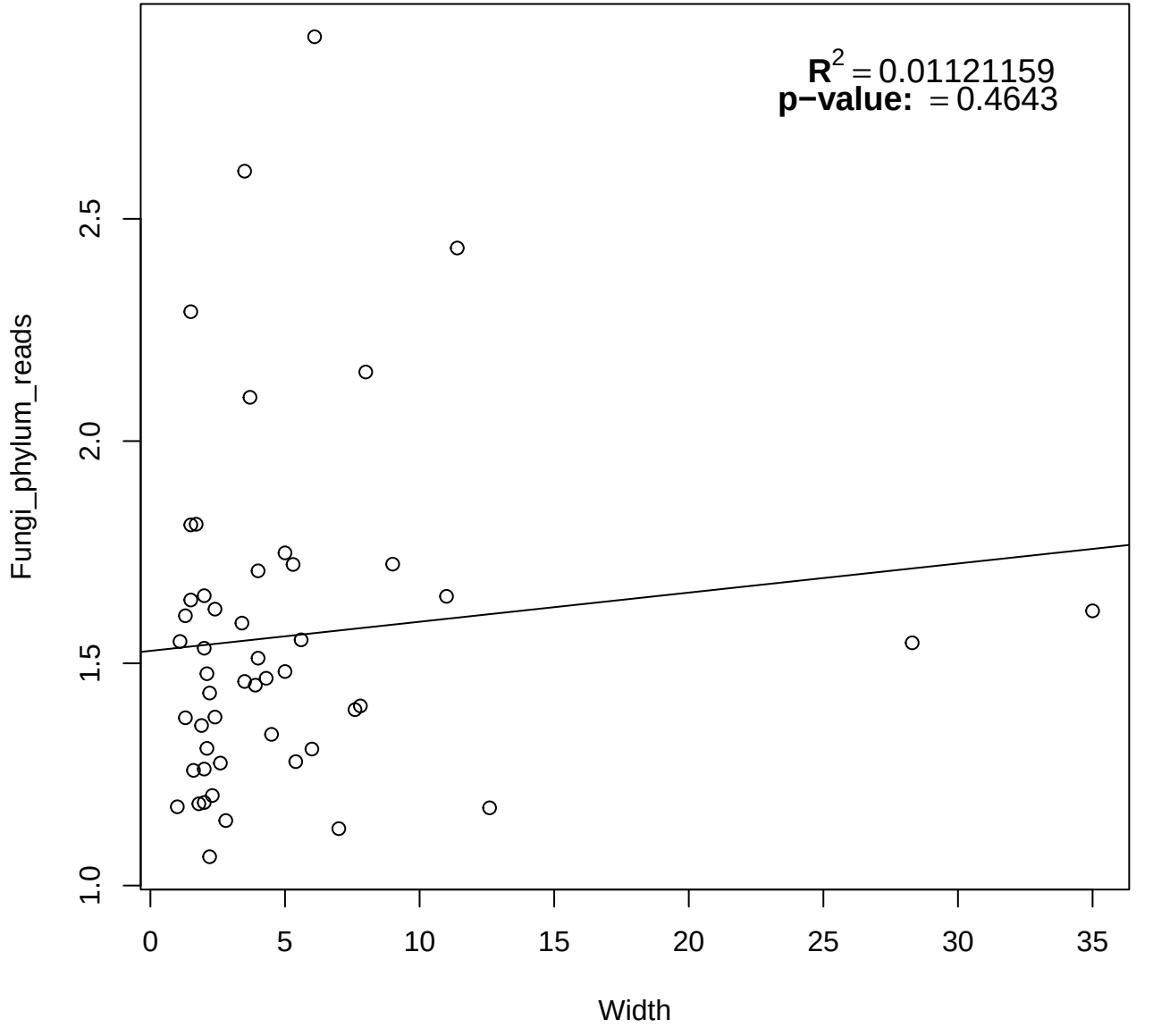

Residuals vs Fitted
Residuals
Fitted values
ERM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
COV1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
COV1
LAB1
Cook's distance
1
0.5

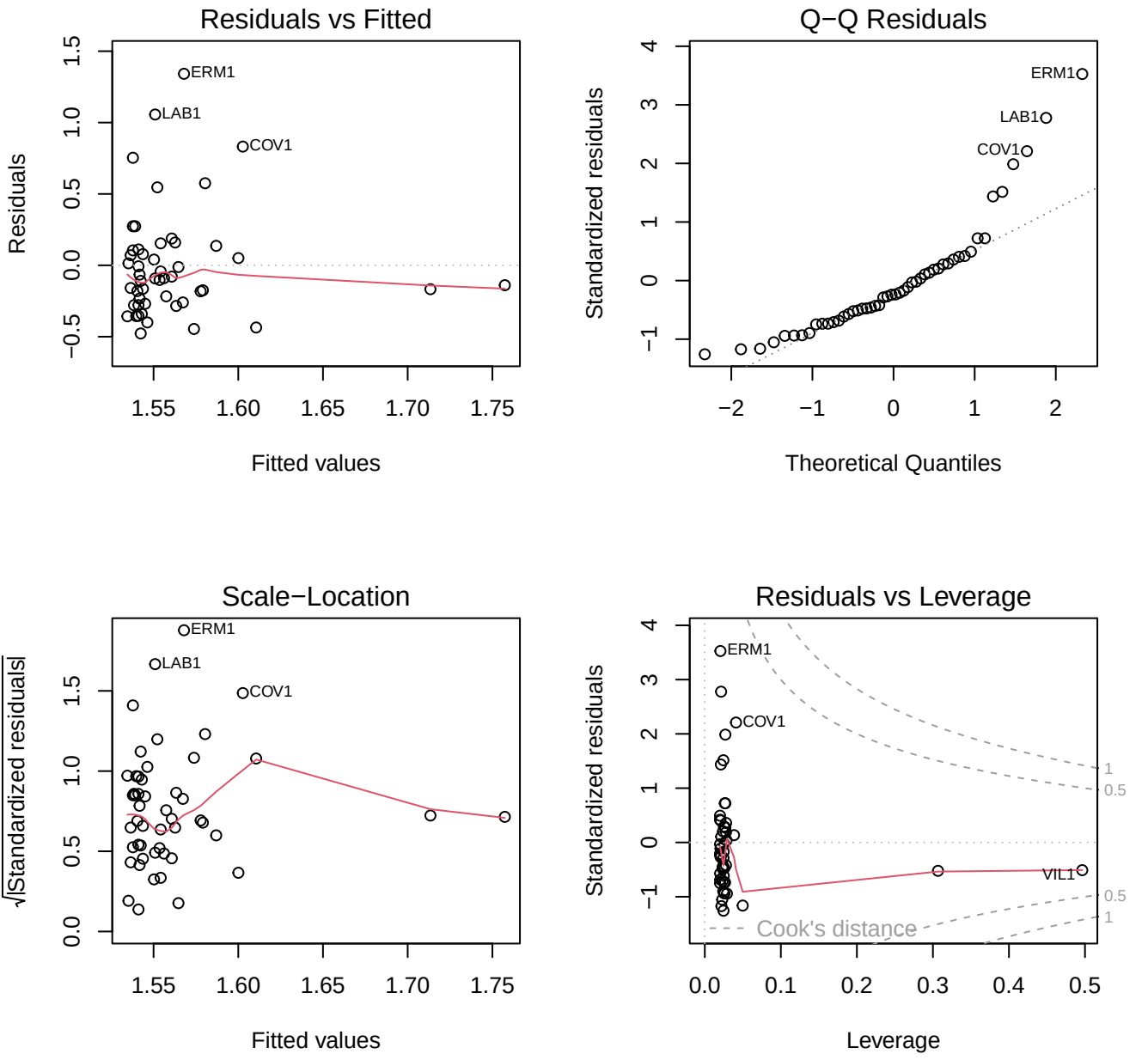

$R^2 = 0.04500821$
p−value: = 0.1391
Fungi_phylum_reads
mean.Depth
1.0
1.5
2.0
2.5
3.0
3.5
4.0

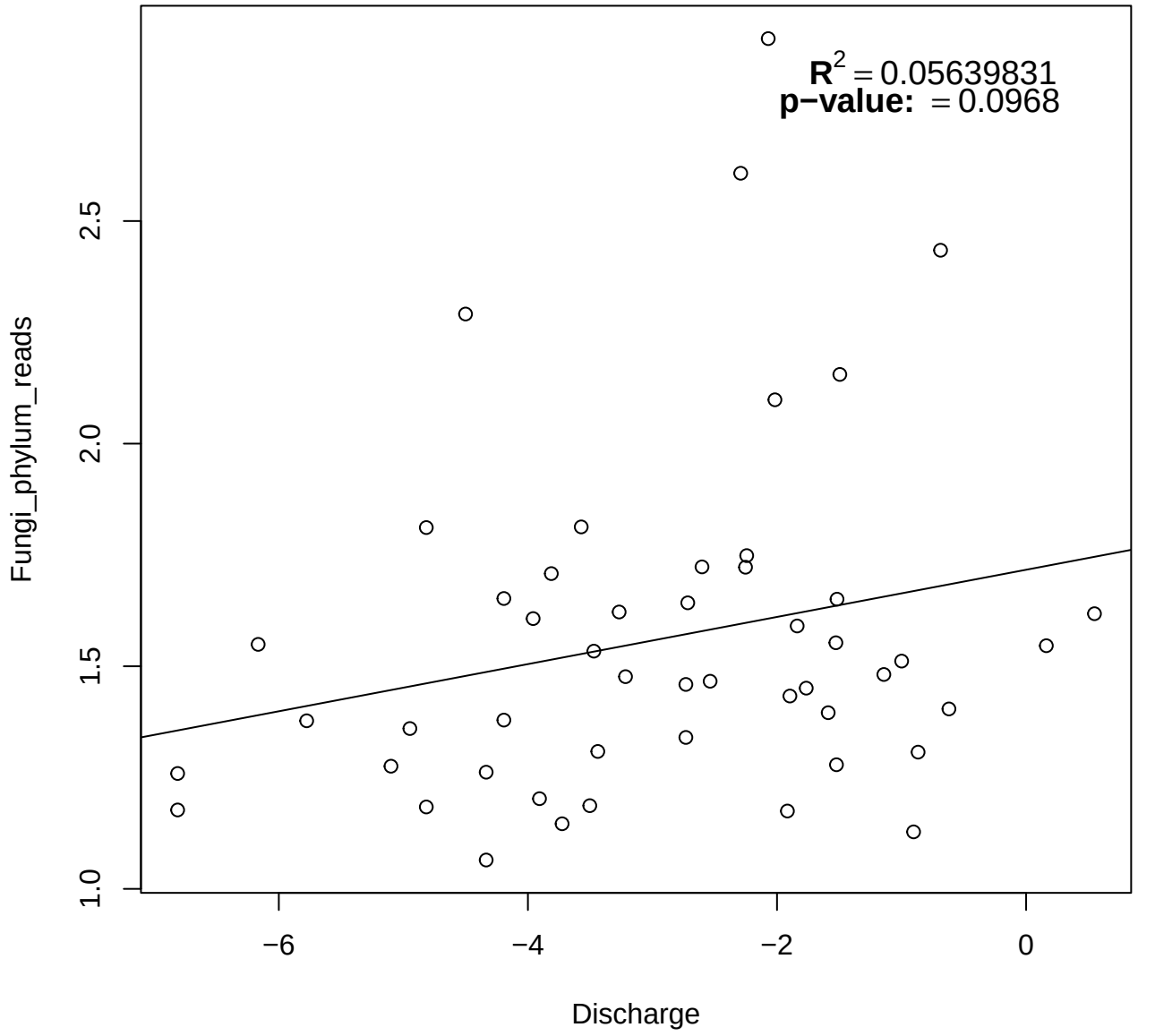

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
ROD1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
ROD1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
ROD1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
ROD1
1
0.5
Cook's distance

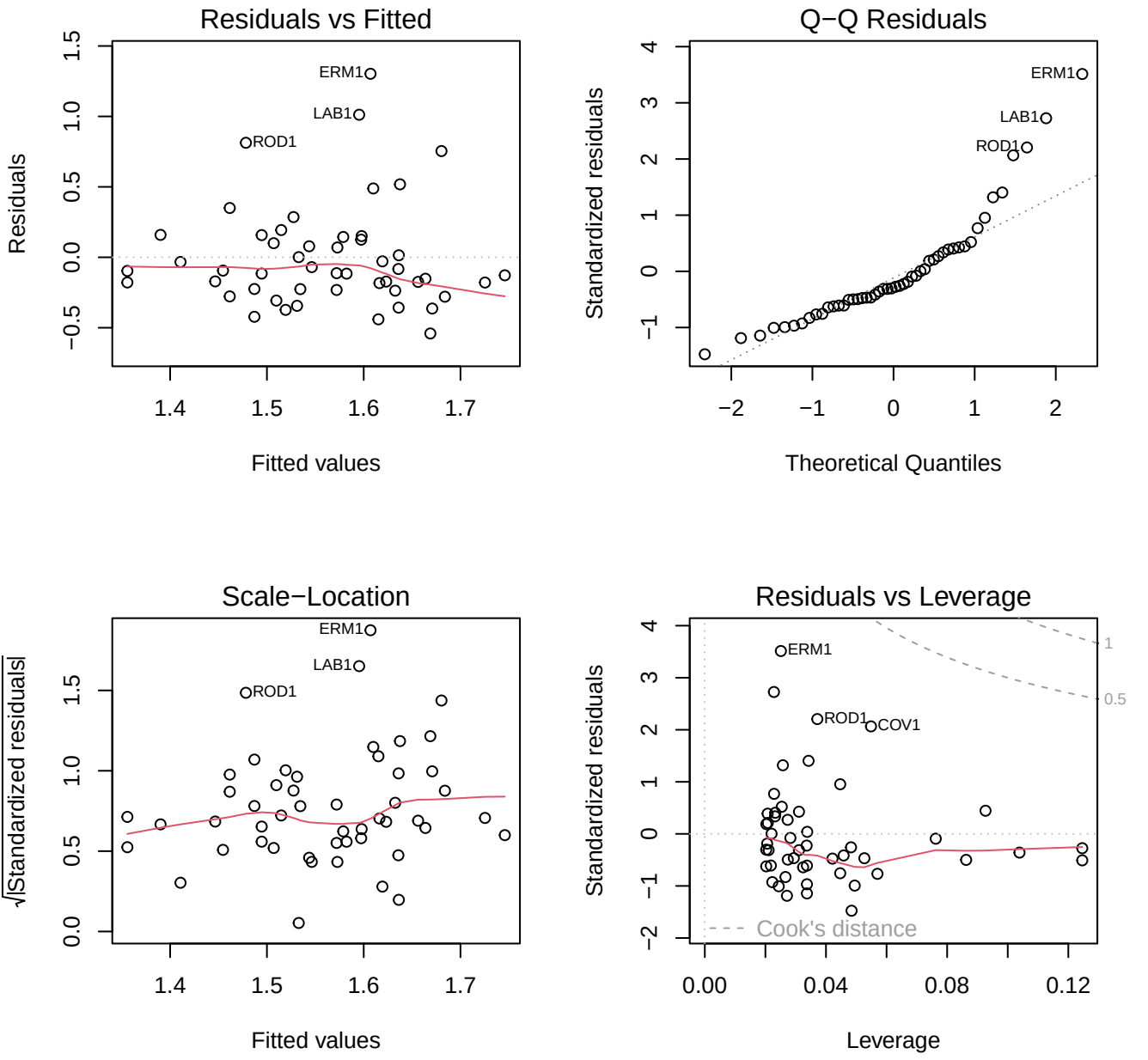

$R^2 = 0.00521655$
p−value: = 0.6182
Fungi_phylum_reads
1.0
1.5
2.0
2.5
0.1
0.2
0.3
0.4
0.5
mean.Velocity

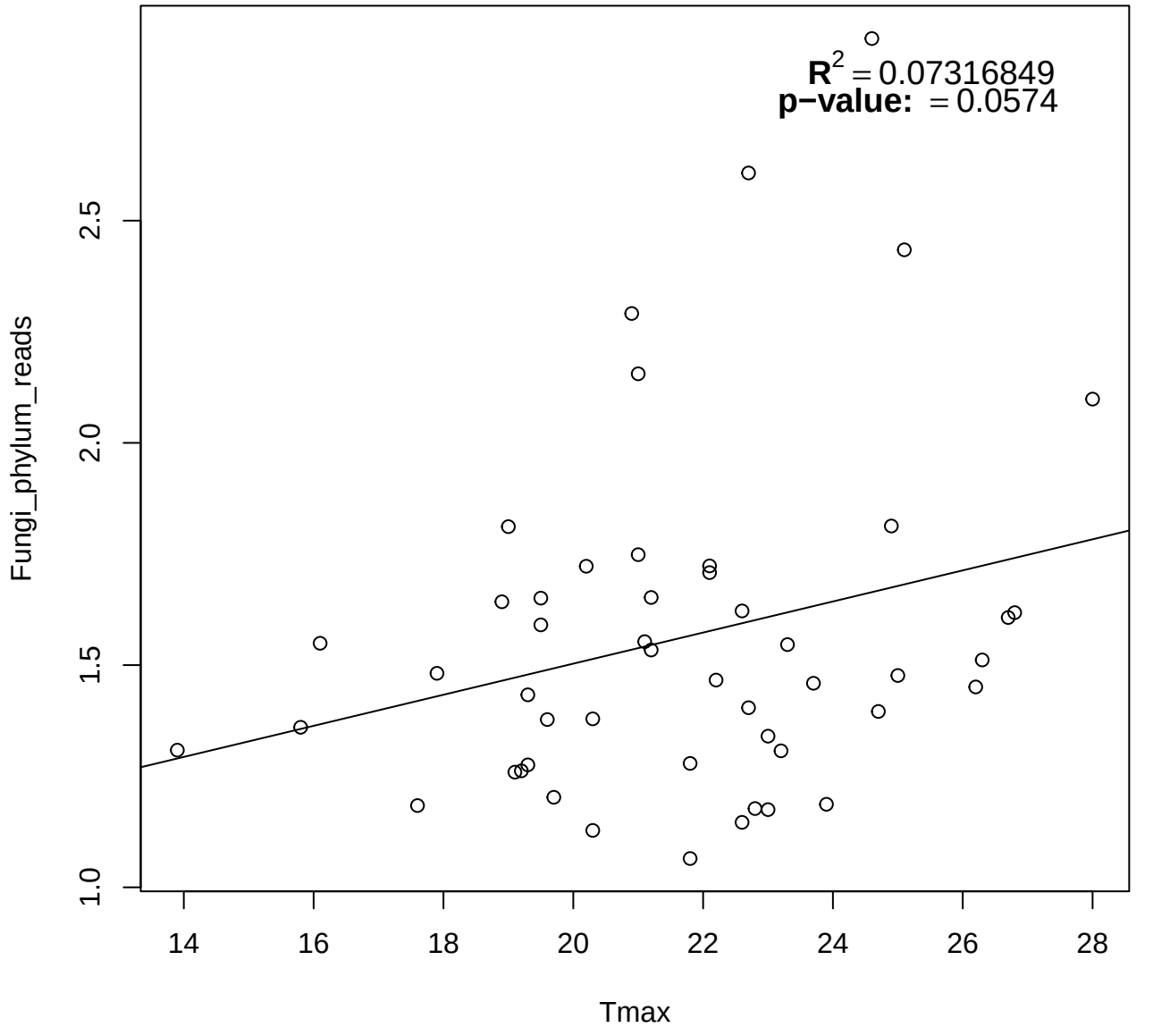

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
SOU1
Cook's distance
1
0.5

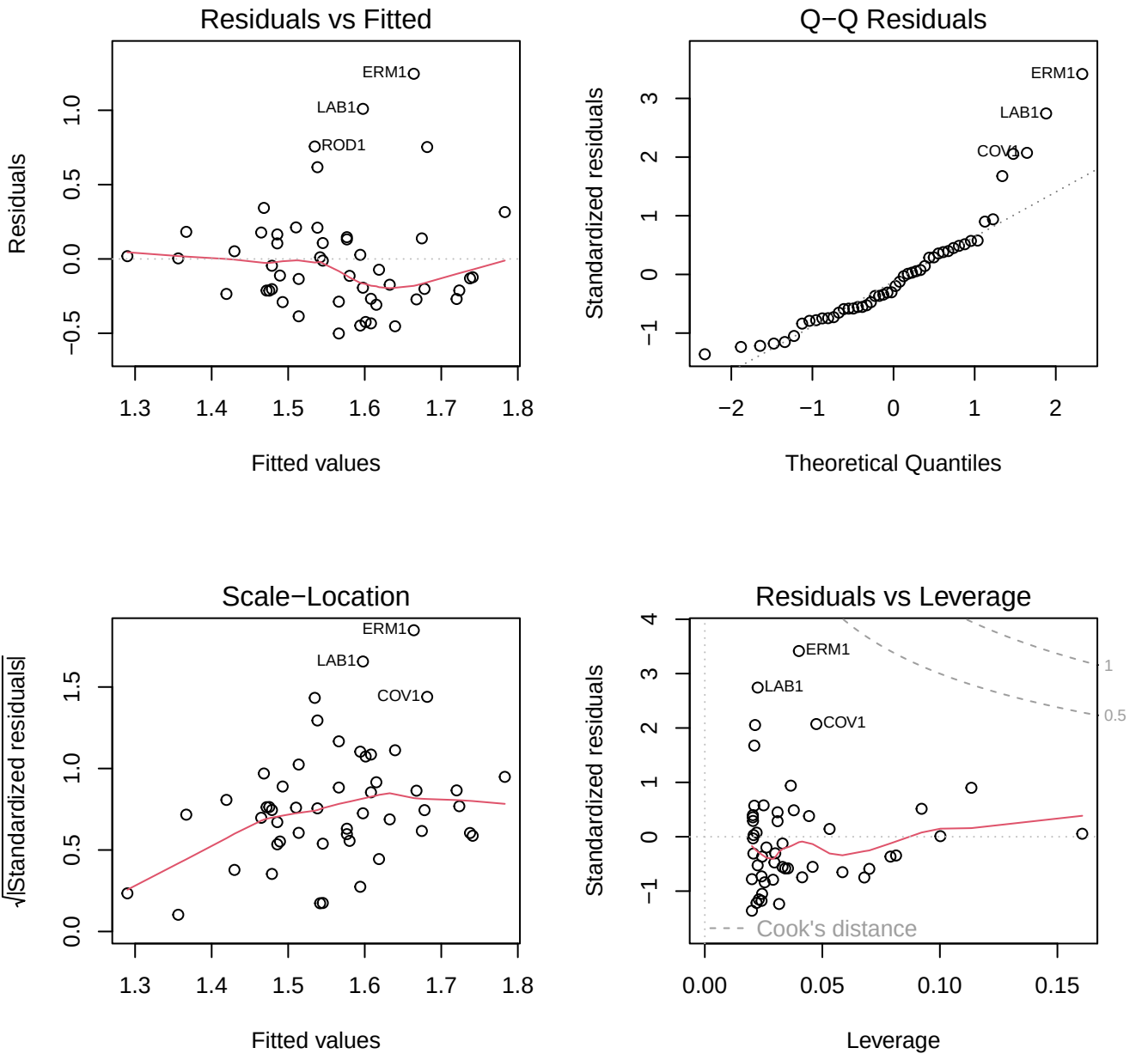

$R^2 = 0.01121159$
p−value: = 0.4643
Fungi_phylum_reads
1.0
1.5
2.0
2.5
0
5
10
15
20
25
30
35
Width

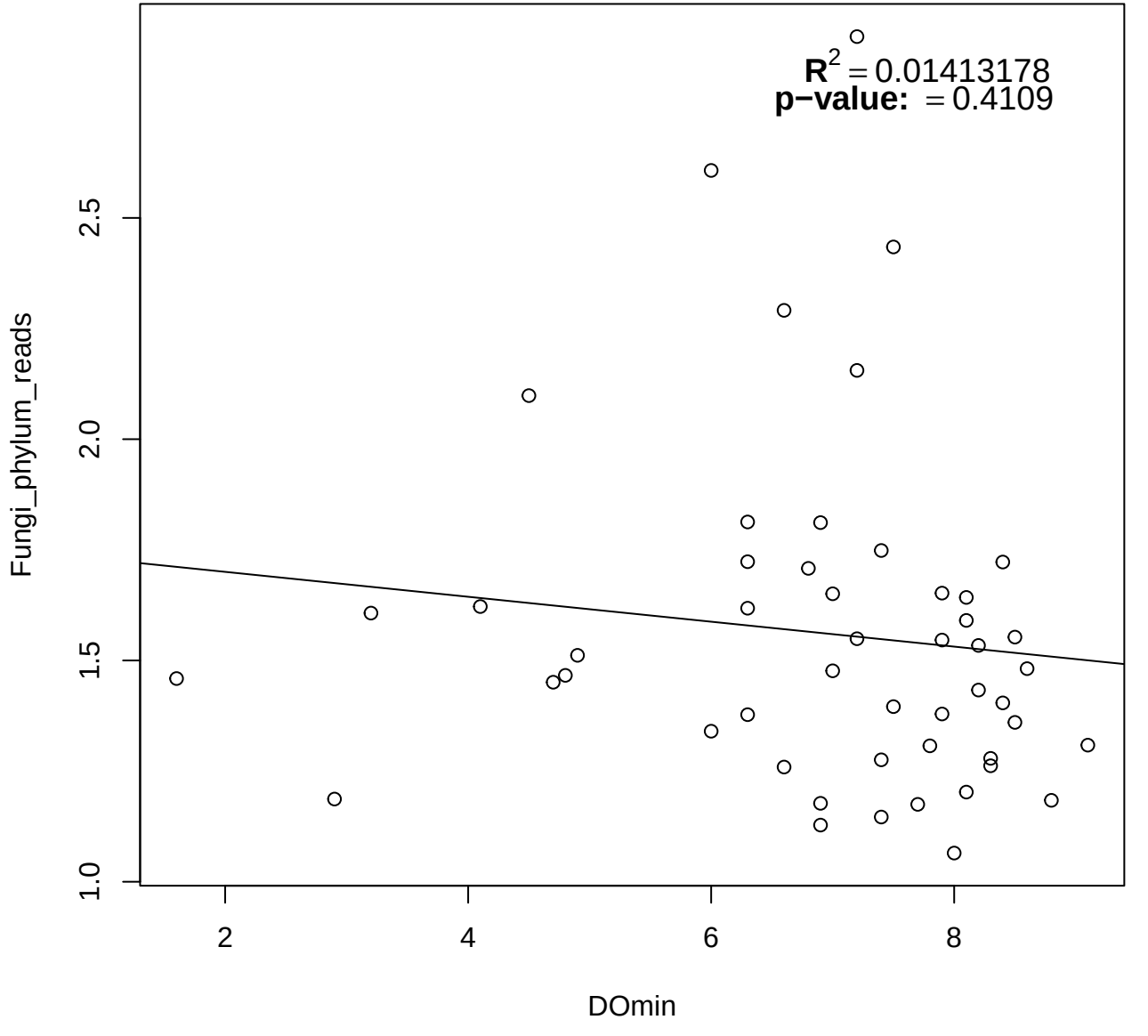

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
COV1
VIL1
Cook's distance

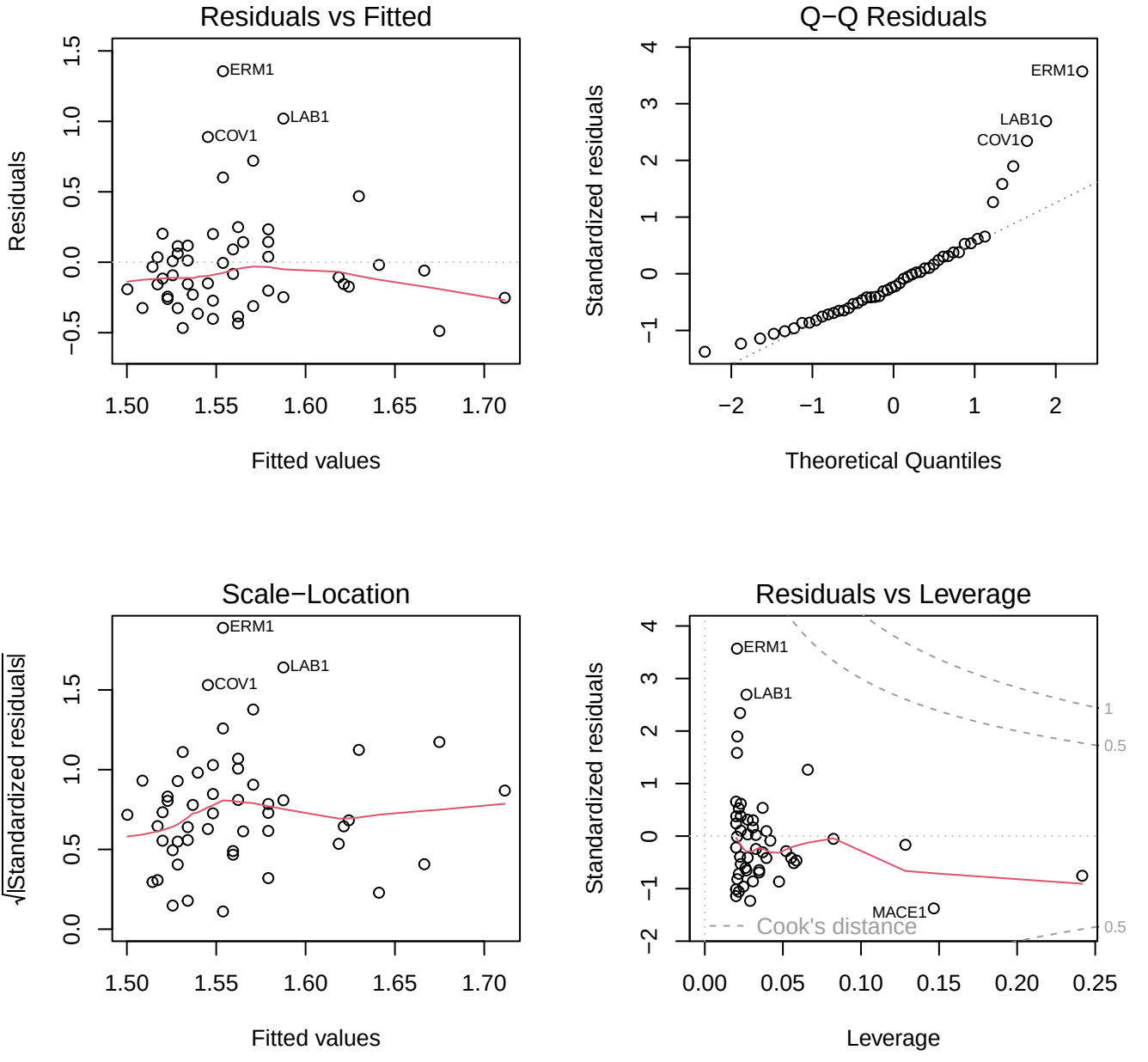

$R^2 = 0.05639831$
p−value: = 0.0968
Fungi_phylum_reads
1.0
1.5
2.0
2.5
−6
−4
−2
0
Discharge

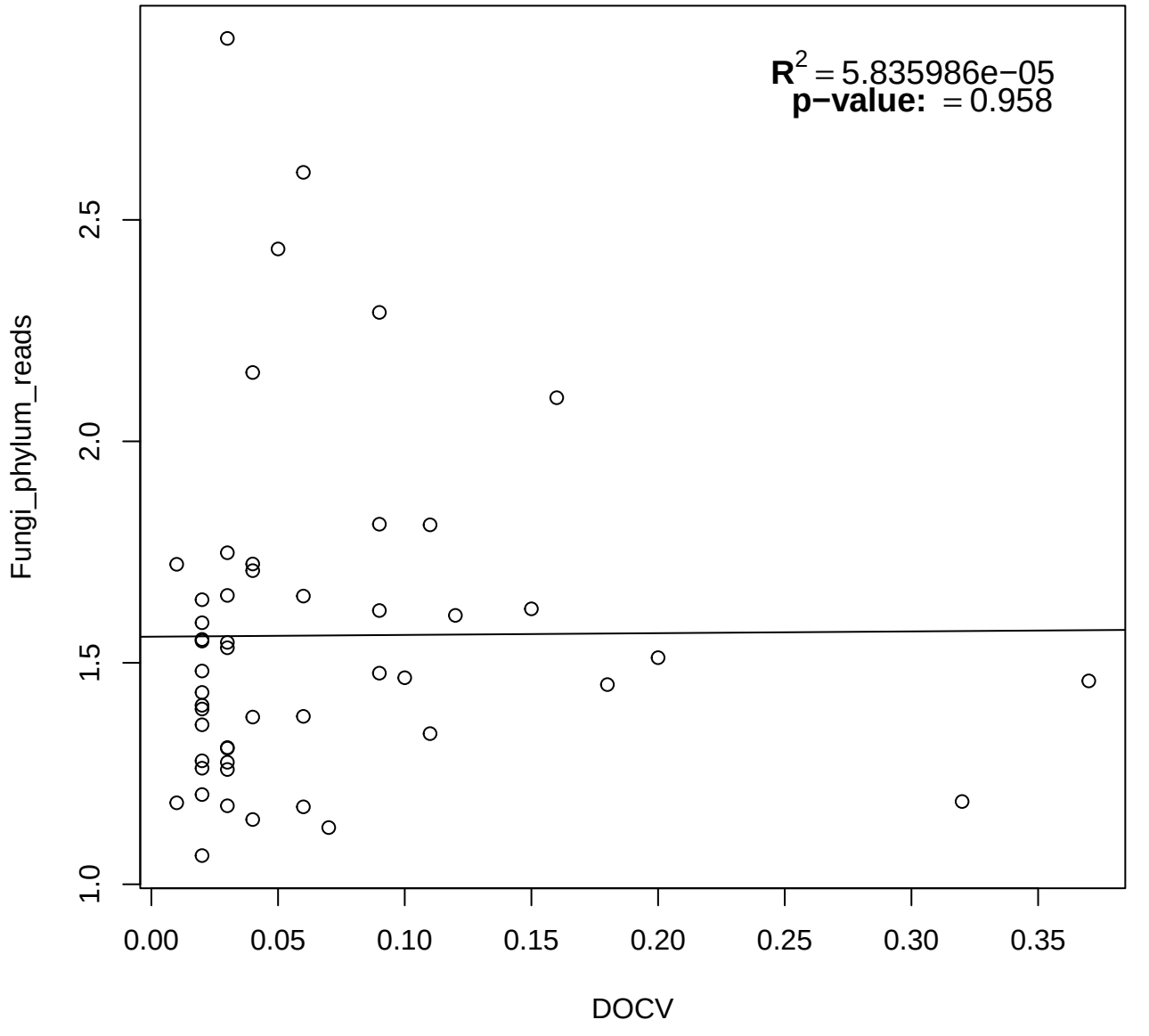

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
ROD1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
ROD1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
ROD1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
ROD1
COV1
Cook's distance
1
0.5

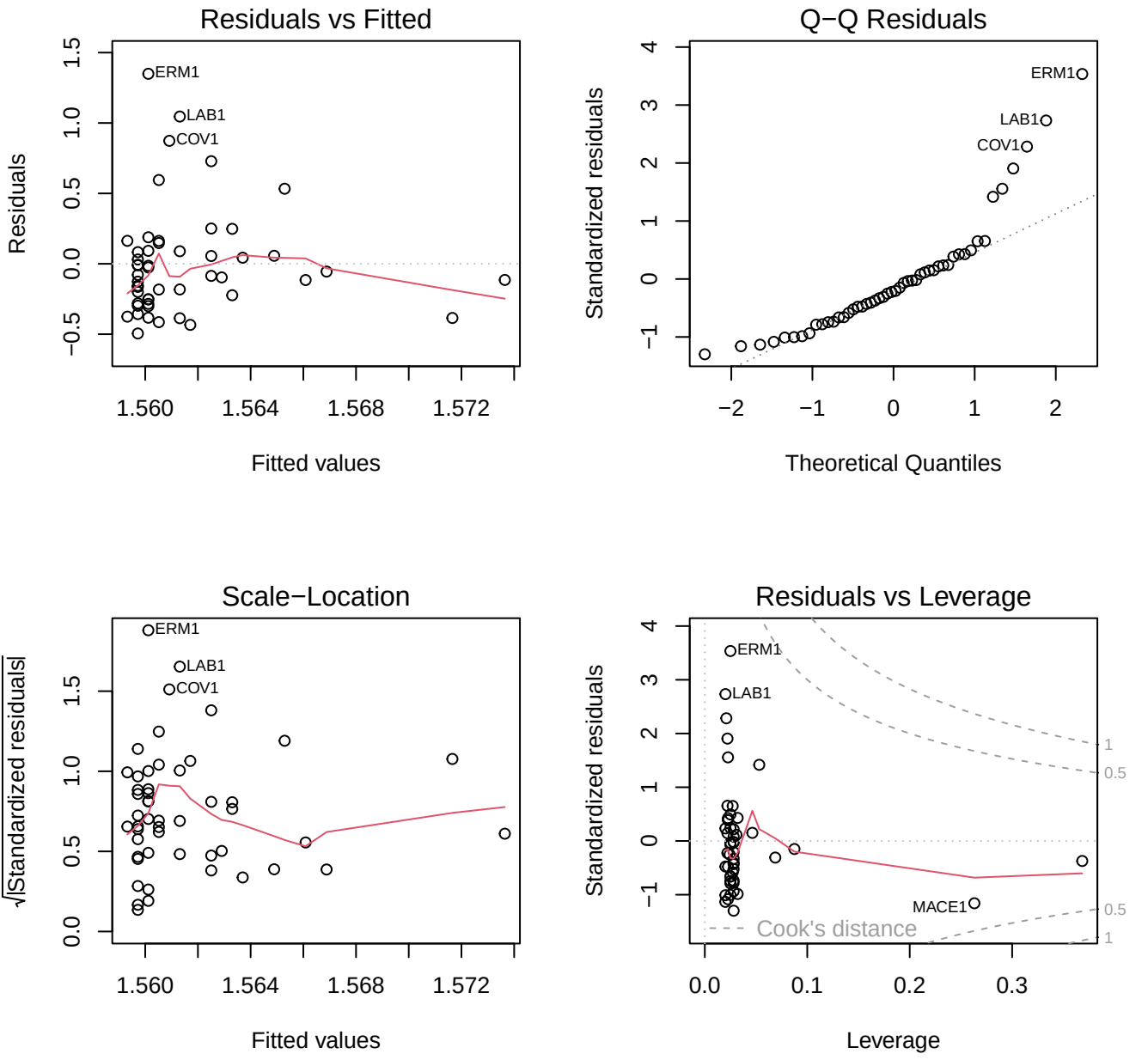

$R^2 = 0.07316849$
p−value: = 0.0574
Fungi_phylum_reads
1.0
1.5
2.0
2.5
14
16
18
20
22
24
26
28
Tmax

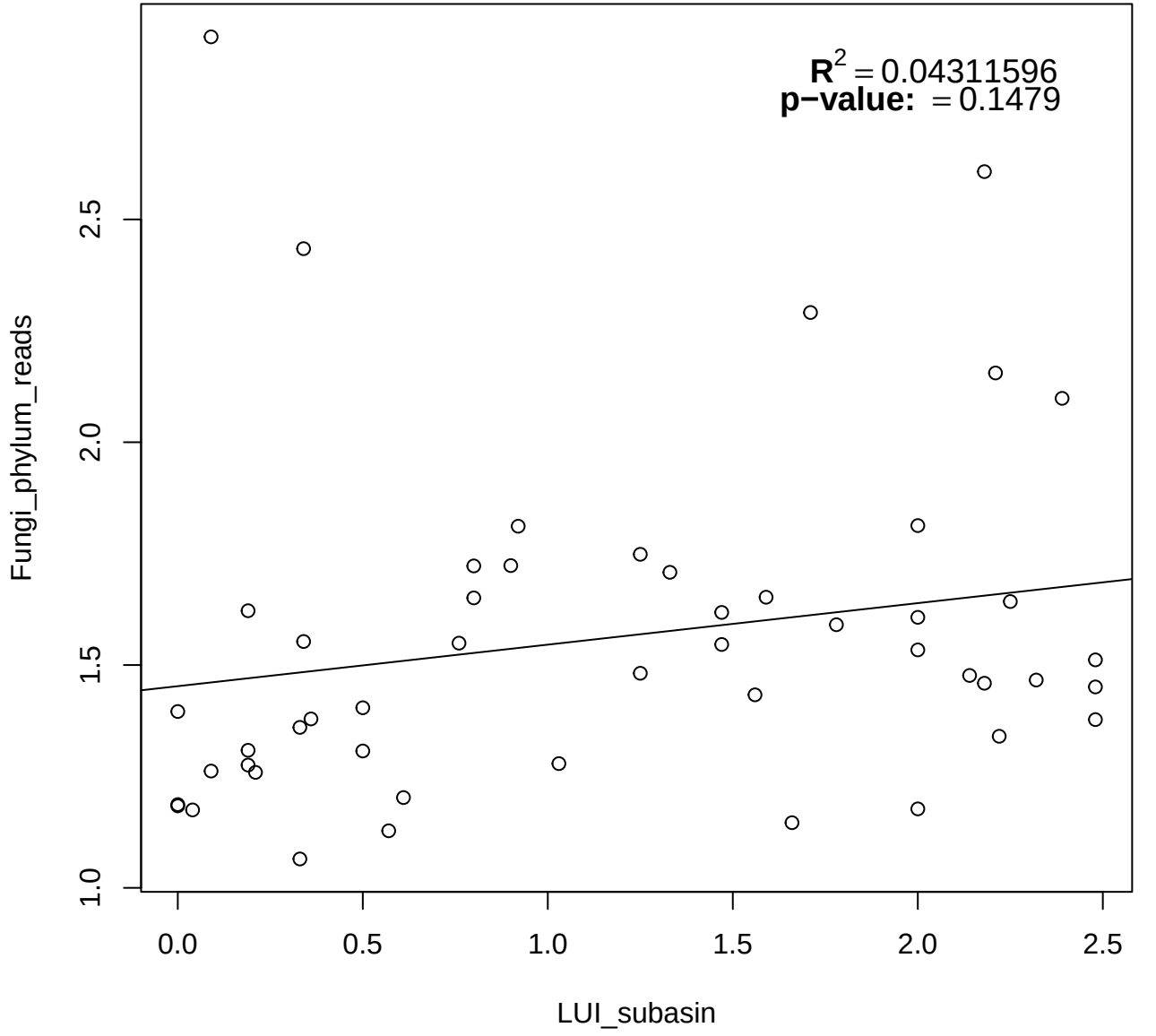

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
ROD1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
COV1
1
0.5
Cook's distance

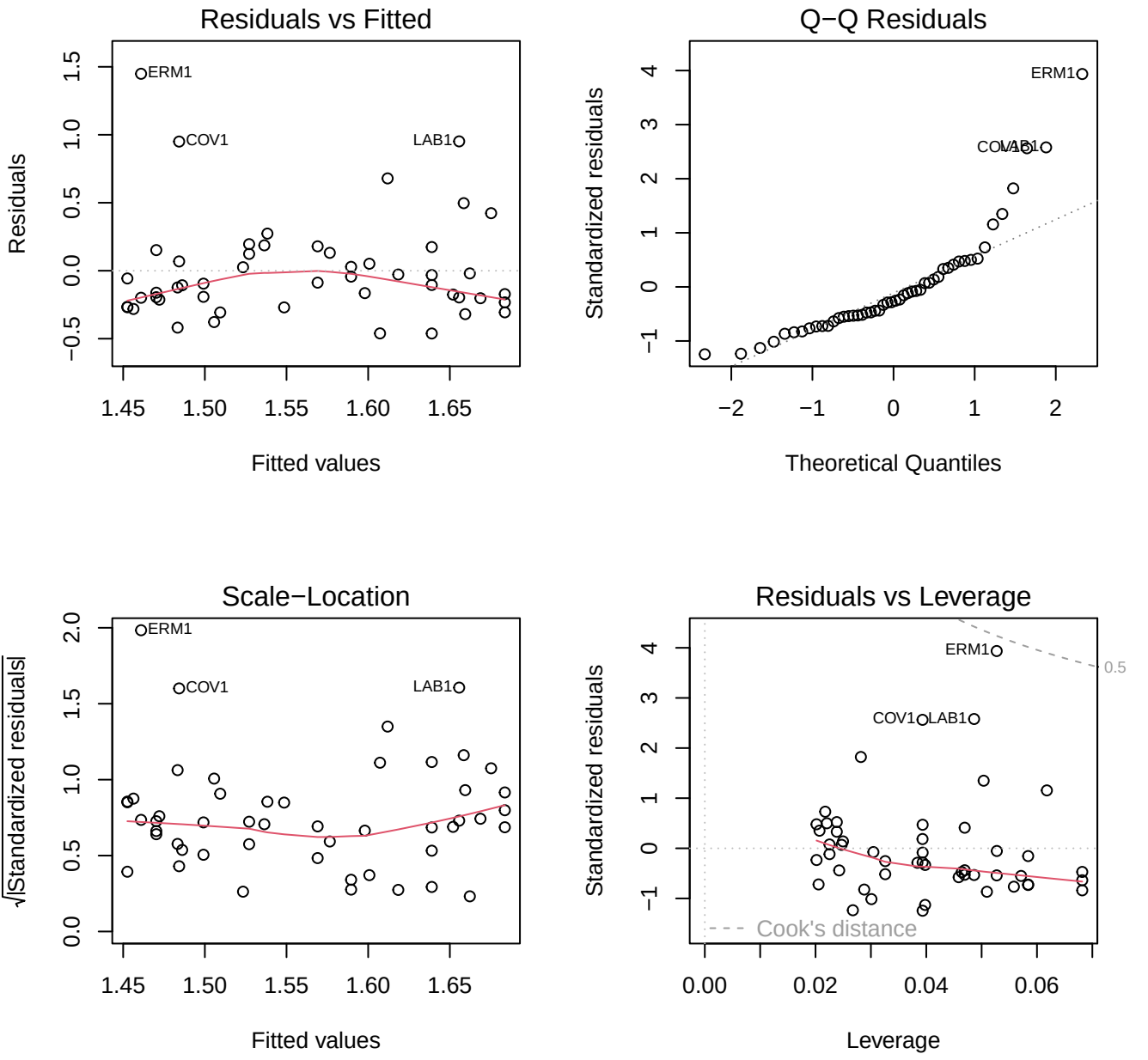

$R^2 = 0.01413178$
p−value: = 0.4109
Fungi_phylum_reads
1.0
1.5
2.0
2.5
2
4
6
8
DOmin

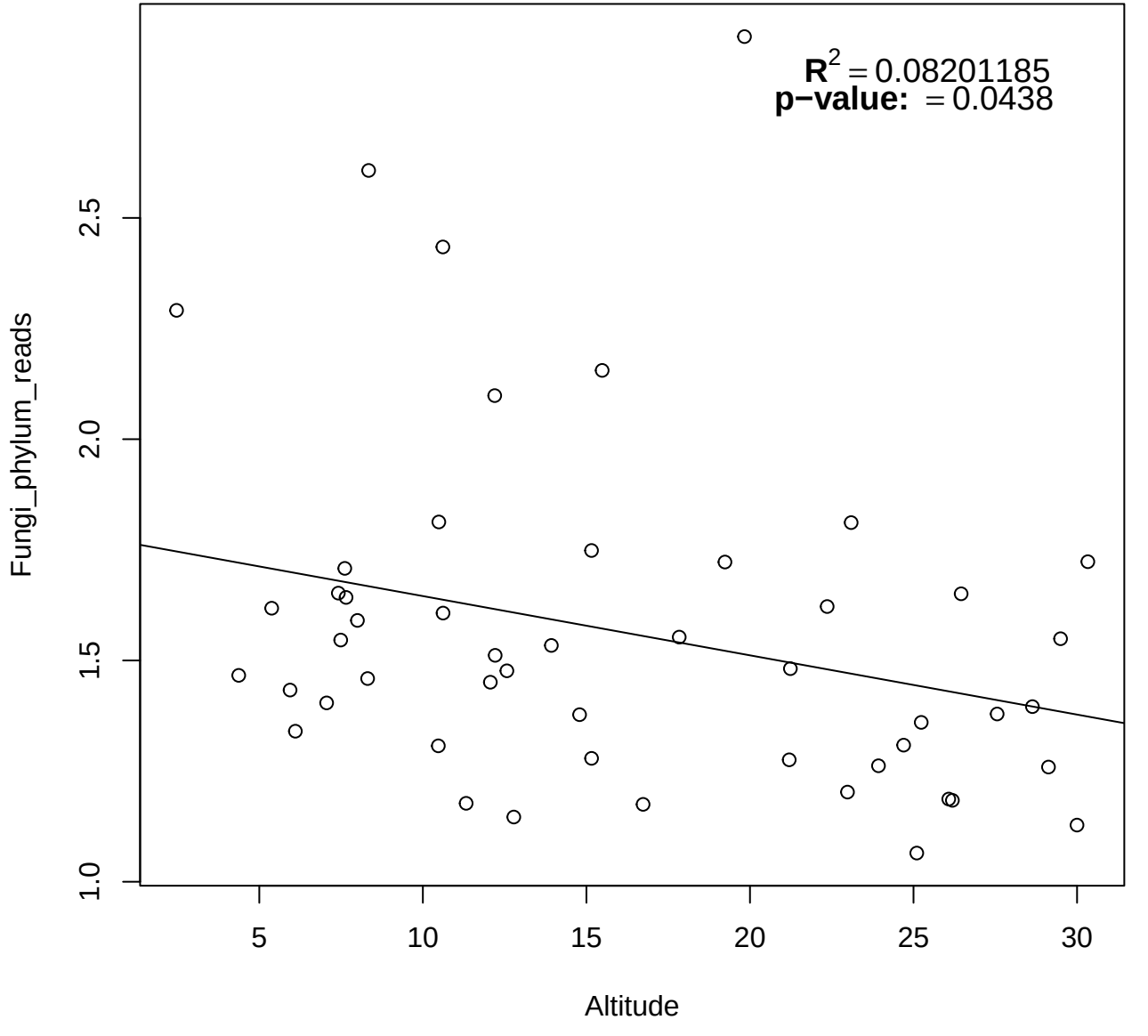

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
MACE1
Cook's distance
1
0.5
0.5

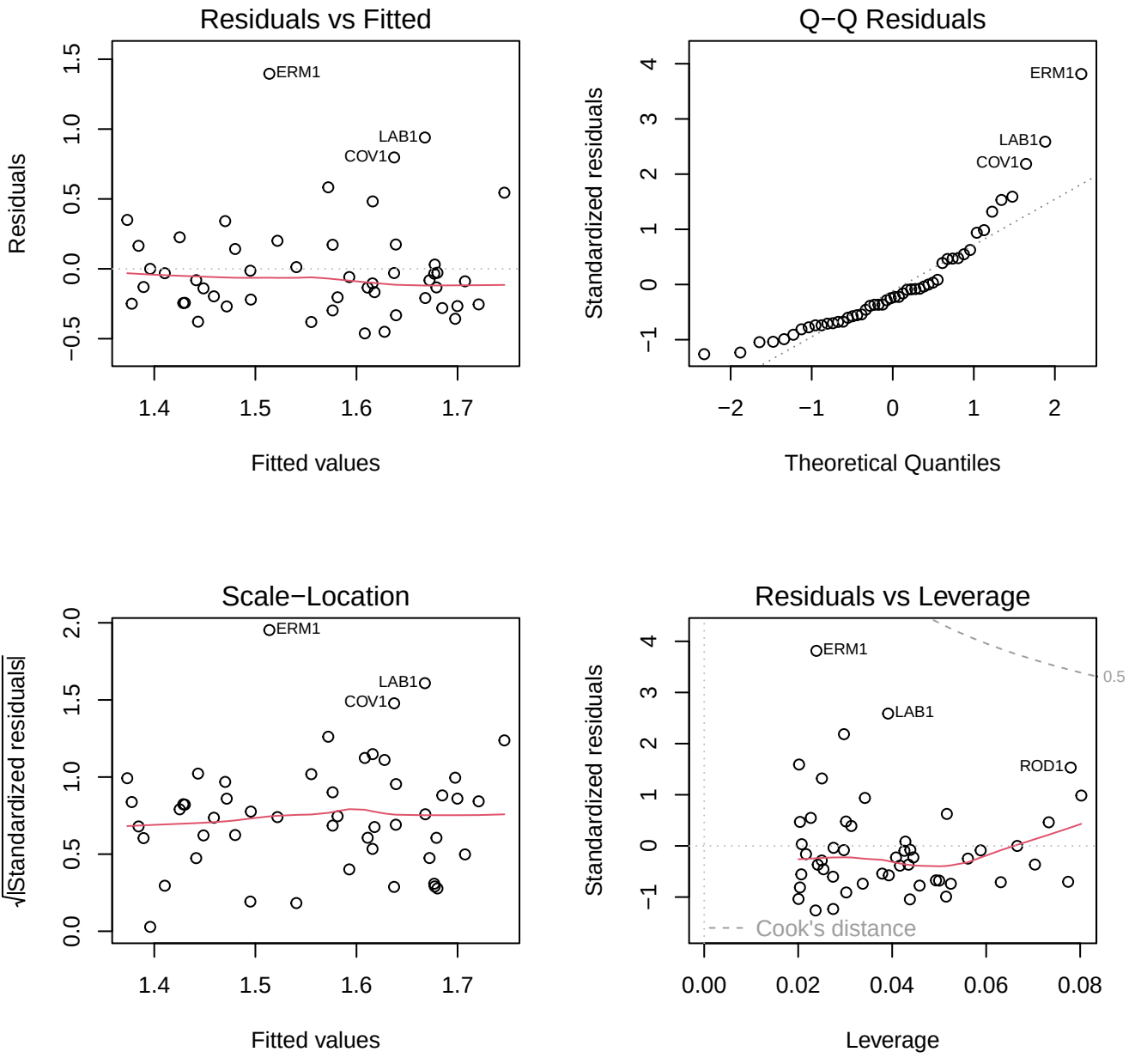

$R^2 = 5.835986e-05$
p−value: = 0.958
Fungi_phylum_reads
1.0
1.5
2.0
2.5
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
DOCV

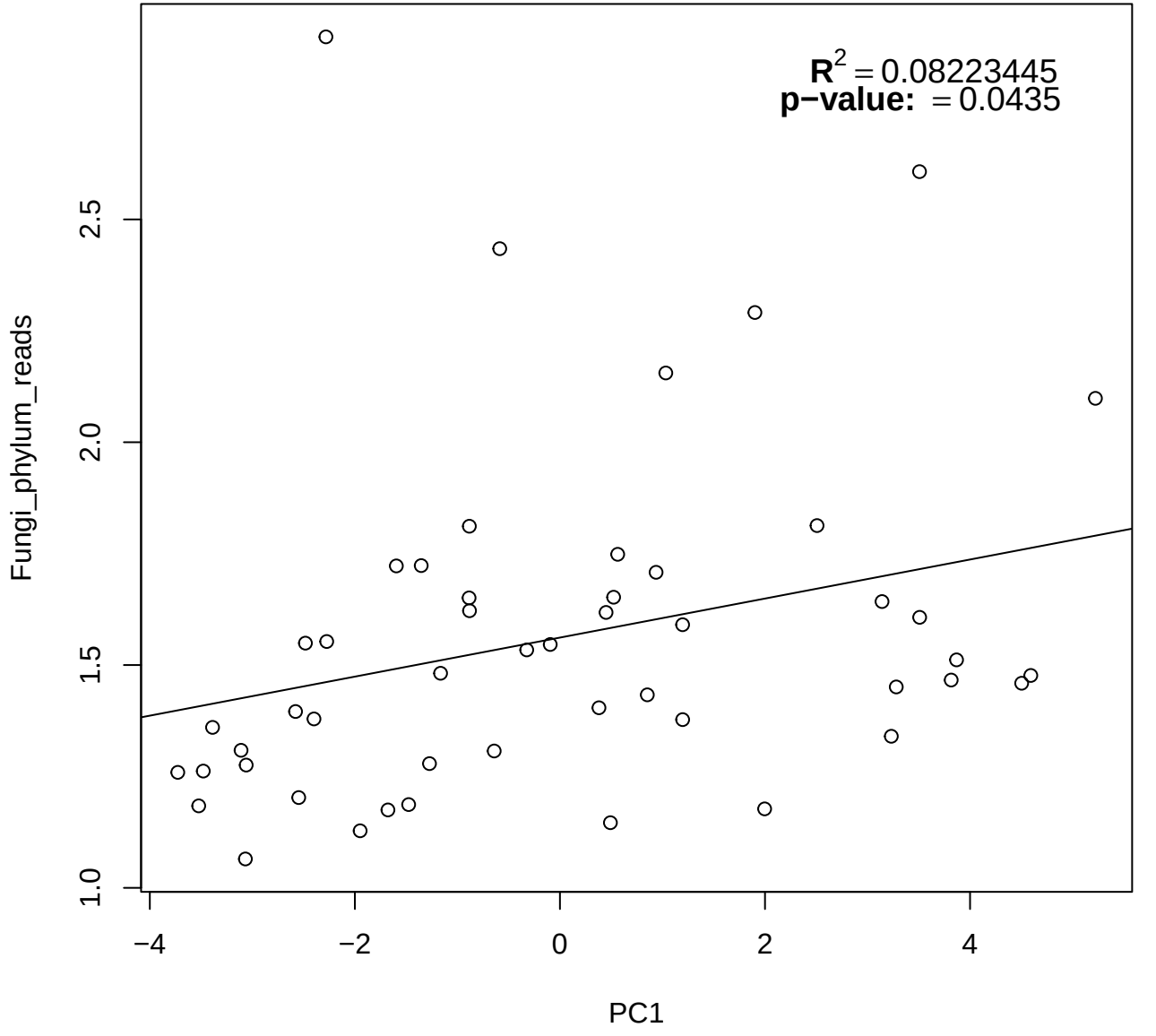

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
MACE1
Cook's distance
1
0.5
0.5
1

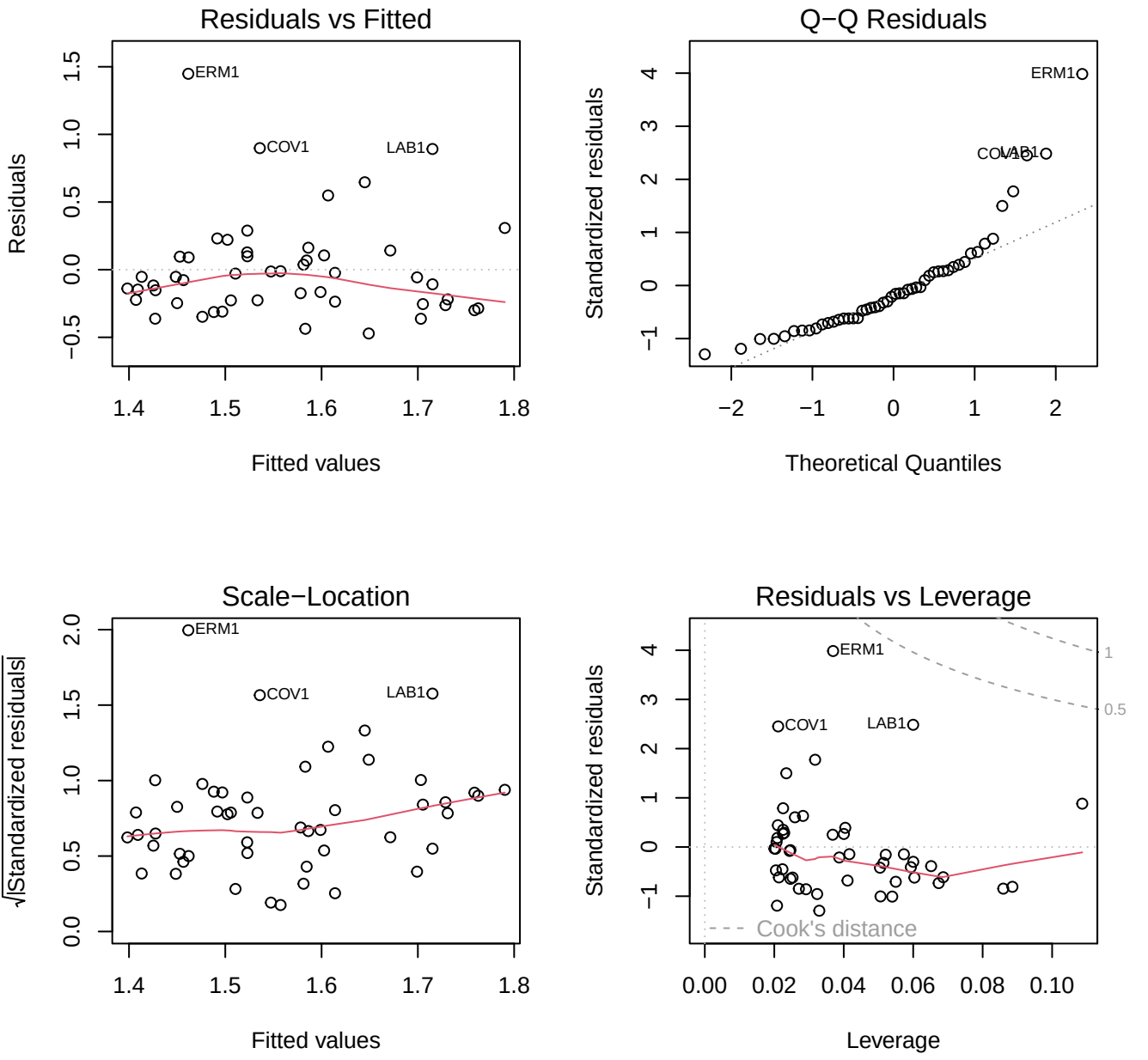

$R^2 = 0.04311596$
p−value: = 0.1479
Fungi_phylum_reads
LUI_subasin
1.0
1.5
2.0
2.5
0.0
0.5
1.0
1.5
2.0
2.5

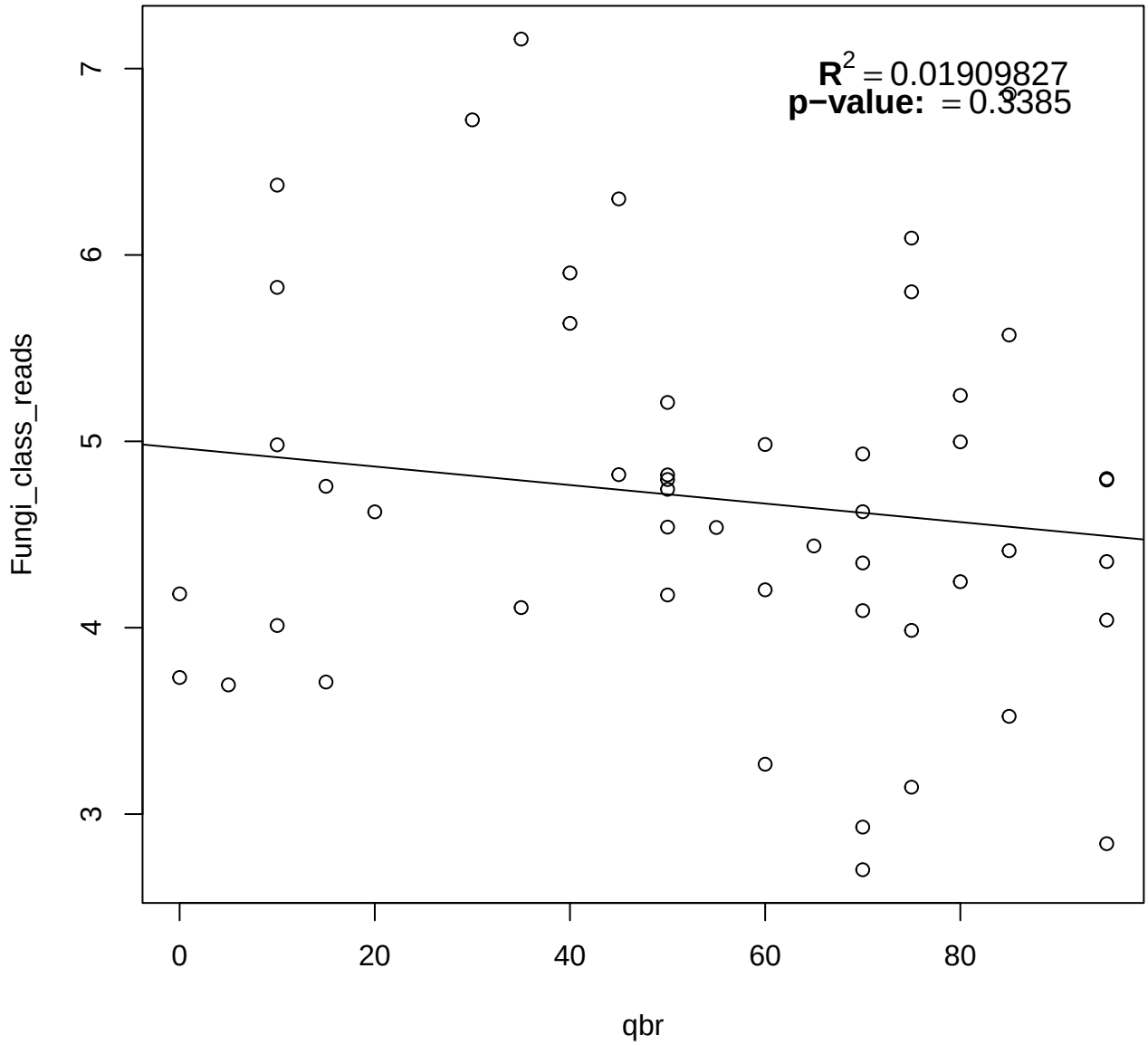

Residuals vs Fitted
Residuals
Fitted values
ERM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
COV1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
COV1
LAB1
0.5
Cook's distance

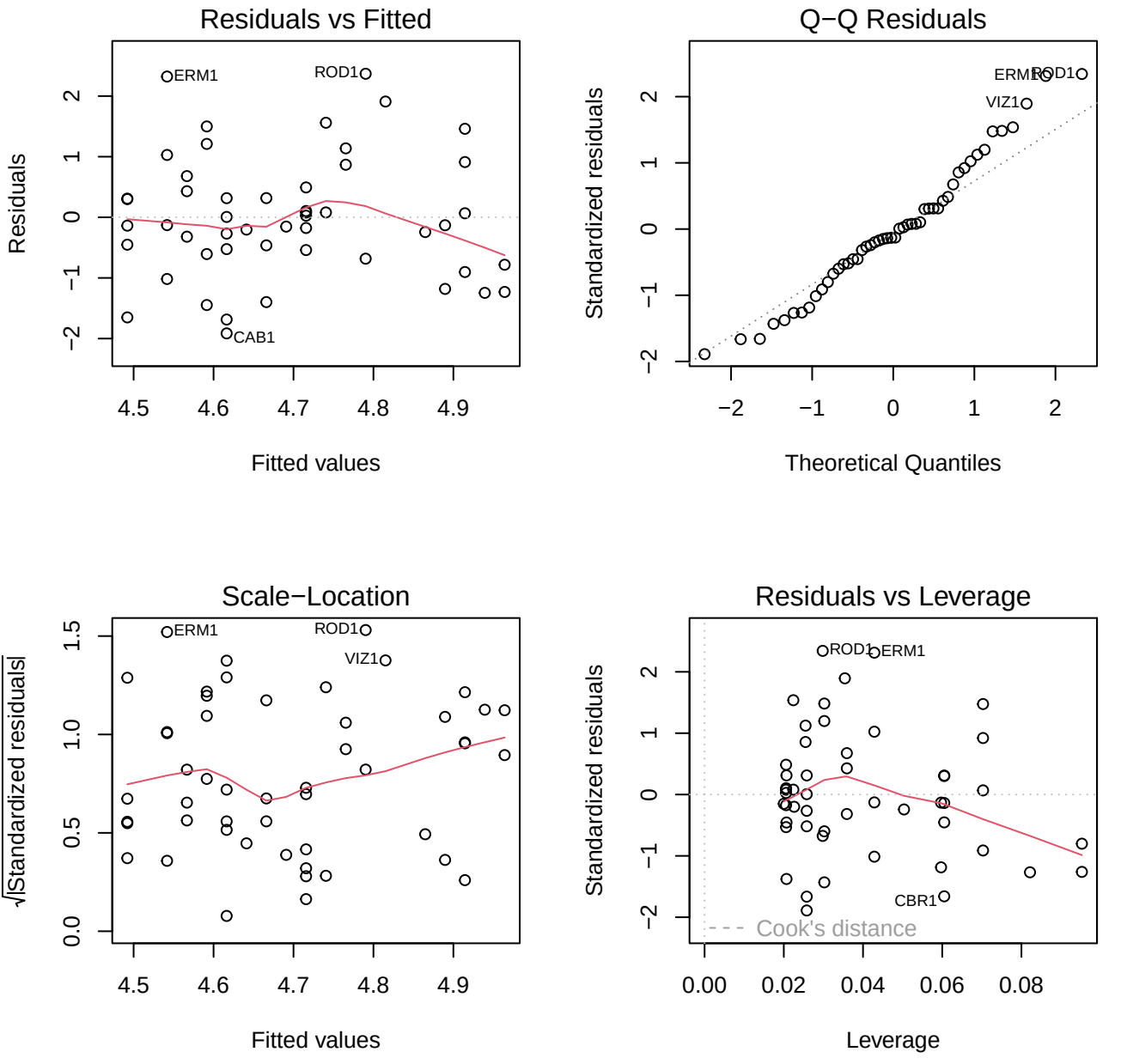

$R^2 = 0.08201185$
p−value: = 0.0438
Fungi_phylum_reads
1.0
1.5
2.0
2.5
5
10
15
20
25
30
Altitude

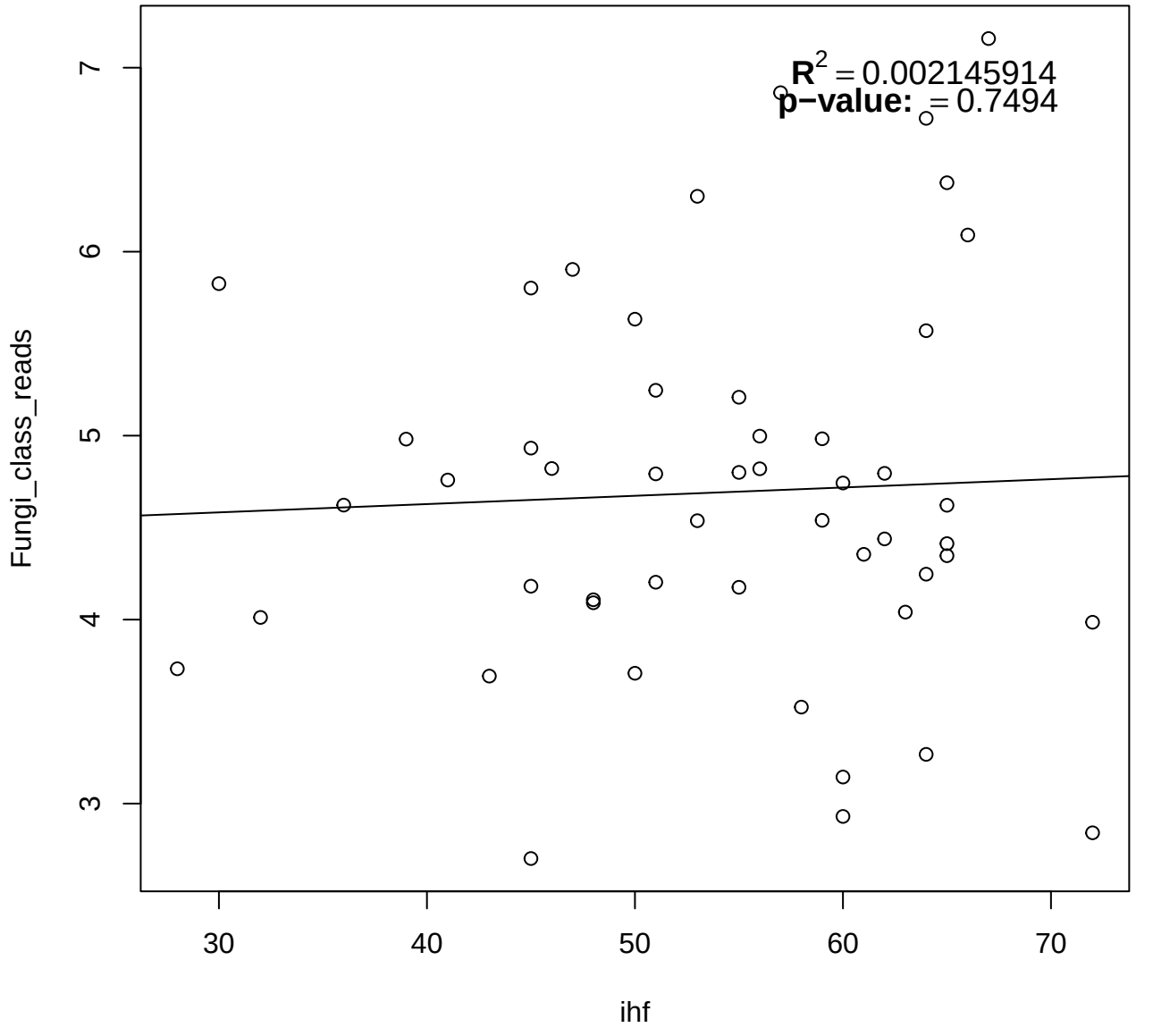

Residuals vs Fitted
Residuals
Fitted values
ERM1
LAB1
COV1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
LAB1
COV1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
LAB1
COV1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
LAB1
ROD1
0.5
Cook's distance

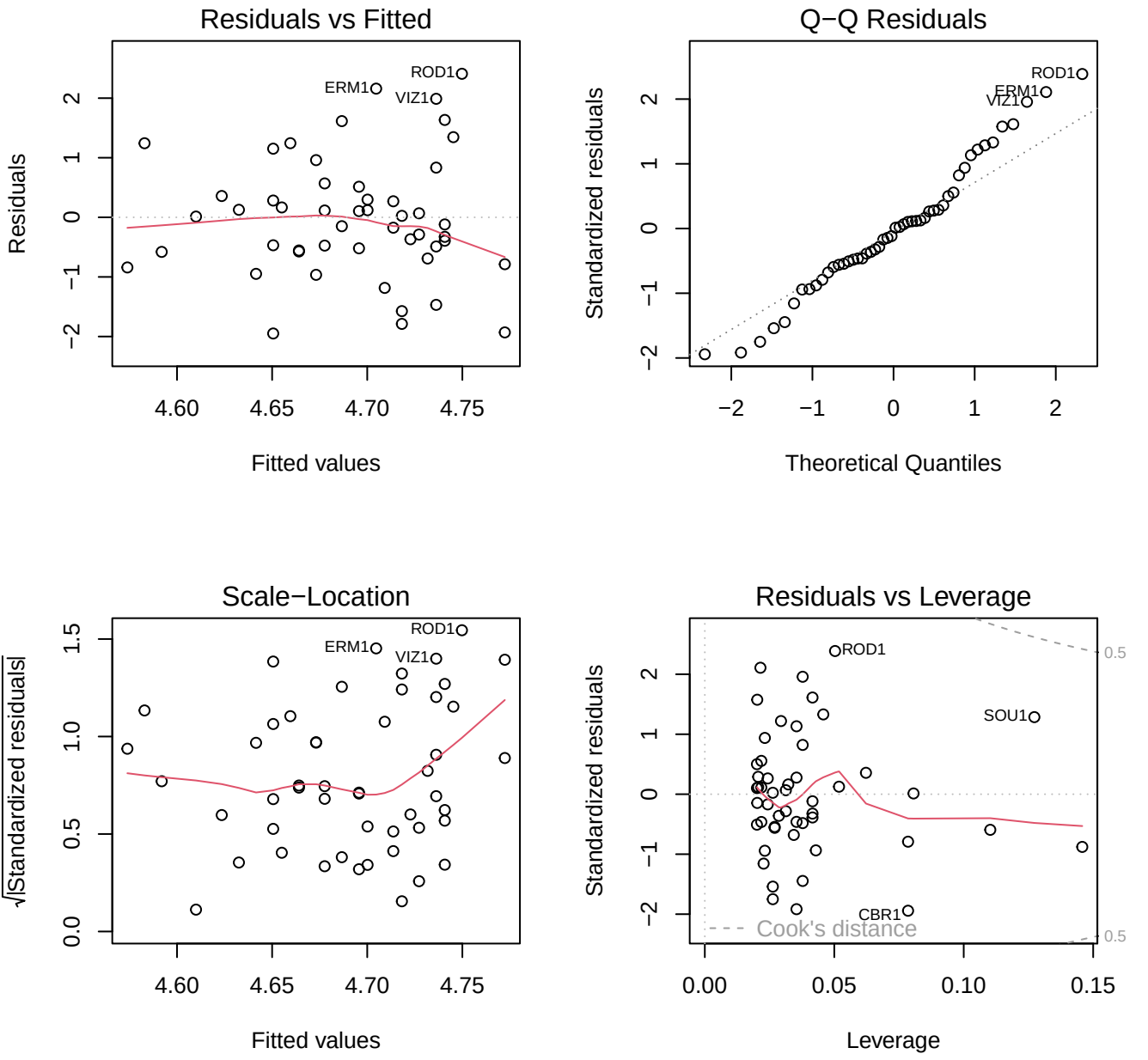

$R^2 = 0.08223445$
p−value: = 0.0435
Fungi_phylum_reads
1.0
1.5
2.0
2.5
−4
−2
0
2
4
PC1

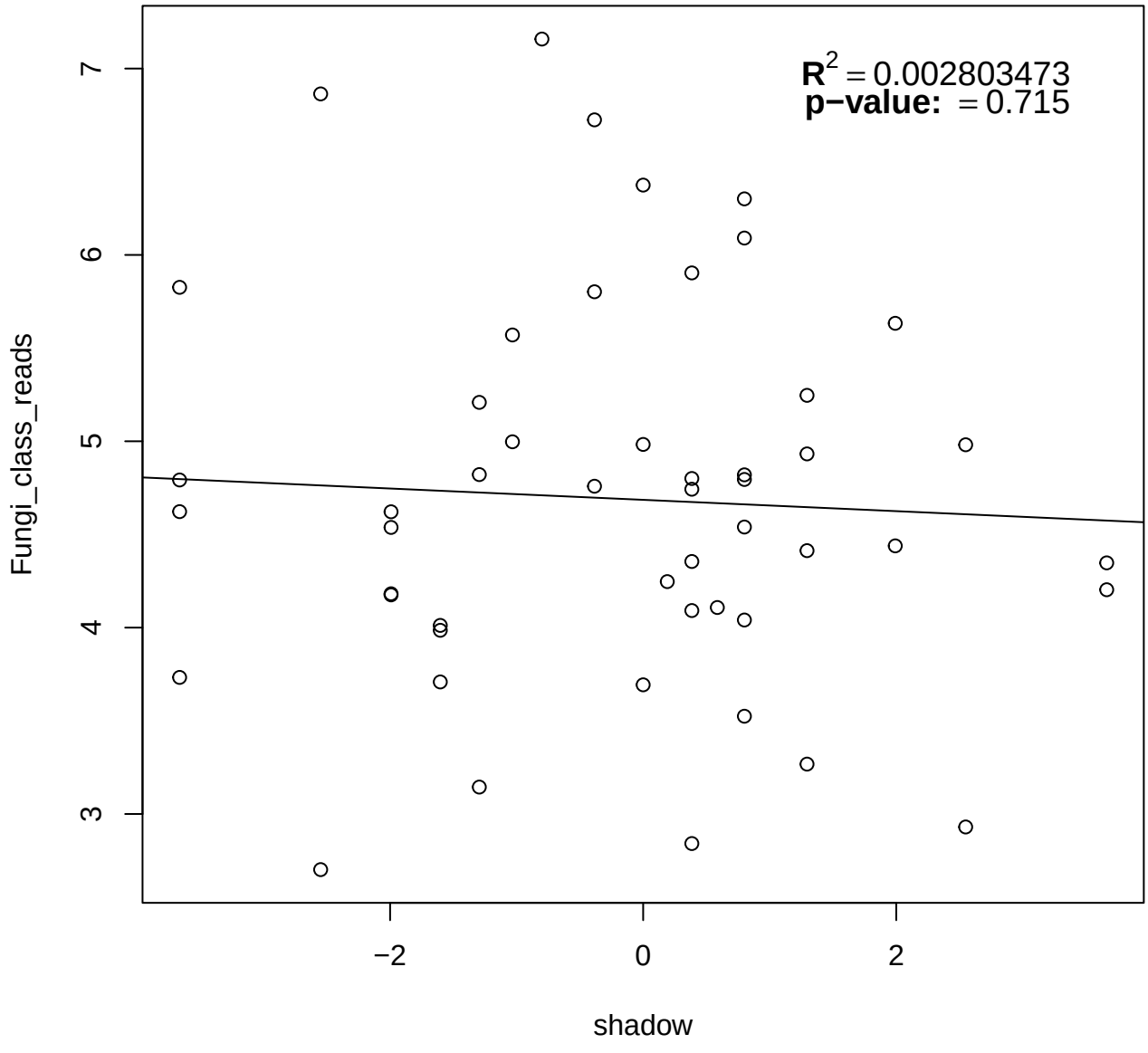

Residuals vs Fitted
Residuals
Fitted values
ERM1
COV1
LAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
COV1
LAB1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
COV1
LAB1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
COV1
LAB1
1
0.5
Cook's distance


$R^2 = 0.01909827$
p−value: = 0.3385
Fungi_class_reads
qbr
3
4
5
6
7
0
20
40
60
80


Residuals vs Fitted
Residuals
Fitted values
ERM1
ROD1
CAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
ROD1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
ROD1
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
ERM1
CBR1
Cook's distance


$R^2 = 0.002145914$
p−value: = 0.7494
Fungi_class_reads
ihf
3
4
5
6
7
30
40
50
60
70


Residuals vs Fitted
Residuals
Fitted values
ROD1
ERM1
VIZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
ERM1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
ERM1
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
SOU1
CBR1
Cook's distance
0.5
0.5


$R^2 = 0.002803473$
p−value: $= 0.715$
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shadow
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4
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6
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−2
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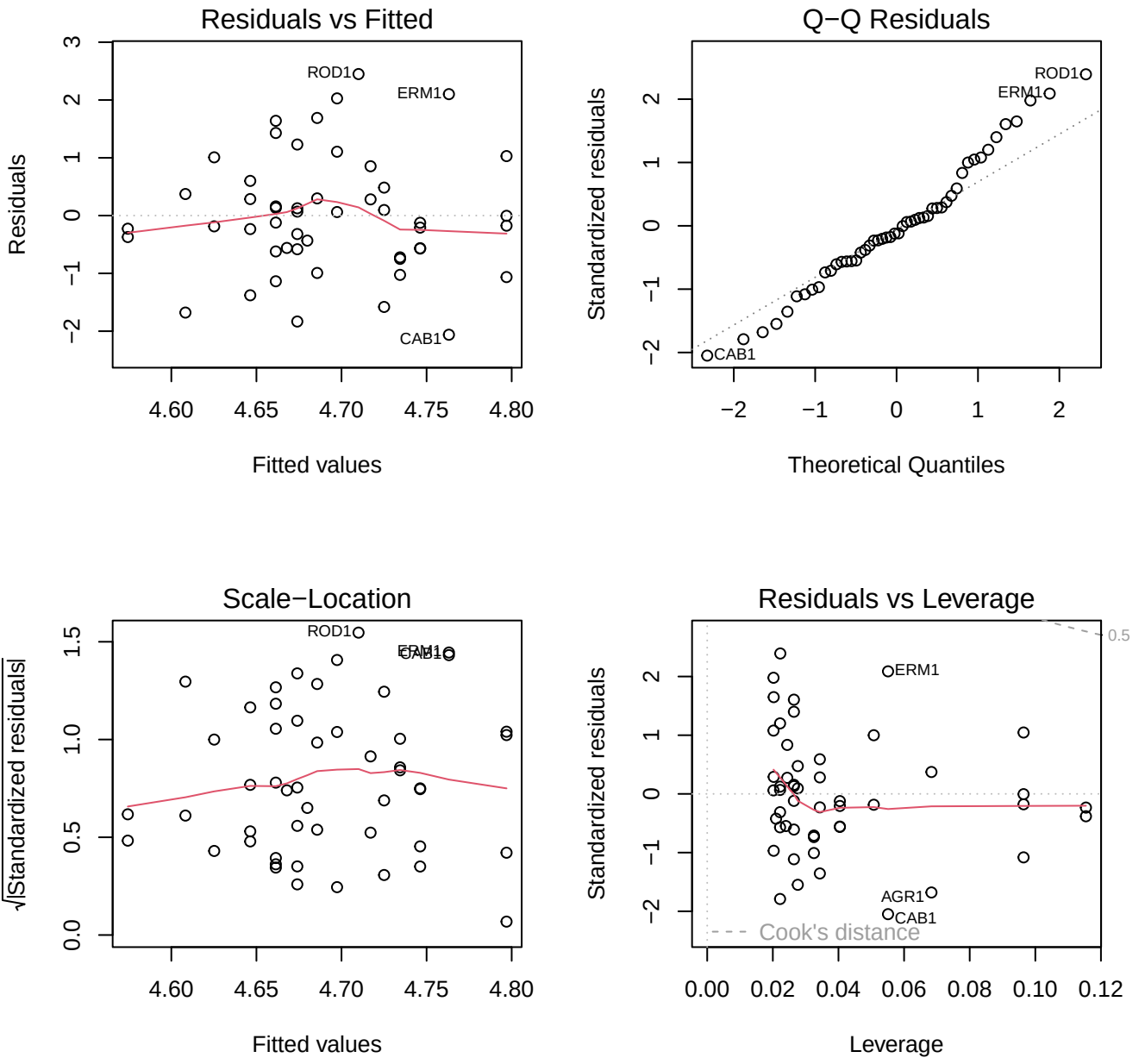
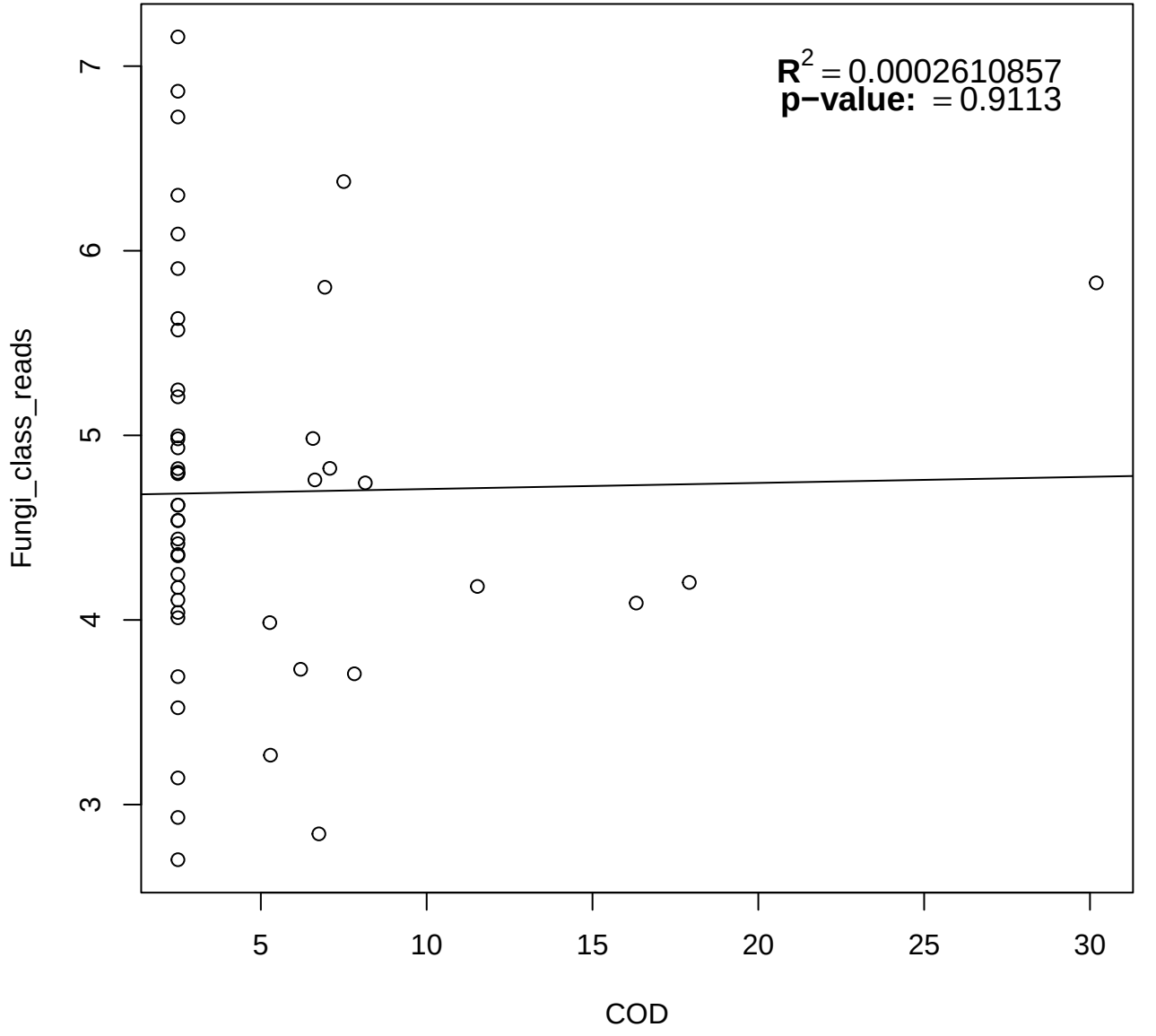
2


Residuals vs Fitted
Residuals
Fitted values
ROD1
ERM1
CAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
ERM1
CAB1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
ERM1
CAB1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
AGR1
CAB1
Cook's distance
0.5


$R^2 = 0.0002610857$
p−value: = 0.9113
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COD
3
4
5
6
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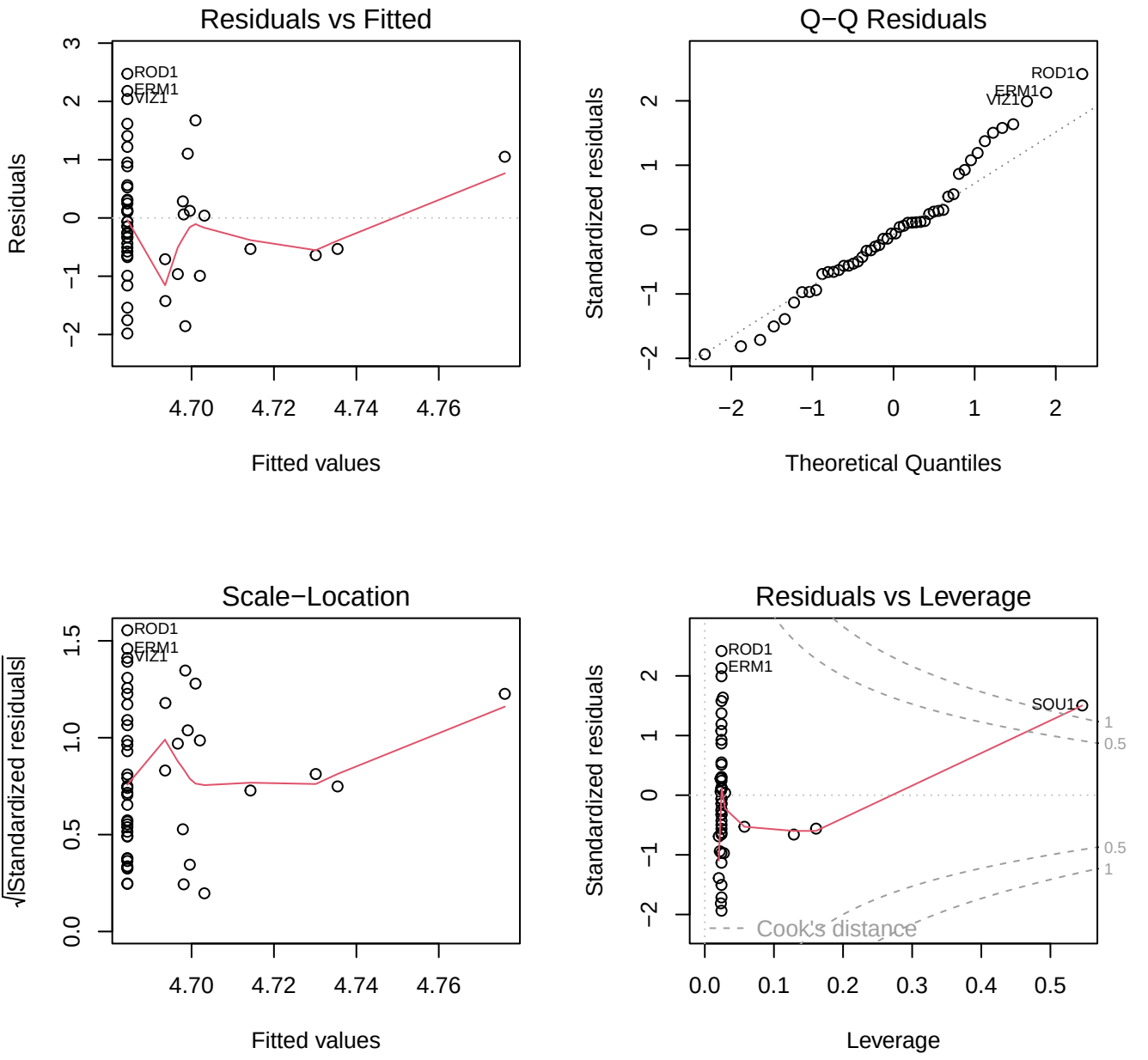
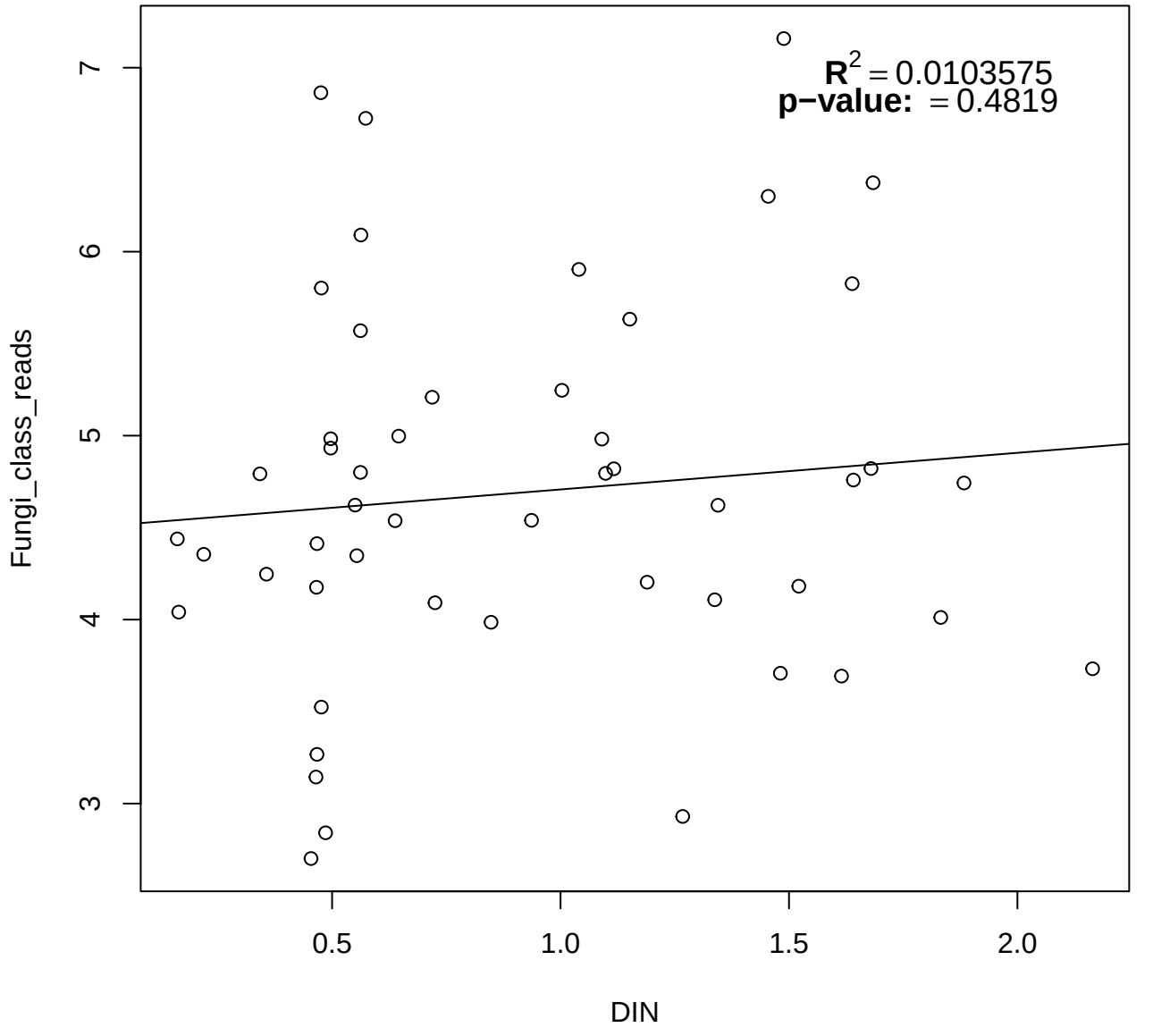
15
20
25
30


Residuals vs Fitted
Residuals
Fitted values
ROD1
ERM1
VIZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
ERM1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
ERM1
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
ERM1
SOU1
Cook's distance


$R^2 = 0.0103575$
p−value: = 0.4819
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DIN
3
4
5
6
7
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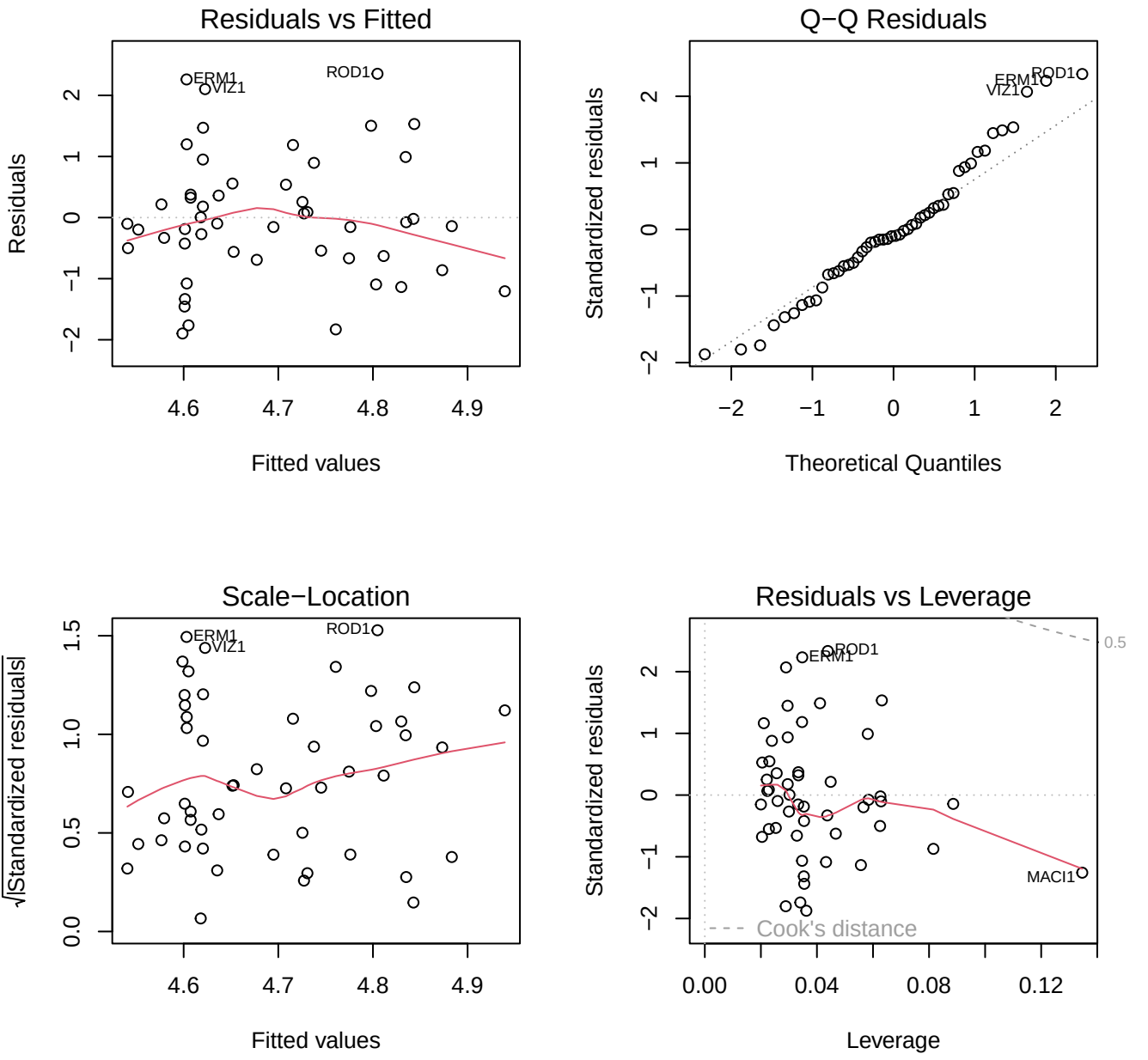
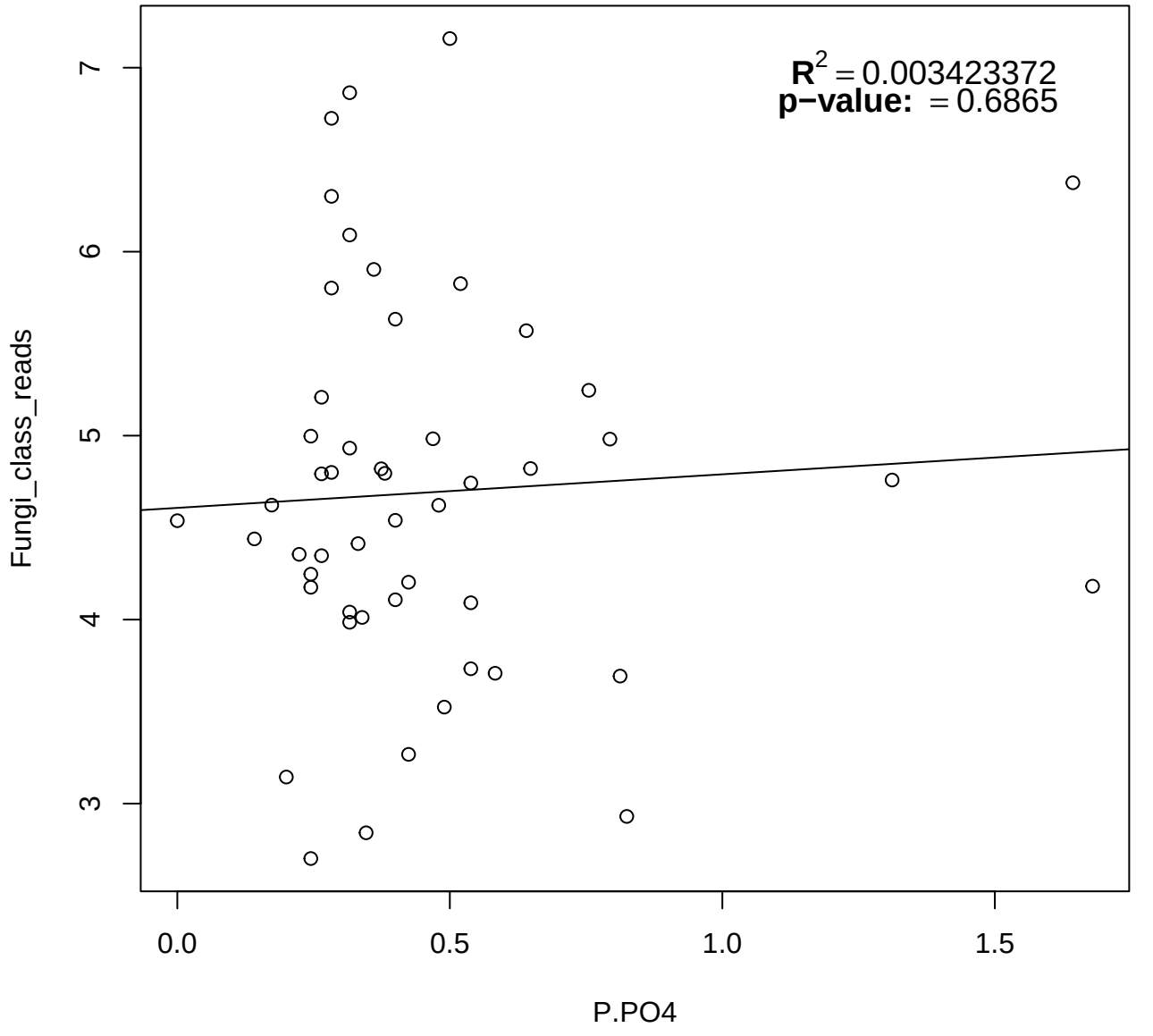
1.0
1.5
2.0


Residuals vs Fitted
Residuals
Fitted values
ERM1
VIZ1
ROD1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
VIZ1
ROD1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
VIZ1
ROD1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
ERM1
MACI1
0.5
Cook's distance


$R^2 = 0.003423372$
p−value: = 0.6865
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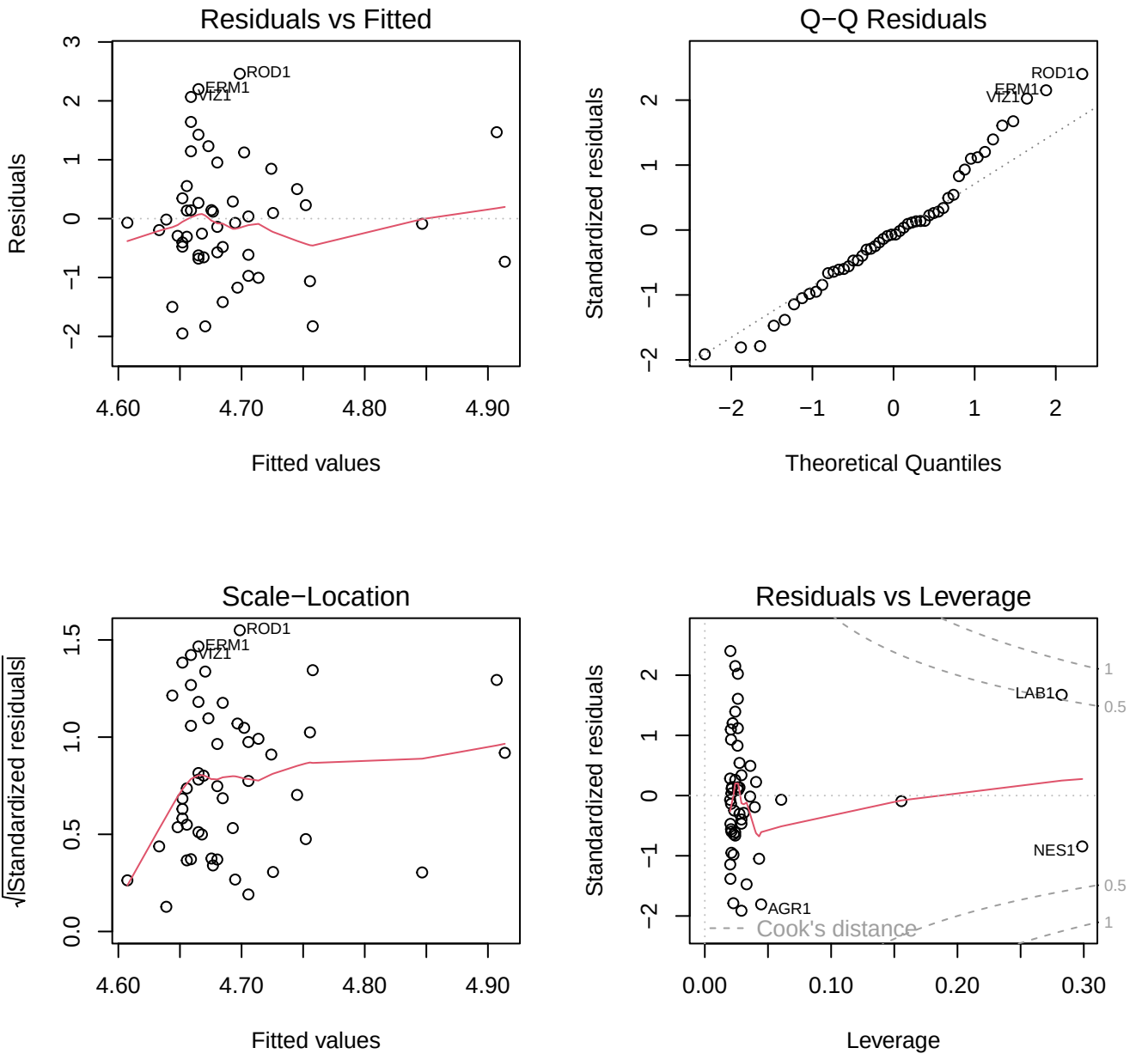
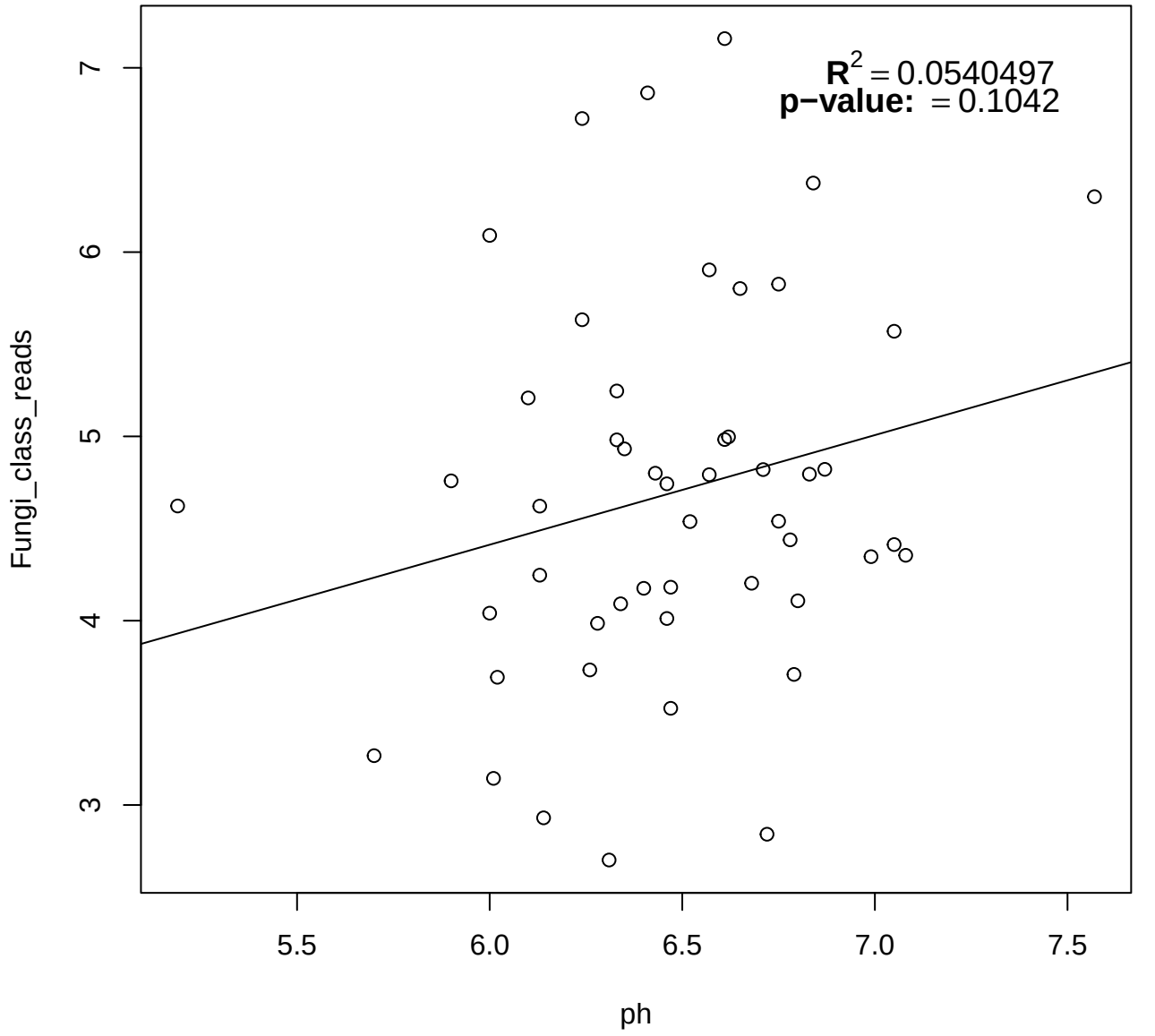
P.PO4
3
4
5
6
7
0.0
0.5
1.0
1.5


Residuals vs Fitted
Residuals
Fitted values
ROD1
ERM1
VIZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
ERM1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
ERM1
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
LAB1
NES1
AGR1
Cook's distance
1
0.5
0.5
1


$R^2 = 0.0540497$
p−value: = 0.1042
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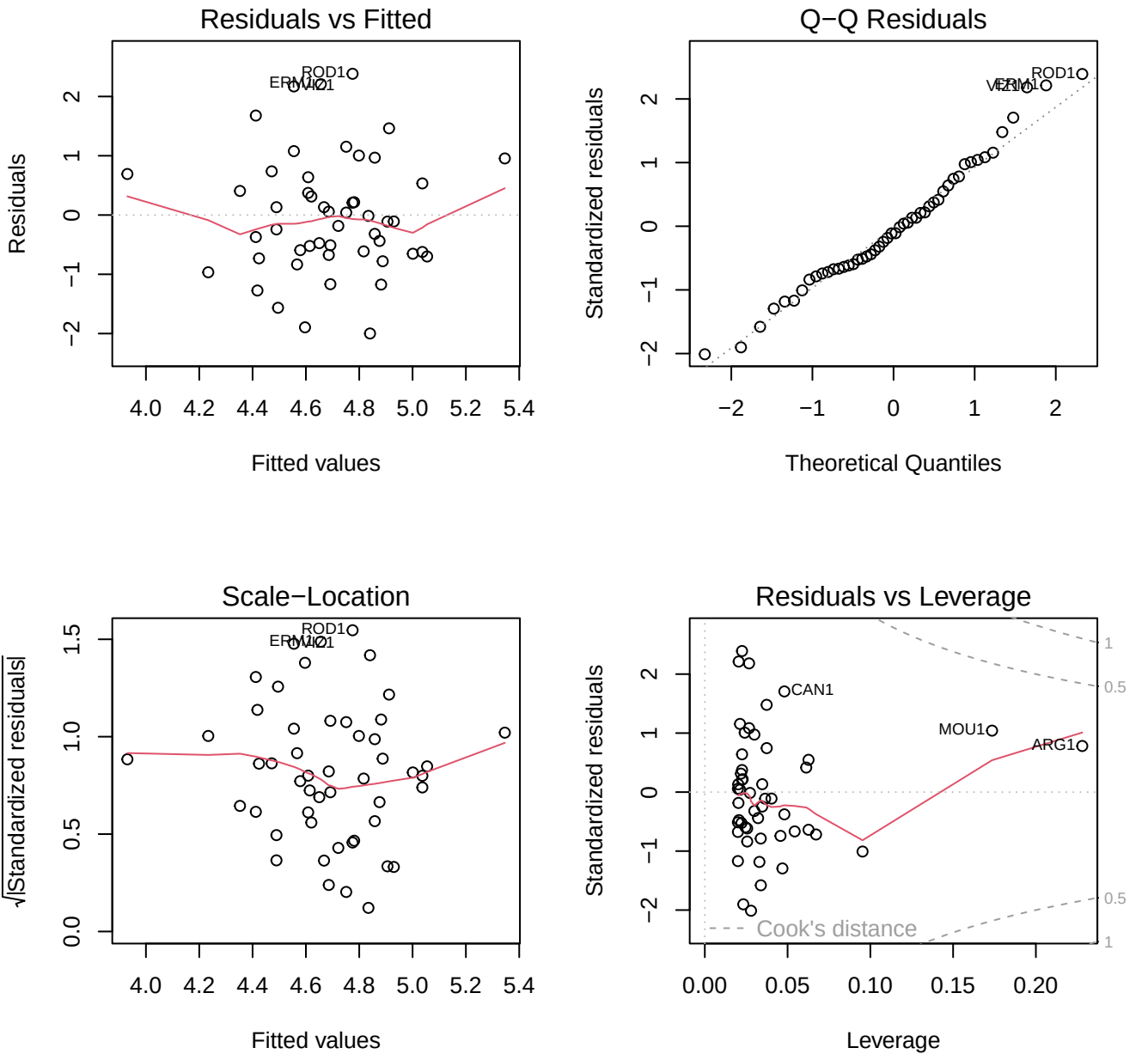
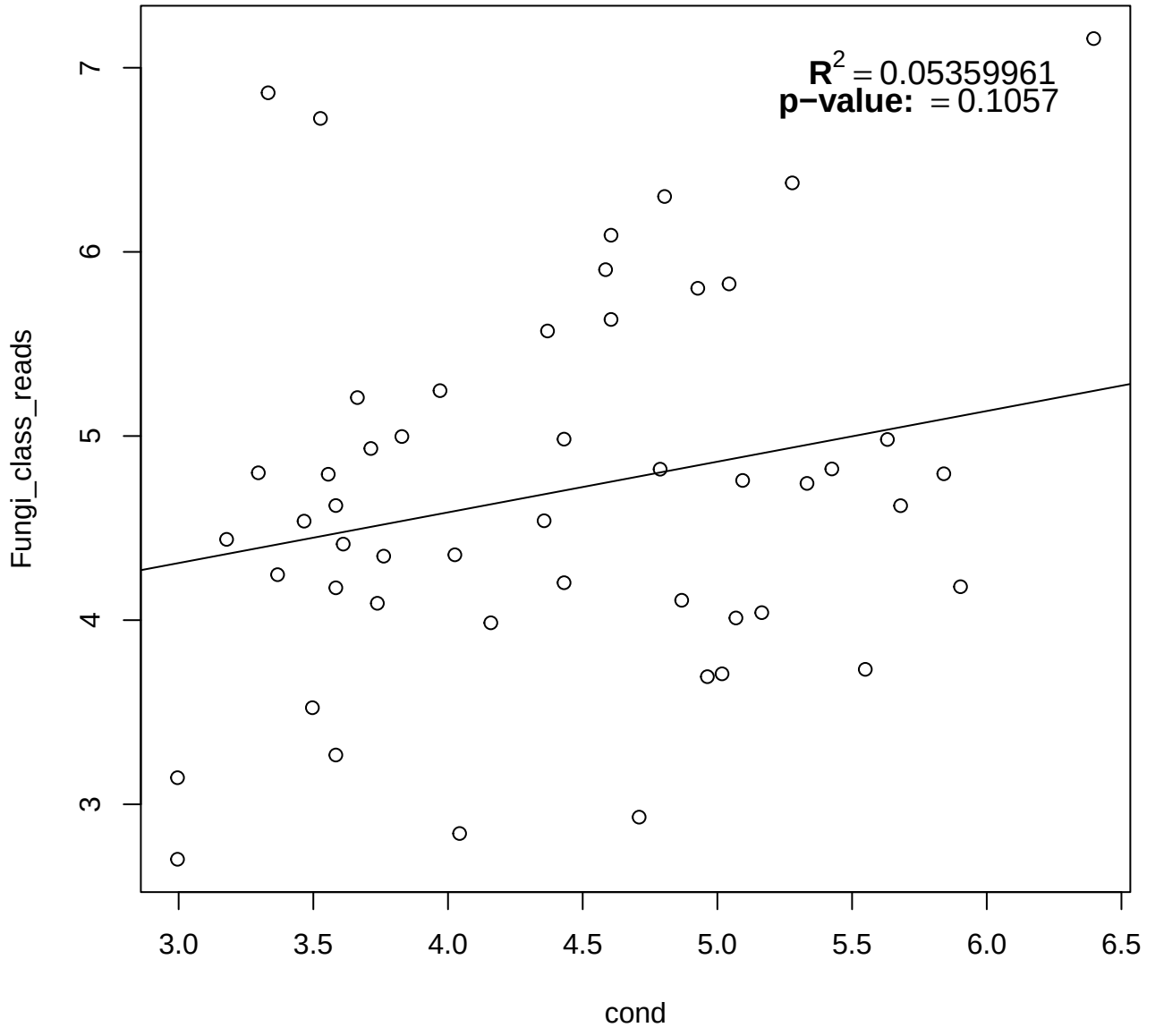
ph
3
4
5
6
7
5.5
6.0
6.5
7.0
7.5


Residuals vs Fitted
Residuals
Fitted values
ROD1
ERM1
VIZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
CAN1
MOU1
ARG1
Cook's distance


$R^2 = 0.05359961$
p−value: = 0.1057
Fungi_class_reads
cond
3
4
5
6
7
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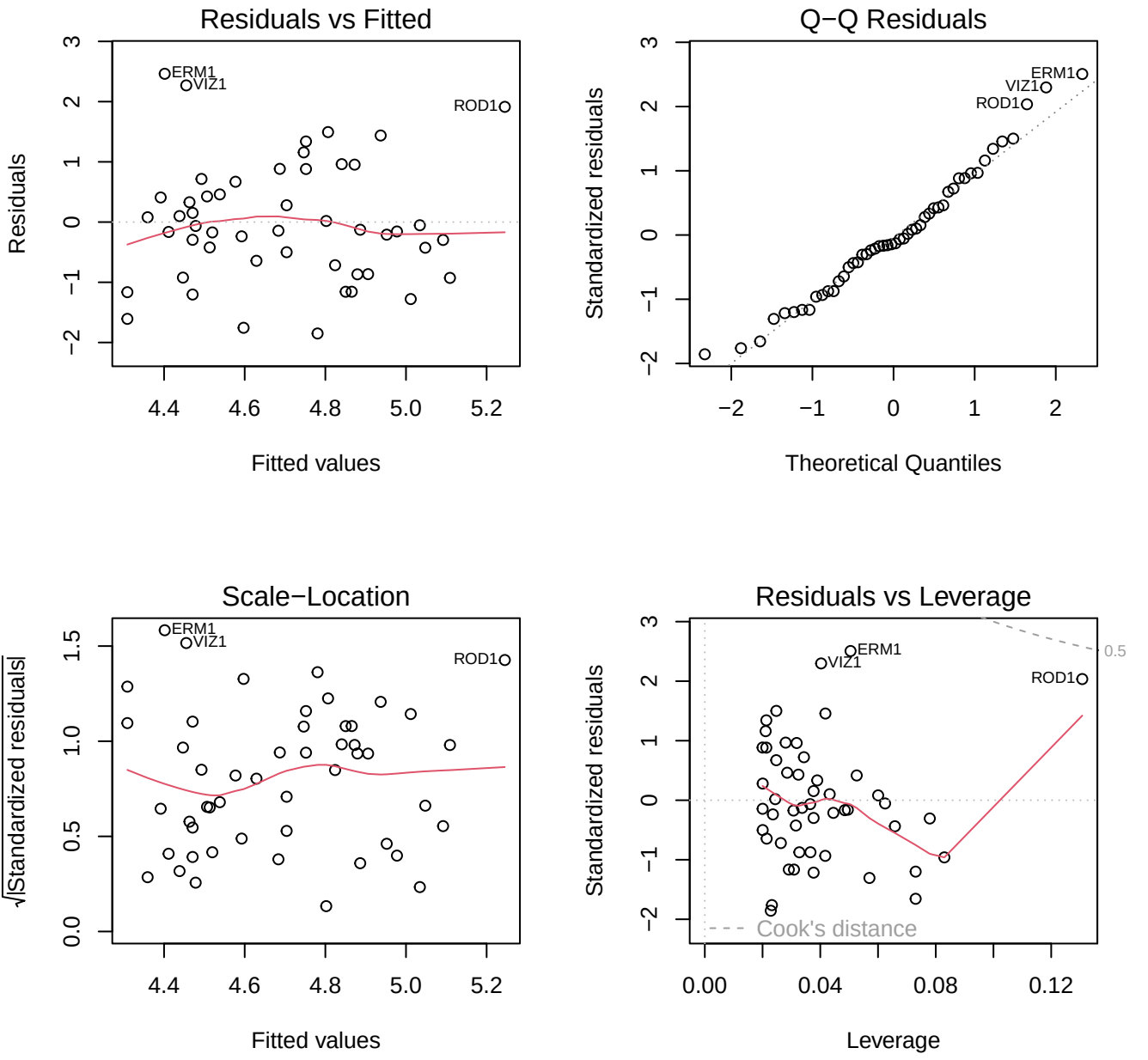
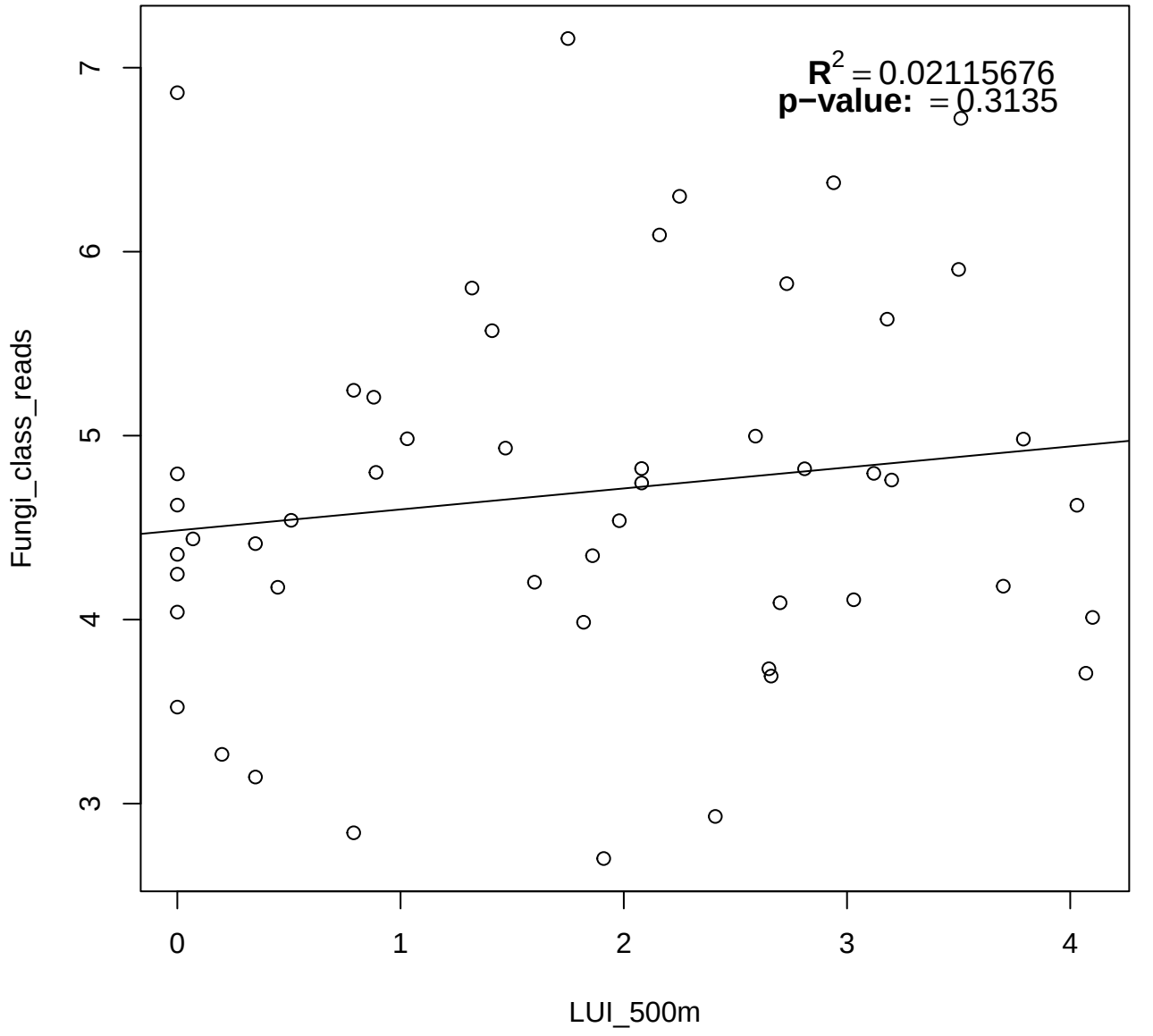
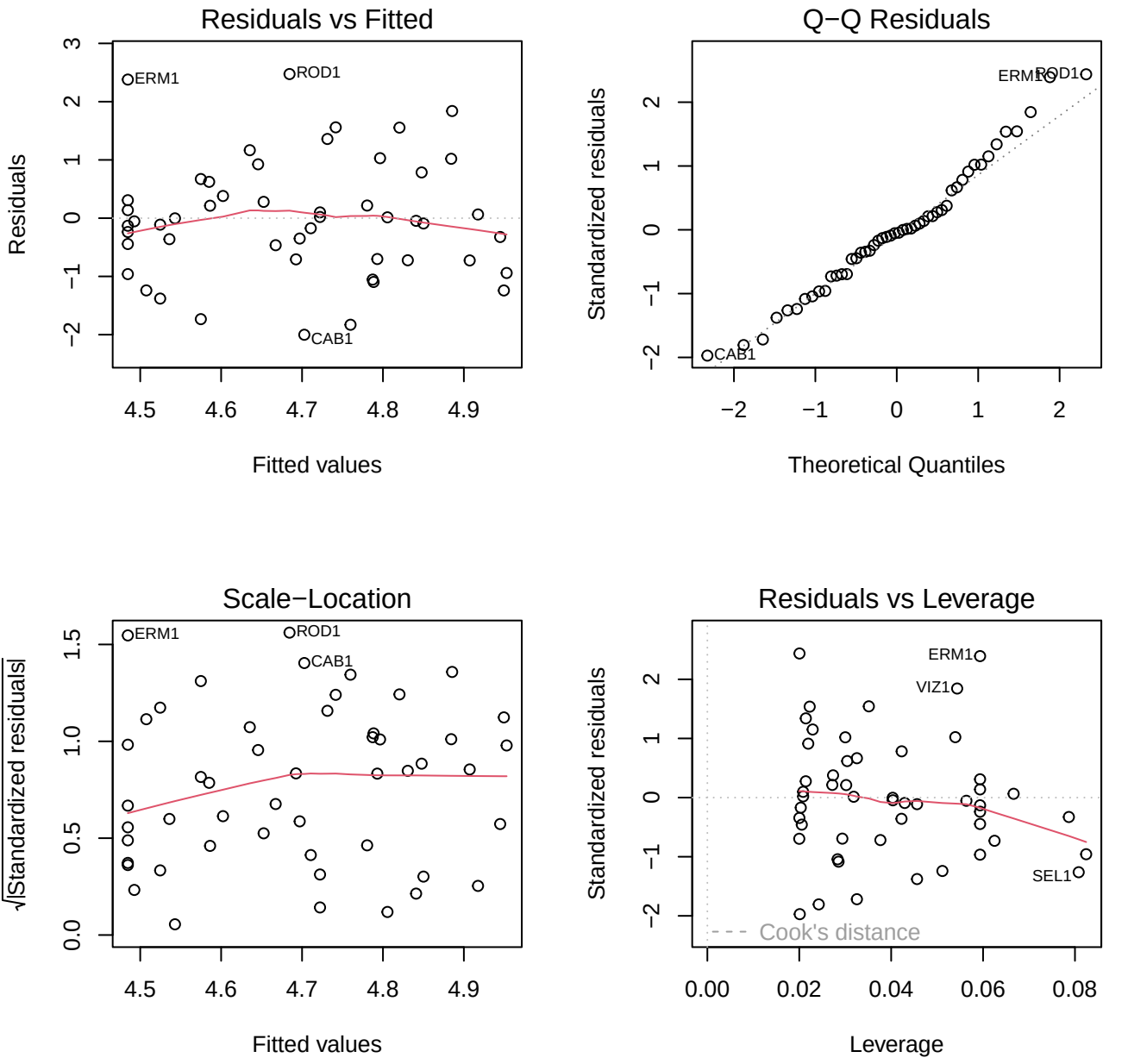
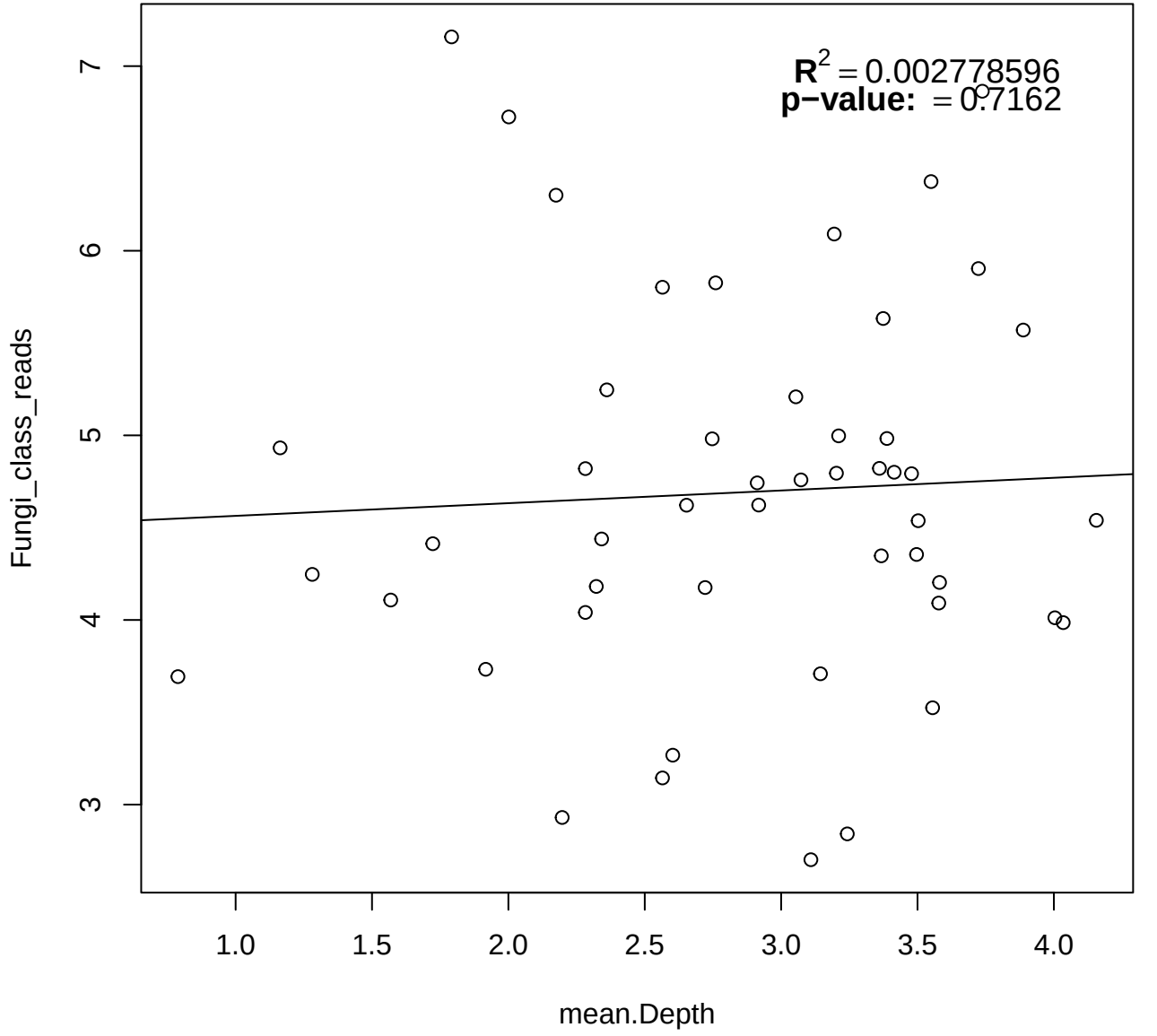
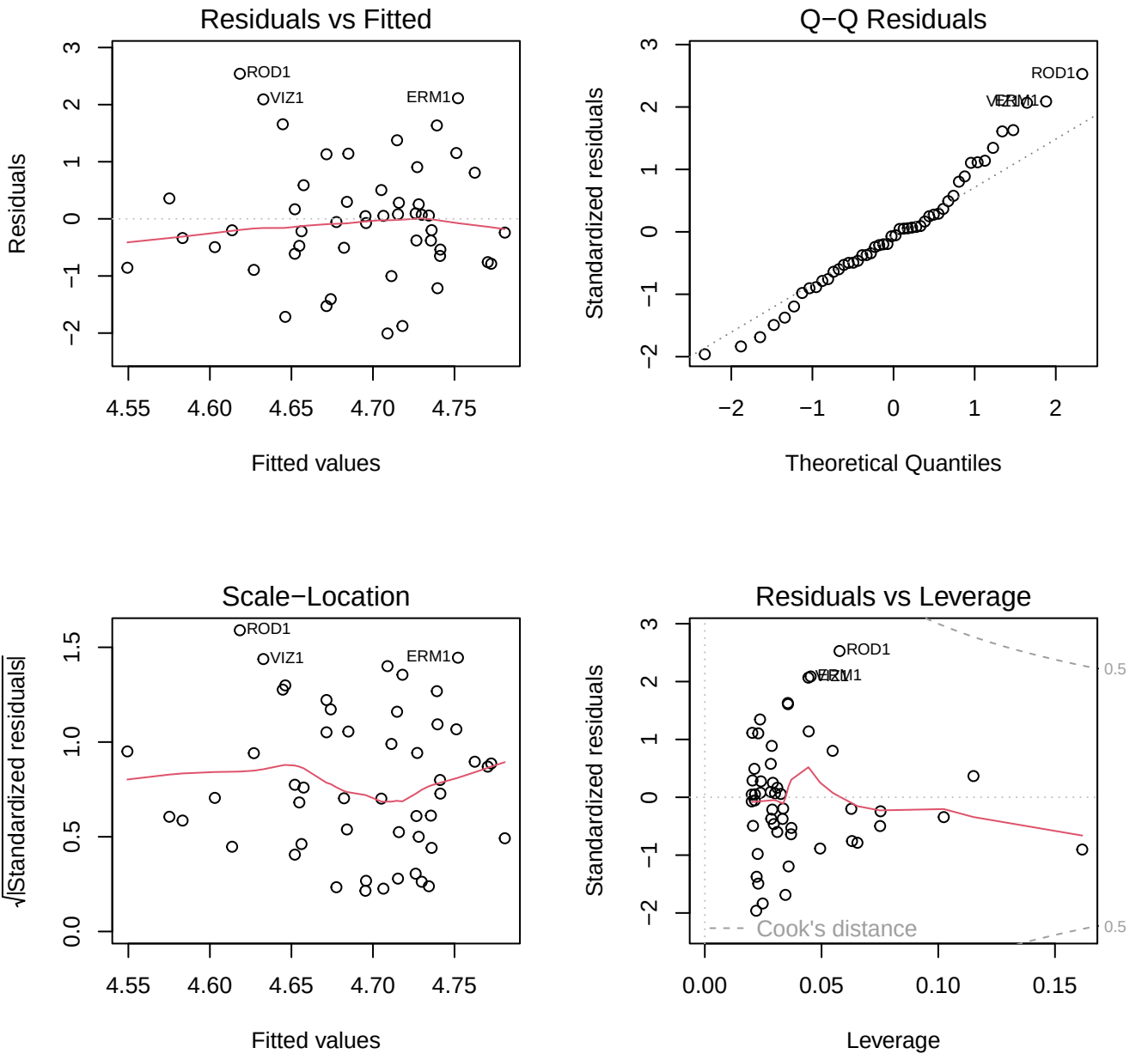
3.5
4.0
4.5
5.0
5.5
6.0
6.5

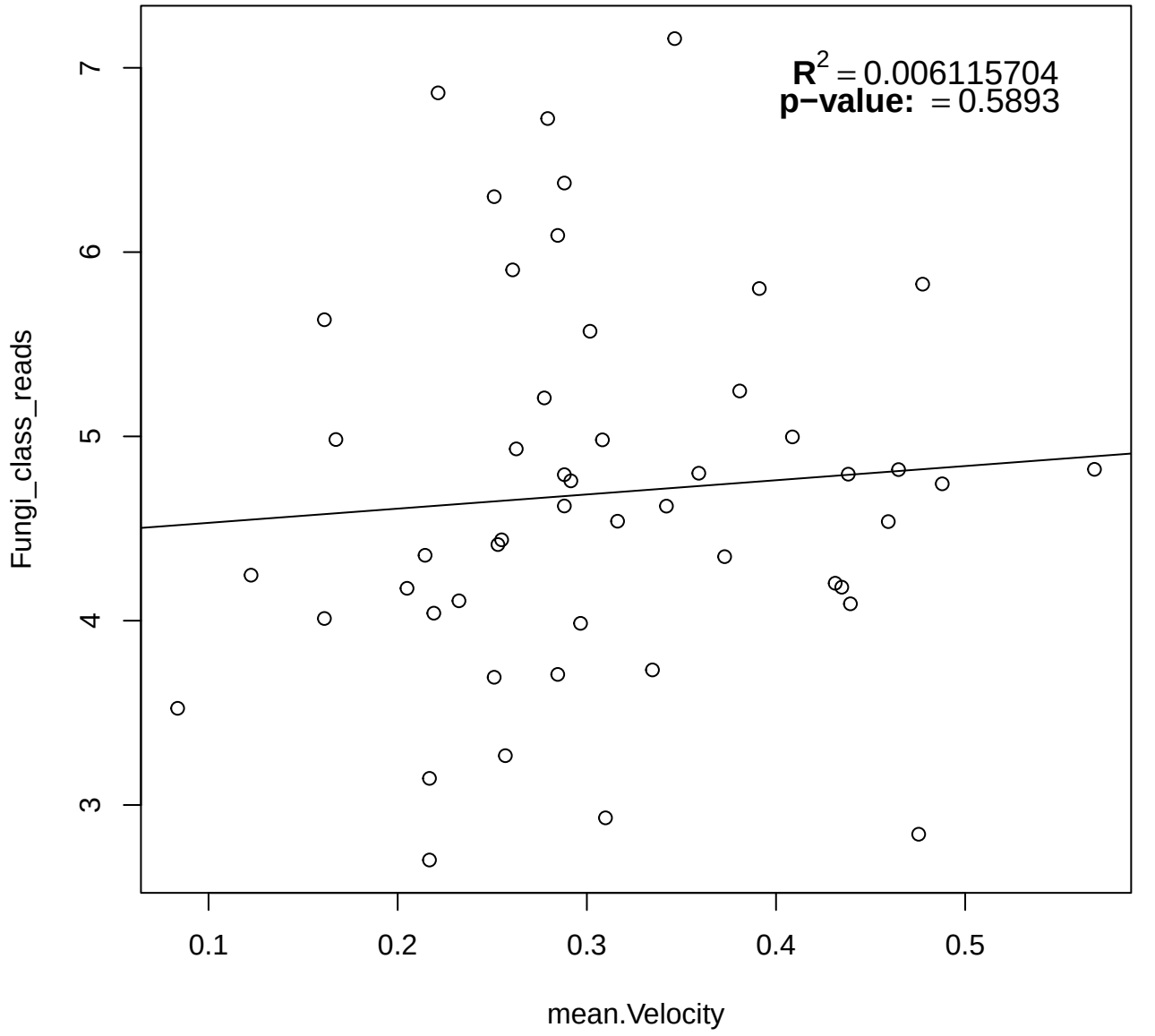

Residuals vs Fitted
Residuals
Fitted values
ERM1
VIZ1
ROD1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
VIZ1
ROD1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
VIZ1
ROD1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
VIZ1
ROD1
0.5
Cook's distance

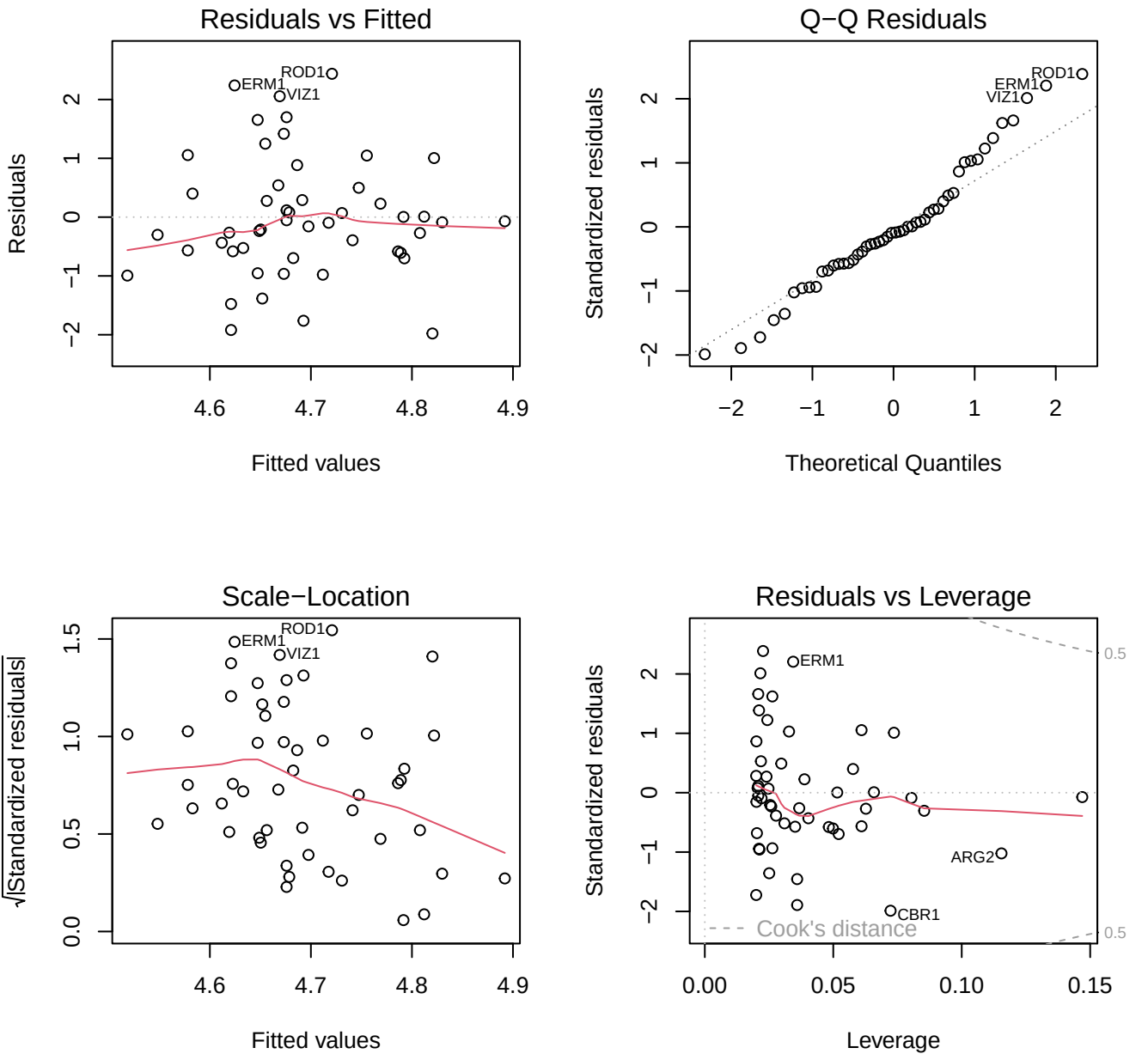

$R^2 = 0.02115676$
p−value: = 0.3135
Fungi_class_reads
LUI_500m
3
4
5
6
7
0
1
2
3
4

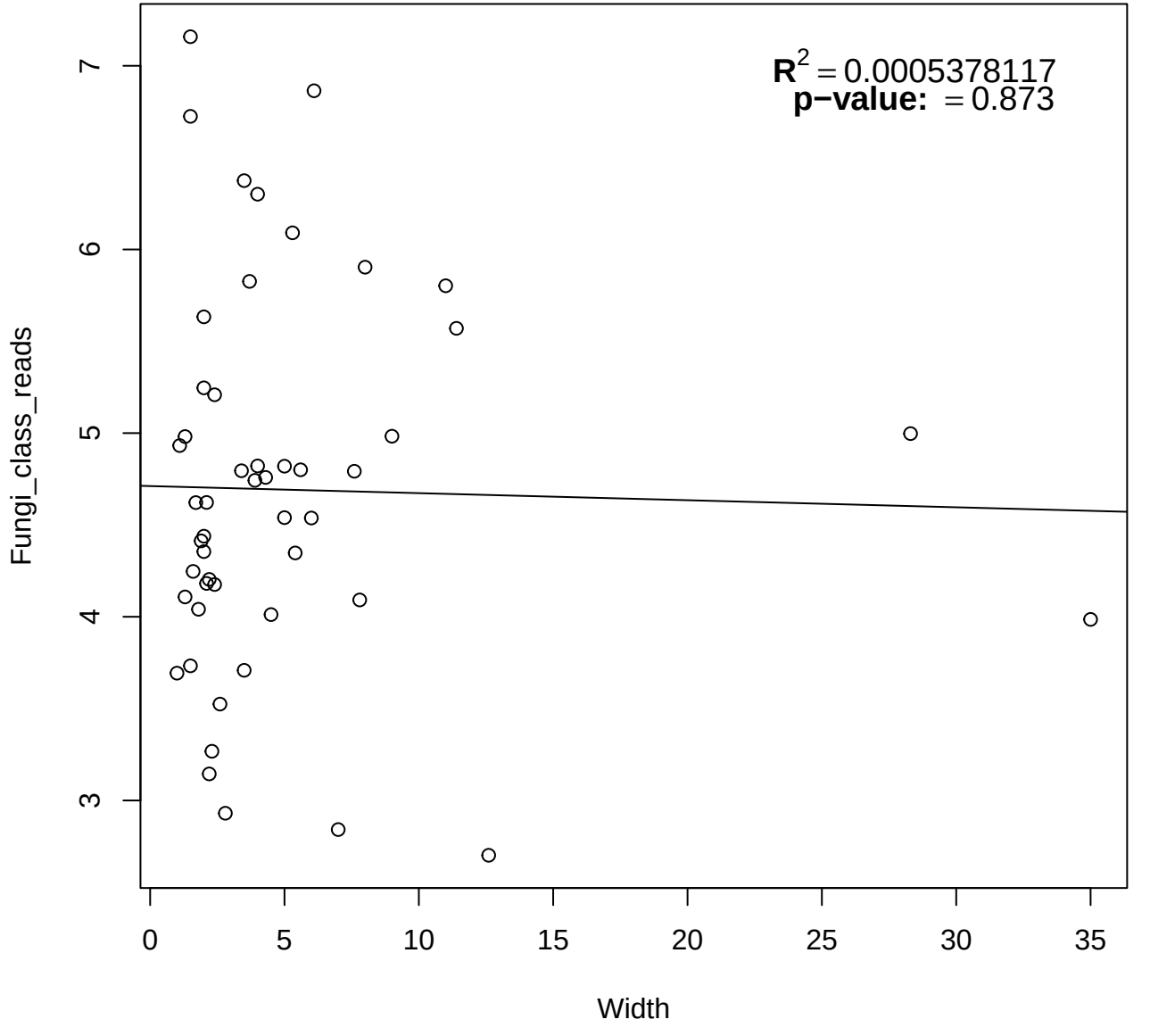

Residuals vs Fitted
Residuals
Fitted values
ERM1
ROD1
CAB1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
ROD1
CAB1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
ROD1
CAB1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
VIZ1
SEL1
Cook's distance


$R^2 = 0.002778596$
p−value: = 0.7162
Fungi_class_reads
mean.Depth
3
4
5
6
7
1.0
1.5
2.0
2.5
3.0
3.5
4.0


Residuals vs Fitted
Residuals
Fitted values
ROD1
VIZ1
ERM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
Cook's distance
0.5


$R^2 = 0.006115704$
p−value: = 0.5893
Fungi_class_reads
mean.Velocity
3
4
5
6
7
0.1
0.2
0.3
0.4
0.5


Residuals vs Fitted
Residuals
Fitted values
ROD1
ERM1
VIZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
ERM1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
ERM1
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
ERM1
ARG2
CBR1
Cook's distance
0.5
0.5


$R^2 = 0.0005378117$
p−value: $= 0.873$
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Width
0
5
10
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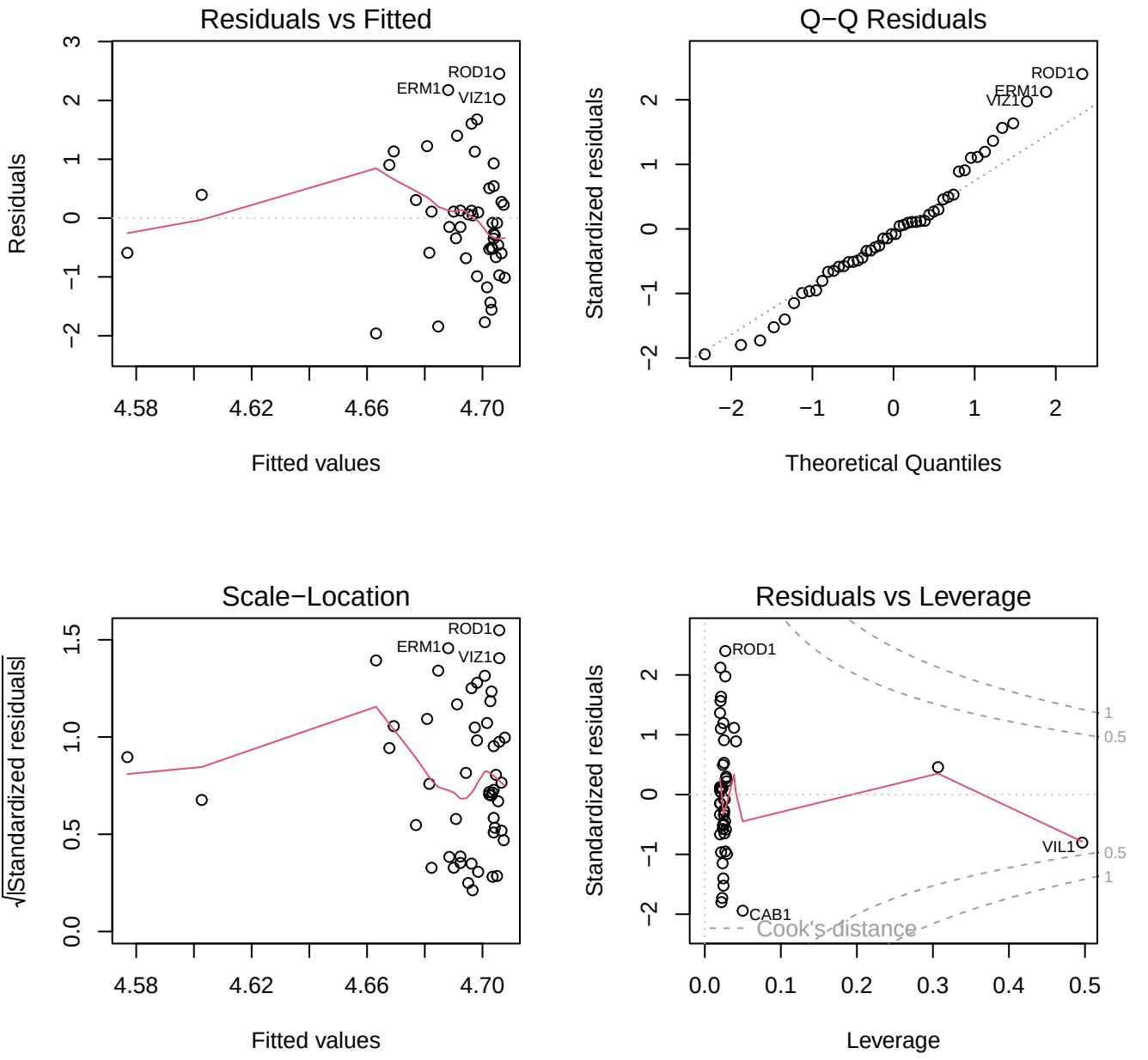
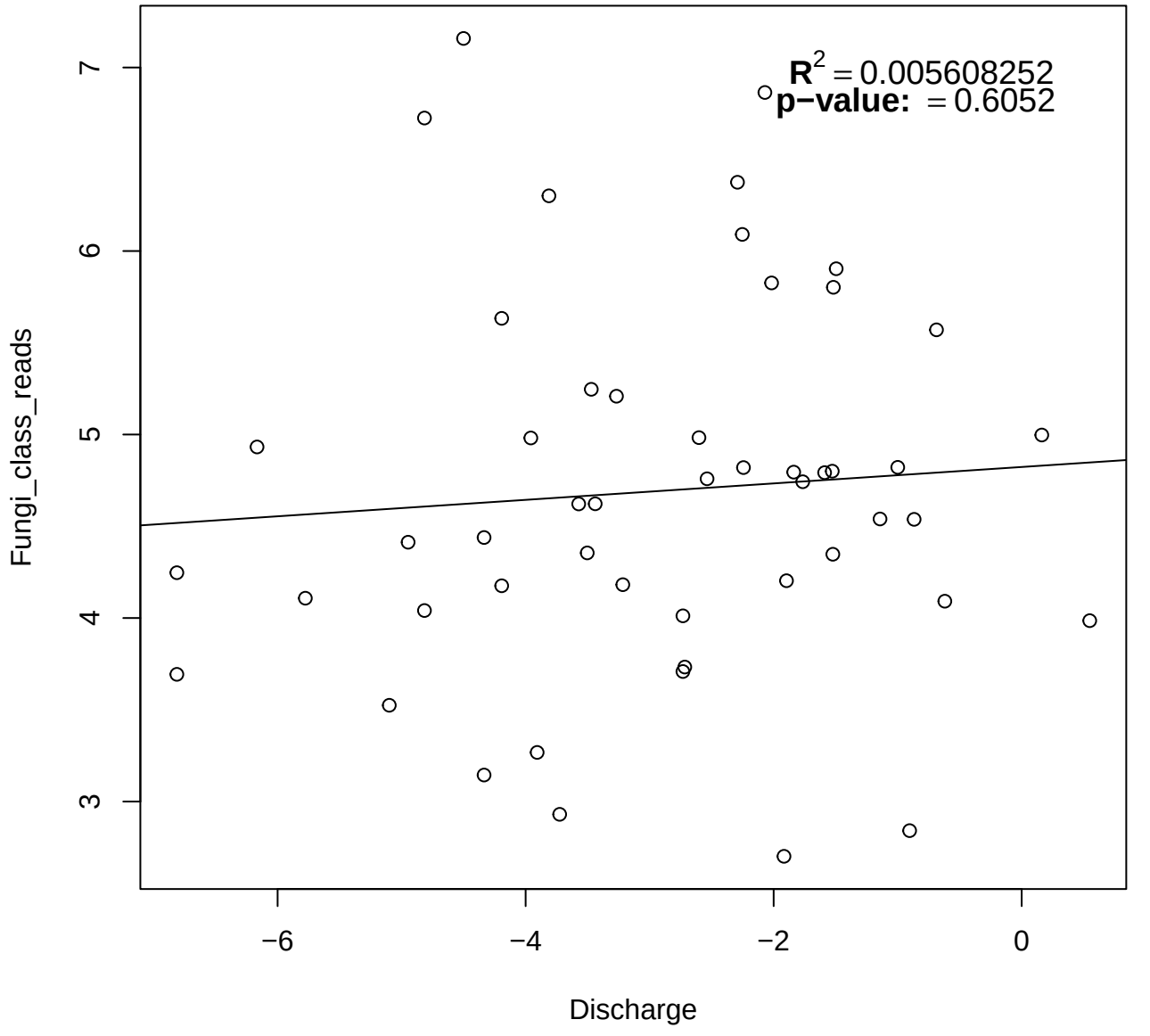
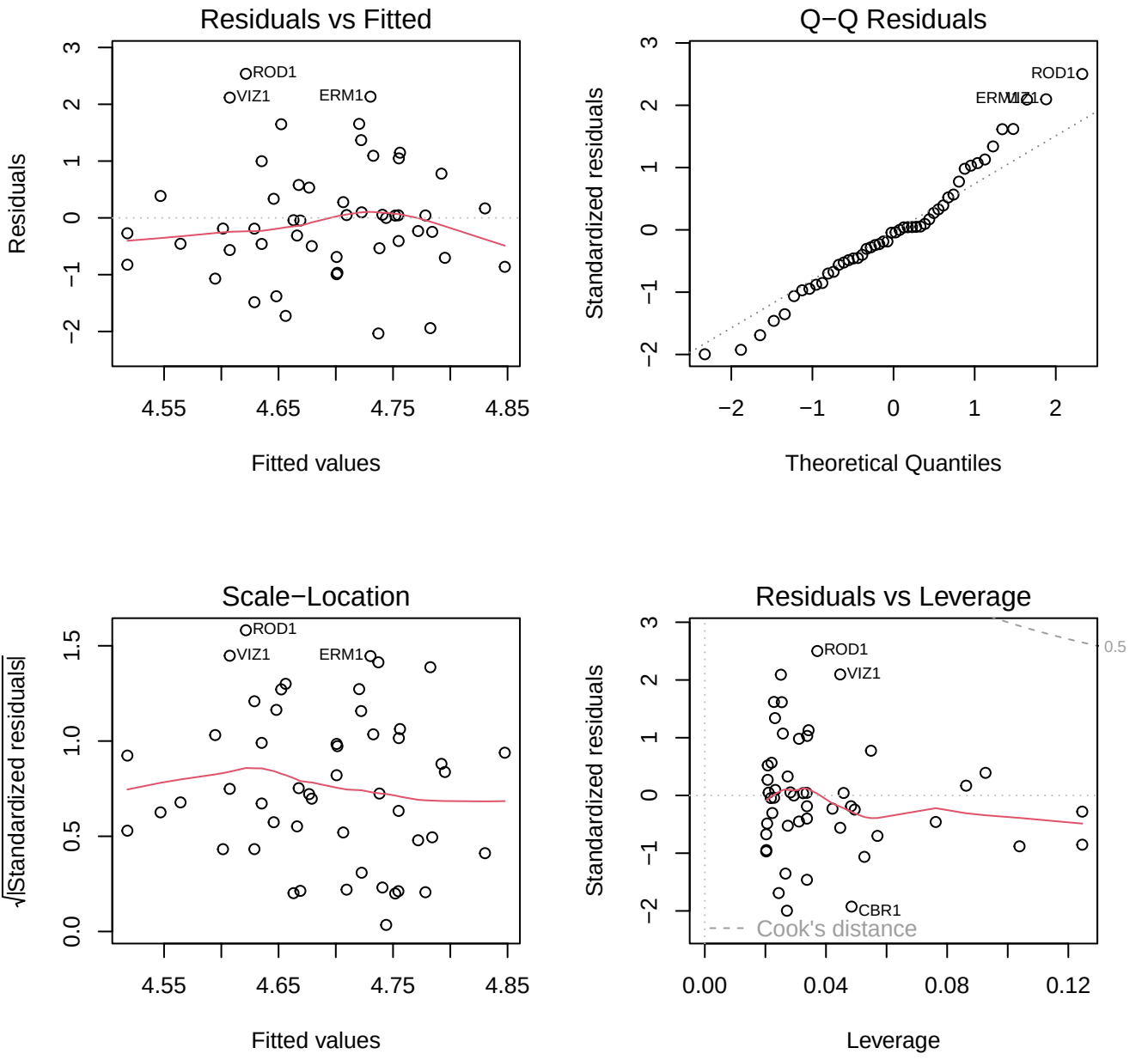
20
25
30
35
3
4
5
6
7


Residuals vs Fitted
Residuals
Fitted values
ROD1
ERM1
VIZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Residuals vs Leverage
Standardized residuals
Leverage
VIL1
CAB1
Cook's distance


$R^2 = 0.005608252$
p−value: = 0.6052
Fungi_class_reads
Discharge
7
6
5
4
3
−6
−4
−2
0


Residuals vs Fitted
Residuals
Fitted values
ROD1
VIZ1
ERM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
ERM1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
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VIZ1
ERM1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
VIZ1
CBR1
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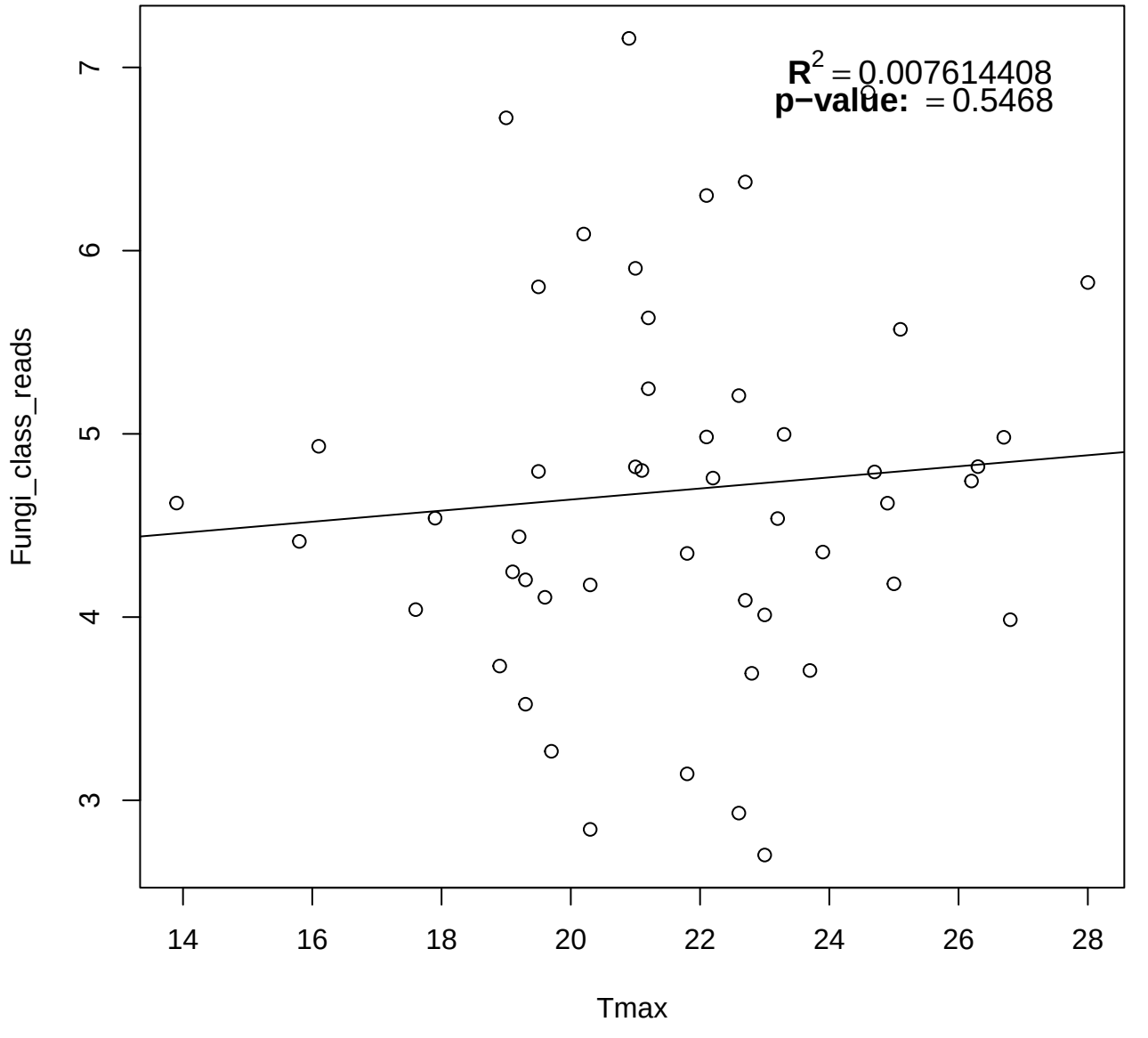
Cook's distance


$R^2 = 0.007614408$
p−value: = 0.5468
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Tmax
3
4
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14
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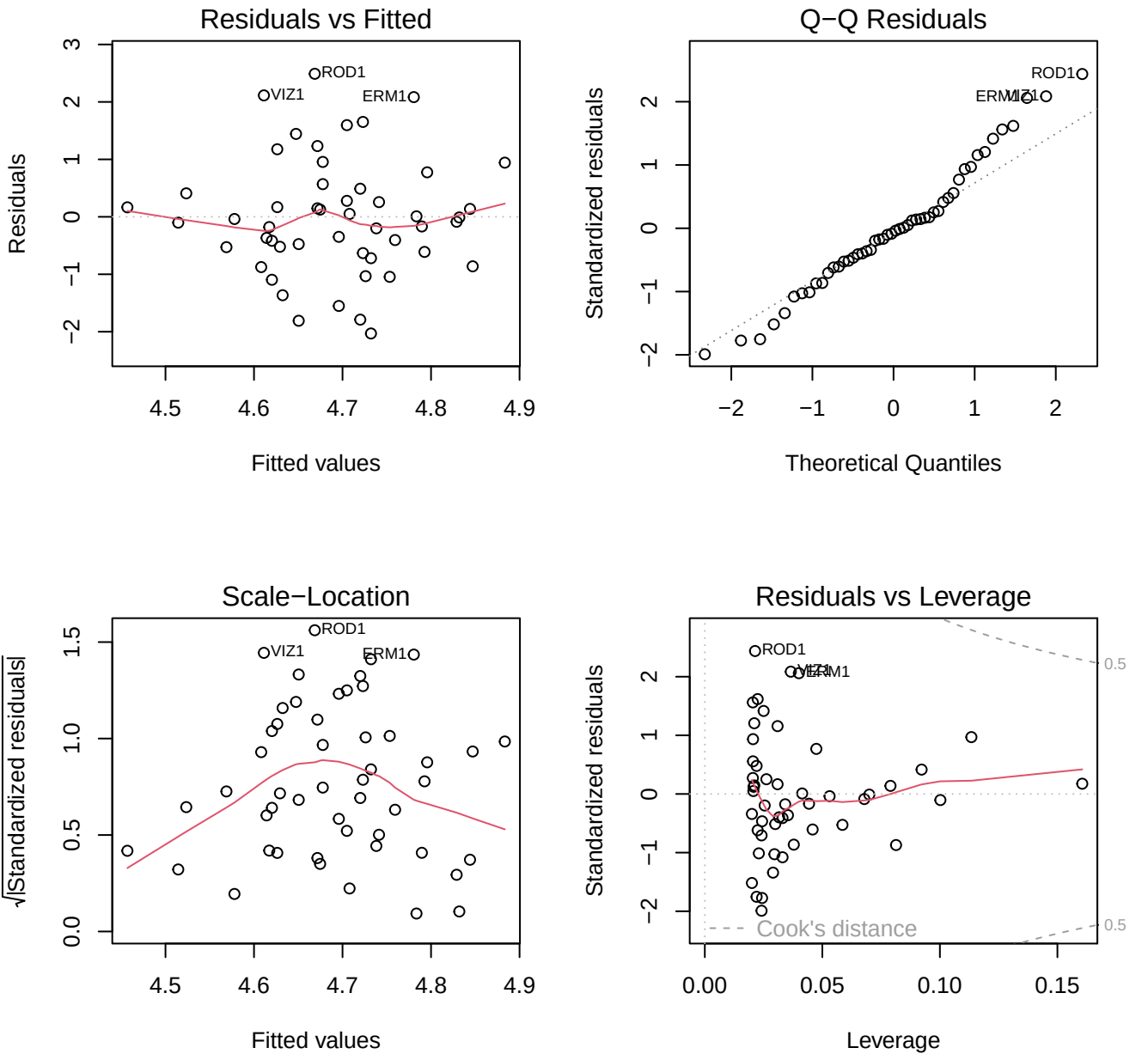
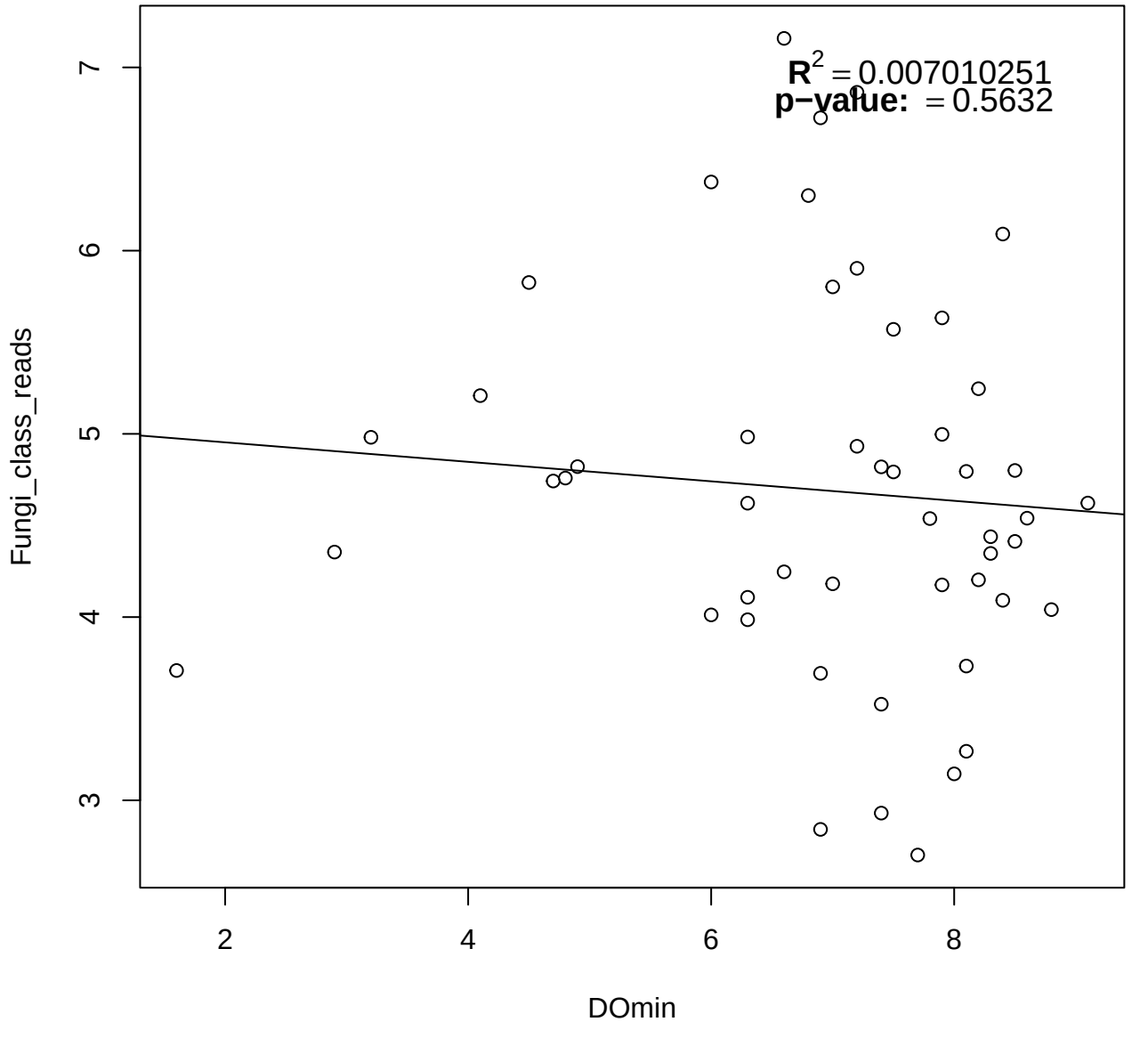
22
24
26
28


Residuals vs Fitted
Residuals
Fitted values
ROD1
VIZ1
ERM1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
ERM1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
VIZ1
ERM1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
VIZ1
ERM1
Cook's distance
0.5
0.5


$R^2 = 0.007010251$
p−value: = 0.5632
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DOmin
3
4
5
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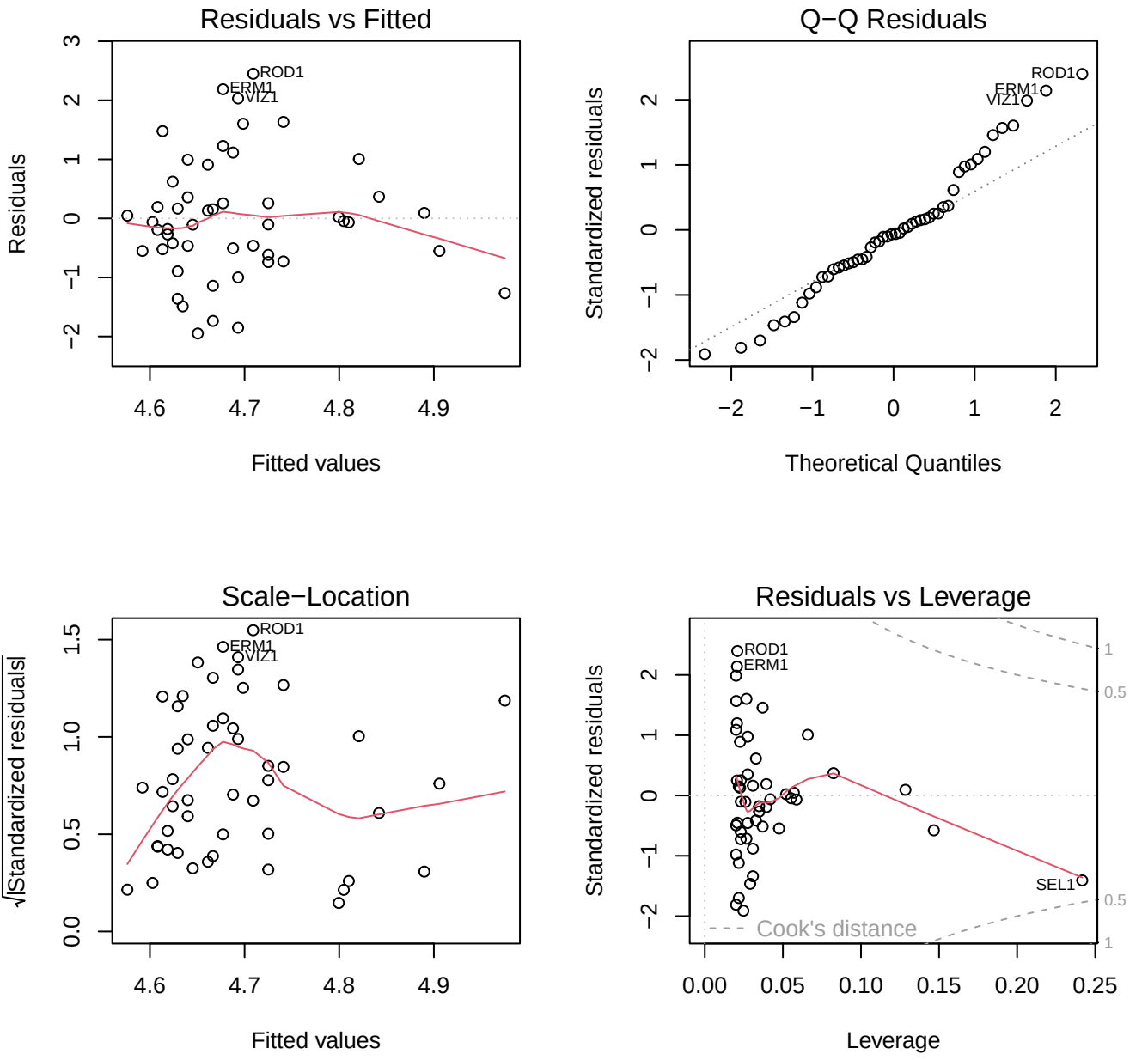
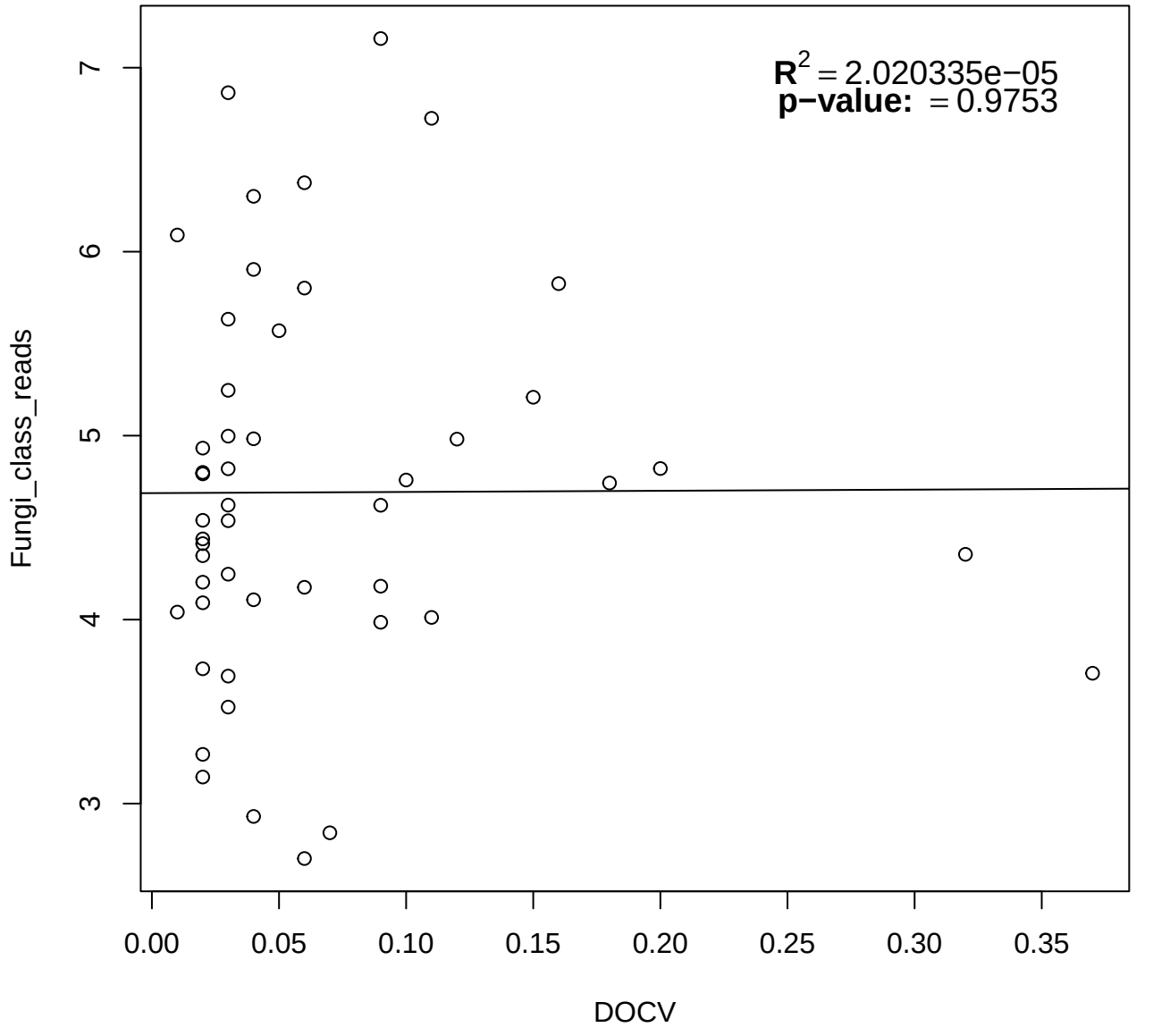
7
2
4
6
8


Residuals vs Fitted
Residuals
Fitted values
ROD1
ERM1
VIZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
ERM1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
ROD1
ERM1
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
ERM1
SEL1
Cook's distance
1
0.5
0.5
1


$R^2 = 2.020335e-05$
p−value: = 0.9753
Fungi_class_reads
DOCV
3
4
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6
7
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0.10
0.15
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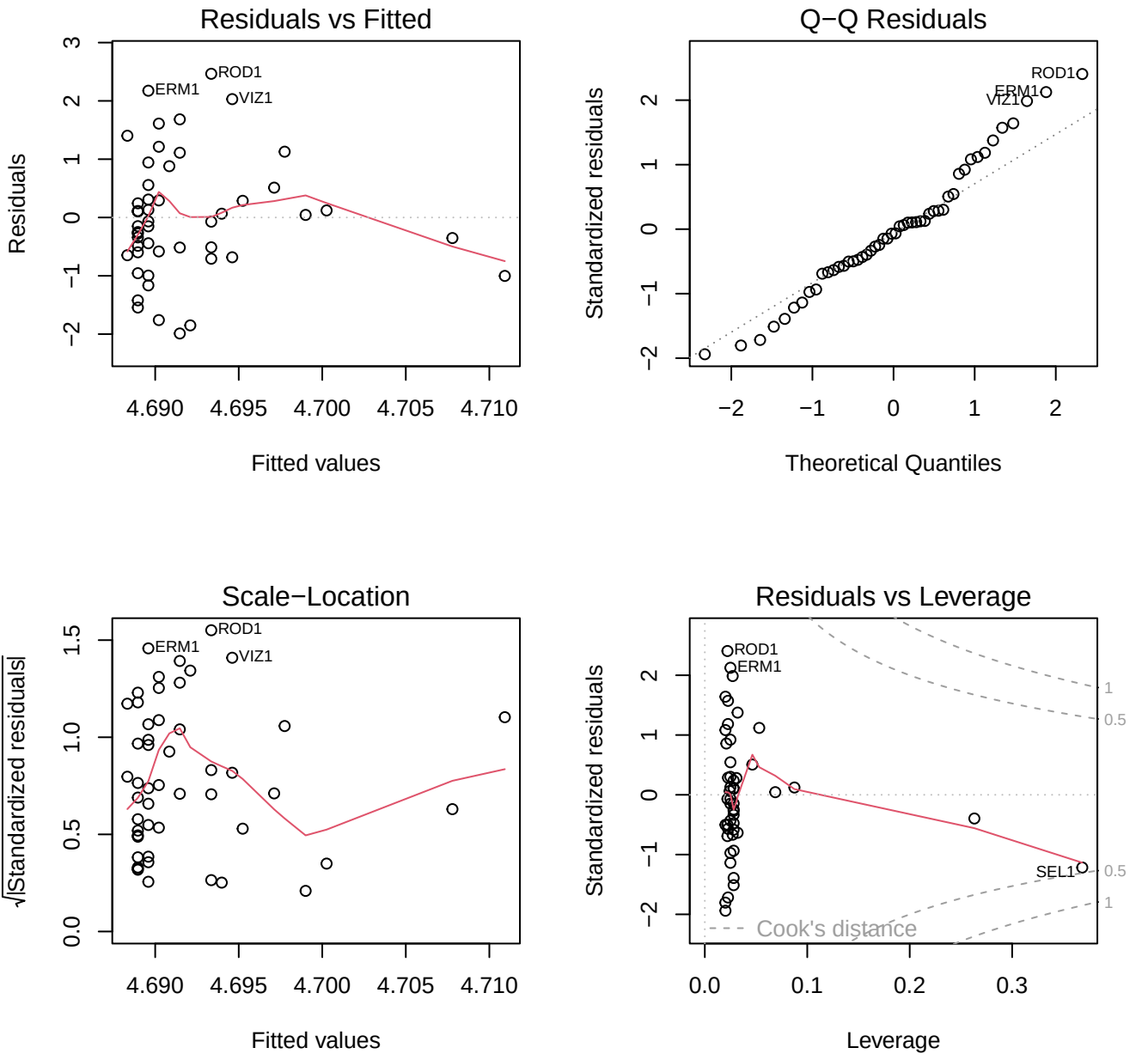
0.30
0.35


Residuals vs Fitted
Residuals
Fitted values
ROD1
ERM1
VIZ1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ROD1
ERM1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
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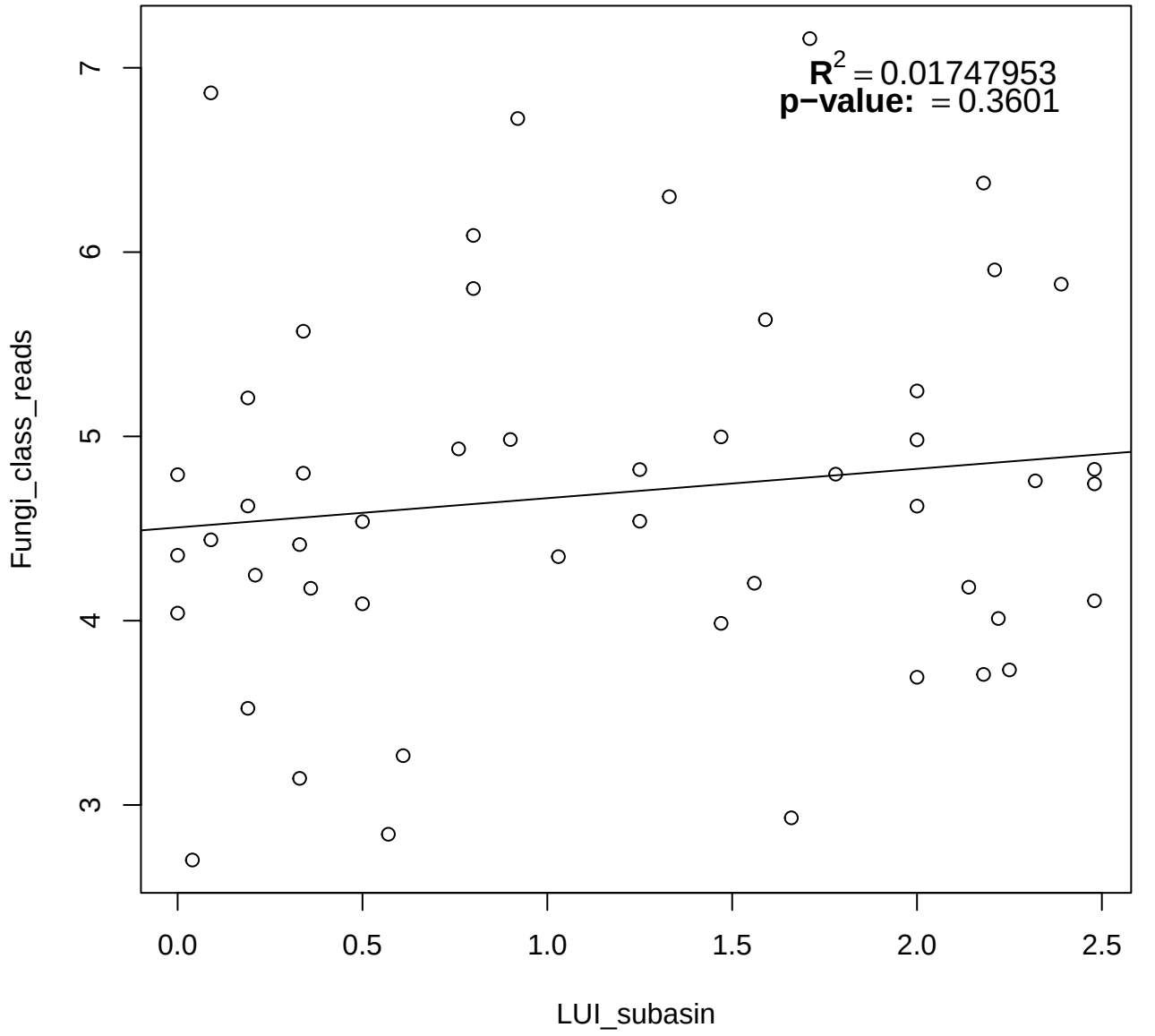
VIZ1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
ERM1
SEL1
Cook's distance


$R^2 = 0.01747953$
p−value: = 0.3601
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LUI_subasin
3
4
5
6
7
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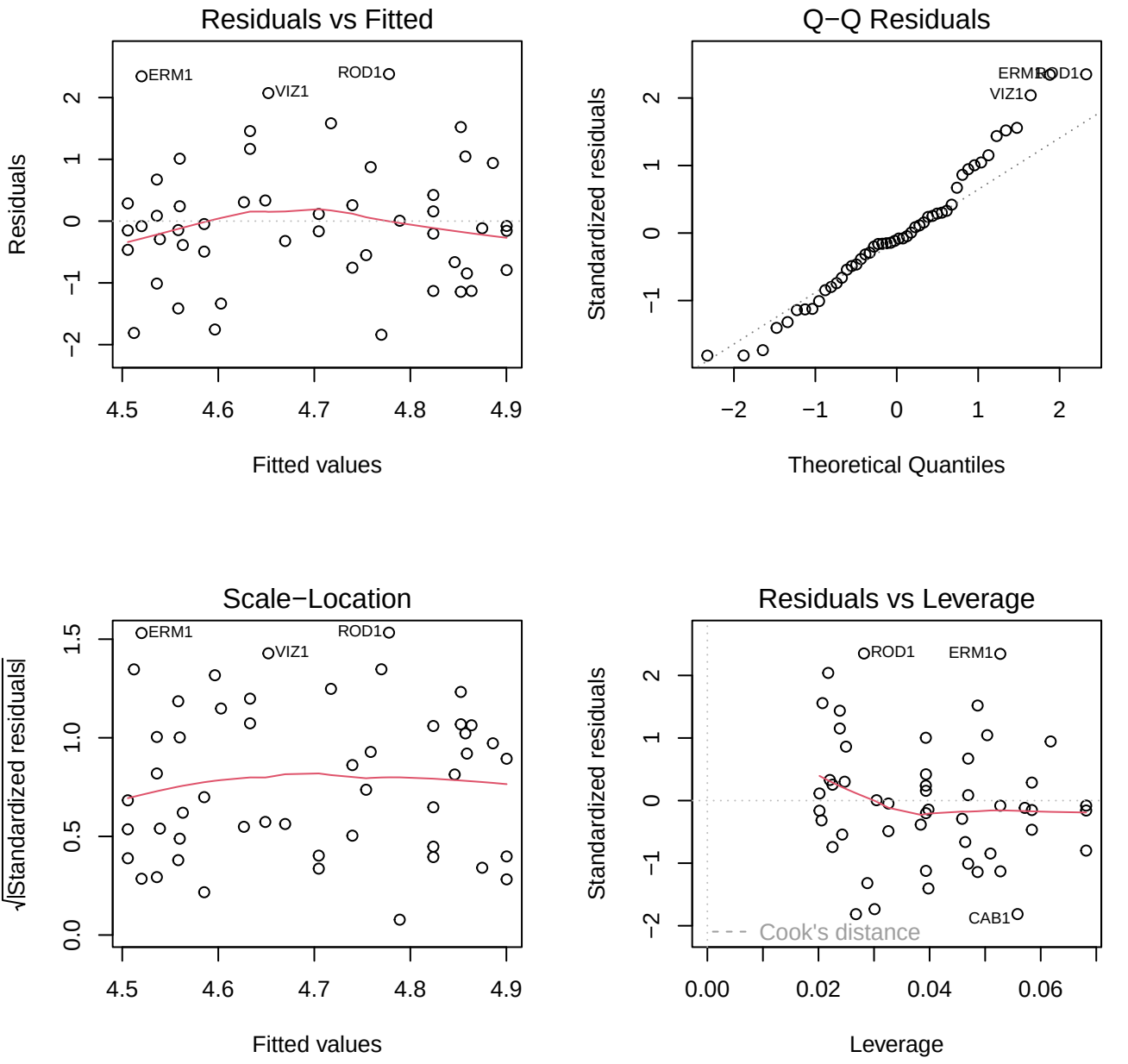
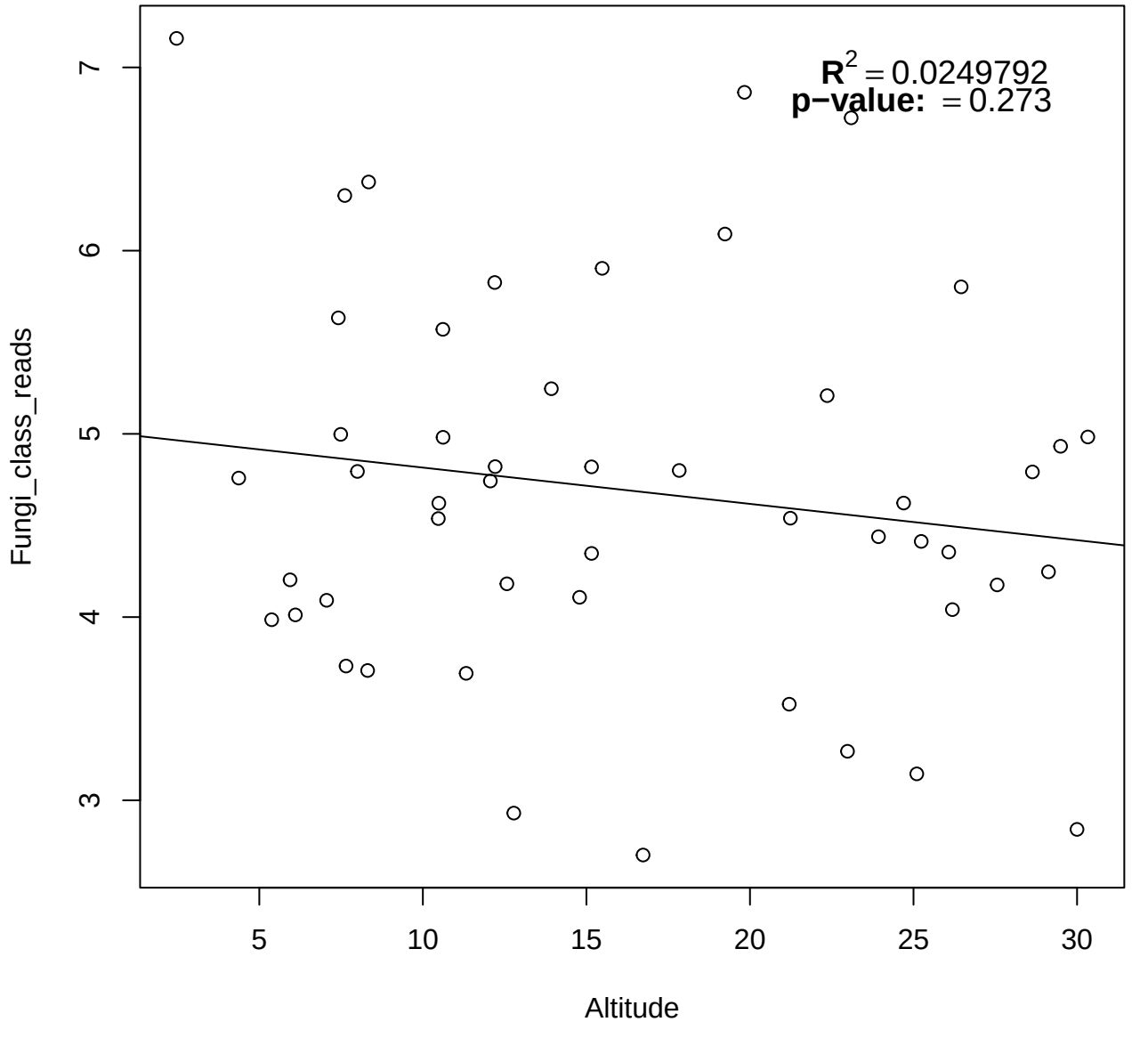
0.5
1.0
1.5
2.0
2.5


Residuals vs Fitted
Residuals
Fitted values
ERM1
VIZ1
ROD1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
ROD1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
VIZ1
ROD1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
ERM1
CAB1
Cook's distance


$R^2 = 0.0249792$
p−value: $= 0.273$
Fungi_class_reads
Altitude
3
4
5
6
7
5
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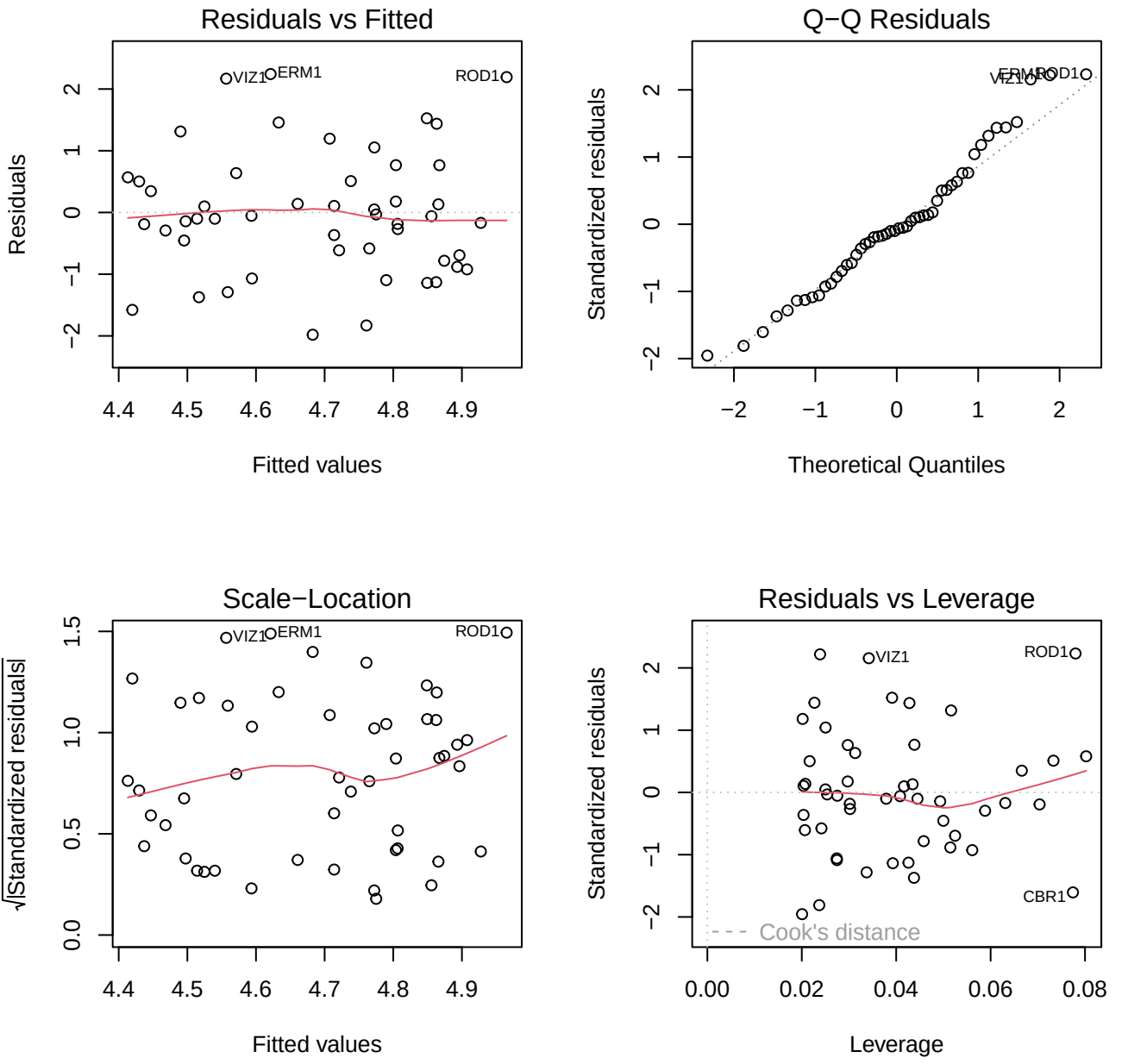
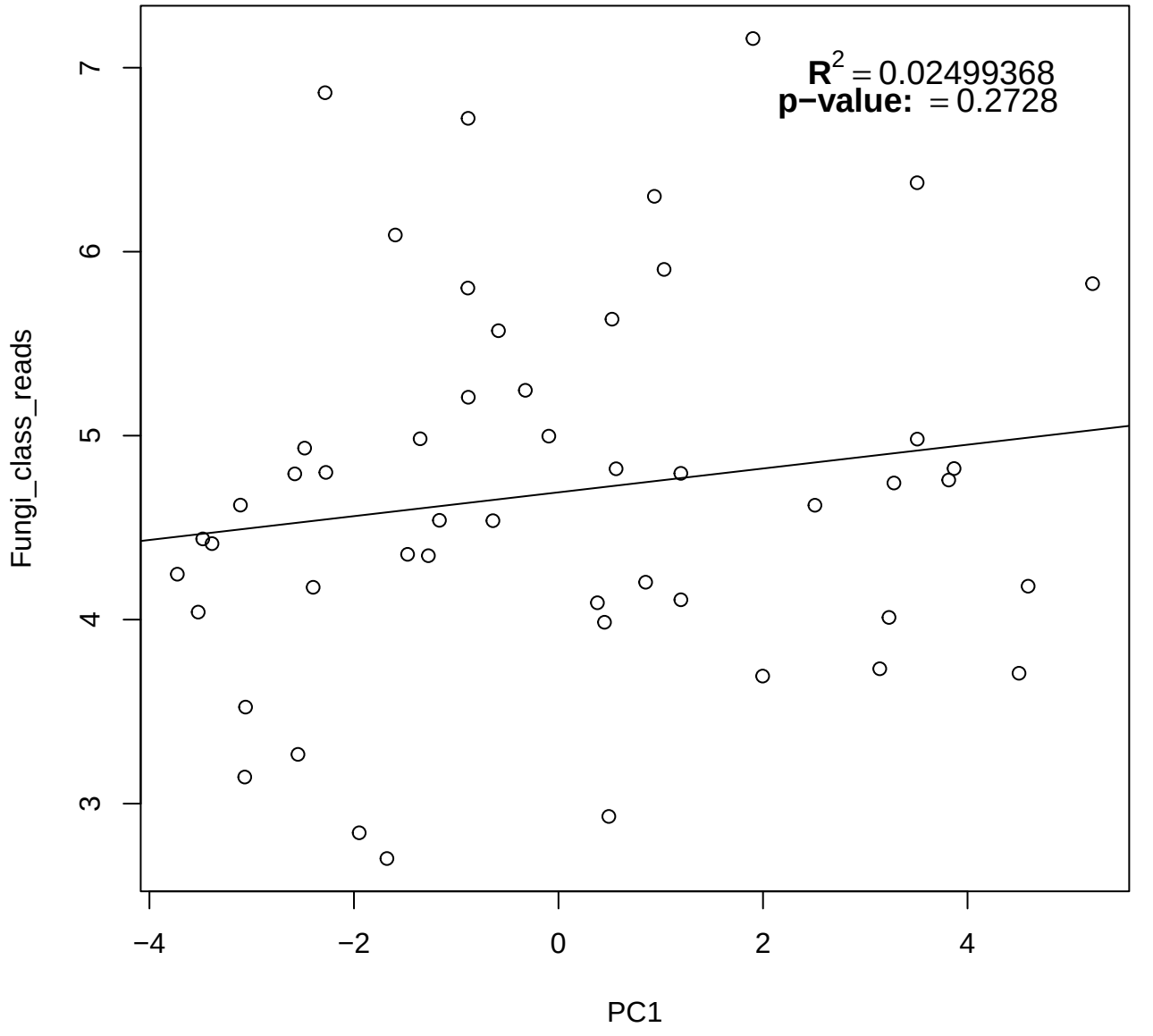
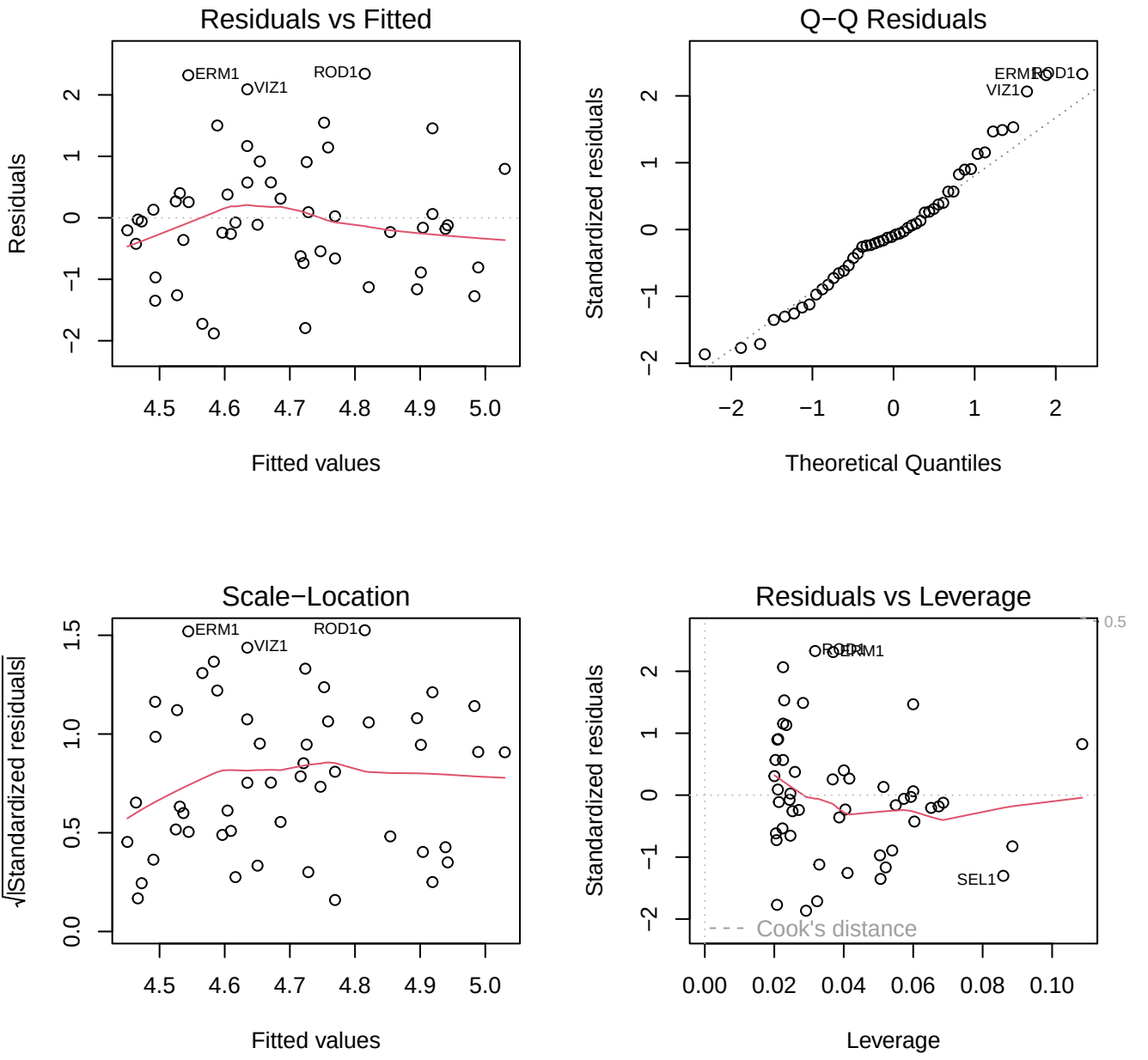
15
20
25
30


Residuals vs Fitted
Residuals
Fitted values
VIZ1
ERM1
ROD1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
VIZ1
ROD1
CBR1
Cook's distance


$R^2 = 0.02499368$
p−value: = 0.2728
Fungi_class_reads
PC1
7
6
5
4
3
−4
−2
0
2
4


Residuals vs Fitted
Residuals
Fitted values
ERM1
VIZ1
ROD1
Q−Q Residuals
Standardized residuals
Theoretical Quantiles
ERM1
ROD1
VIZ1
Scale−Location
√|Standardized residuals|
Fitted values
ERM1
VIZ1
ROD1
Residuals vs Leverage
Standardized residuals
Leverage
ROD1
ERM1
SEL1
Cook's distance
0.5