MLR

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December 1, 2019

```
set.seed(10035)
remove_singularities <- function(dataset, gene_name){
  dataset_copy <- dataset
  item <- paste(gene_name, "~.", sep="")
  full_formula <- as.formula(item)
  fit <- lm(full_formula, data=dataset)
  singularities <- attributes(alias(fit)$Complete)$dimnames[[1]]
  for (singularity in singularities){
    dataset_copy[singularity] <- NULL
  }
  return(dataset_copy)
}
read_in_pruned_datasets_for_gene_0.8 <- function(gene_name, path){
  full_path0.8 <- paste(path, gene_name, "_for_r_0.8.txt", sep="")
  Data0.8 <- read.table(full_path0.8, header=TRUE, sep=',')
  Data0.8 <- remove_singularities(Data0.8, gene_name)
  return(Data0.8)
}
#install.packages("DAAG")
#install.packages("caret")
#install.packages("lmtest")
#install.packages("MASS")
#install.packages("car")
#install.packages("reshape")
#install.packages("plotmo")
#install.packages("olsrr")
library(caret)
```

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

```
## Loading required package: ggplot2
```

```
library(lmtest)
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```r
library(MASS)
library(car)
```

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

```r
library(reshape)
library(plotmo)
```

```
## Loading required package: Formula
```

```
## Loading required package: plotrix
```

```
## Loading required package: TeachingDemos
```

```r
library(olsrr)
```

```
##
## Attaching package: 'olsrr'
```

```
## The following object is masked from 'package:MASS':
##
##     cement
```

```
## The following object is masked from 'package:datasets':
##
##     rivers
```

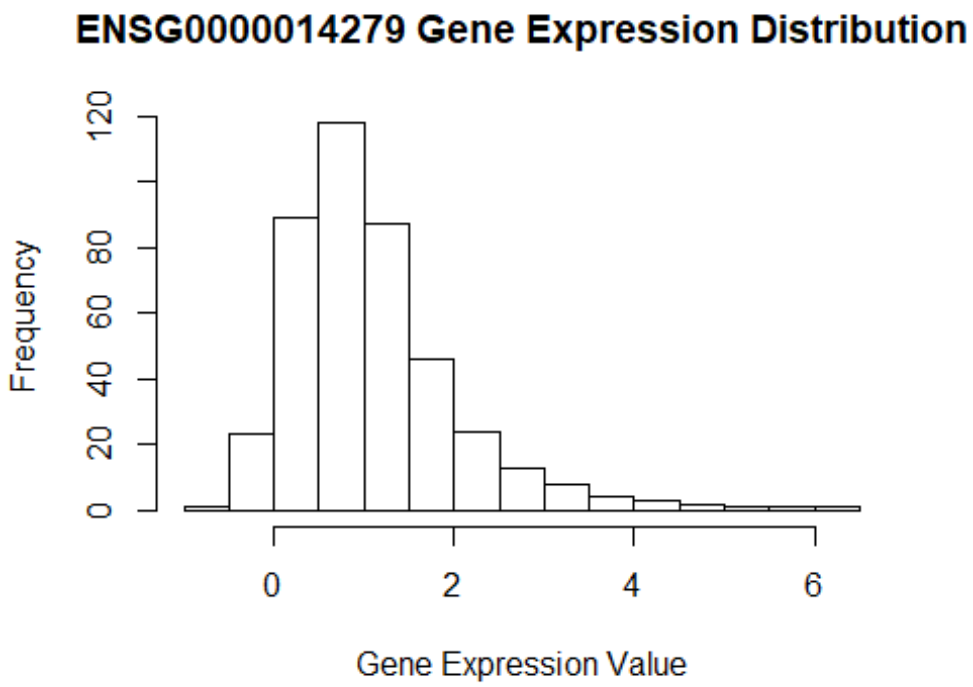
```r
library(DAAG)
```

```
##
## Attaching package: 'DAAG'
```

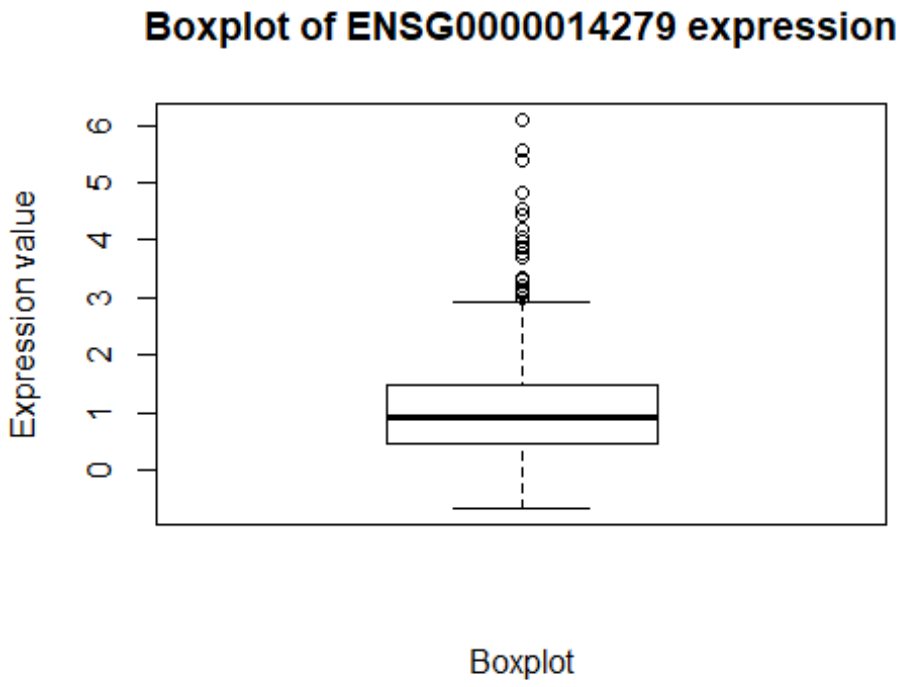
```
## The following object is masked from 'package:car':
##
##     vif
```

```
## The following object is masked from 'package:MASS':
##
##     hills
```

```r
gene_data <- read_in_pruned_datasets_for_gene_0.8("ENSG00000142794", "D:\\Pro
ject\\GitStash\\Applied_regression_project\\")
gene_data <- as.data.frame(gene_data)
hist(gene_data[["ENSG00000142794"]], main="ENSG0000014279 Gene Expression Dis
tribution", ylab="Frequency", xlab="Gene Expression Value")
```



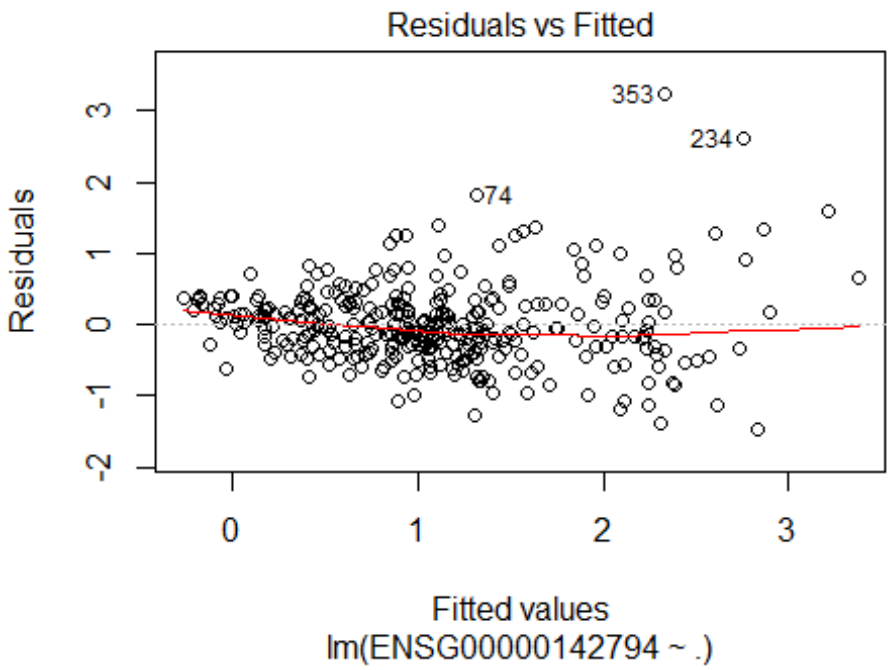

```r
boxplot(gene_data[["ENSG00000142794"]], main="Boxplot of ENSG0000014279 expre
ssion", ylab="Expression value", xlab="Boxplot")
```



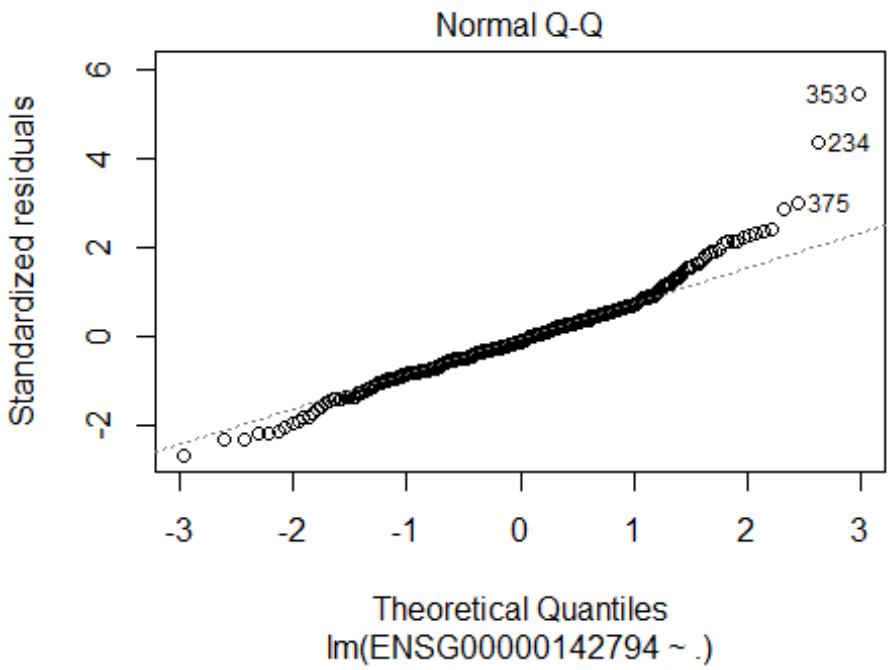
```r
# We notice that the Expression Data is skewed to the right.
trainIndex <- createDataPartition(gene_data[["ENSG00000142794"]], p=.8, list
= FALSE, times=1)

# We do test train split and explicitly create the data partition indexs
# because of the difference seed values produce in different R versions

gene_data <- gene_data[train_index,]
gene_test <- gene_data[-train_index,]
#We do a train validation split here.

model <- lm(ENSG00000142794~., data=gene_data)
summary(model)

##
## Call:
## lm(formula = ENSG00000142794 ~ ., data = gene_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.4584 -0.3311 -0.0545  0.2781  3.2295
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.0773438  0.8375846   1.286   0.1996
## rs12734589  -0.2426399  0.3650244  -0.665   0.5069
## rs2004380    0.1102502  1.0093512   0.109   0.9131
## rs10737456  -0.1014757  0.2853902  -0.356   0.7225
## rs10799692   0.0890538  0.5131390   0.174   0.8624
## rs3820296   -0.2600382  0.3517204  -0.739   0.4604
## rs10916988   0.1944314  0.1744793   1.114   0.2663
## rs1976403    0.5034704  0.4112980   1.224   0.2222
## rs1780324    0.4284627  0.2894724   1.480   0.1402
## rs4654753   -0.4658774  0.4593801  -1.014   0.3116
## rs79760554   0.0278784  0.1362679   0.205   0.8381
## rs12729540  -0.0386049  0.2499062  -0.154   0.8774
## rs12043777  -0.1137017  0.1445647  -0.787   0.4324
## rs10799702   0.1519789  0.2212533   0.687   0.4928
## rs4061838   -0.1683068  0.1846747  -0.911   0.3630
## rs7545635    0.0693701  0.2444405   0.284   0.7768
## rs4654946   -0.0593146  0.5275433  -0.112   0.9106
## rs2047653   -0.0215676  0.4805840  -0.045   0.9642
## rs4079441    0.0160076  0.5254259   0.030   0.9757
## rs12034222   0.1939562  0.1212573   1.600   0.1111
## rs3820292   -0.0718418  0.1268148  -0.567   0.5716
## rs75417796   0.1798876  0.3004644   0.599   0.5500
## rs7541779    0.0238033  0.2965717   0.080   0.9361
## rs75417790   0.0475355  0.2394576   0.199   0.8428
## rs10799691  -0.0251948  0.2950647  -0.085   0.9320
## rs1971328    0.2014015  0.2281684   0.883   0.3783
```

```
## rs12744514   0.6974904  0.5034685   1.385   0.1673
## rs41310392  -0.4924510  0.3108441  -1.584   0.1145
## rs75056920   0.0976996  0.1316812   0.742   0.4589
## rs1697421   -0.2674773  0.2314293  -1.156   0.2490
## rs146767219  0.0388611  0.1074221   0.362   0.7179
## rs12132412   0.0488435  0.1550308   0.315   0.7530
## rs112985962 -0.1747530  0.6483509  -0.270   0.7878
## rs147900768  0.1793372  0.2227159   0.805   0.4215
## rs1814737   -0.6478764  0.7304950  -0.887   0.3760
## rs56286426  -0.0108865  0.1338131  -0.081   0.9352
## rs17420195   1.2040546  0.9058701   1.329   0.1851
## rs113548640  0.1619209  0.3515875   0.461   0.6456
## rs146564096 -0.1459169  0.1311852  -1.112   0.2672
## rs10916989   0.0113086  0.2306912   0.049   0.9609
## rs150401191  0.0091174  0.6004537   0.015   0.9879
## rs3010180   -0.1346392  0.1276371  -1.055   0.2926
## rs78885464   0.1262377  0.1141166   1.106   0.2698
## rs6694671    0.0356021  0.3917338   0.091   0.9277
## rs144522615 -0.0696422  0.1296253  -0.537   0.5916
## rs61775934  -0.1628478  0.4170355  -0.390   0.6965
## rs3010181    0.1408603  0.1079256   1.305   0.1931
## rs1780323   -0.0641018  0.1257974  -0.510   0.6108
## rs61778366  -0.3494258  0.2960935  -1.180   0.2392
## rs79659018   0.0159360  0.1274369   0.125   0.9006
## rs10737458  -0.3630167  0.4858445  -0.747   0.4557
## rs11584744   0.5002325  0.3351833   1.492   0.1369
## rs201590042 -0.0149337  0.1038923  -0.144   0.8858
## rs1566524   -0.1873926  0.4552565  -0.412   0.6810
## rs61775950   0.0831508  0.0978564   0.850   0.3964
## rs144443608  0.0877285  0.1013082   0.866   0.3874
## rs10916986   0.3573069  0.2995042   1.193   0.2341
## rs904927     0.1363907  0.3373079   0.404   0.6863
## rs190849739  0.0054703  0.1267022   0.043   0.9656
## rs143561157  0.1553284  0.1161436   1.337   0.1824
## rs12740648  -0.0110182  0.1509227  -0.073   0.9419
## rs12118362   0.0390582  0.1495256   0.261   0.7942
## rs1809914   -0.4849652  0.2207155  -2.197   0.0290 *
## rs41310412   0.0082098  0.2822820   0.029   0.9768
## rs6423191    0.0007244  0.1983363   0.004   0.9971
## rs140609058 -0.2737547  0.3502827  -0.782   0.4353
## rs7555005   -0.1160461  0.2698248  -0.430   0.6675
## rs71512991  -0.0922331  0.1062848  -0.868   0.3864
## rs139043162 -0.0988816  0.3860193  -0.256   0.7981
## rs2800935   -0.0890408  0.1292364  -0.689   0.4915
## rs113324018  0.1567611  0.2392068   0.655   0.5129
## rs904928     0.0440956  0.1553133   0.284   0.7767
## rs7533048    0.1191272  0.2959662   0.403   0.6877
## rs12239666  -0.1800842  0.2227685  -0.808   0.4197
## rs972662     0.1707553  0.2390314   0.714   0.4757
## rs9726624   -0.0631679  0.1772911  -0.356   0.7219
```

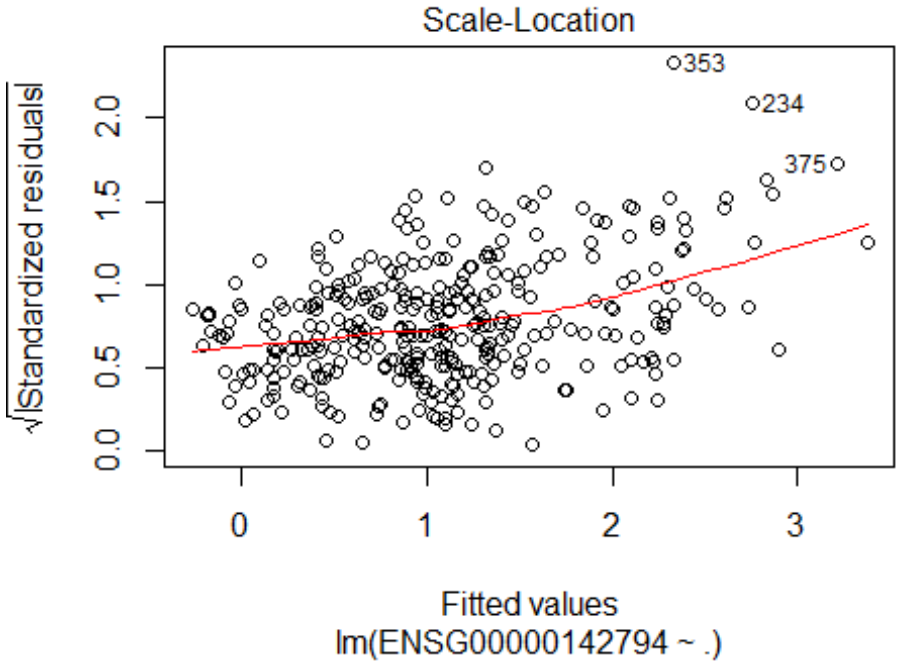
```
## rs2800774    0.0266631  0.0939158   0.284   0.7767
## rs56268398   0.0605925  0.1983985   0.305   0.7603
## rs12082914   0.1894957  0.3400845   0.557   0.5779
## rs78566499   0.0775510  0.2753531   0.282   0.7785
## rs1809915    0.2982296  0.1990040   1.499   0.1353
## rs7547671    0.2785216  0.8860444   0.314   0.7535
## rs146549873 -0.0763266  0.0938884  -0.813   0.4171
## rs113934925 -0.1689566  0.9265713  -0.182   0.8555
## rs200384063 -0.0353196  0.2725797  -0.130   0.8970
## rs4654930    0.3933332  0.3124555   1.259   0.2093
## rs3855556    0.0959987  0.1545367   0.621   0.5351
## rs35836191  -0.6655432  0.5295844  -1.257   0.2101
## rs60803995   0.1947940  0.1536928   1.267   0.2063
## rs12037596  -0.1170011  0.1806859  -0.648   0.5179
## rs2651402    0.4172604  0.3110401   1.342   0.1811
## rs41290414  -0.3163552  0.4893582  -0.646   0.5186
## rs72476502   0.0790231  0.2649570   0.298   0.7658
## rs58090121  -0.0165627  0.1430192  -0.116   0.9079
## rs904937    -0.1079859  0.1691946  -0.638   0.5239
## rs41265985  -0.3857862  0.2618278  -1.473   0.1420
## rs77025042  -0.0157810  0.1191521  -0.132   0.8947
## rs7417849   -0.1141053  0.1663477  -0.686   0.4934
## rs113558389 -0.1506948  0.2873036  -0.525   0.6004
## rs904929     0.1129374  0.1973569   0.572   0.5677
## rs10799704  -0.0001877  0.0840813  -0.002   0.9982
## rs148061397  0.0406450  0.2051900   0.198   0.8432
## rs115933091  0.1055186  0.3592554   0.294   0.7692
## rs143553186  0.5298658  0.2947059   1.798   0.0735 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6711 on 233 degrees of freedom
## Multiple R-squared:  0.6148, Adjusted R-squared:  0.4446
## F-statistic: 3.611 on 103 and 233 DF,  p-value: 2.972e-16

plot(model, which=1)
```



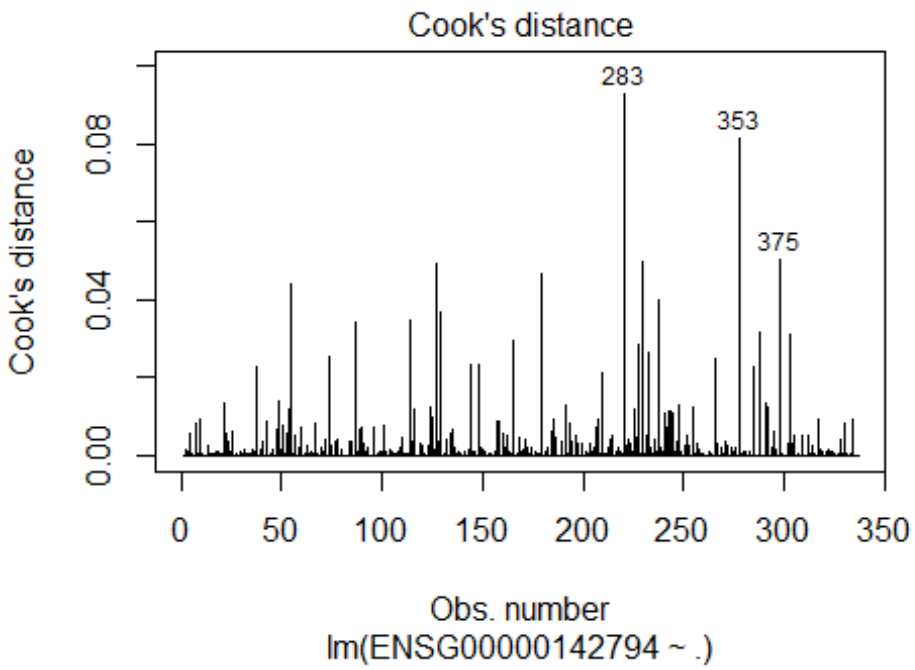

```
bptest(model)

##
##  studentized Breusch-Pagan test
##
## data:  model
## BP = 96.199, df = 103, p-value = 0.6693

# We note from the Residuals Vs Fitted Plot that there
#might be a slight concern with nonconstant variance but for the Breusch-Paga
n test
# we fail to reject with an alpha of 0.05.

plot(model, which=2)
```



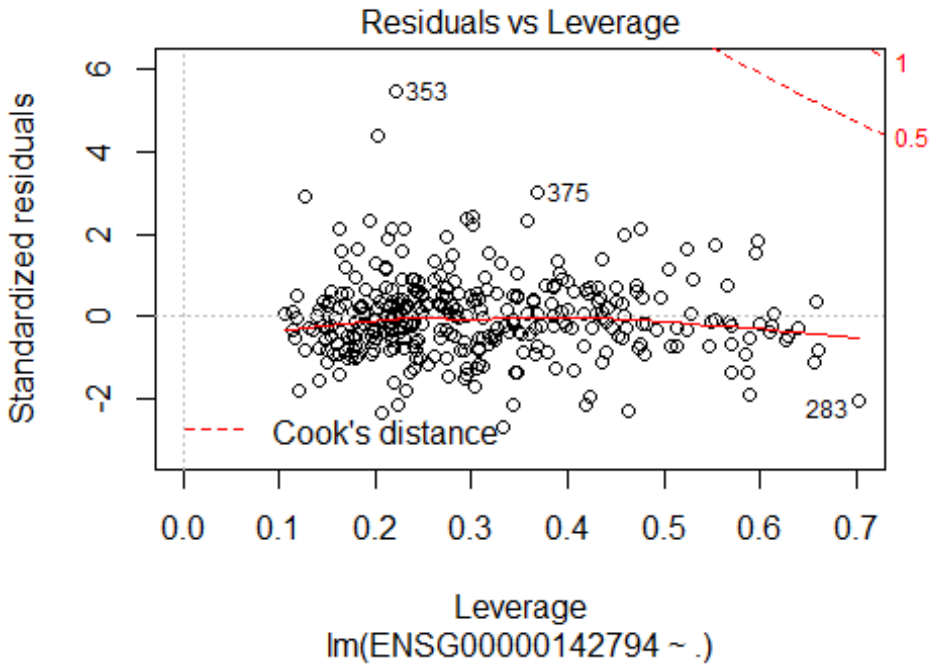

```
shapiro.test(model$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model$residuals
## W = 0.94027, p-value = 2.08e-10

# However, we notice an issue with normality from a QQPlot that
# suggests the data is skewed and we reject the shapiro-wilks test with an al
pha of 0.05

plot(model, which=3)
```




```
#The Scale-Location plot has a slope most likely because there isn't enough d
ata for the fitted values.

plot(model, which=4)
```



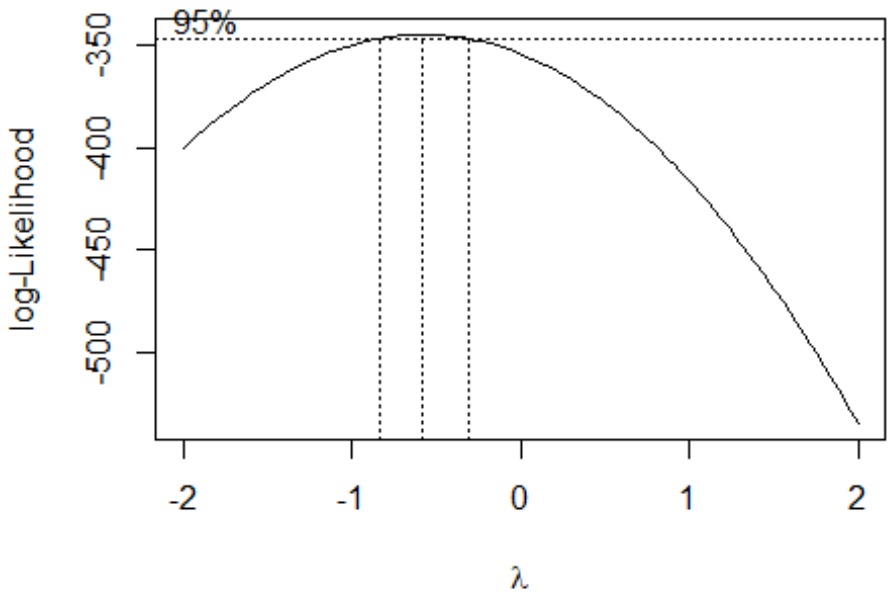

```r
plot(model, which=5)
```



```r
# We don't notice an issues with overly influential points in the residuals v
s Leverage Plot.
# However, we do note some points are considered to have high leverage later
on. But these points
# are actually important to the variation we want to capture in our data.

summary(model)$adj.r.squared
```

```
## [1] 0.444552
```

```r
# We have an adjusted R-squared of 0.44452.

test <- model <- lm(ENSG00000142794+2~., data=gene_data)
# We do a Boxcox on the model and note that we should do a transformation on
Y(1/sqrt(Y+2))
boxcox(test)
```

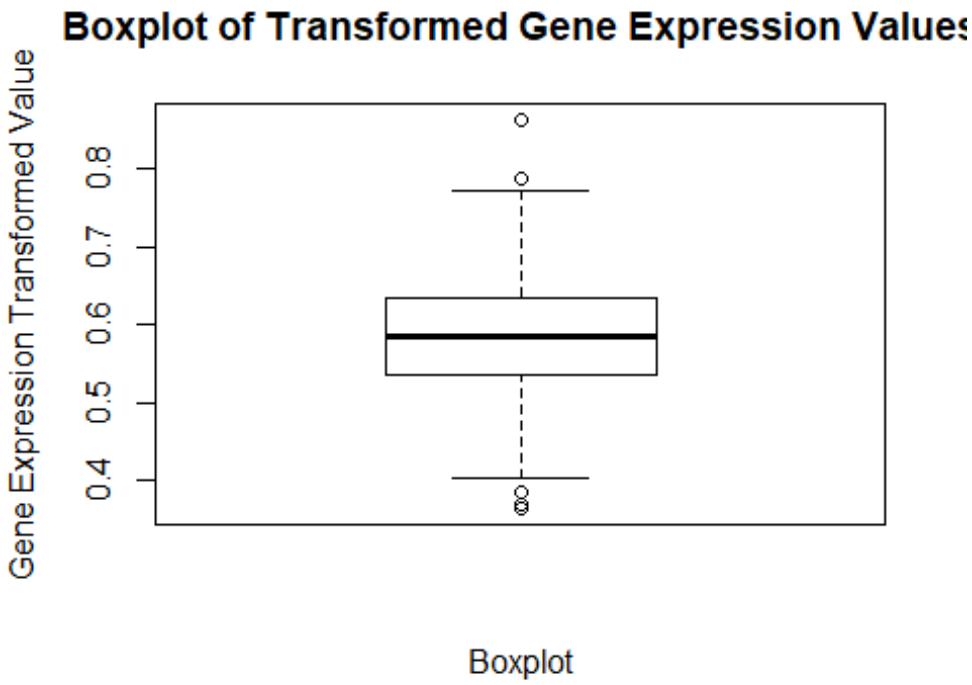



```r
# VIF Calculation and setting N and P
n <- nrow(gene_data)
p <- length(model$coefficients)

# There is an indication of severe multicolinearity.
car::vif(model)
test <- lm(ENSG00000142794+2~., data=gene_data)
```

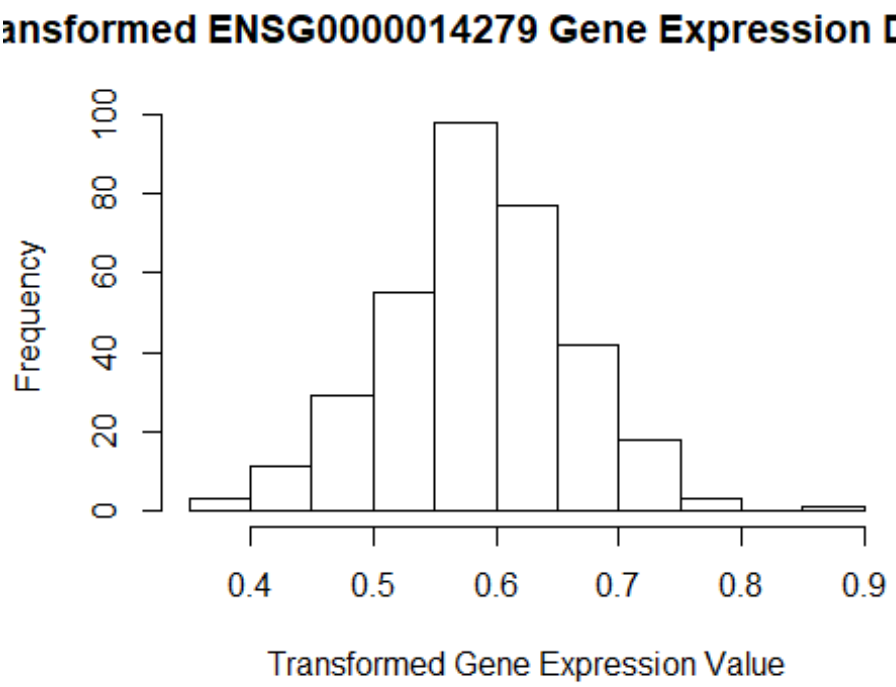
```r
# The added variable plots suggest a lot of the predictors do not
# add new information when the other predictors are included in the model.
pdf("AddedVariablesBeforeSelection.pdf")
avPlots(model, ask=FALSE)
dev.off()
```

```
## png
##   2
```

```r
# We do the transform on the train and test datasets. # We also set n.
# Additionally, we also plot the transformed values and note they appear to b
e normally distributed.
transformed_gene_data <- gene_data
transformed_gene_test <- gene_test
n <- nrow(transformed_gene_data)
transformed_gene_data[["ENSG00000142794"]] <- 1/(sqrt(transformed_gene_data[[
"ENSG00000142794"]]+2))
transformed_gene_test[["ENSG00000142794"]] <- 1/(sqrt(transformed_gene_test[[
"ENSG00000142794"]]+2))
boxplot(transformed_gene_data["ENSG00000142794"], main="Boxplot of Transforme
d Gene Expression Values", ylab="Gene Expression Transformed Value", xlab="Bo
xplot")
```




```r
hist(transformed_gene_data[["ENSG00000142794"]], main="Transformed ENSG000001
4279 Gene Expression Distribution", ylab="Frequency", xlab="Transformed Gene
Expression Value")
```




```
# We do variable selection and we do a strict variable selection with a p-val
ue of 0.01. Step-Forward BIC, and Step-Backward BIC.
# We then put the selected variables for each model together and do a best su
bset exhaustive search over just these variables.

naieve_model <- lm(ENSG00000142794~., data=transformed_gene_data)
naieve_model_empty <- lm(ENSG00000142794~1, data=transformed_gene_data)


selected_p <- ols_step_backward_p(naieve_model, prem=0.01)
selected_p_model <- selected_p$model
p <- length(selected_p_model$coefficients)
RSS_selected <- c(crossprod(selected_p_model$residuals))
MSE <- RSS_selected / length(selected_p_model$residuals)
selected_p_stats <- rbind(sqrt(MSE), BIC(selected_p_model), summary(selected_
p_model)$adj.r.squared, DAAG::press(selected_p_model))




selected<- stepAIC(naieve_model, k=log(n))
p <- length(selected$coefficients)
RSS_selected <- c(crossprod(selected$residuals))
MSE <- RSS_selected / length(selected$residuals)
selected_stats <- rbind(sqrt(MSE), BIC(selected), summary(selected)$adj.r.squ
ared, DAAG::press(selected))
```

```r
forward_bic <- stepAIC(naieve_model_empty, scope = list(upper=naieve_model, l
ower=naieve_model_empty), direction="forward", k=log(n))
p <- length(forward_bic$coefficients)
RSS_selected <- c(crossprod(forward_bic$residuals))
MSE <- RSS_selected / length(forward_bic$residuals)
forward_bic_stats <- rbind(sqrt(MSE), BIC(forward_bic), summary(forward_bic)$
adj.r.squared, DAAG::press(forward_bic))

car::vif(selected)

##  rs12734589  rs10799692 rs113548640   rs6694671   rs1566524  rs35836191
##    5.036327    4.997166    2.697843    3.118706    3.069425    1.694852
##  rs60803995
##    2.351035

car::vif(selected_p_model)

##  rs12734589 rs113548640   rs6694671   rs1566524  rs35836191  rs60803995
##    3.283511    2.146153    2.669397    3.068997    1.694835    2.347506

car::vif(forward_bic)

##  rs12734589   rs1976403   rs4654753   rs6694671 rs113548640  rs10916989
##    3.192661    2.848736    4.706859    3.299466    5.526336    3.981726

# We now do not see any issues with multicolinearity which suggests
# we do not need to use ridge regression on these reduced variable models.

search_full_model <- lm(ENSG00000142794~rs12734589 + rs1976403 + rs4654753 +
rs6694671 + rs113548640 + rs10916989 + rs1566524, rs35836191 + rs60803995 + r
s10799692, data=transformed_gene_data)

all_possible <- ols_step_best_subset(search_full_model)
all_possible

##                                 Best Subsets Regression
## --------------------------------------------------------------------------
--------------
## Model Index    Predictors
## --------------------------------------------------------------------------
--------------
##      1         rs12734589
##      2         rs6694671 rs113548640
##      3         rs12734589 rs6694671 rs113548640
##      4         rs12734589 rs1976403 rs6694671 rs113548640
##      5         rs12734589 rs4654753 rs6694671 rs113548640 rs10916989
##      6         rs12734589 rs1976403 rs4654753 rs6694671 rs113548640 rs1091
6989
##      7         rs12734589 rs1976403 rs4654753 rs6694671 rs113548640 rs1091
6989 rs1566524
## --------------------------------------------------------------------------
```

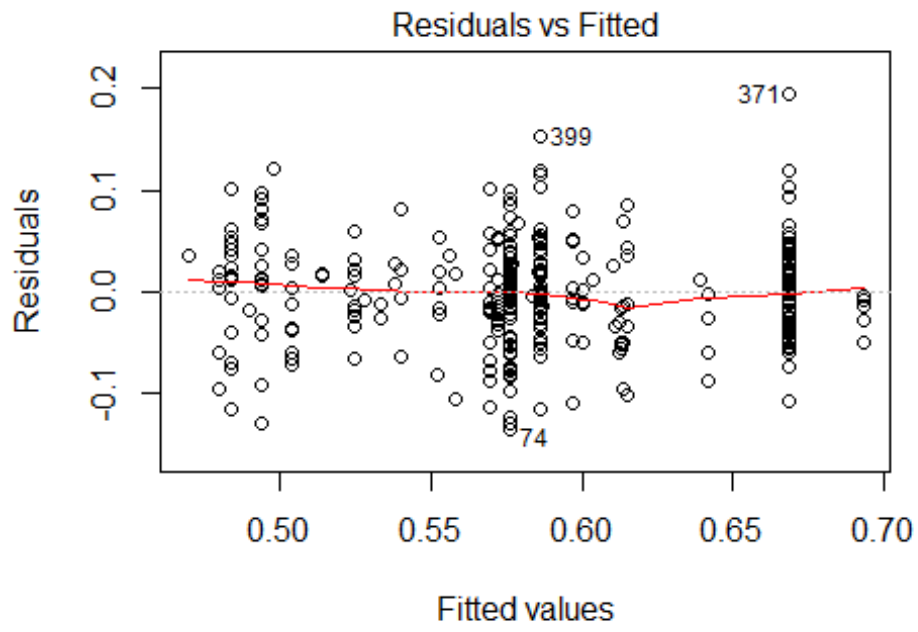
```
--------------
##
##                                                       Subsets Regression Sum
mary
## ------------------------------------------------------------------------
-------------------------------------------------------
##                         Adj.        Pred
## Model    R-Square    R-Square    R-Square       C(p)          AIC        S
BIC       SBC          MSEP      FPE        HSP       APC
## ------------------------------------------------------------------------
-------------------------------------------------------
##   1        0.4428      0.4412      0.4356    12886.6397     -972.0540
NA     -960.5938    0.0033    0.0033    0.0000    0.5638
##   2        0.5173      0.5144      0.5077    11122.3098    -1018.3882
NA    -1003.1079    0.0028    0.0028    0.0000    0.4914
##   3        0.5479      0.5438      0.5357    10397.7557    -1038.4744
NA    -1019.3740    0.0027    0.0027    0.0000    0.4630
##   4        0.5550      0.5496      0.5398    10231.6838    -1041.7965
NA    -1018.8760    0.0026    0.0026    0.0000    0.4584
##   5        0.5639      0.5573      0.5477    10021.9716    -1046.6223
NA    -1019.8817    0.0026    0.0026    0.0000    0.4519
##   6        0.5751      0.5674       0.556     9758.9045    -1053.3680
NA    -1022.8074    0.0026    0.0026    0.0000    0.4429
##   7        0.5798      0.5709      0.5588     9649.2532    -1055.1209
NA    -1020.7402    0.0025    0.0025    0.0000    0.4406
## ------------------------------------------------------------------------
-------------------------------------------------------
## AIC: Akaike Information Criteria
##  SBIC: Sawa's Bayesian Information Criteria
##  SBC: Schwarz Bayesian Criteria
##  MSEP: Estimated error of prediction, assuming multivariate normality
##  FPE: Final Prediction Error
##  HSP: Hocking's Sp
##  APC: Amemiya Prediction Criteria
```

```
final_stats <- cbind(selected_p_stats,selected_stats,forward_bic_stats)
row.names(final_stats) <- c("RMSE", "BIC", "ADJ-R-Squared", "PRESS")
colnames(final_stats) <- c("BackwardSelected_By_P_0.01", "Backward_BIC", "For
wardBIC")
knitr::kable(final_stats)
```

	BackwardSelected_By_P_0.01	Backward_BIC	ForwardBIC
RMSE	0.0498458	0.0493727	0.0495121
BIC	-1018.2806629	-1018.8876841	-1022.8073740
ADJ-R-Squared	0.5615122	0.5684880	0.5673627
PRESS	0.8735692	0.8599983	0.8632144

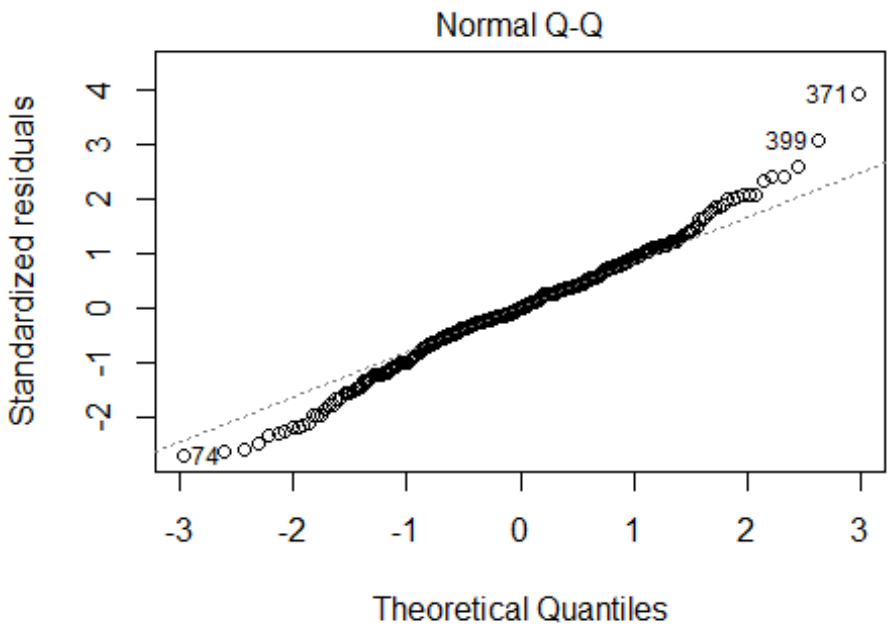
```
# We note that the optimal model is the one selected by forward_bic
# if we consider all the variables all these models give us and their best po
```

```
ssible subsets.
# We try to minimize SBC(BIC) and keep a reasonable Adj-R-Squared(>0.55) and
MSE.
# We note that MSE is near minmal at 4 predictors. But we have a lower SBC wi
th 6 predictors and a slightly higher R-squared.
model <- forward_bic

# We redo the model diagnostics from the beginning on the selected model.
# We will then compare this to one of the other models in our testing.
summary(model)

##
## Call:
## lm(formula = ENSG00000142794 ~ rs12734589 + rs1976403 + rs4654753 +
##     rs6694671 + rs113548640 + rs10916989, data = transformed_gene_data)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.134598 -0.026933  0.000069  0.028130  0.194233
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.524253   0.010447  50.183  < 2e-16 ***
## rs12734589   0.027072   0.006622   4.088 5.46e-05 ***
## rs1976403   -0.019831   0.006733  -2.946 0.003453 **
## rs4654753    0.033980   0.008821   3.852 0.000141 ***
## rs6694671    0.035719   0.007743   4.613 5.68e-06 ***
## rs113548640 -0.036296   0.011122  -3.263 0.001216 **
## rs10916989  -0.024367   0.007821  -3.116 0.001995 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05003 on 330 degrees of freedom
## Multiple R-squared:  0.5751, Adjusted R-squared:  0.5674
## F-statistic: 74.44 on 6 and 330 DF,  p-value: < 2.2e-16

# All variables appear significant




# We note that the residual vs fitted plot appears to be random.
plot(model, which=1)
```



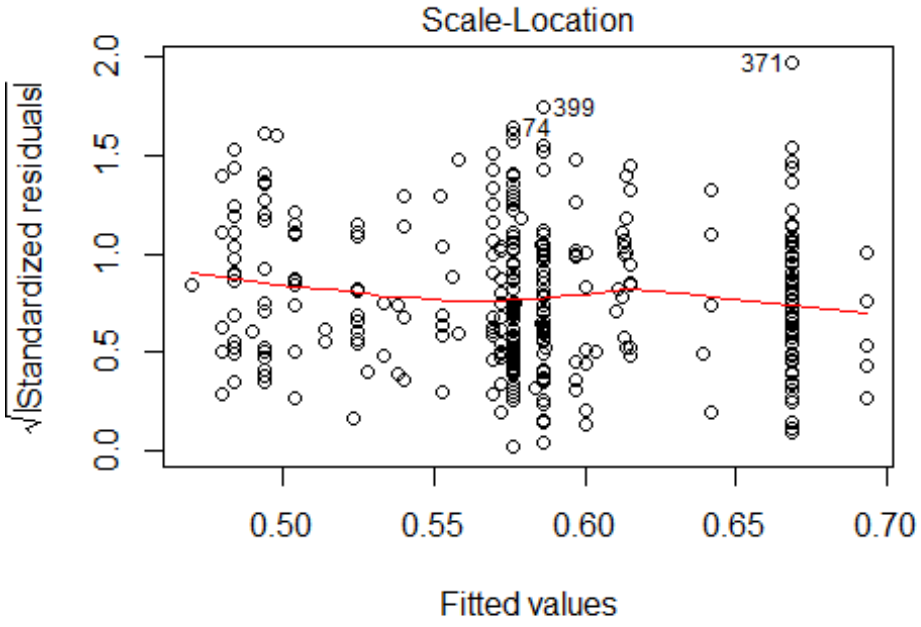
ŚG00000142794 ~ rs12734589 + rs1976403 + rs4654753 + rs66946

```
# We notice a small issue with normality still but this can probably be ignored.
# There is no issue with non constant error variance which is more important.
plot(model, which=2)
```

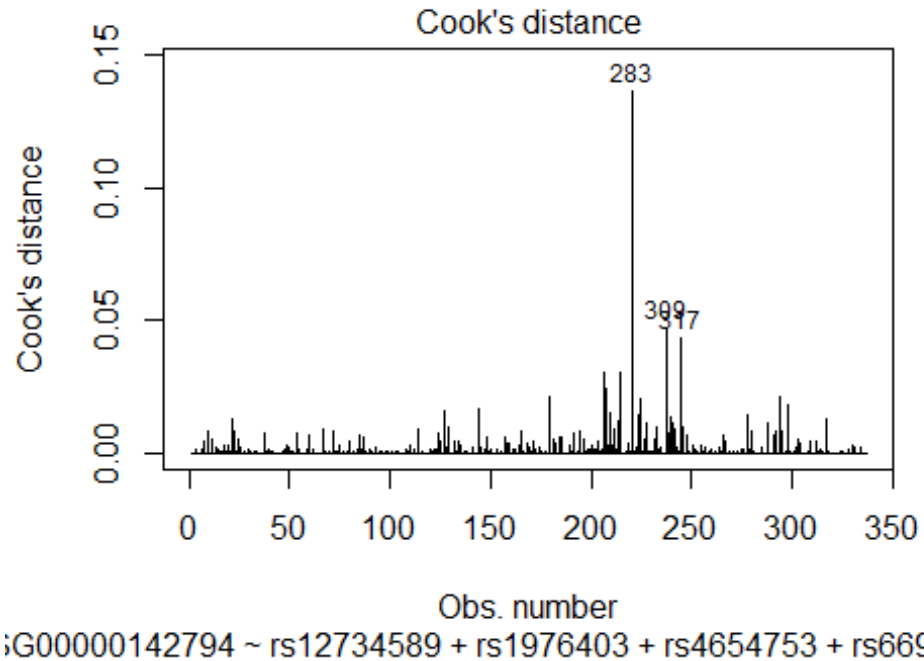


ENSG00000142794 ~ rs12734589 + rs1976403 + rs4654753 + rs66946

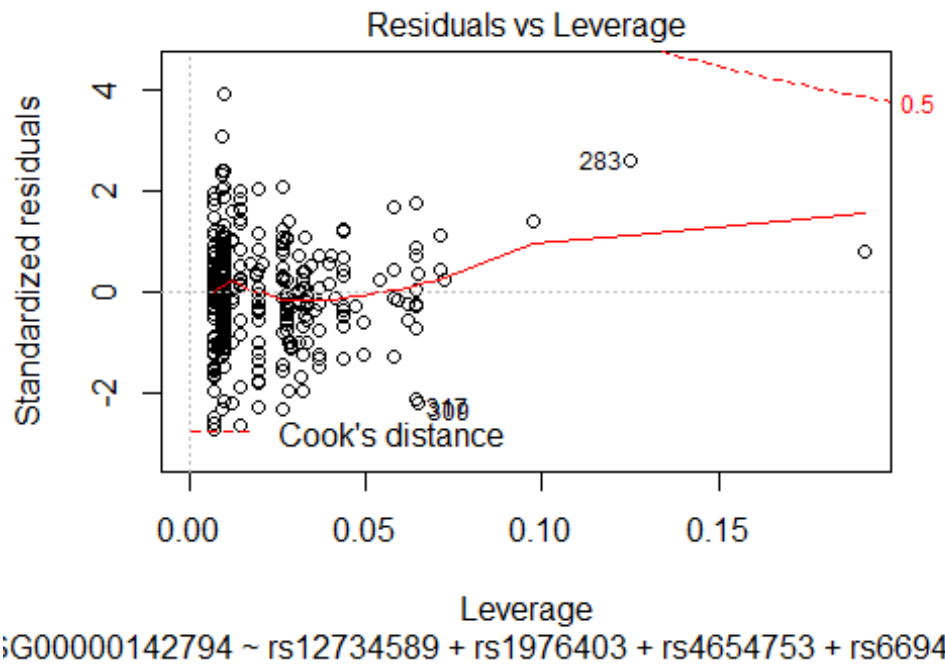
```
shapiro.test(model$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model$residuals
## W = 0.98986, p-value = 0.01963

bptest(model)

##
##  studentized Breusch-Pagan test
##
## data:  model
## BP = 2.7847, df = 6, p-value = 0.8353

# We notice potential outliers in the Cook's Distance Plot and Residuals vs L
everage Plot
# so we will do further analysis on these points.
# Particulary points 283, 309, and 317 have a high cook's distance and are ca
ndidate outliers.
# The Scale Location Plot doesn't appear to have a slope which is good.
plot(model, which=3)
```




```
plot(model, which=4)
```




```
plot(model, which=5)
```



ENSG00000142794 ~ rs12734589 + rs1976403 + rs4654753 + rs66946

```
# The added variable plots look much better.

pdf("AddedVariablesAfterSelection.pdf")
avPlots(model, ask=FALSE)
dev.off()

## png
##   2

# All variables appear significant.
# MSE looks very good.
knitr::kable(anova(model))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
rs12734589	1	0.8610066	0.8610066	343.928080	0.0000000
rs1976403	1	0.1251881	0.1251881	50.006228	0.0000000
rs4654753	1	0.0464546	0.0464546	18.556256	0.0000218
rs6694671	1	0.0403177	0.0403177	16.104843	0.0000742
rs113548640	1	0.0208500	0.0208500	8.328506	0.0041598
rs10916989	1	0.0243041	0.0243041	9.708235	0.0019954
Residuals	330	0.8261383	0.0025034	NA	NA

```
# We do outlier analysis here

cd <- cooks.distance(model)
```

```r
transformed_gene_dropped <- model$model[-c(which(cd > 4 / (n-p))),]
cooks_distance_model <- lm(ENSG00000142794~., data=transformed_gene_dropped)


# We note that we would like to retain these points regardless as they are in
teresting and represent variation
# in the population that can be informative in clinical situations.
# We opt to not use Robust Regression since the effect on the final model is
not serious enough.



leverage_threshold <- (3*(p))/n
leverage_values <- hatvalues(model)
transformed_gene_dropped_leverage <- model$model[-c(which(leverage_values > l
everage_threshold)),]
leverage_model <- lm(ENSG00000142794~., data=transformed_gene_dropped_leverag
e)

betas <- as.data.frame(dfbetas(model))

# We print the largest DFBeta for each parameter and the index of that DFBeta
.
to_remove <- c()
for(column in betas){
  outliers <- which(abs(column) > 0.11)
  print(max(abs(column)))
  print(which(abs(column) == max(abs(column))))
  to_remove <- union(to_remove, outliers)
}
```

```
## [1] 0.4216956
## [1] 238
## [1] 0.5156542
## [1] 245
## [1] 0.8014485
## [1] 221
## [1] 0.3773799
## [1] 221
## [1] 0.7861822
## [1] 221
## [1] 0.8713133
## [1] 221
## [1] 0.3917799
## [1] 238
```

```r
# One of 238, 245, and 221 give the max DFBetas the coefficients. These are t
he greatest outliers for DFBetas.
transformed_gene_dropped_betas <- model$model[-c(to_remove),]
new_model_betas <- lm(ENSG00000142794~., data=transformed_gene_dropped_betas)
```

```
coefficients <- rbind(model$coefficients,new_model_betas$coefficients,cooks_d
istance_model$coefficients, leverage_model$coefficients)
row.names(coefficients) <- c("Normal Model", "DroppedHighDFBetas", "DroppedHi
ghCooks", "DroppedHighLeverage")

# We make a summary table that shows what happens when we drop high DFBetas,
highCooks, and High Leverage Points from the model.
model_data <- c()
add_to_coefficients_data <- function(model, model_data){
  current_model <- model
  RSS_selected <- c(crossprod(current_model$residuals))
  MSE <- RSS_selected / length(current_model$residuals)
  current_model_stats <- cbind(sqrt(MSE), BIC(current_model), summary(current
_model)$adj.r.squared, DAAG::press(current_model), shapiro.test(model$residua
ls)$p.value, bptest(model)$p.value)
  colnames(current_model_stats) <- c("RMSE", "BIC", "ADJ-R-Squared", "PRESS",
"Shapiro_Wilks_Test_P_value", "Breusch-Pagan_Test_P_value")
  model_data <- rbind(model_data, current_model_stats)
  shapiro.test(model$residuals)
  return(model_data)
}
model_data <- add_to_coefficients_data(model, model_data)
model_data <- add_to_coefficients_data(cooks_distance_model, model_data)
model_data <- add_to_coefficients_data(new_model_betas, model_data)
model_data <- add_to_coefficients_data(leverage_model, model_data)

# Here is the summary table
summary_of_excluding_points <- cbind(coefficients, model_data)
knitr::kable(summary_of_excluding_points)
```

	(Intercept)	rs1273	rs19764	rs465347	rs669466	rs1354862	rs1091698	RMSE	BIC	ADJ-R-Squared	PRESS	Shapiro_Wilks_Test_P_value	Breusch-Pagan_Test_P_value
Normal Model	0.524	0.0270	-0.0198311	0.0033	0.0035	-0.00362	-0.00243	0.04951	-1022.8074	0.56736	0.86321	0.0196253	0.8353379
DroppedHighDFBetas	0.524	0.0268	-0.0151579	0.0037	0.0037	-0.00397	-0.00286	0.04417	-1038.9073	0.60712	0.86145	0.1451441	0.9307043

Dropp	0.5	0.0	-	0.0	0.0	-	-	0.0	-	0.6	0.5	0.00062	0.046
edHig	28	291	0.0	29	34	0.0	0.0	43	94	31	61	52	5953
hCook	85	684	17	84	55	387	245	42	7.5	36	80		
s	62		00	46	75	295	814	63	29	59	19		
			19						5				
Dropp	0.5	0.0	-	0.0	0.0	-	-	0.0	-	0.5	0.7	0.02083	0.859
edHig	28	369	0.0	31	30	0.0	0.0	48	98	85	97	70	8845
hLever	24	003	15	27	90	392	287	83	1.2	25	56		
age	15		04	38	58	810	681	92	10	52	38		
			14						4				

```
# We only would consider dropping HighDF Betas since dropping the other eleme
nts hurts BIC and might
# even cause the non constant error vairance assumption not to hold. We choos
e not to drop any points.
#The coefficients are not changed greatly enough to warrant us to exclude so
many
# points that contain valuable variation from the overall population.

# Dropping the High DFBetas points might be something we would consider if
# we had more data to represent the true diversity of the population but drop
ping
# these points might exclude points that include important variation.

# We compare the validation model and original model and get MSPR and compare
it to MSE.

predictions <- predict(model, transformed_gene_test)
validation_model_one <- lm(formula(model), data=transformed_gene_test)

# Comparison of Model Stats
model_stats <- cbind(sigma(model)^2, summary(model)$adj.r.squared, DAAG::pres
s(model))
validation_model_stats <- cbind(sigma(validation_model_one)^2, summary(valida
tion_model_one)$adj.r.squared, DAAG::press(validation_model_one))
comparison_of_stats <- rbind(model_stats, validation_model_stats)
colnames(comparison_of_stats) <- c("MSE", "Adj-R-Squared","PRESS")
rownames(comparison_of_stats) <- c("Original Model", "Validation Model")
comparison_of_stats

##                            MSE Adj-R-Squared     PRESS
## Original Model   0.002503449     0.5673627 0.8632144
## Validation Model 0.002299010     0.5480023 0.1912980

knitr::kable(comparison_of_stats)
```

	MSE	Adj-R-Squared	PRESS
Original Model	0.0025034	0.5673627	0.8632144
Validation Model	0.0022990	0.5480023	0.1912980

```r
# MSE vs MSPR
mspr_vs_mse <- cbind(sigma(model)^2, mean((transformed_gene_test[["ENSG00000142794"]]-predictions)^2))
colnames(mspr_vs_mse) <- c("MSE", "MSPR")
knitr::kable(mspr_vs_mse)
```

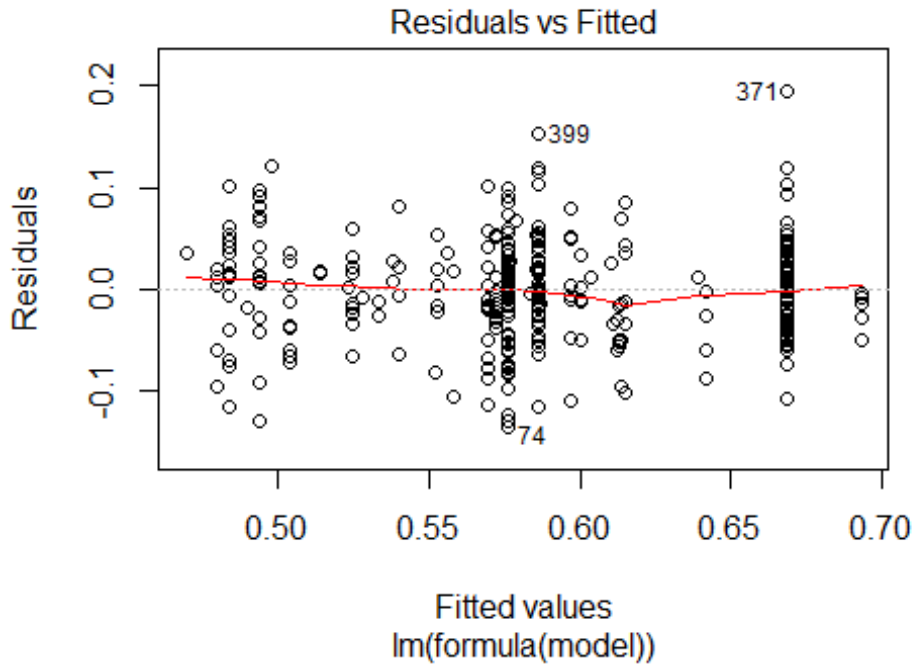
MSE	MSPR
0.0025034	0.0021703

```r
# Fitting the Final Multiple Linear Regression Model :)
final_gene_data <- read_in_pruned_datasets_for_gene_0.8("ENSG00000142794", "D:\\Project\\GitStash\\Applied_regression_project\\")
transformed_final_gene_data <- final_gene_data
transformed_final_gene_data[["ENSG00000142794"]] <- 1/(sqrt(transformed_final_gene_data[["ENSG00000142794"]]+2))
final_model <- lm(formula(model), data=transformed_gene_data)
summary(final_model)

##
## Call:
## lm(formula = formula(model), data = transformed_gene_data)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.134598 -0.026933  0.000069  0.028130  0.194233
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.524253   0.010447  50.183  < 2e-16 ***
## rs12734589   0.027072   0.006622   4.088 5.46e-05 ***
## rs1976403   -0.019831   0.006733  -2.946 0.003453 **
## rs4654753    0.033980   0.008821   3.852 0.000141 ***
## rs6694671    0.035719   0.007743   4.613 5.68e-06 ***
## rs113548640 -0.036296   0.011122  -3.263 0.001216 **
## rs10916989  -0.024367   0.007821  -3.116 0.001995 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05003 on 330 degrees of freedom
## Multiple R-squared:  0.5751, Adjusted R-squared:  0.5674
## F-statistic: 74.44 on 6 and 330 DF,  p-value: < 2.2e-16

knitr::kable(anova(final_model))
```

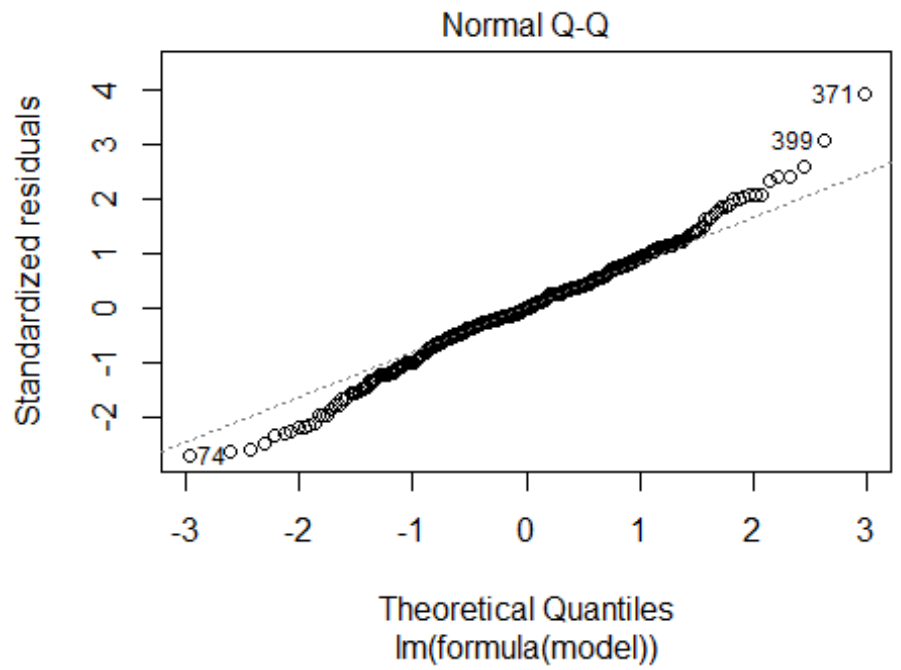
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
rs12734589	1	0.8610066	0.8610066	343.928080	0.0000000
rs1976403	1	0.1251881	0.1251881	50.006228	0.0000000
rs4654753	1	0.0464546	0.0464546	18.556256	0.0000218
rs6694671	1	0.0403177	0.0403177	16.104843	0.0000742

rs113548640	1	0.0208500	0.0208500	8.328506	0.0041598
rs10916989	1	0.0243041	0.0243041	9.708235	0.0019954
Residuals	330	0.8261383	0.0025034	NA	NA

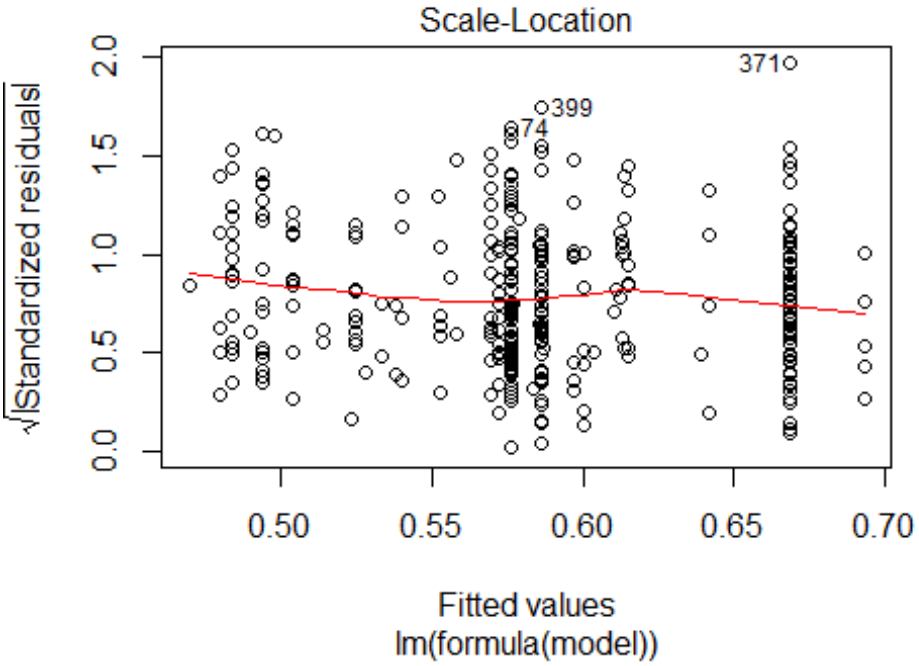
```
plot(final_model, which=1)
```



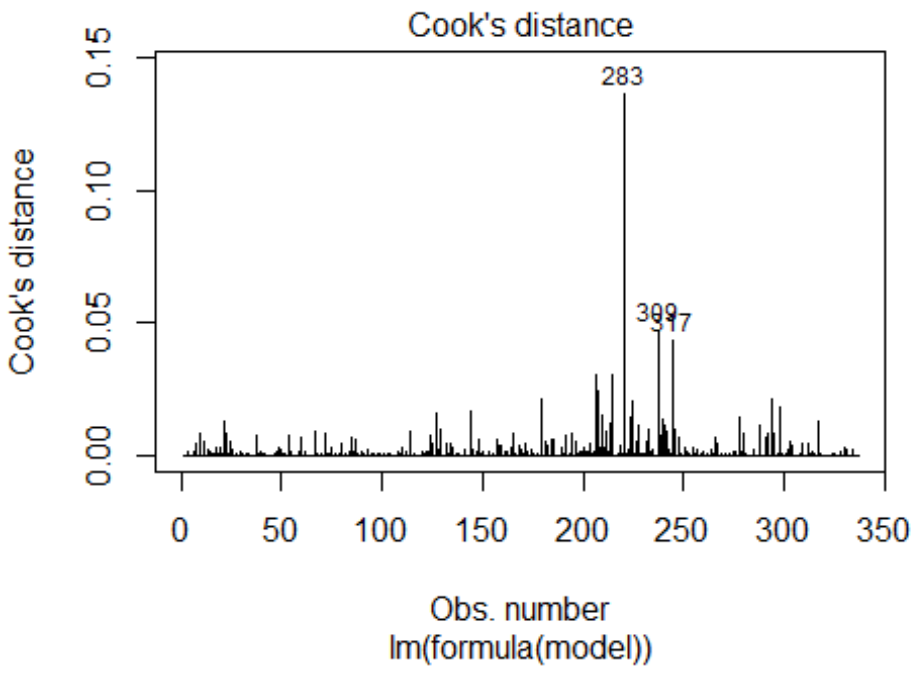

```
plot(final_model, which=2)
```



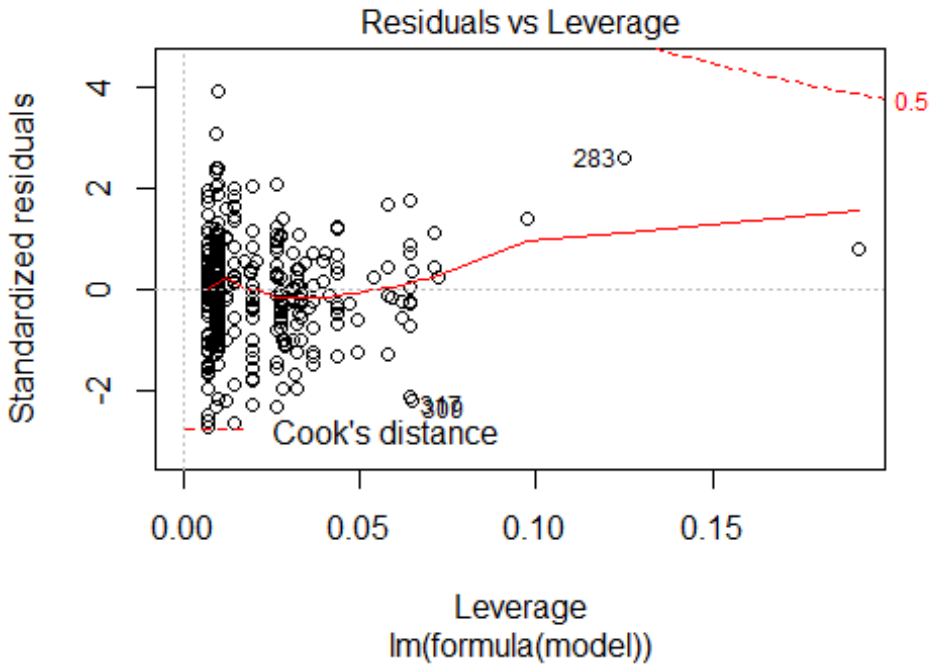

```
plot(final_model, which=3)
```




```
plot(final_model, which=4)
```




```r
plot(final_model, which=5)
```




```r
shapiro.test(model$residuals)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  model$residuals
## W = 0.98986, p-value = 0.01963
```

```
bptest(final_model)
```

```
##
##  studentized Breusch-Pagan test
##
## data:  final_model
## BP = 2.7847, df = 6, p-value = 0.8353
```

```
# We note the same diagnostic findings as we did from the selected model. The
re is a slight issue with normality and some outliers.

n <- nrow(transformed_final_gene_data)
p <- length(final_model$coefficients)
model <- final_model
# We do outlier analysis here

cd <- cooks.distance(model)
transformed_gene_dropped <- model$model[-c(which(cd > 4 / (n-p))),]
cooks_distance_model <- lm(ENSG00000142794~., data=transformed_gene_dropped)



leverage_threshold <- (3*(p))/n
leverage_values <- hatvalues(model)
transformed_gene_dropped_leverage <- model$model[-c(which(leverage_values > l
everage_threshold)),]
leverage_model <- lm(ENSG00000142794~., data=transformed_gene_dropped_leverag
e)

betas <- as.data.frame(dfbetas(model))

# We print the largest DFBeta for each parameter and the index of that DFBeta
.
to_remove <- c()
for(column in betas){
  outliers <- which(abs(column) > 2/sqrt(n))
  print(max(abs(column)))
  print(which(abs(column) == max(abs(column))))
  to_remove <- union(to_remove, outliers)
}
```

```
## [1] 0.4216956
## [1] 238
## [1] 0.5156542
```

```
## [1] 245
## [1] 0.8014485
## [1] 221
## [1] 0.3773799
## [1] 221
## [1] 0.7861822
## [1] 221
## [1] 0.8713133
## [1] 221
## [1] 0.3917799
## [1] 238

#238, 221, and 245 are possible massive outliers
transformed_gene_dropped_betas <- model$model[-c(to_remove),]
new_model_betas <- lm(ENSG00000142794~., data=transformed_gene_dropped_betas)
coefficients <- rbind(model$coefficients,new_model_betas$coefficients, cooks_
distance_model$coefficients, leverage_model$coefficients)
row.names(coefficients) <- c("Normal Model", "DroppedHighDFBetas", "DroppedHi
ghCooks", "DroppedHighLeverage")

# We make a summary table that shows what happens when we drop high DFBetas,
highCooks, and High Leverage Points from the model.
model_data <- c()
add_to_coefficients_data <- function(model, model_data){
  current_model <- model
  RSS_selected <- c(crossprod(current_model$residuals))
  MSE <- RSS_selected / length(current_model$residuals)
  current_model_stats <- cbind(sqrt(MSE), BIC(current_model), summary(current
_model)$adj.r.squared, DAAG::press(current_model), shapiro.test(model$residua
ls)$p.value, bptest(model)$p.value)
  colnames(current_model_stats) <- c("RMSE", "BIC", "ADJ-R-Squared", "PRESS",
"Shapiro_Wilks_Test_P_value", "Breusch-Pagan_Test_P_value")
  model_data <- rbind(model_data, current_model_stats)
  shapiro.test(model$residuals)
  return(model_data)
}
model_data <- add_to_coefficients_data(model, model_data)
model_data <- add_to_coefficients_data(cooks_distance_model, model_data)
model_data <- add_to_coefficients_data(new_model_betas, model_data)
model_data <- add_to_coefficients_data(leverage_model, model_data)

# Here is the summary table
summary_of_excluding_points <- cbind(coefficients, model_data)
knitr::kable(summary_of_excluding_points)
```

	(Intercept)	rs12734589	rs1976403	rs4654753	rs6694671	rs113548640	rs10916989	RMSE	BIC	ADJ-R-Sq	PRESS	Shapiro_Wilks_Test_P_value	Breusch-Pagan_Test_

										uared			P_value
Normal Model	0.524 2534	0.0270 721	-0.0198 3111	0.0339 8071	0.0357 1185	-0.0362 962	-0.0243 674	0.0495 1021	-10 22.8074	0.5673 6327	0.8632 1444	0.0196253	0.8353379
DroppedHighDFBetas	0.524 4619	0.0294 151	-0.0164 7000	0.0376 9858	0.0330 1030	-0.0355 336	-0.0282 190	0.0434 3086	-10 29.1651	0.6157 5703	0.6111 5164	0.0857069	0.6765788
DroppedHighCooks	0.524 2282	0.0298 767	-0.0116 8687	0.0281 4222	0.0370 1616	-0.0447 463	-0.0243 940	0.0425 1774	-92 1.8093	0.6437 6677	0.5179 5535	0.0002389	0.0167372
DroppedHighLeverage	0.528 2157	0.0376 963	-0.0170 7575	0.0327 2019	0.0280 0078	-0.0343 316	-0.0281 172	0.0490 7226	-95 2.8234	0.5846 7680	0.7864 0494	0.0226870	0.8651839

```
#We note that dropping the high DFBetas again results in a satisfied normalit
y assumption but we choose to retain these points.
```