STAT I512, Honglang Wang (hlwang)

Final Exam

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Problem 1:

```
library(MASS)
library(ggplot2)
library(corrplot)
```

```
## Warning: package 'corrplot' was built under R version 4.4.2
```

```
## corrplot 0.95 loaded
```

```
library(splines)
set.seed(42)

load("G:/Other computers/My Laptop/Google Drive/STAT512 Projects/Final Exam/meps512.RData")

# Predictors:
# AGE42X, ADBMI42, MNHLTH42, FAMINC18, RACETHX, SEX
# age, BMI, perceived mental health status, family income, race and gender

# Response:
# TOTEXP18 = total adult medical expenditures.

# Convert to factors
data$MNHLTH42 = as.factor(data$MNHLTH42)
data$RACETHX = as.factor(data$RACETHX)
data$SEX = as.factor(data$SEX)

colSums(is.na(data))
```

```
## TOTEXP18   AGE42X  ADBMI42 MNHLTH42 FAMINC18  RACETHX      SEX
##        0        0        0        0        0        0        0
```

```
m1 = lm(TOTEXP18 ~ AGE42X, data=data)
cat('\nMODEL 1:')
```

```
##
## MODEL 1:
```

```
summary(m1)
```

```
##
## Call:
## lm(formula = TOTEXP18 ~ AGE42X, data = data)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -14904  -6955  -3807   -538 801046
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -2385.134    407.137  -5.858 4.76e-09 ***
## AGE42X        203.406      7.691  26.448  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18930 on 18250 degrees of freedom
## Multiple R-squared:  0.03691,    Adjusted R-squared:  0.03686
## F-statistic: 699.5 on 1 and 18250 DF,  p-value: < 2.2e-16
```

```
m2 = lm(TOTEXP18 ~ AGE42X + SEX, data=data)
cat('\nMODEL 2:')
```

```
##
## MODEL 2:
```

```
summary(m2)
```

```
##
## Call:
## lm(formula = TOTEXP18 ~ AGE42X + SEX, data = data)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -15414  -6908  -3791   -465 800523
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1848.028    428.466  -4.313 1.62e-05 ***
## AGE42X        203.081      7.688  26.415  < 2e-16 ***
## SEXMALE     -1125.788    280.895  -4.008 6.15e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18920 on 18249 degrees of freedom
## Multiple R-squared:  0.03776,    Adjusted R-squared:  0.03765
## F-statistic: 358.1 on 2 and 18249 DF,  p-value: < 2.2e-16
```

```
m3 = lm(TOTEXP18 ~ AGE42X * SEX, data=data)
cat('\nMODEL 3:')
```

```
##
## MODEL 3:
```

```
summary(m3)
```

```
##
## Call:
## lm(formula = TOTEXP18 ~ AGE42X * SEX, data = data)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -15308  -6963  -3830   -181 800381
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -643.38     554.06  -1.161  0.24557
## AGE42X           178.93      10.43  17.162  < 2e-16 ***
## SEXMALE        -3752.99     816.28  -4.598  4.3e-06 ***
## AGE42X:SEXMALE    52.89      15.43   3.428  0.00061 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18920 on 18248 degrees of freedom
## Multiple R-squared:  0.03838,    Adjusted R-squared:  0.03822
## F-statistic: 242.8 on 3 and 18248 DF,  p-value: < 2.2e-16
```

a)

In model 1, β1 represents the change in medical expenditure for an increase in age of 1 year. This captures the relationship between age and medical expenditure without accounting for the potential influence of any other variables.

In model 2, β1 represents the change in medical expenditure for an increase in age of 1 year while holding gender constant. This isolates the effects of each predictor from the other which gives a more precise understanding of each predictors contribution to the response.

b)

The change in expected response if age increases by 1 while sex held fixed for Model 2 is an increase of $203.08

c)

The change in expected response if age increases by 1 while sex held fixed for Model 3 is an increase of… for females (X2=0): β1 = $178.93 for males (X2=1): β1 + β3 = 178.93 + 52.89 = $231.82

Problem 2:

###Print summary statistics

```
# summary statistics
cat('\nContinuous variables:\n')
```

```
##
## Continuous variables:
```

```
summary(data[, c("TOTEXP18", "AGE42X", "ADBMI42", "FAMINC18")])
```

```
##     TOTEXP18          AGE42X        ADBMI42         FAMINC18
##  Min.   :     0   Min.   :18.0   Min.   : 0.10   Min.   :-309948
##  1st Qu.:   400   1st Qu.:34.0   1st Qu.:23.70   1st Qu.:  27130
##  Median :  2024   Median :50.0   Median :27.30   Median :  56838
##  Mean   :  7725   Mean   :49.7   Mean   :28.15   Mean   :  75915
##  3rd Qu.:  7087   3rd Qu.:64.0   3rd Qu.:31.90   3rd Qu.: 104718
##  Max.   :807611   Max.   :85.0   Max.   :71.10   Max.   : 583219
```

```
cat('\nMental health:')
```

```
##
## Mental health:
```

```
table(data$MNHLTH42)
```

```
##
## EXCELLENT      FAIR      GOOD   INVALID      POOR VERY GOOD
##      5868      1405      4904         6       301      5768
```

```
cat('\nRace:')
```

```
##
## Race:
```

```
table(data$RACETHX)
```

```
##
##        ASIAN ONLY        BLACK ONLY          HISPANIC OTHER OR MULTIPLE
##               900              2633              3642               569
##        WHITE ONLY
##             10508
```

```
cat('\nGender:')
```

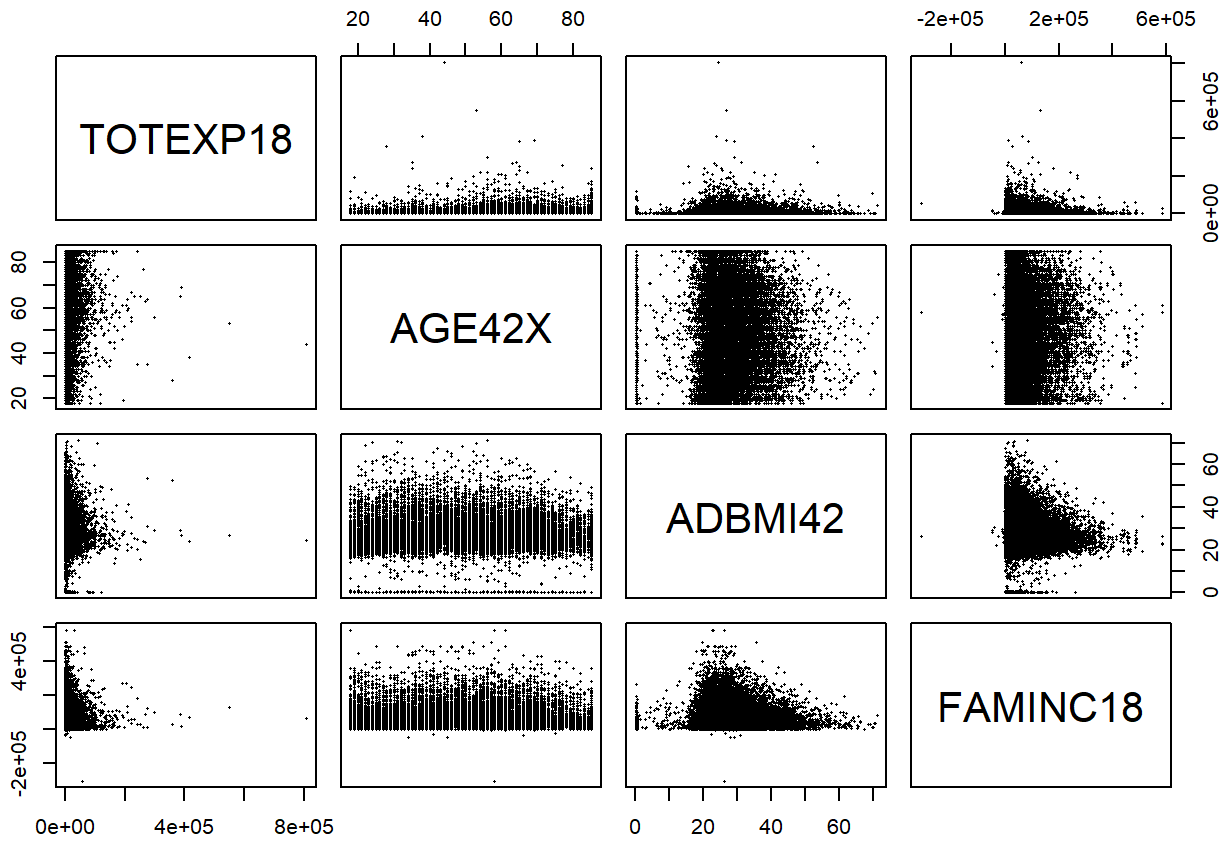
```
##
## Gender:
```

```
table(data$SEX)
```

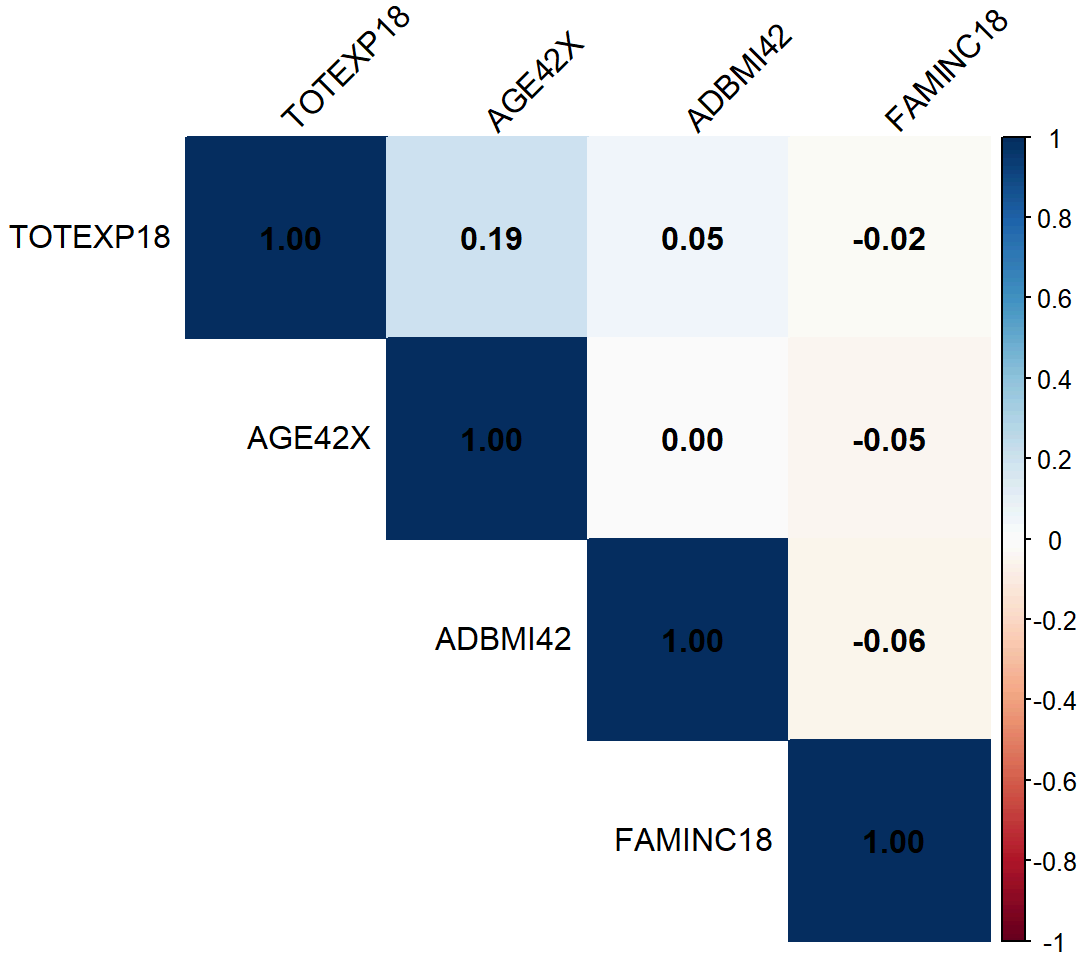
```
##
## FEMALE   MALE
##   9806   8446
```

Investigate distribution of variables using plots

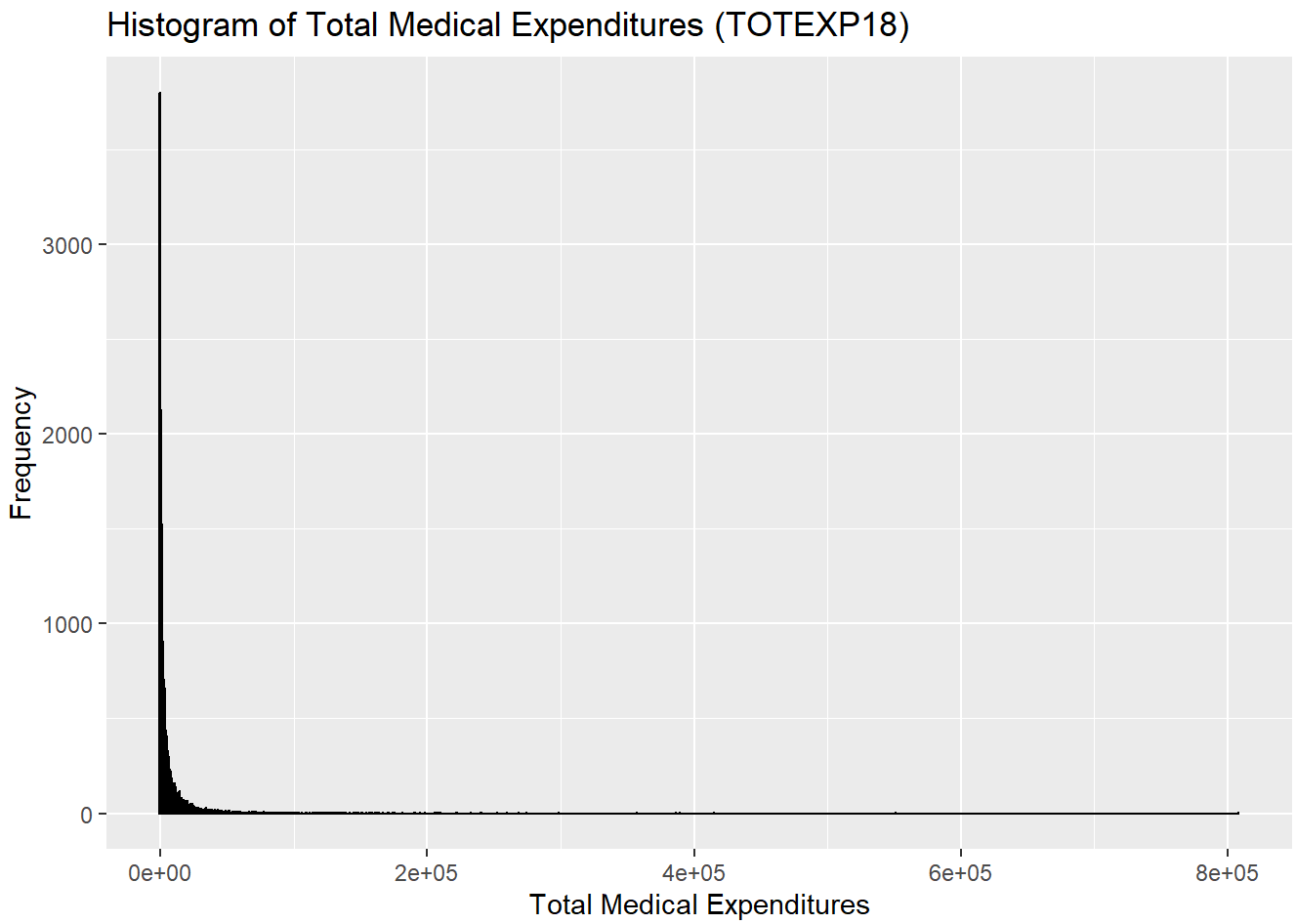
```
# pairwise scatterplot
pairs(data[, c("TOTEXP18", "AGE42X", "ADBMI42", "FAMINC18")],
      pch = 16,
      cex = 0.3)
```



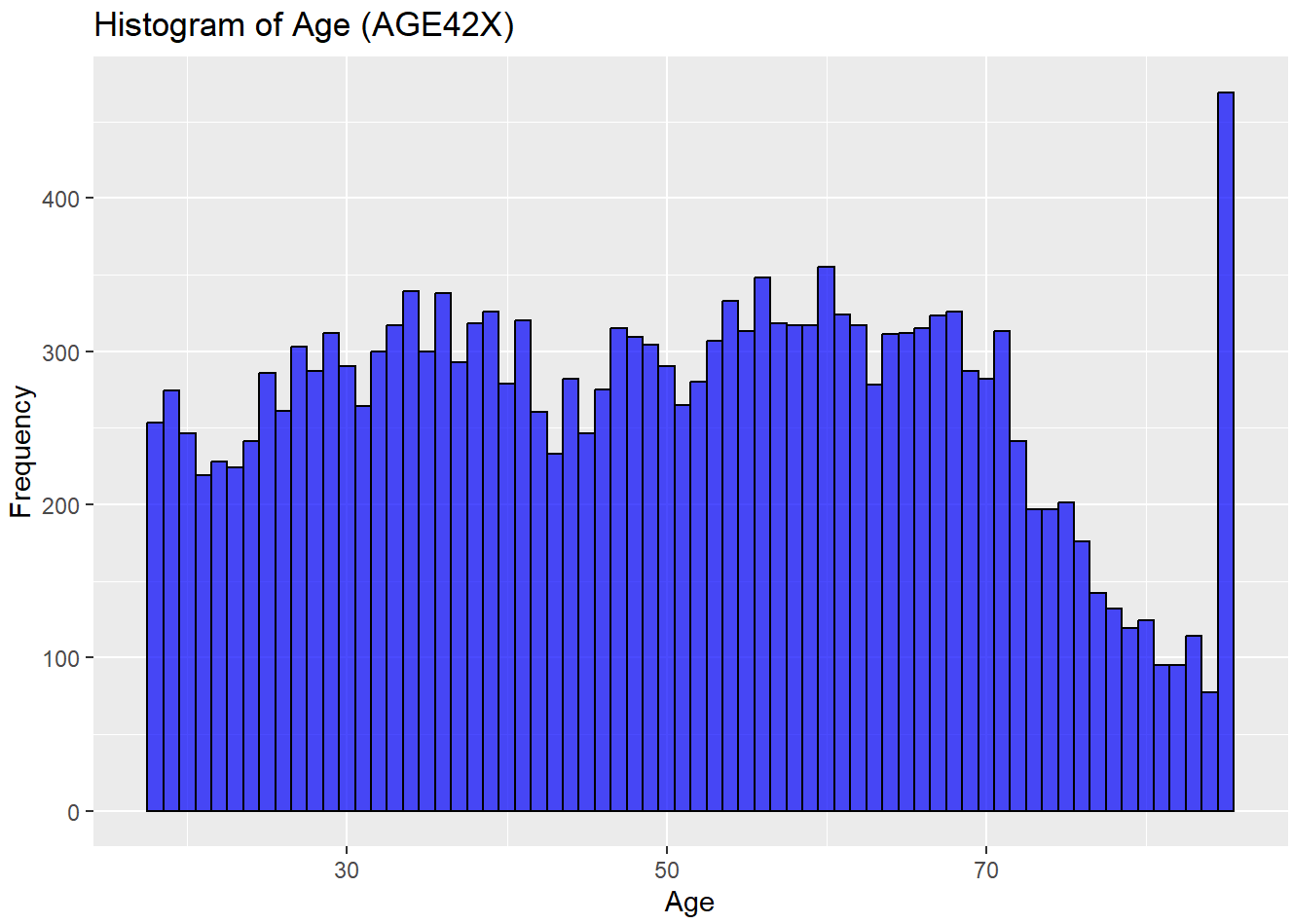
```
# correlation matrix
cor_matrix = cor(data[, c("TOTEXP18", "AGE42X", "ADBMI42", "FAMINC18")], use = "complete.obs")
corrplot(cor_matrix, method = "color", type = "upper", tl.col = "black", tl.srt = 45, addCoef.co
l = "black")
```



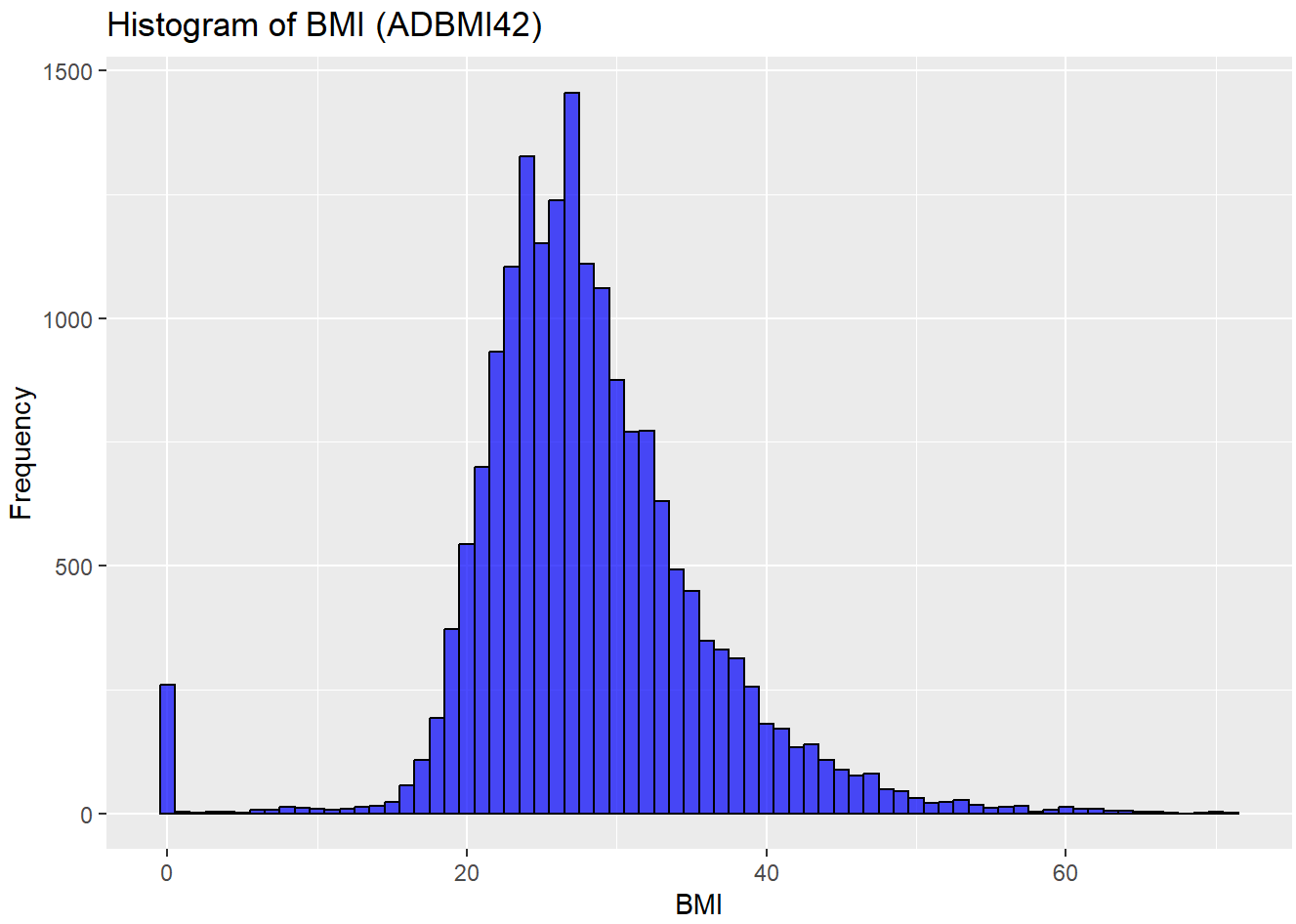

```
# histograms for continuous variables
ggplot(data, aes(x = TOTEXP18)) +
  geom_histogram(binwidth = 500, fill = "blue", color = "black", alpha = 0.7) +
  ggtitle("Histogram of Total Medical Expenditures (TOTEXP18)") +
  xlab("Total Medical Expenditures") +
  ylab("Frequency")
```



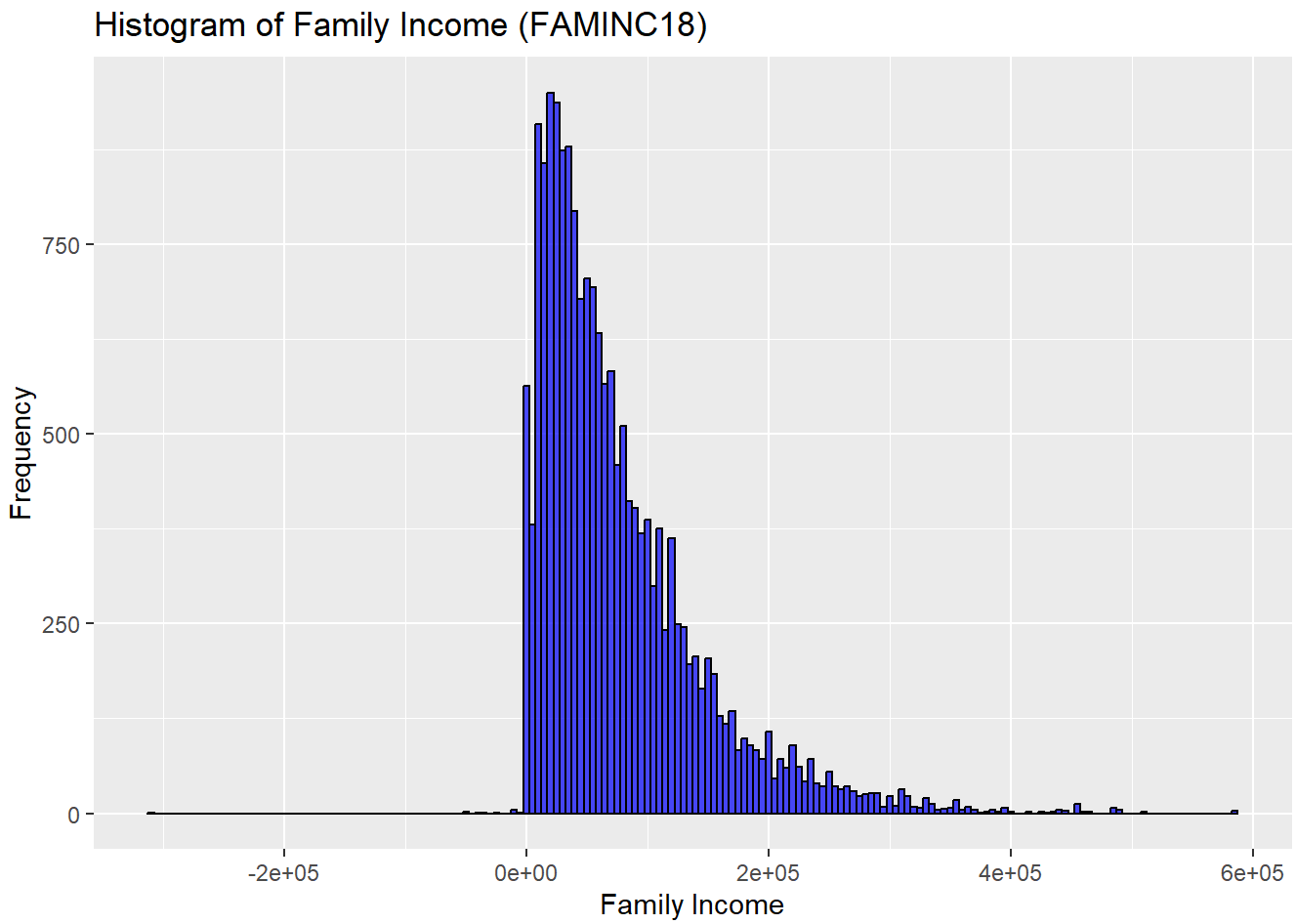

```
ggplot(data, aes(x = AGE42X)) +
  geom_histogram(binwidth = 1, fill = "blue", color = "black", alpha = 0.7) +
  ggtitle("Histogram of Age (AGE42X)") +
  xlab("Age") +
  ylab("Frequency")
```



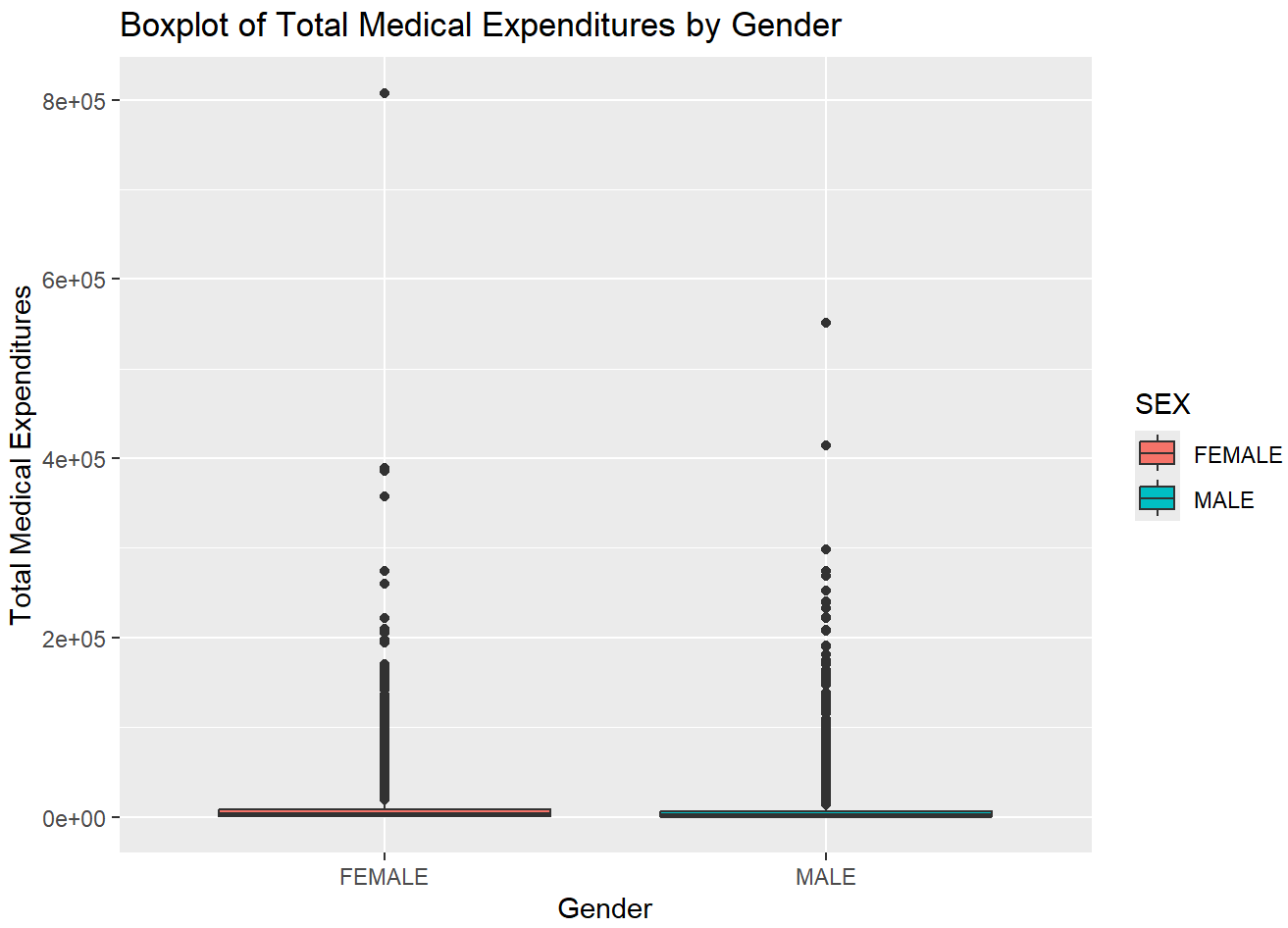

```
ggplot(data, aes(x = ADBMI42)) +
  geom_histogram(binwidth = 1, fill = "blue", color = "black", alpha = 0.7) +
  ggtitle("Histogram of BMI (ADBMI42)") +
  xlab("BMI") +
  ylab("Frequency")
```



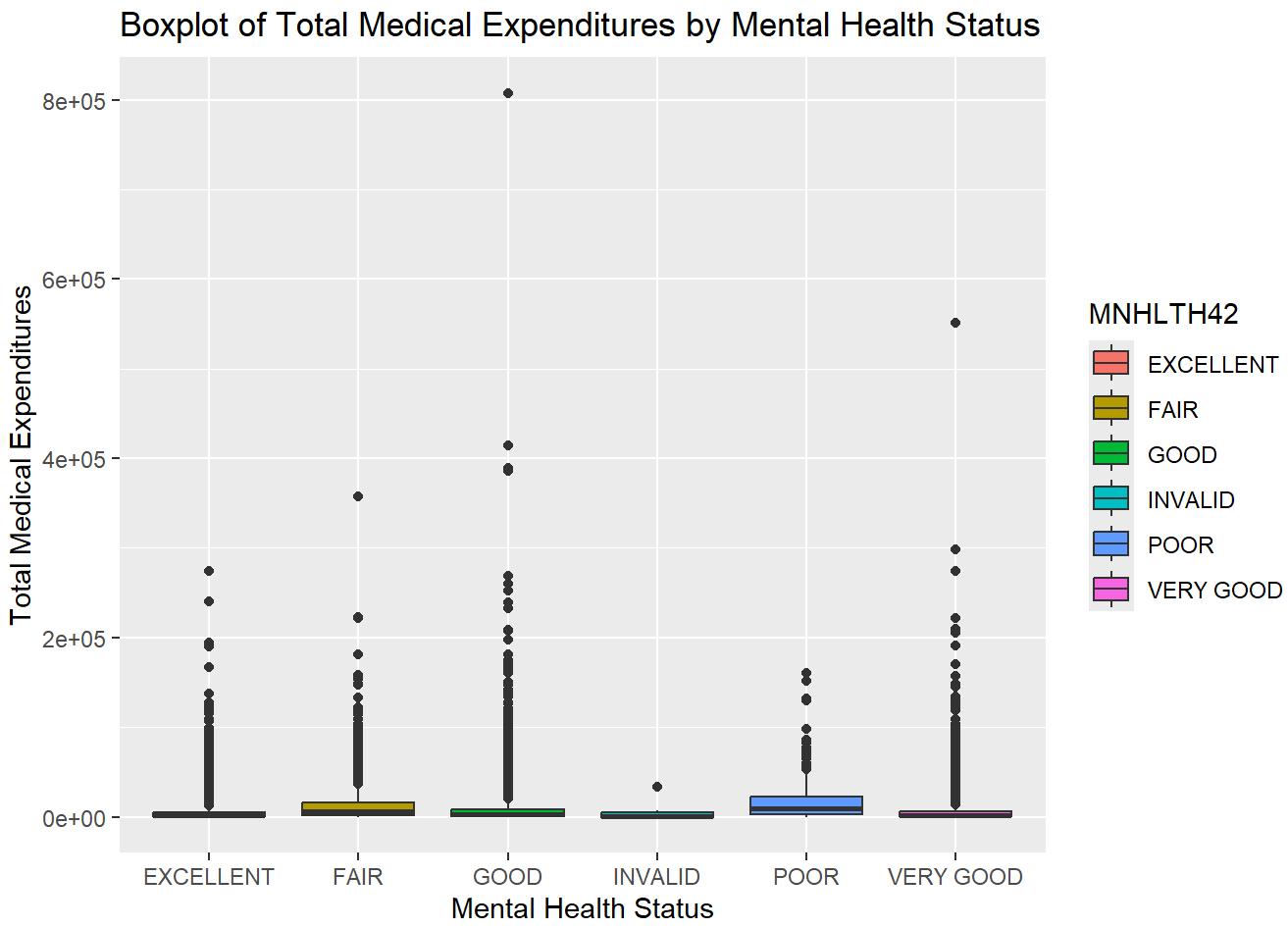

```
ggplot(data, aes(x = FAMINC18)) +
  geom_histogram(binwidth = 5000, fill = "blue", color = "black", alpha = 0.7) +
  ggtitle("Histogram of Family Income (FAMINC18)") +
  xlab("Family Income") +
  ylab("Frequency")
```



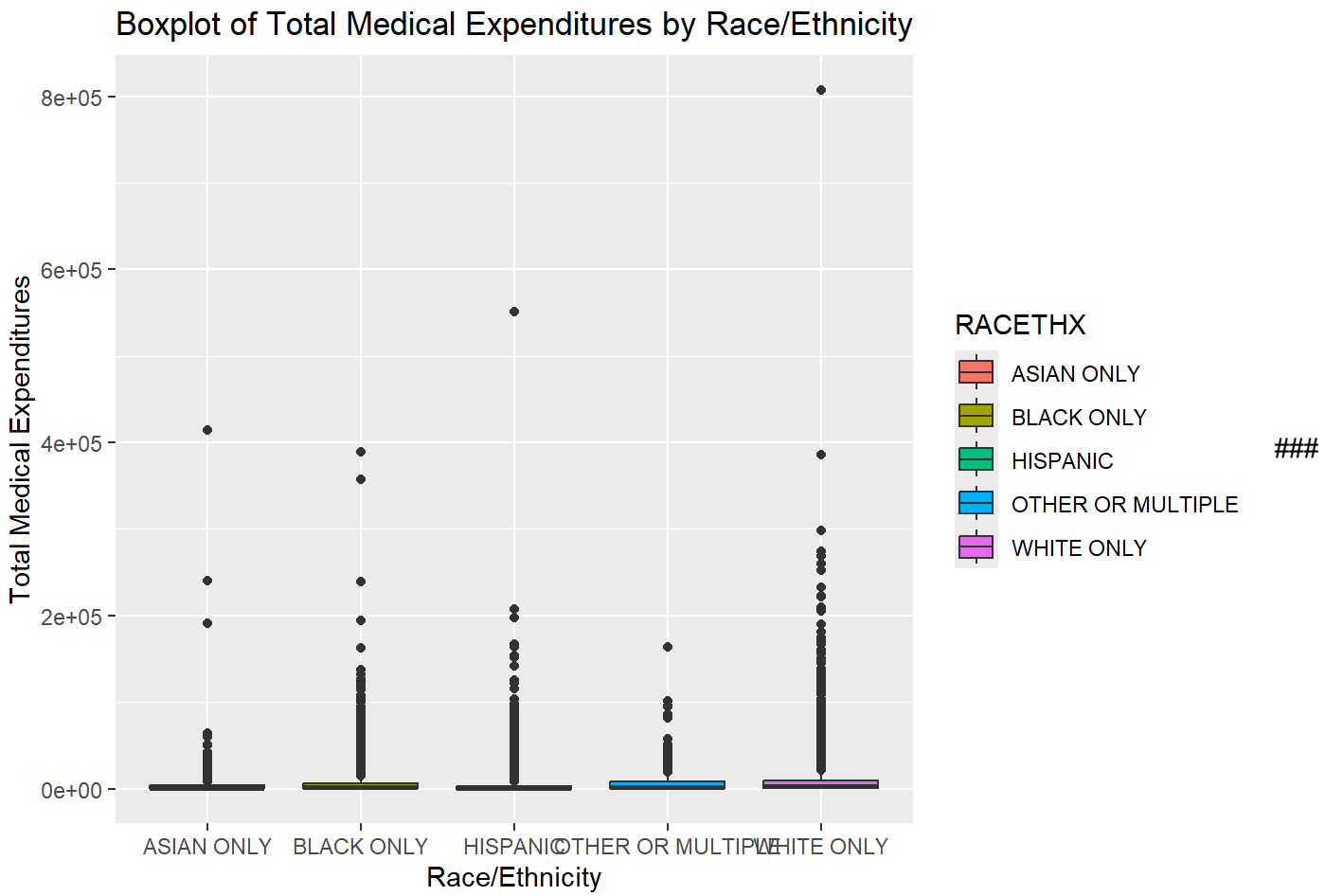

```
# boxplot for `TOTEXP18` by gender
ggplot(data, aes(x = SEX, y = TOTEXP18, fill = SEX)) +
  geom_boxplot() +
  ggtitle("Boxplot of Total Medical Expenditures by Gender") +
  xlab("Gender") +
  ylab("Total Medical Expenditures")
```




```
# boxplot for `TOTEXP18` by perceived mental health status
ggplot(data, aes(x = MNHLTH42, y = TOTEXP18, fill = MNHLTH42)) +
  geom_boxplot() +
  ggtitle("Boxplot of Total Medical Expenditures by Mental Health Status") +
  xlab("Mental Health Status") +
  ylab("Total Medical Expenditures")
```




```
# boxplot for `TOTEXP18` by race
ggplot(data, aes(x = RACETHX, y = TOTEXP18, fill = RACETHX)) +
  geom_boxplot() +
  ggtitle("Boxplot of Total Medical Expenditures by Race/Ethnicity") +
  xlab("Race/Ethnicity") +
  ylab("Total Medical Expenditures")
```



BMI appears to have some invalid data. The histogram bar including BMIs less than 1 does not make sense.

```
data_raw = data
data = data[data$ADBMI42 >= 1, ]
```

Negative family income also does not make sense.

```
data = data[data$FAMINC18 >= 0, ]
```

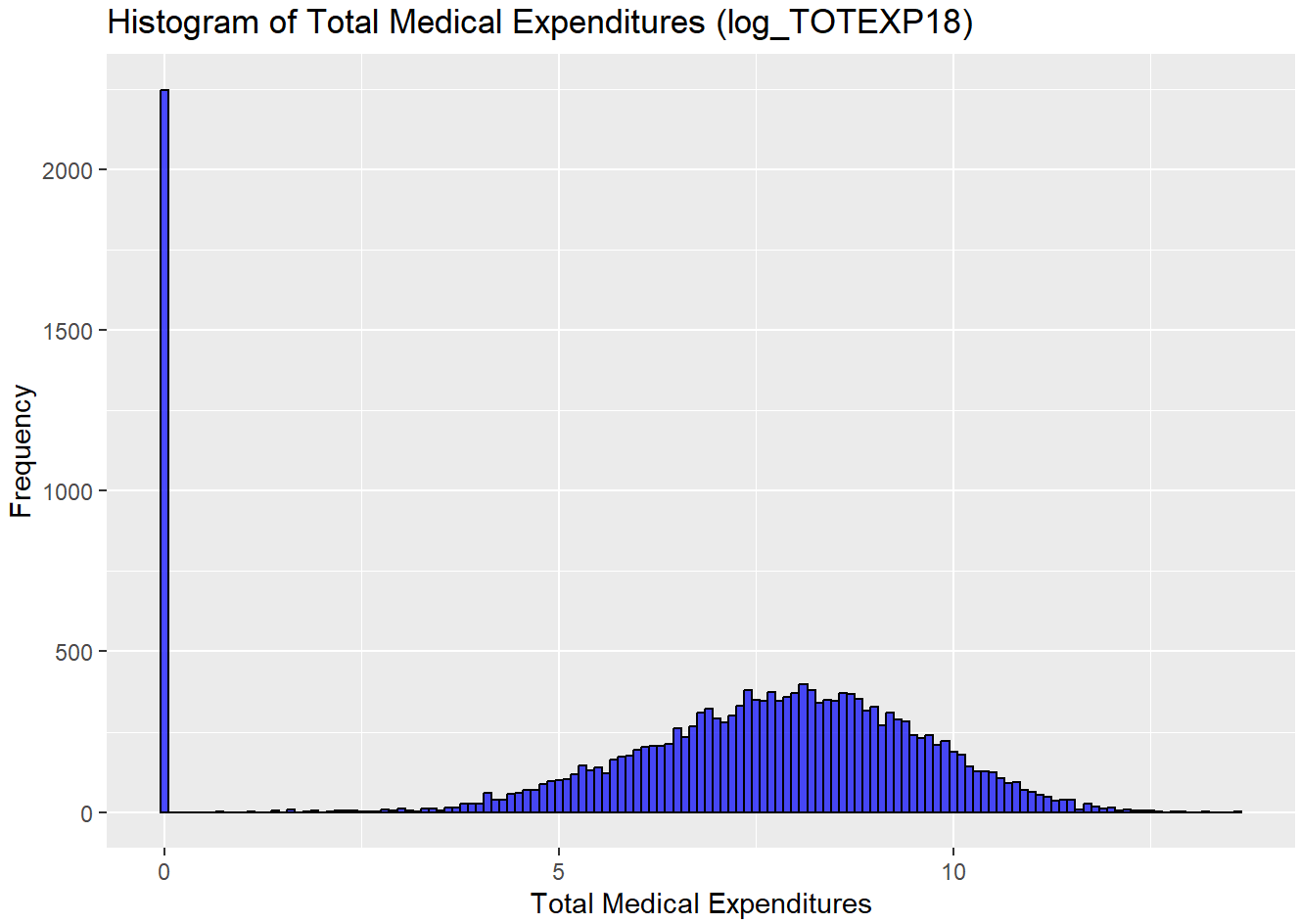
Also going to remove the 6 ‘invalid’ mental health assessments.

```
data = data[data$MNHLTH42 != 'INVALID', ]
```

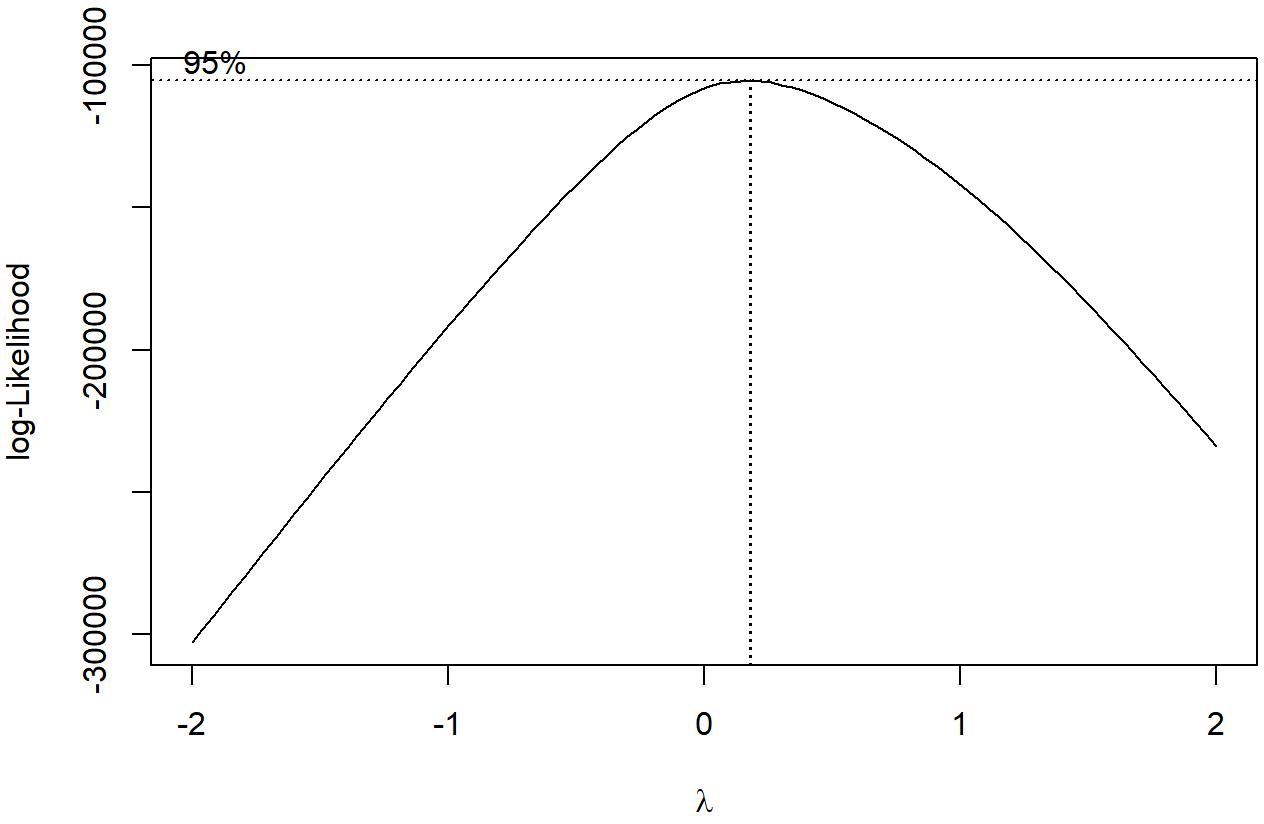
The response is heavily skewed. I want to see what it would look

like with a log or box-cox transformation.

```
# log
data$log_TOTEXP18 = log(data$TOTEXP18+1)
ggplot(data, aes(x = log_TOTEXP18)) +
  geom_histogram(binwidth = .1, fill = "blue", color = "black", alpha = 0.7) +
  ggtitle("Histogram of Total Medical Expenditures (log_TOTEXP18)") +
  xlab("Total Medical Expenditures") +
  ylab("Frequency")
```



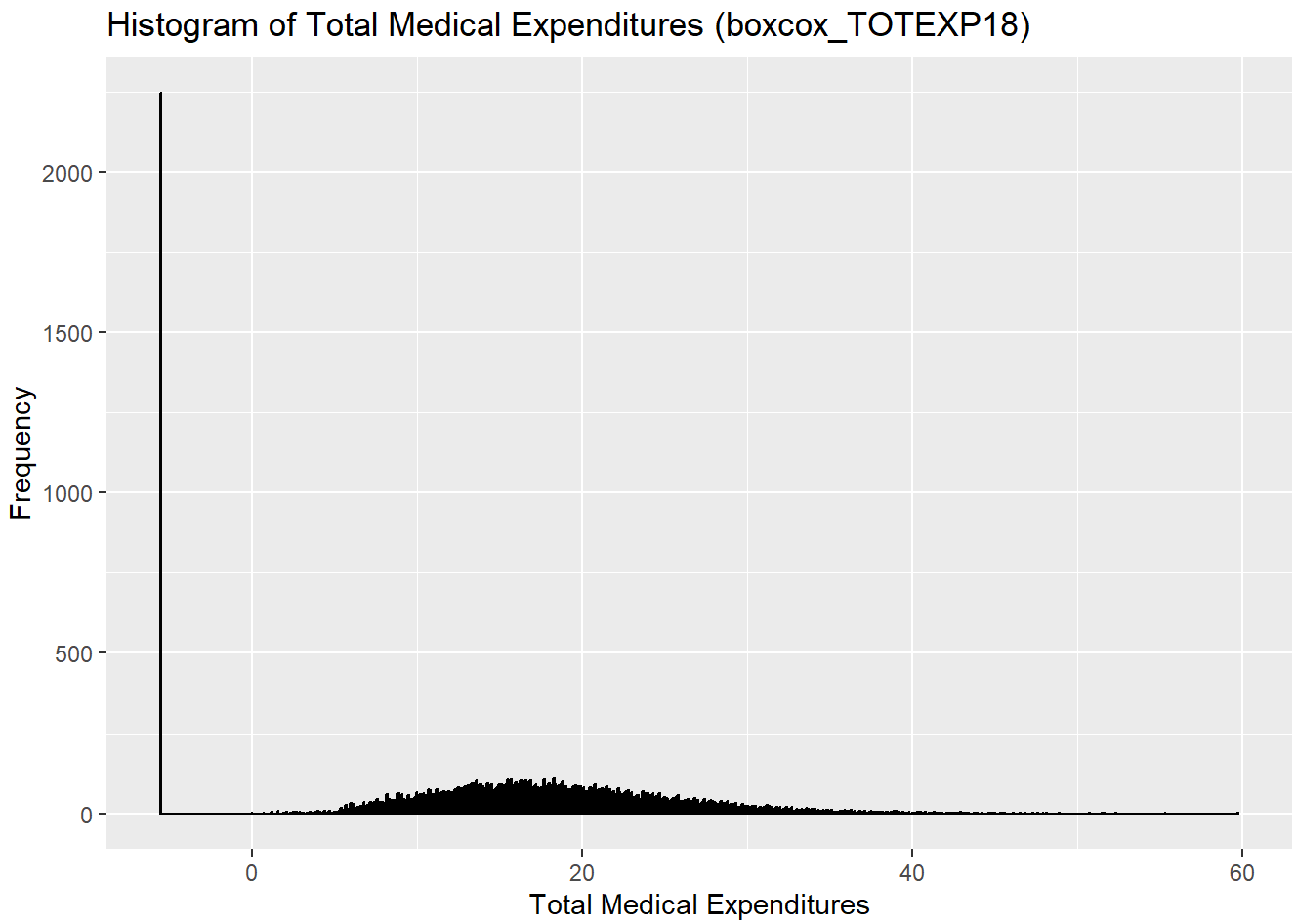

```
# box-cox
boxcox_result <- boxcox(TOTEXP18+1 ~ 1, data = data, lambda = seq(-2, 2, by = 0.1))
```




```
optimal_lambda <- boxcox_result$x[which.max(boxcox_result$y)]
print(optimal_lambda)
```

```
## [1] 0.1818182
```

```
data$boxcox_TOTEXP18 <- (data$TOTEXP18^optimal_lambda - 1) / optimal_lambda
ggplot(data, aes(x = boxcox_TOTEXP18)) +
  geom_histogram(binwidth = .1, fill = "blue", color = "black", alpha = 0.7) +
  ggtitle("Histogram of Total Medical Expenditures (boxcox_TOTEXP18)") +
  xlab("Total Medical Expenditures") +
  ylab("Frequency")
```



There are a lot of people with 0 expenditure. I am going to create a binary indicator variable to consider this.

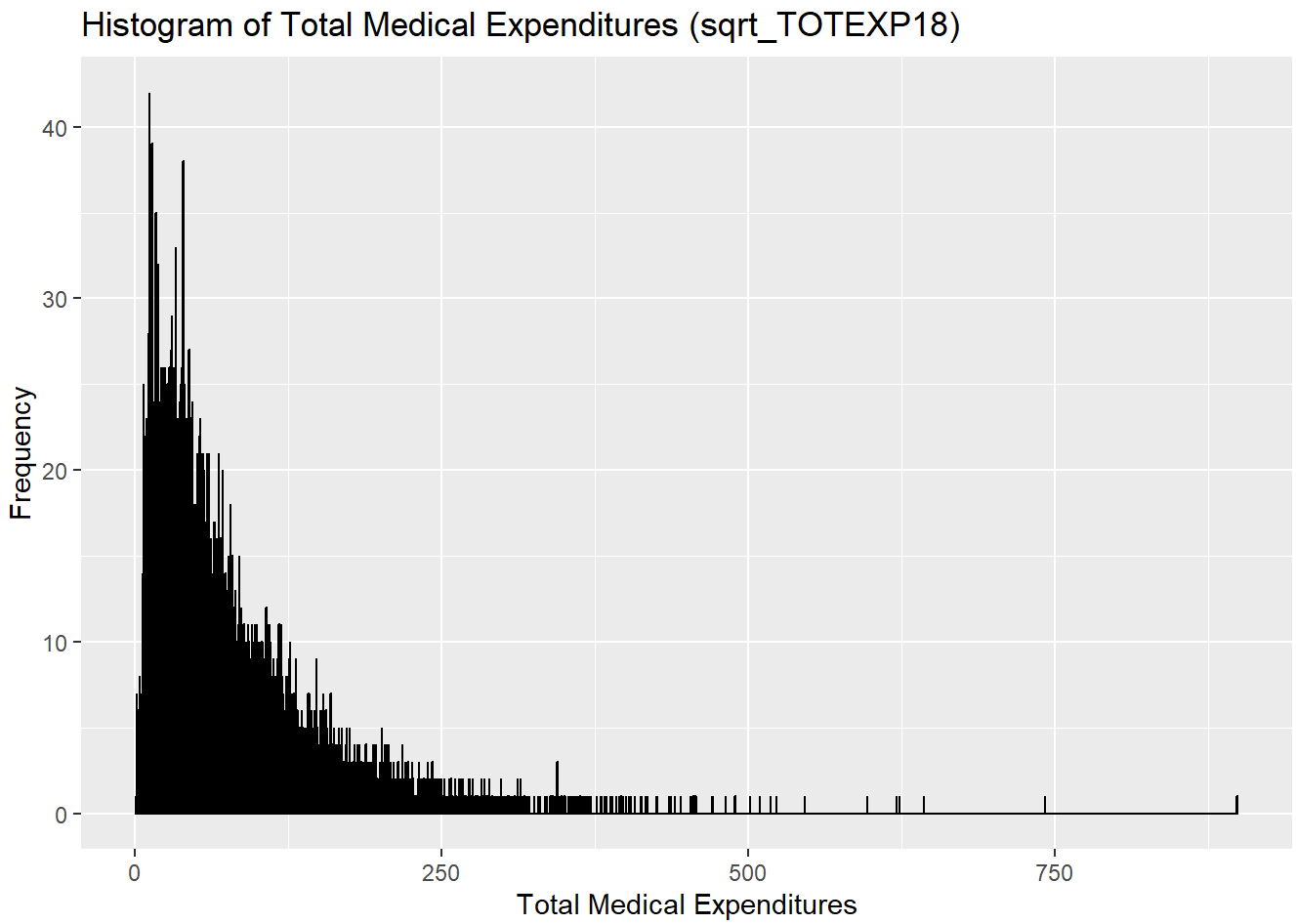
```
# binary variable indicating whether expenditure is zero
# data$NO_EXP <- as.factor(ifelse(data$TOTEXP18 == 0, 1, 0))
```

Actually, I am going to remove the 0 expenditure observations. I am only trying to predict non-zero expenditure amount.

```
data = data[data$TOTEXP18 != 0, ]
```

What about sqrt transfom of response?

```
# sqrt
data$sqrt_TOTEXP18 = sqrt(data$TOTEXP18)
ggplot(data, aes(x = sqrt_TOTEXP18)) +
  geom_histogram(binwidth = .1, fill = "blue", color = "black", alpha = 0.7) +
  ggtitle("Histogram of Total Medical Expenditures (sqrt_TOTEXP18)") +
  xlab("Total Medical Expenditures") +
  ylab("Frequency")
```

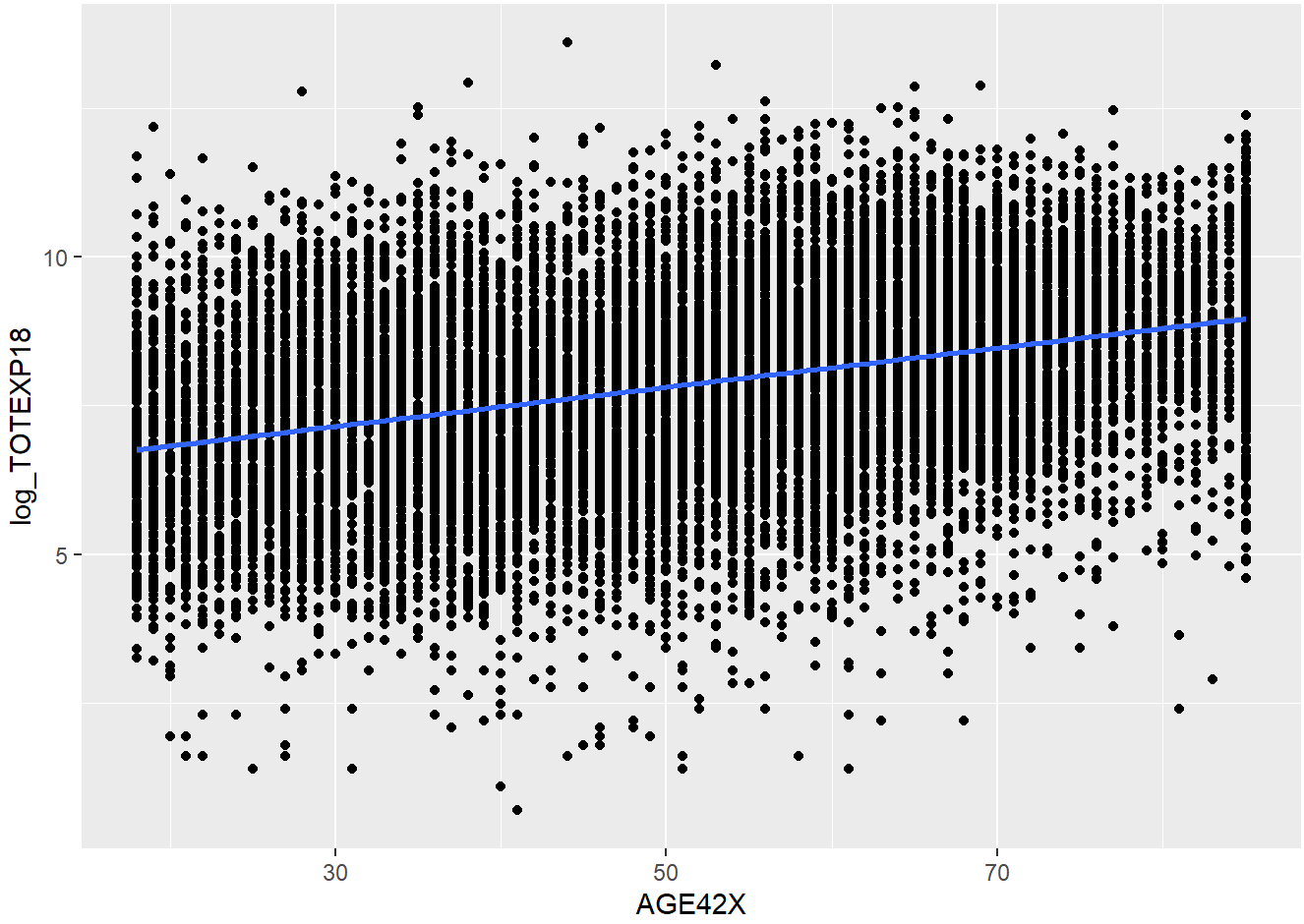



```
# Nope.
data$sqrt_TOTEXP18 = NULL
```

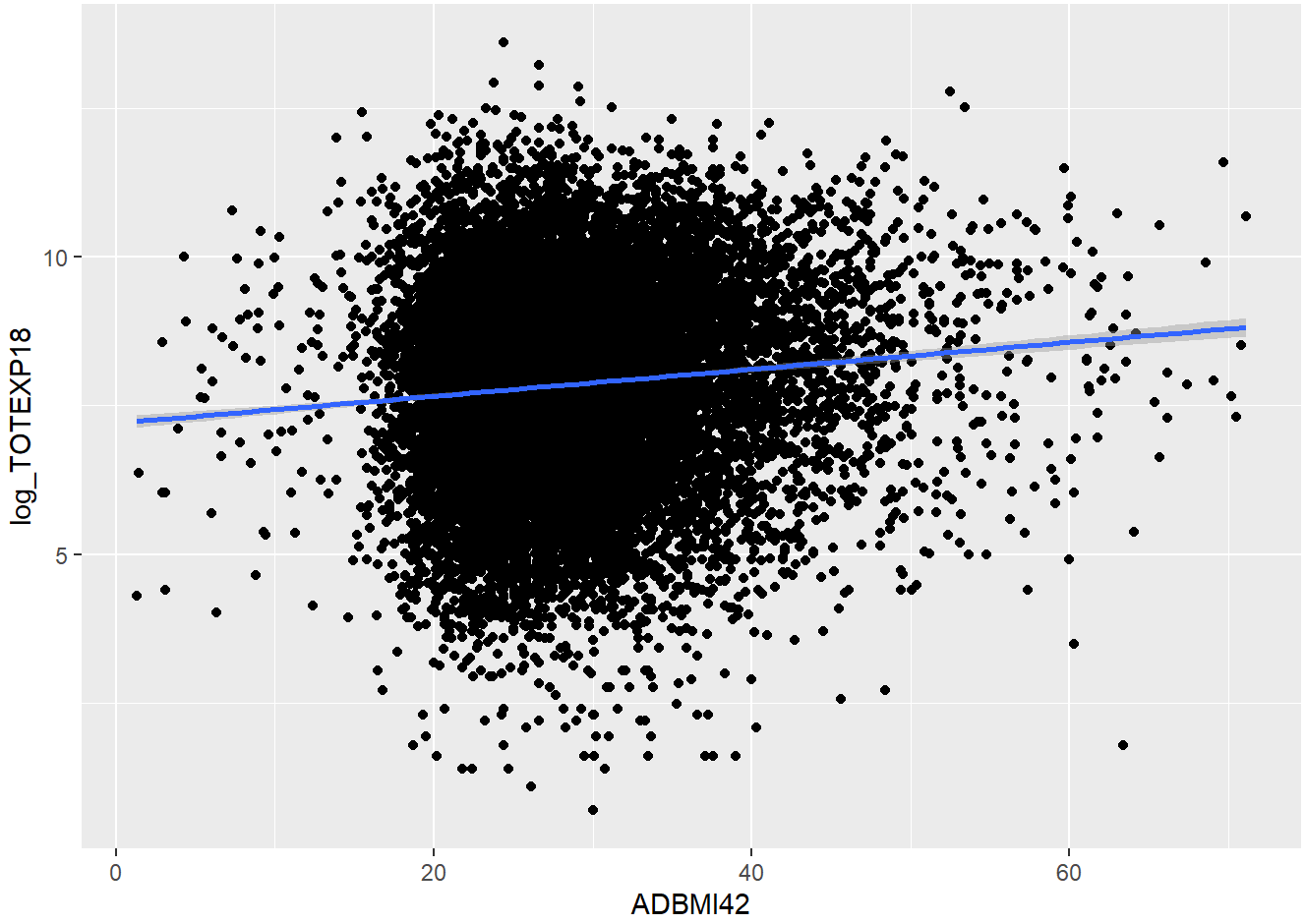
More pairwise scatter plots against log-transformed response

```
for (col in colnames(data)[!colnames(data) %in% c('log_TOTEXP18', 'boxcox_TOTEXP18', 'TOTEXP1
8')]) {
  plot = ggplot(data, aes(x = !!sym(col), y = log_TOTEXP18)) + geom_point() + geom_smooth(method
= "lm")
  print(plot)
}
```

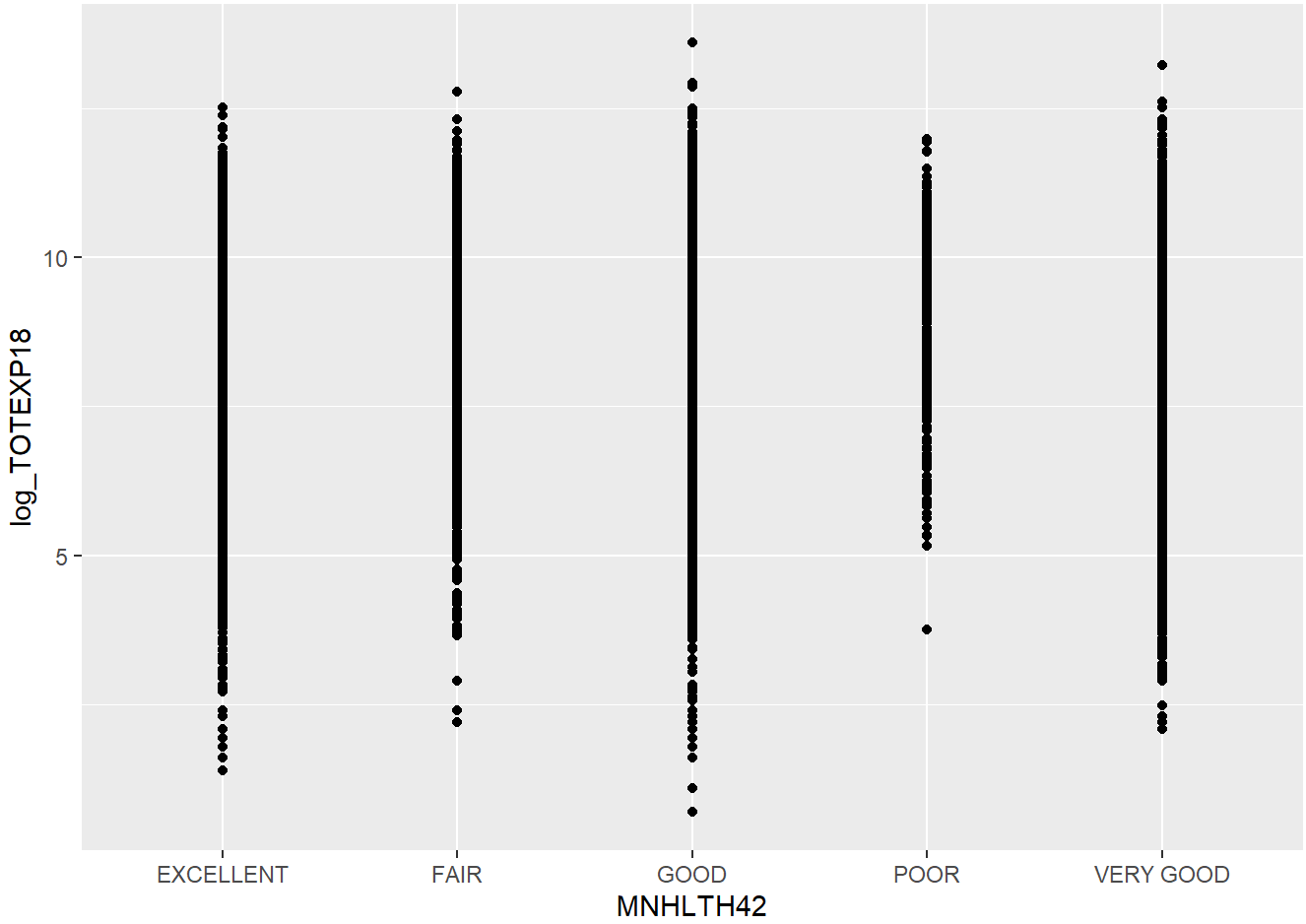
```
## `geom_smooth()` using formula = 'y ~ x'
```



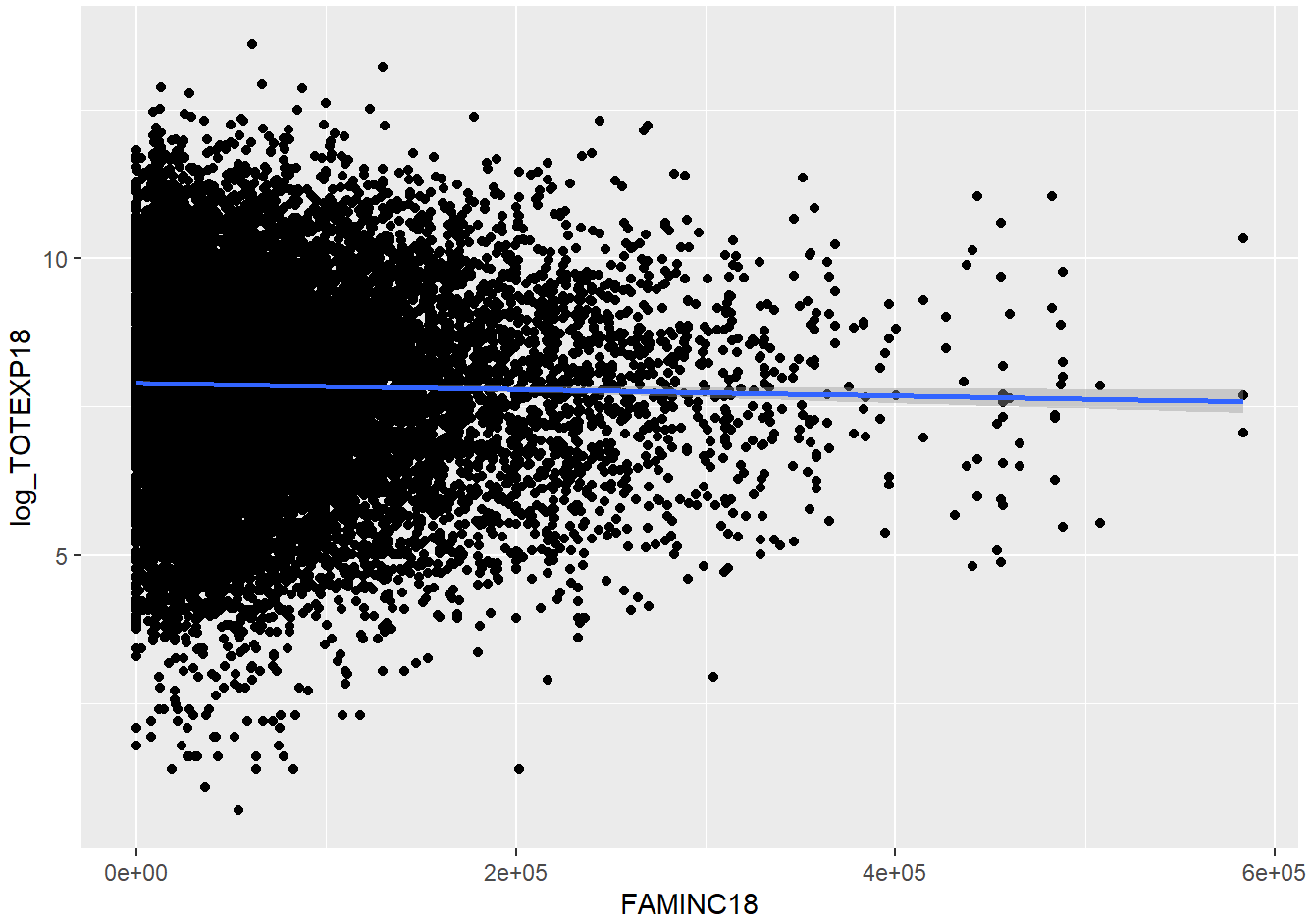

```
## `geom_smooth()` using formula = 'y ~ x'
```



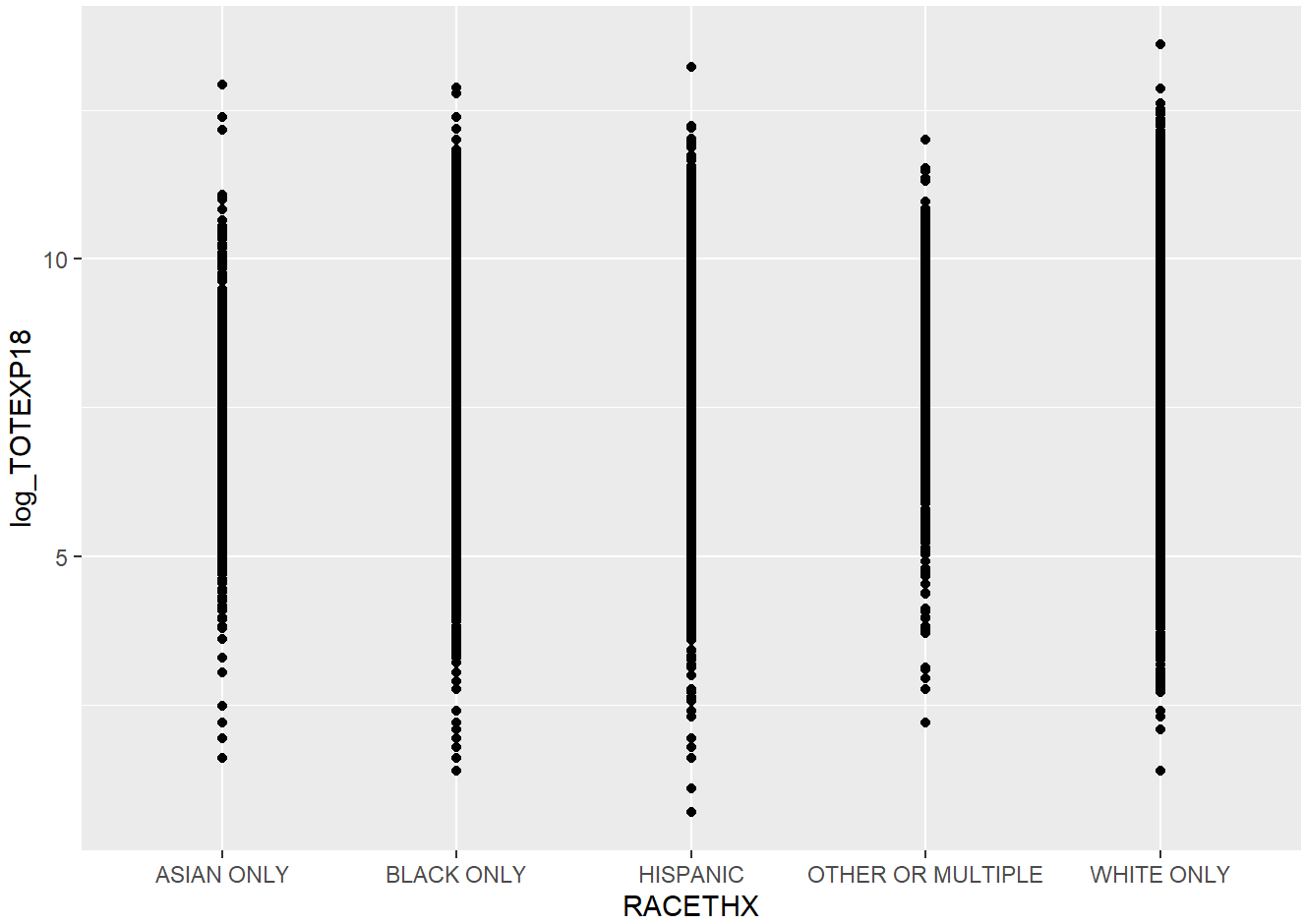

```
## `geom_smooth()` using formula = 'y ~ x'
```



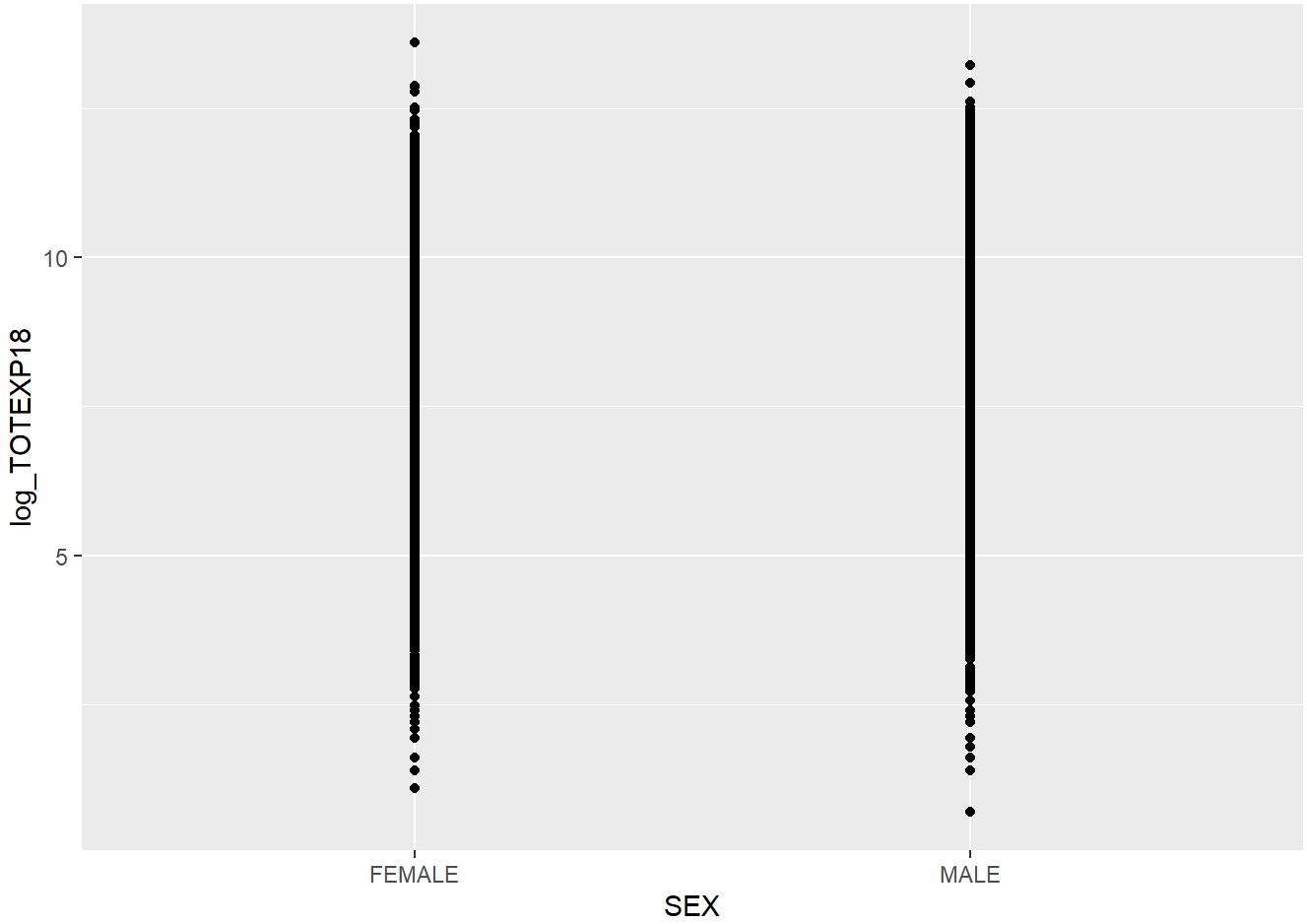

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
## `geom_smooth()` using formula = 'y ~ x'
```




```
## `geom_smooth()` using formula = 'y ~ x'
```

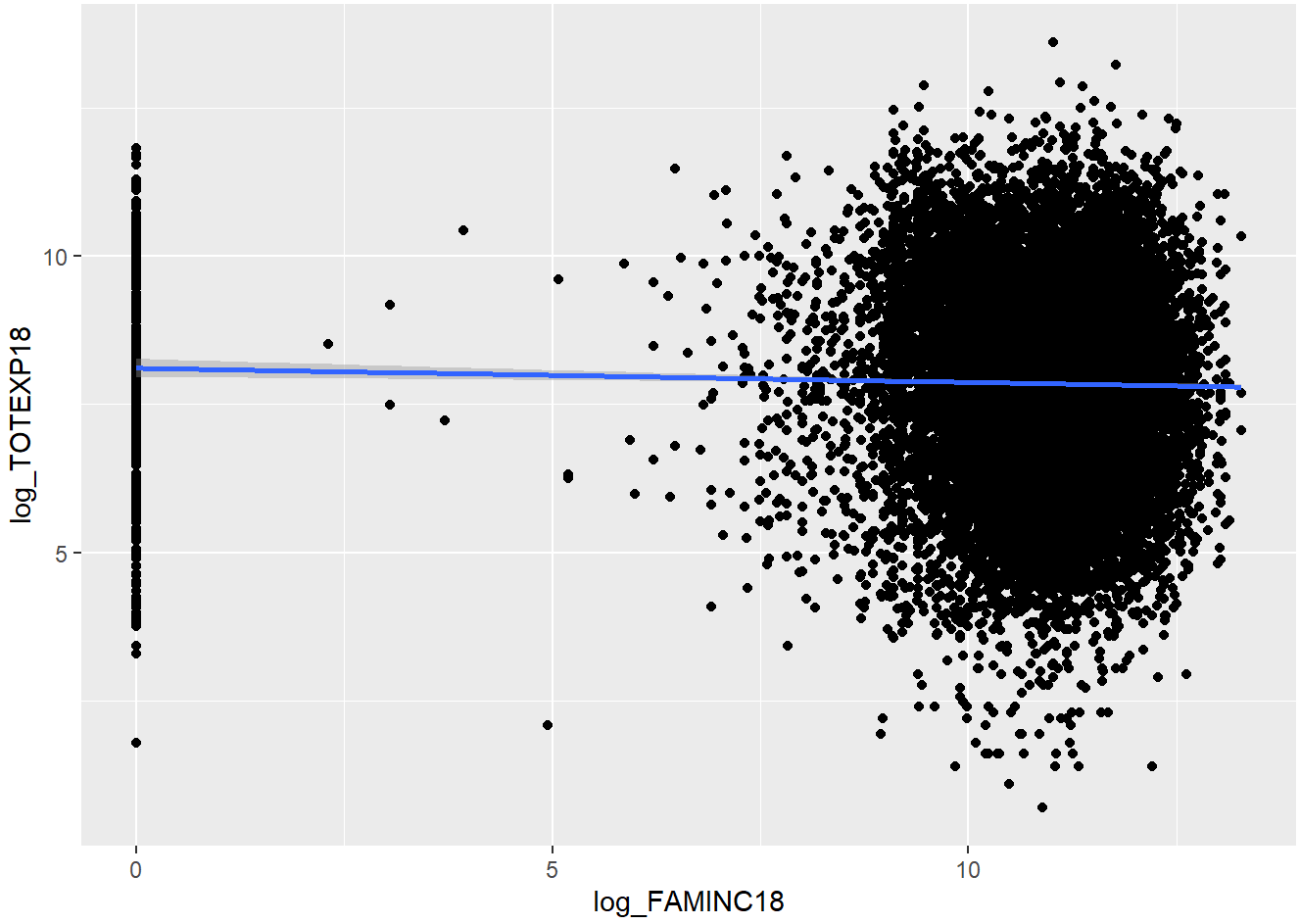


I

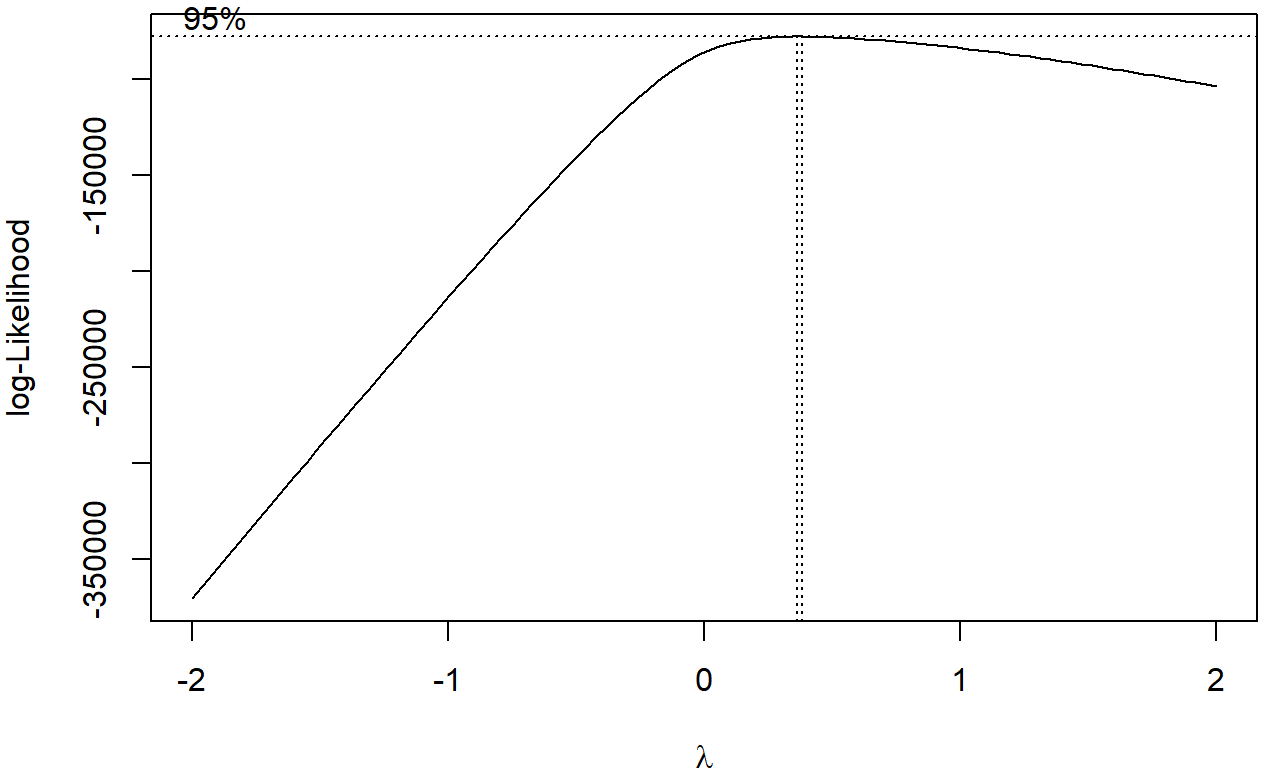
will log transform and box-cox transform family income

```
# log
data$log_FAMINC18 = log(data$FAMINC18+1)
ggplot(data, aes(x = log_FAMINC18, y = log_TOTEXP18)) + geom_point() + geom_smooth(method = "l
m")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
# box-cox
boxcox_result <- boxcox(FAMINC18+1 ~ 1, data = data, lambda = seq(-2, 2, by = 0.1))
```

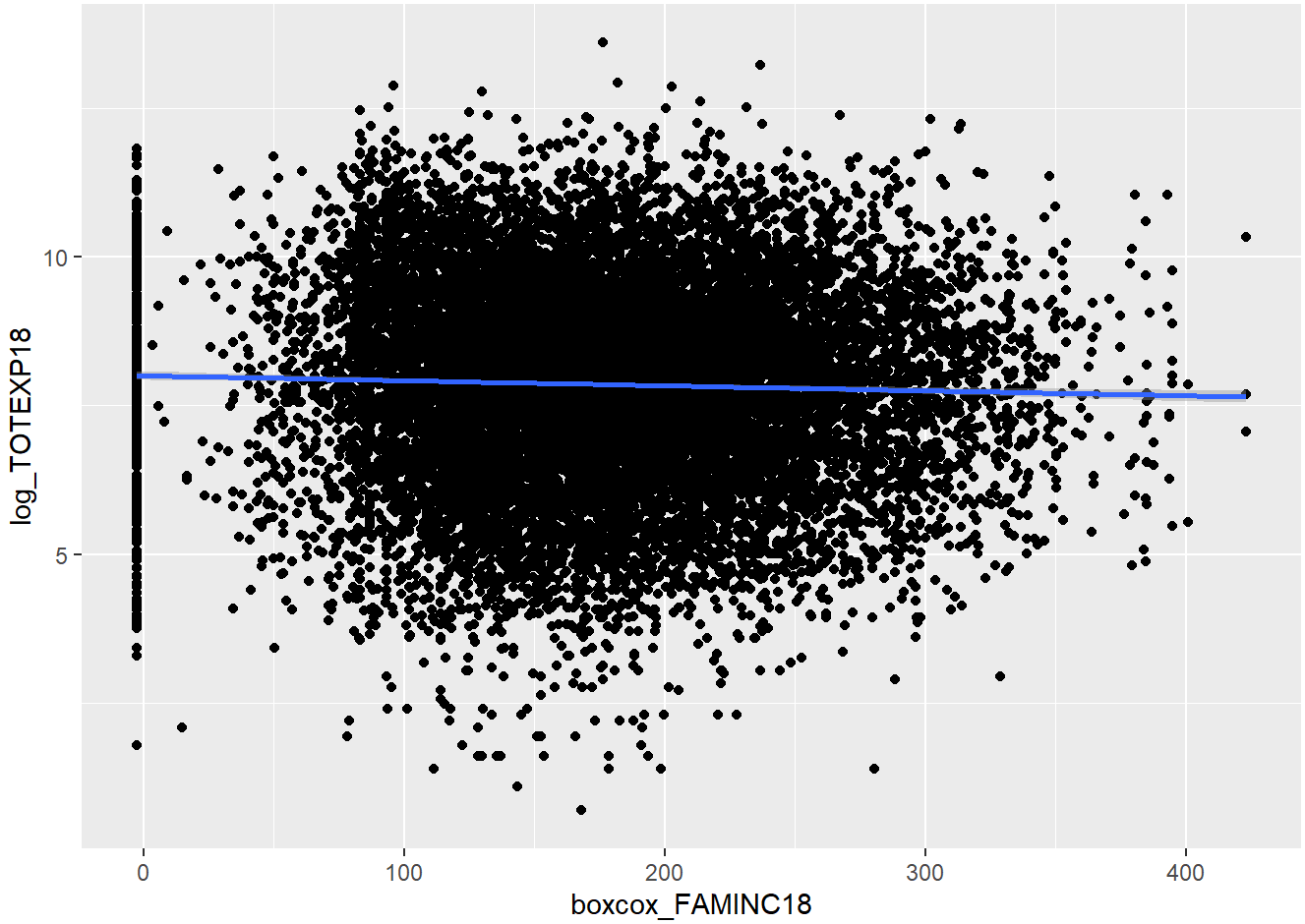



```
optimal_lambda <- boxcox_result$x[which.max(boxcox_result$y)]
print(optimal_lambda)
```

```
## [1] 0.3838384
```

```
data$boxcox_FAMINC18 <- (data$FAMINC18^optimal_lambda - 1) / optimal_lambda
ggplot(data, aes(x = boxcox_FAMINC18, y = log_TOTEXP18)) + geom_point() + geom_smooth(method =
"lm")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
# box-cox looks better
data$log_FAMINC18 = NULL
# data$FAMINC18 = NULL
```

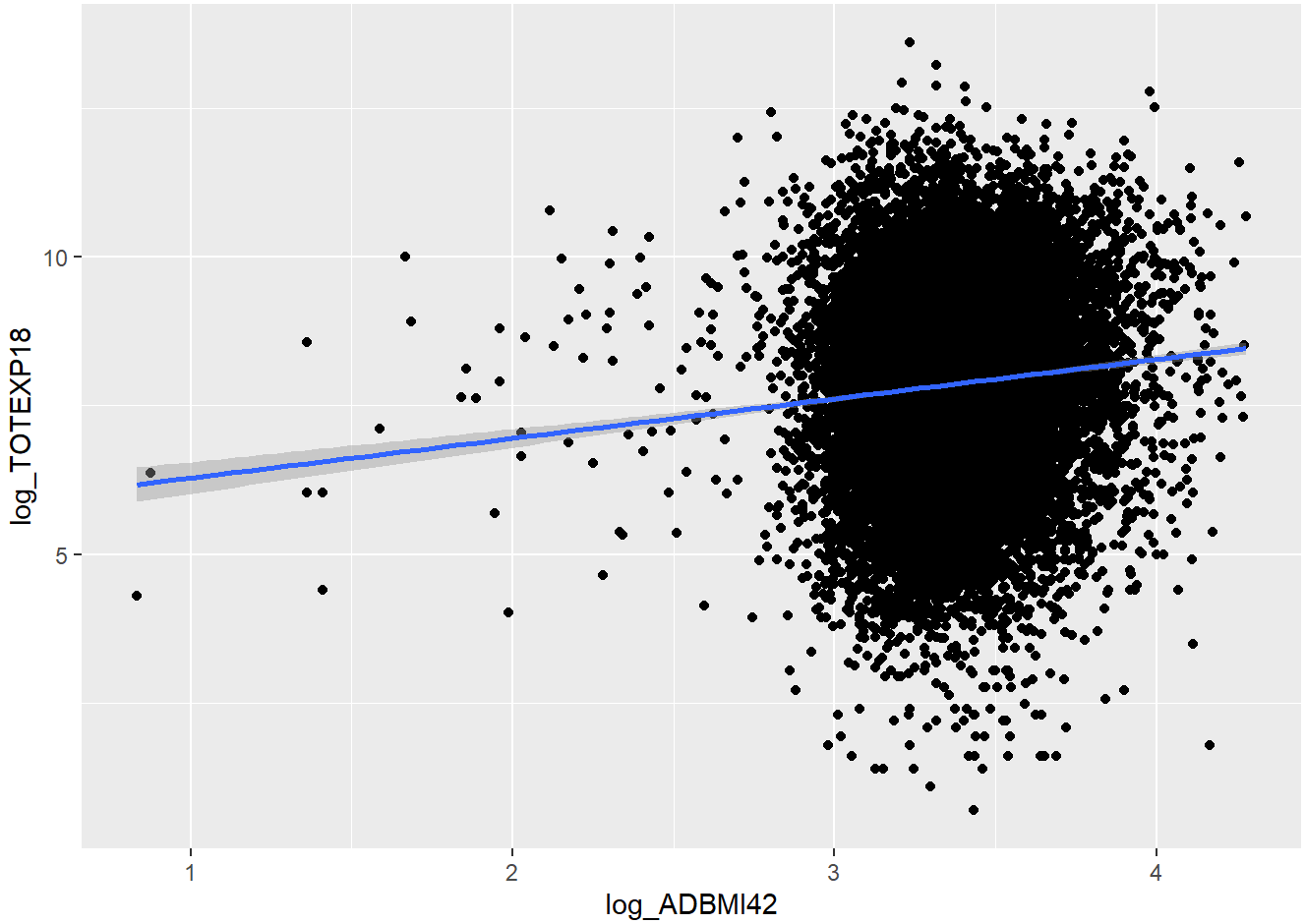
There are a lot of people with very low/no family income. I am going to create a binary indicator variable to consider this.

```
data$NO_INC <- as.factor(ifelse(data$boxcox_FAMINC18 < 0, 1, 0))
```

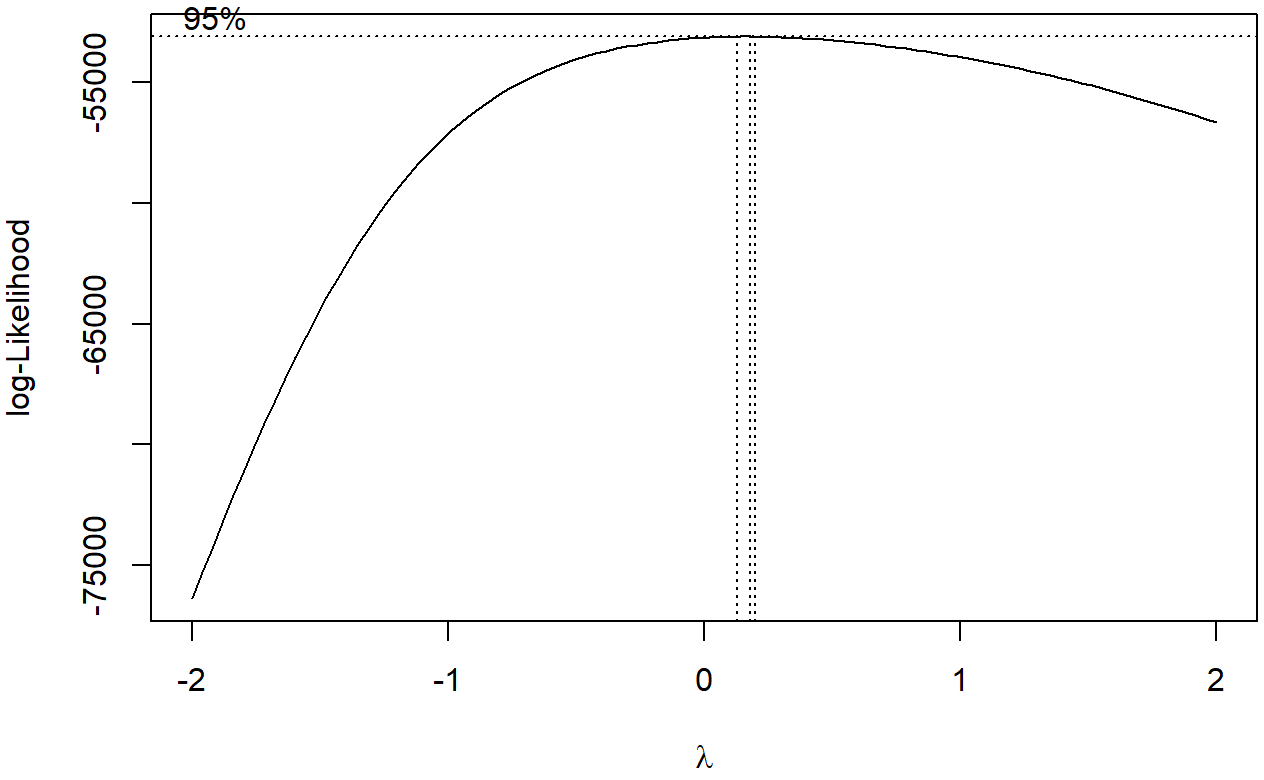
I will log transform and box-cox transform BMI

```
# log
data$log_ADBMI42 = log(data$ADBMI42+1)
ggplot(data, aes(x = log_ADBMI42, y = log_TOTEXP18)) + geom_point() + geom_smooth(method = "lm")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
# box-cox
boxcox_result <- boxcox(ADBMI42+1 ~ 1, data = data, lambda = seq(-2, 2, by = 0.1))
```

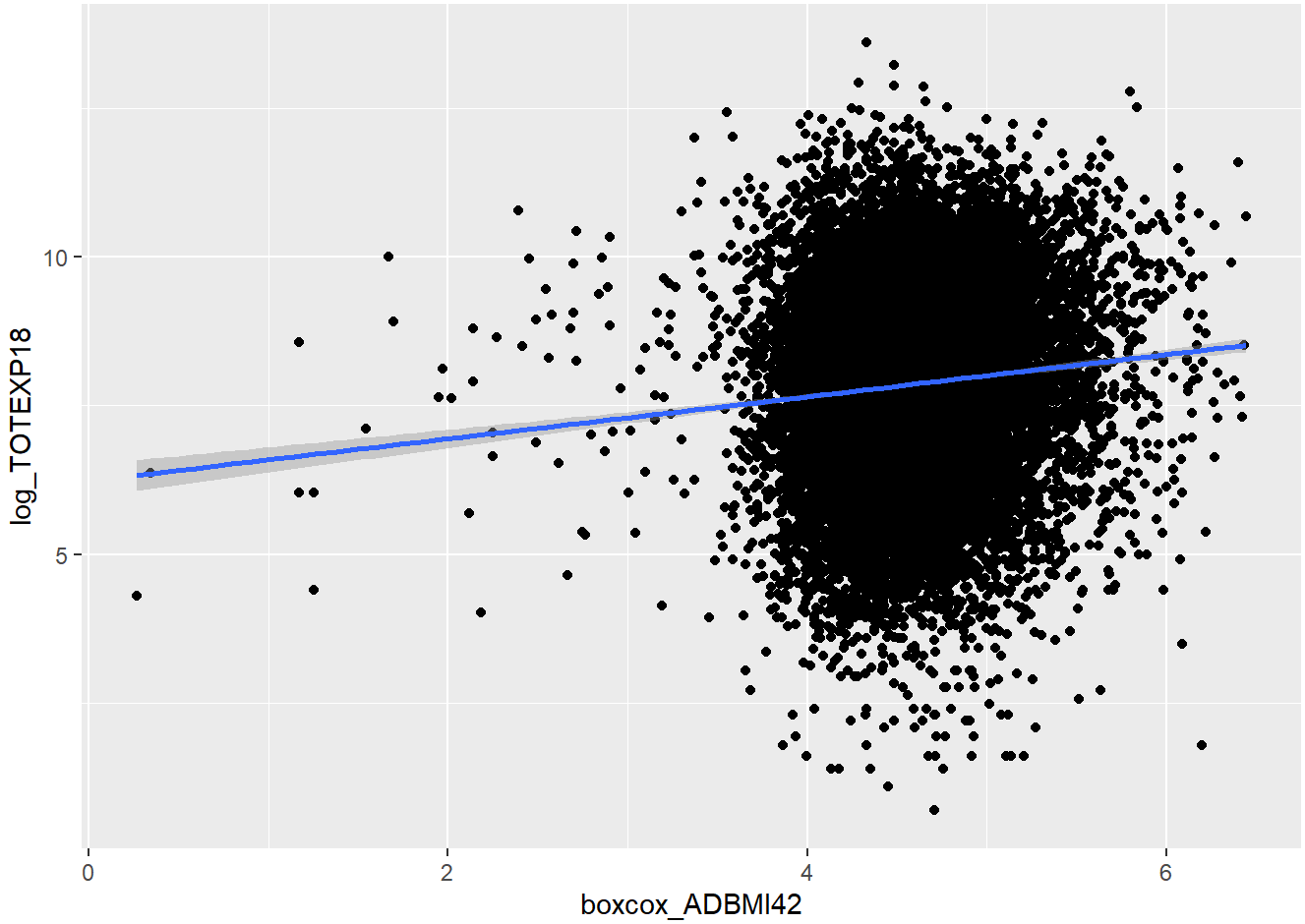



```
optimal_lambda <- boxcox_result$x[which.max(boxcox_result$y)]
print(optimal_lambda)
```

```
## [1] 0.1818182
```

```
data$boxcox_ADBMI42 <- (data$ADBMI42^optimal_lambda - 1) / optimal_lambda
ggplot(data, aes(x = boxcox_ADBMI42, y = log_TOTEXP18)) + geom_point() + geom_smooth(method = "l
m")
```

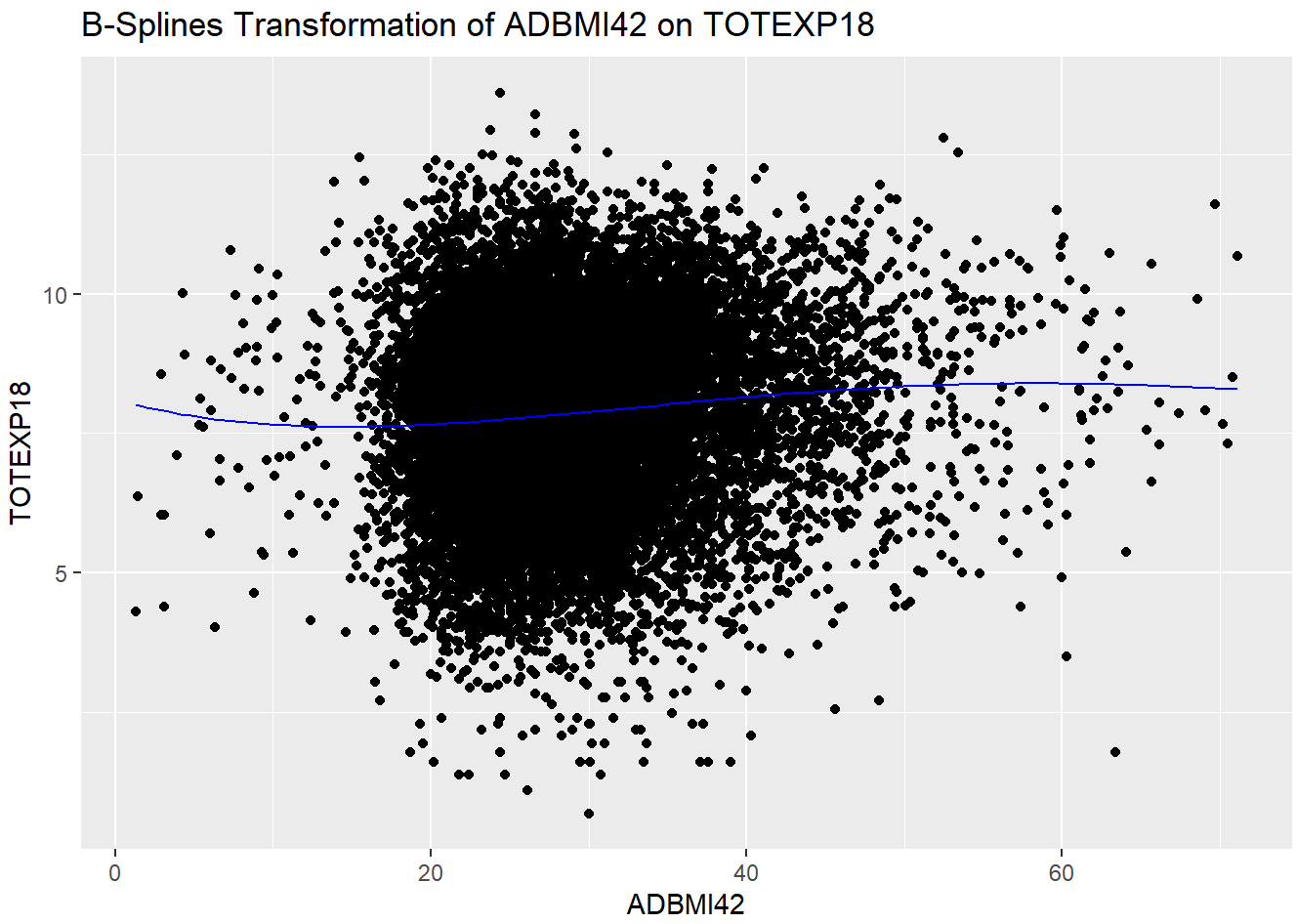
```
## `geom_smooth()` using formula = 'y ~ x'
```



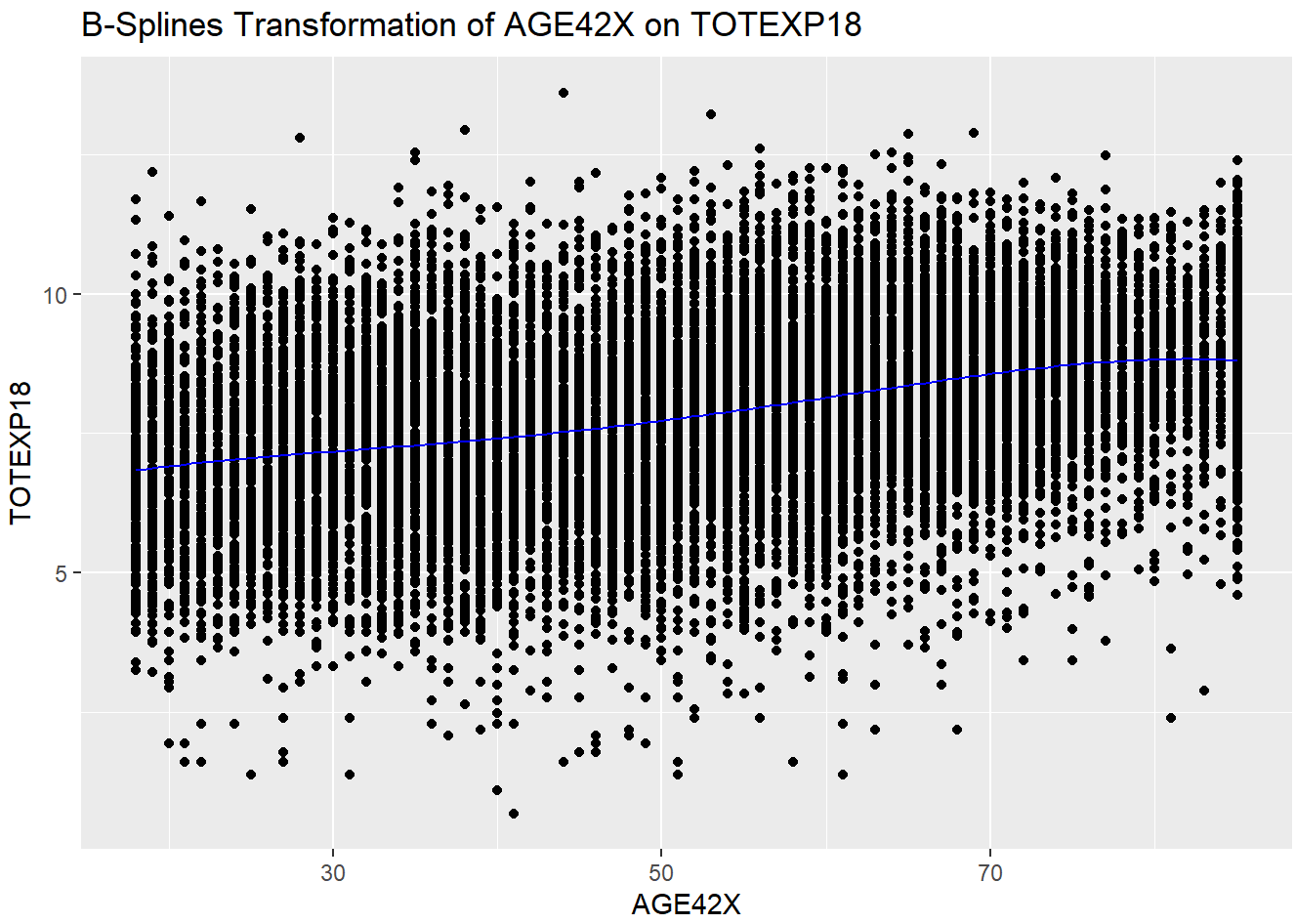

```
# don't love either
data$log_ADBMI42 = NULL
data$boxcox_ADBMI42 = NULL
```

I will try to b-spline transform the BMI, Age, and Income predictors

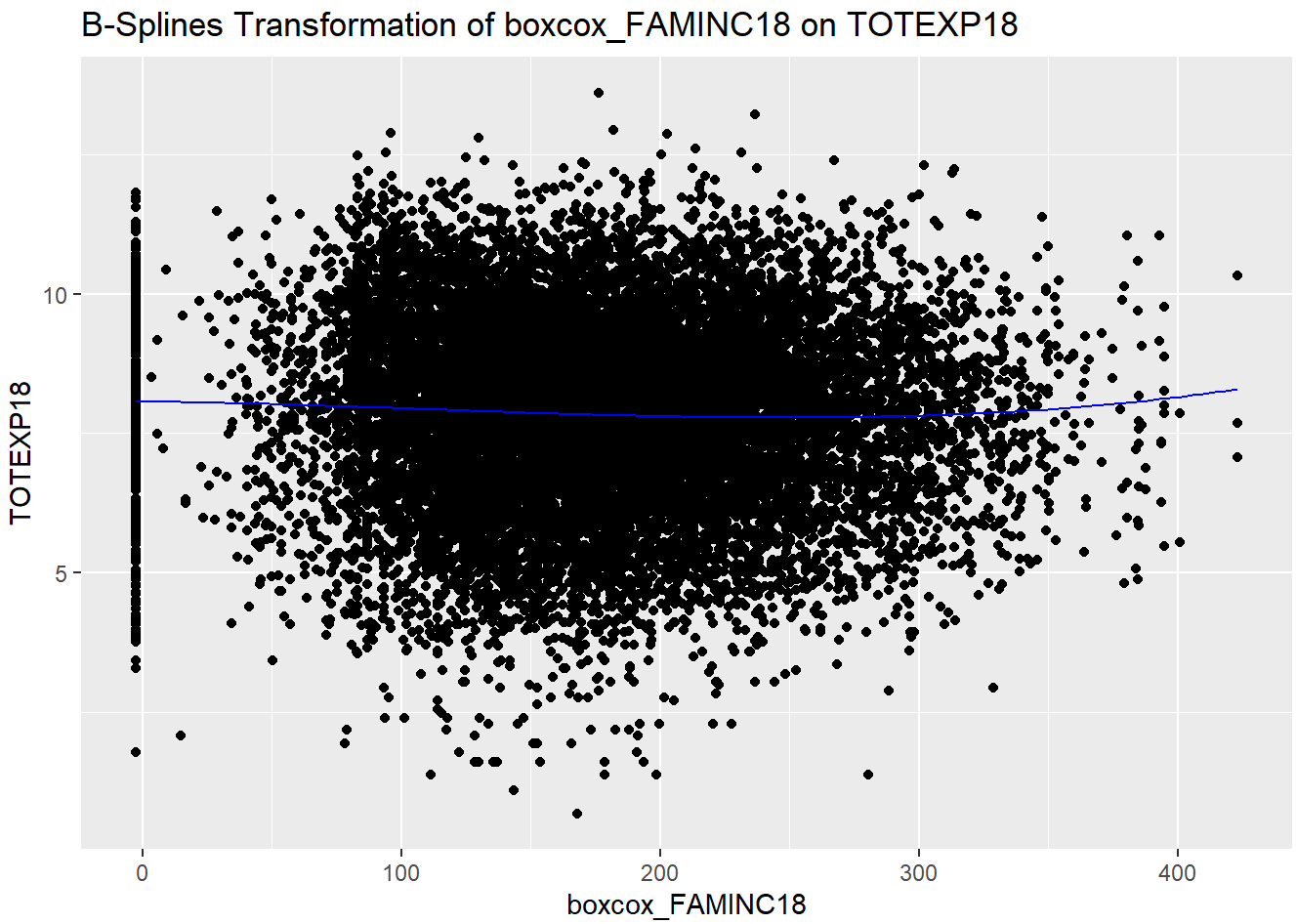
```
# BMI
bs_model = lm(log_TOTEXP18 ~ bs(ADBMI42, degree = 4), data = data) # degree 4 looks good
new_data = data.frame(ADBMI42 = seq(min(data$ADBMI42), max(data$ADBMI42), length.out = 100))
new_data$log_TOTEXP18_pred = predict(bs_model, newdata = new_data)

# Plot the data and the fitted curve
library(ggplot2)
ggplot(data, aes(x = ADBMI42, y = log_TOTEXP18)) +
  geom_point() +
  geom_line(data = new_data, aes(x = ADBMI42, y = log_TOTEXP18_pred), color = "blue") +
  labs(title = "B-Splines Transformation of ADBMI42 on TOTEXP18",
       x = "ADBMI42", y = "TOTEXP18")
```




```
# AGE
bs_model = lm(log_TOTEXP18 ~ bs(AGE42X, degree = 4), data = data) # degree 4 looks good
new_data = data.frame(AGE42X = seq(min(data$AGE42X), max(data$AGE42X), length.out = 100))
new_data$log_TOTEXP18_pred = predict(bs_model, newdata = new_data)

# Plot the data and the fitted curve
library(ggplot2)
ggplot(data, aes(x = AGE42X, y = log_TOTEXP18)) +
  geom_point() +
  geom_line(data = new_data, aes(x = AGE42X, y = log_TOTEXP18_pred), color = "blue") +
  labs(title = "B-Splines Transformation of AGE42X on TOTEXP18",
       x = "AGE42X", y = "TOTEXP18")
```

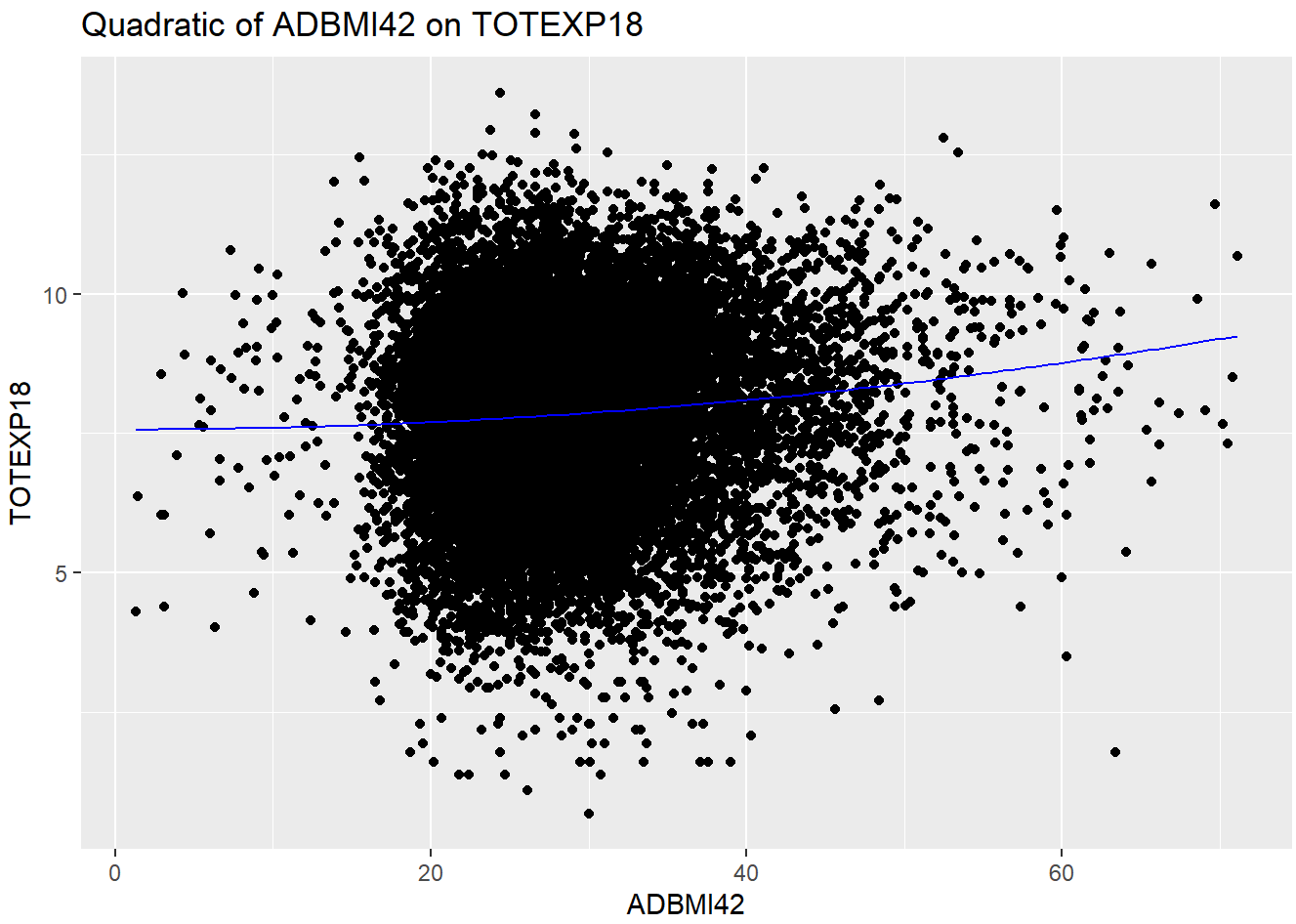



```
# INCOME
bs_model = lm(log_TOTEXP18 ~ bs(boxcox_FAMINC18, degree = 3), data = data) # degree 3 looks good
new_data = data.frame(boxcox_FAMINC18 = seq(min(data$boxcox_FAMINC18), max(data$boxcox_FAMINC1
8), length.out = 100))
new_data$log_TOTEXP18_pred = predict(bs_model, newdata = new_data)

# Plot the data and the fitted curve
library(ggplot2)
ggplot(data, aes(x = boxcox_FAMINC18, y = log_TOTEXP18)) +
  geom_point() +
  geom_line(data = new_data, aes(x = boxcox_FAMINC18, y = log_TOTEXP18_pred), color = "blue") +
  labs(title = "B-Splines Transformation of boxcox_FAMINC18 on TOTEXP18",
       x = "boxcox_FAMINC18", y = "TOTEXP18")
```



I will also try to quadratic transform the BMI predictor

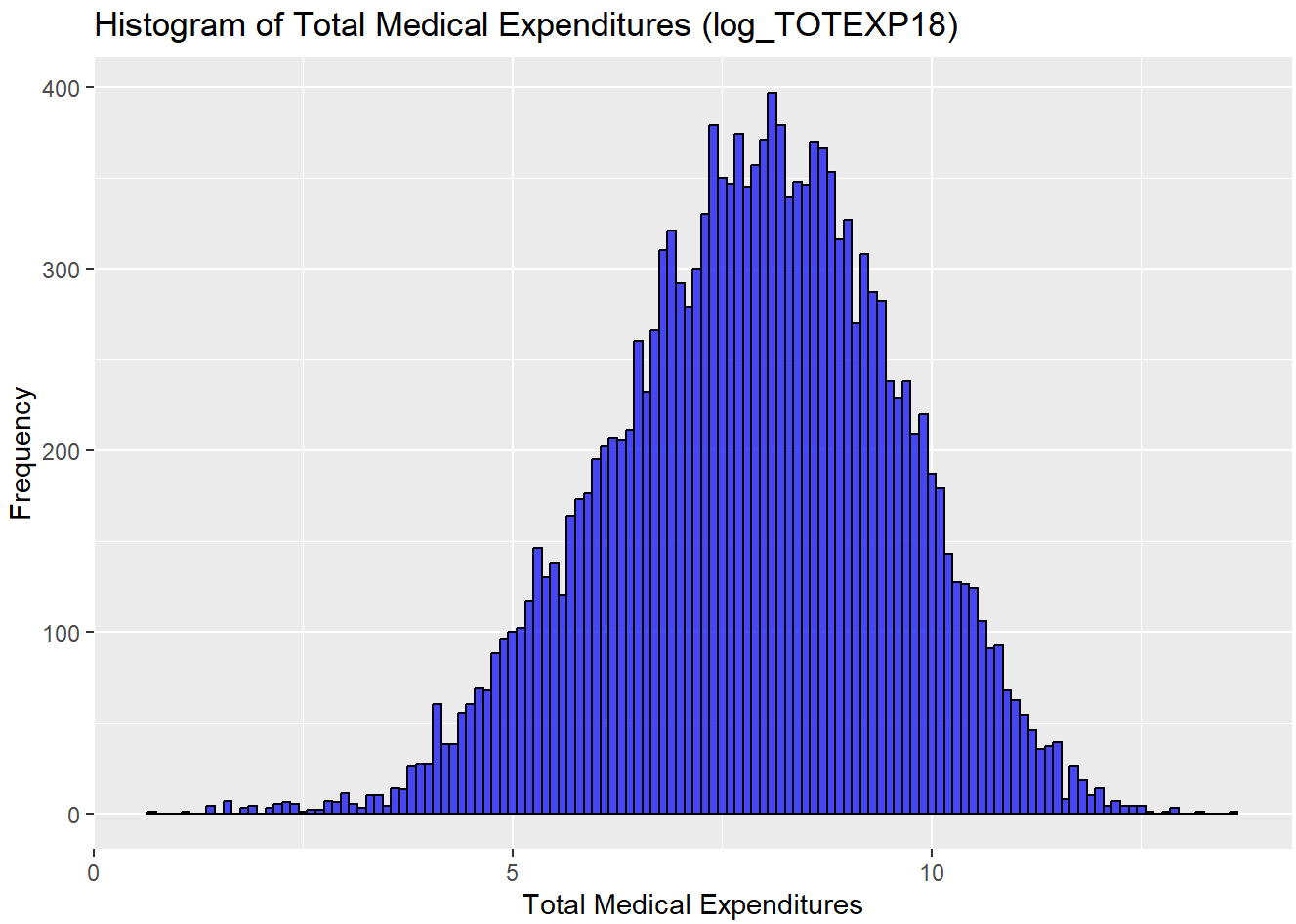
```
bs_model = lm(log_TOTEXP18 ~ I(ADBMI42^2), data = data)
new_data = data.frame(ADBMI42 = seq(min(data$ADBMI42), max(data$ADBMI42), length.out = 100))
new_data$log_TOTEXP18_pred = predict(bs_model, newdata = new_data)

# Plot the data and the fitted curve
library(ggplot2)
ggplot(data, aes(x = ADBMI42, y = log_TOTEXP18)) +
  geom_point() +
  geom_line(data = new_data, aes(x = ADBMI42, y = log_TOTEXP18_pred), color = "blue") +
  labs(title = "Quadratic of ADBMI42 on TOTEXP18",
       x = "ADBMI42", y = "TOTEXP18")
```



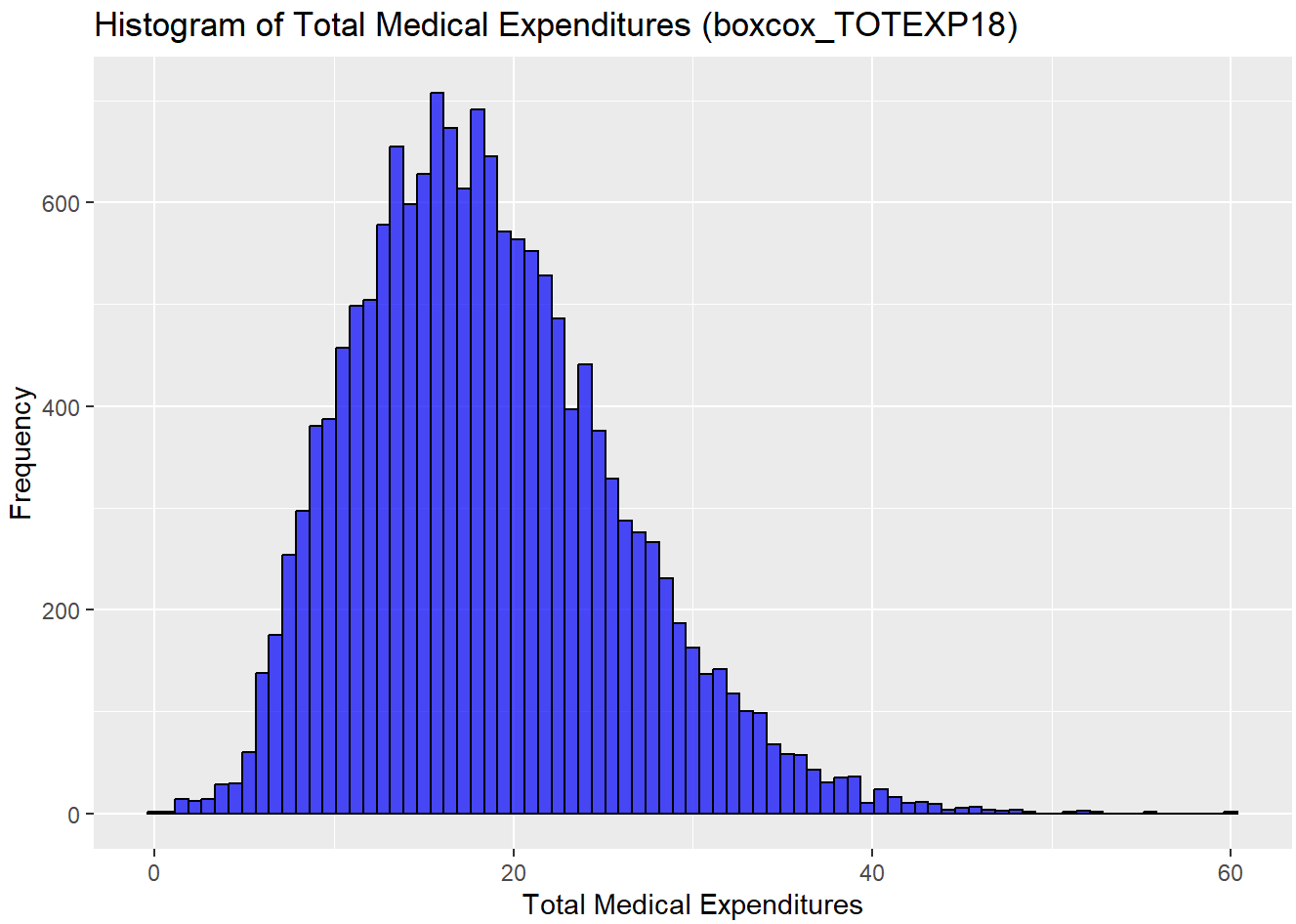

```
# This might be better than the b-spline
```

Final plots of transformed variables

```
ggplot(data, aes(x = log_TOTEXP18)) +
  geom_histogram(binwidth = .1, fill = "blue", color = "black", alpha = 0.7) +
  ggtitle("Histogram of Total Medical Expenditures (log_TOTEXP18)") +
  xlab("Total Medical Expenditures") +
  ylab("Frequency")
```

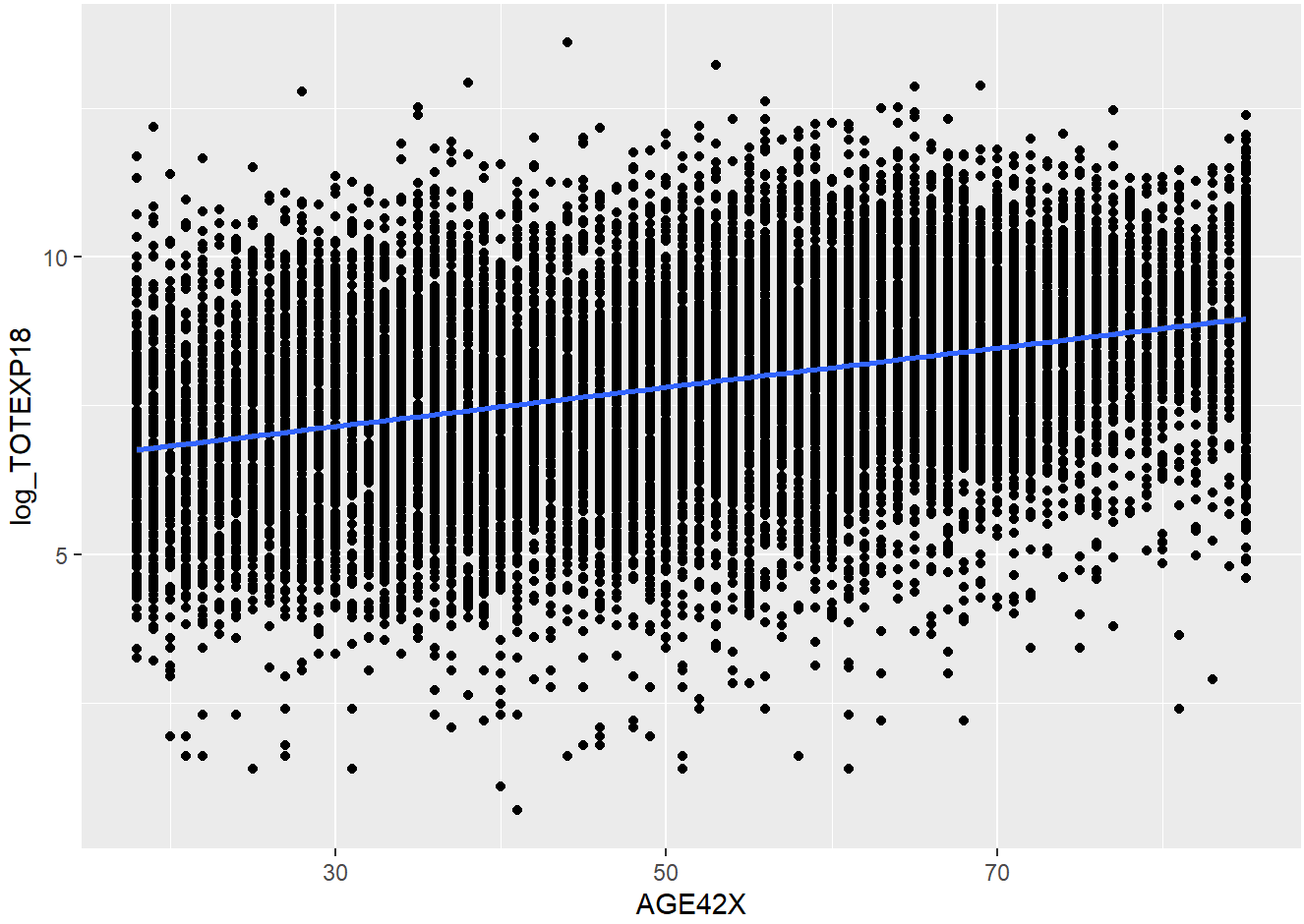



```
ggplot(data, aes(x = boxcox_TOTEXP18)) +
  geom_histogram(binwidth = .75, fill = "blue", color = "black", alpha = 0.7) +
  ggtitle("Histogram of Total Medical Expenditures (boxcox_TOTEXP18)") +
  xlab("Total Medical Expenditures") +
  ylab("Frequency")
```

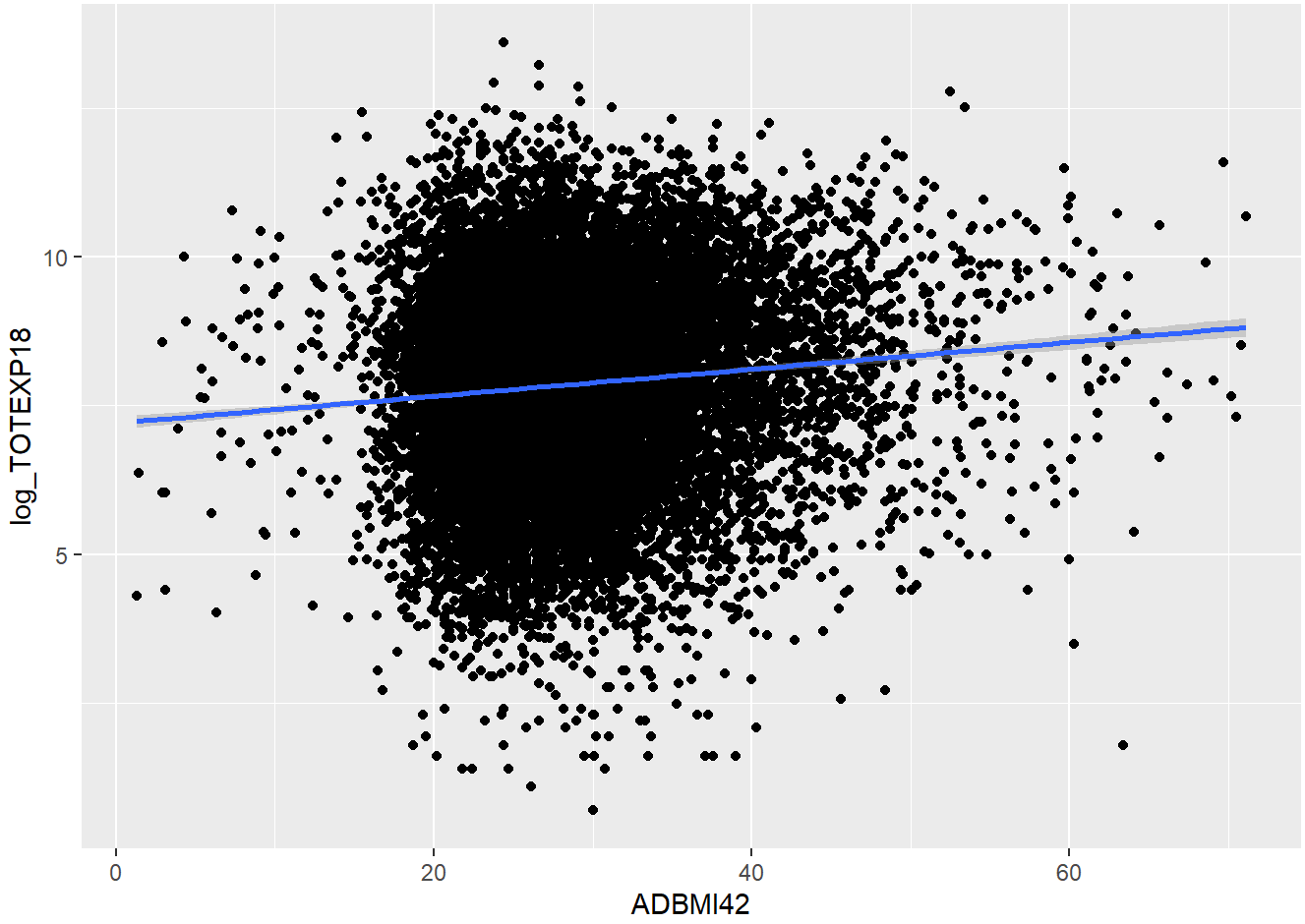



```
for (col in colnames(data)[!colnames(data) %in% c('log_TOTEXP18','boxcox_TOTEXP18','TOTEXP18','FAMINC18')]) {
  plot = ggplot(data, aes(x = !!sym(col), y = log_TOTEXP18)) + geom_point() + geom_smooth(method = "lm")
  print(plot)
}
```

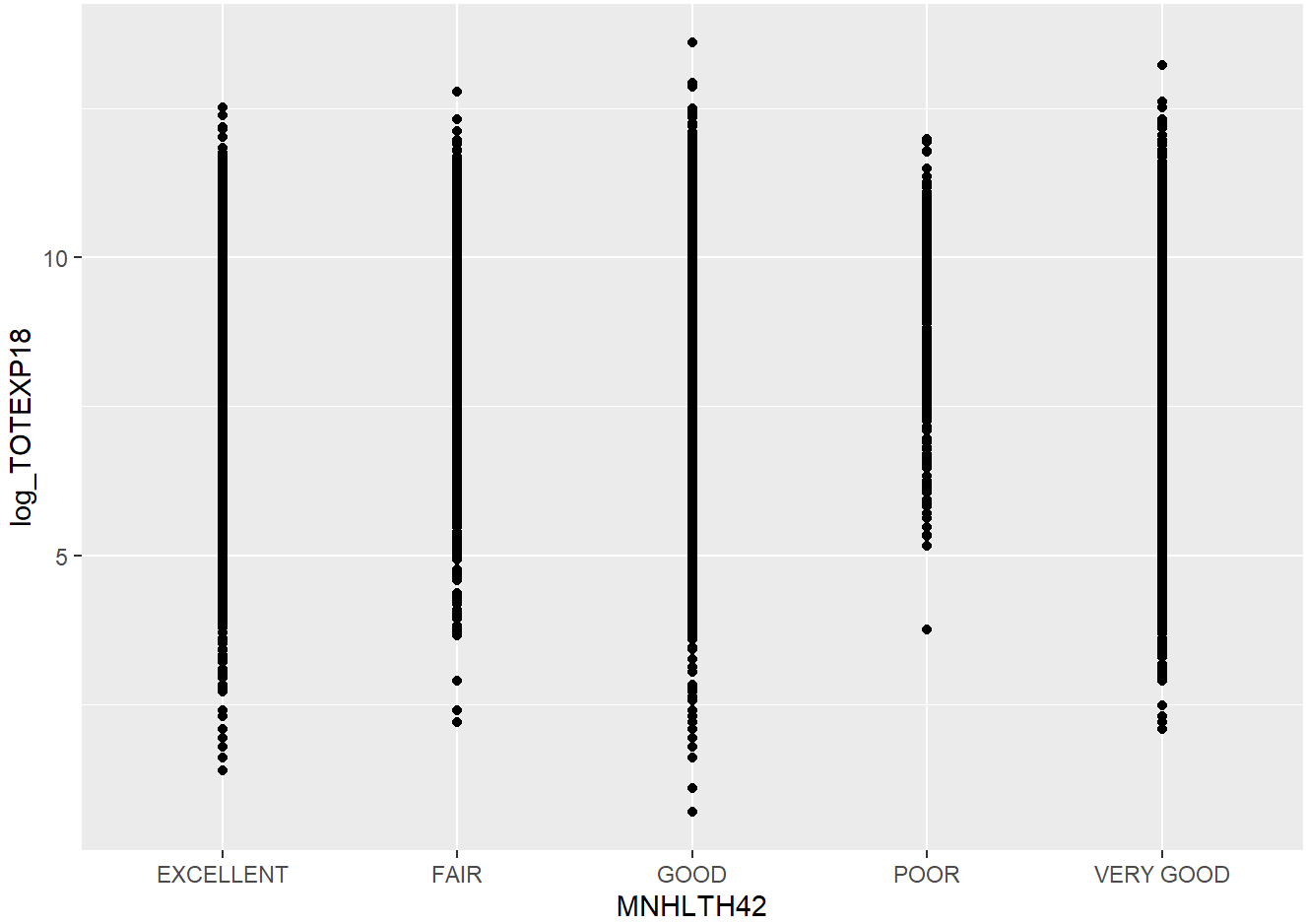
```
## `geom_smooth()` using formula = 'y ~ x'
```



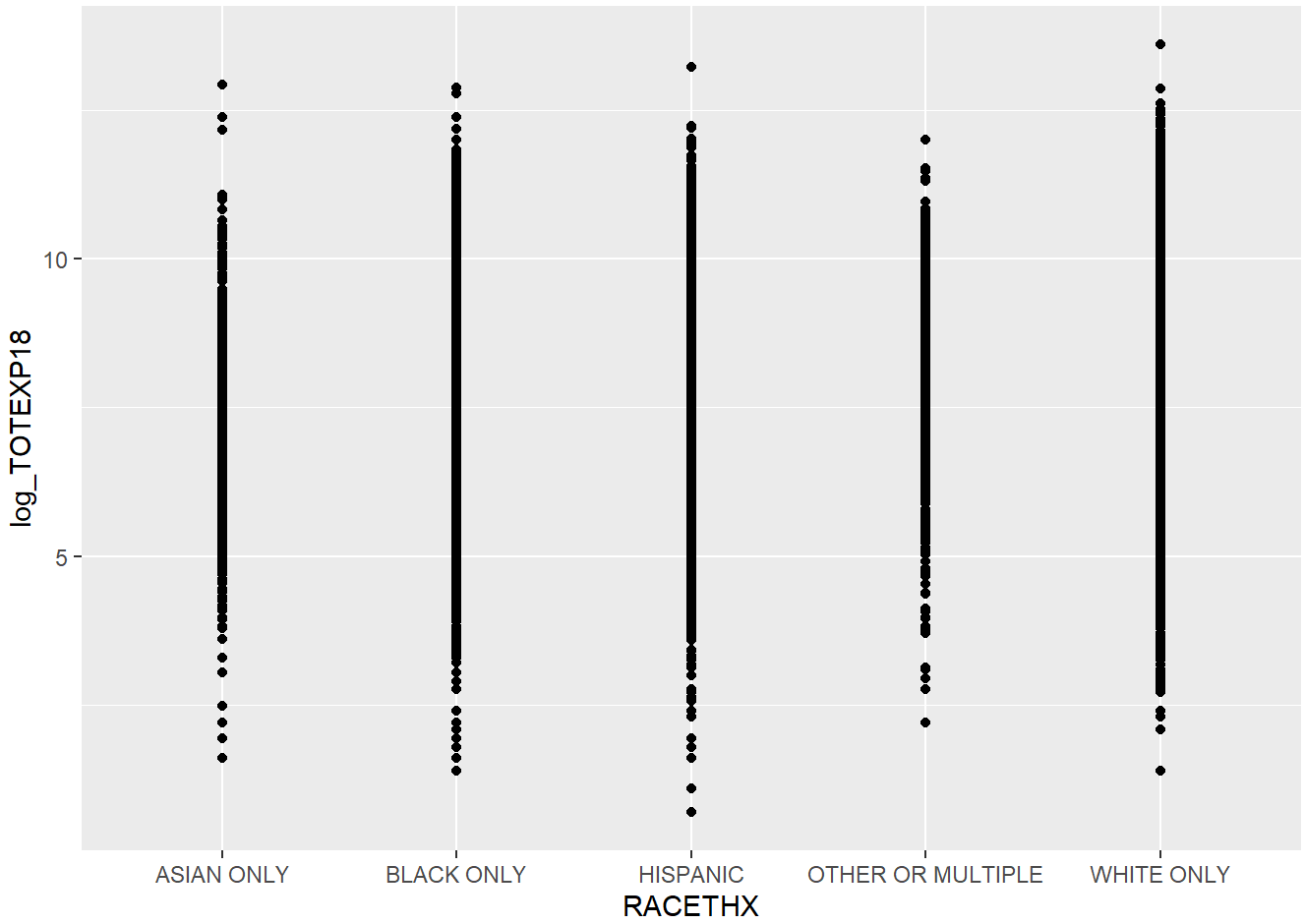

```
## `geom_smooth()` using formula = 'y ~ x'
```



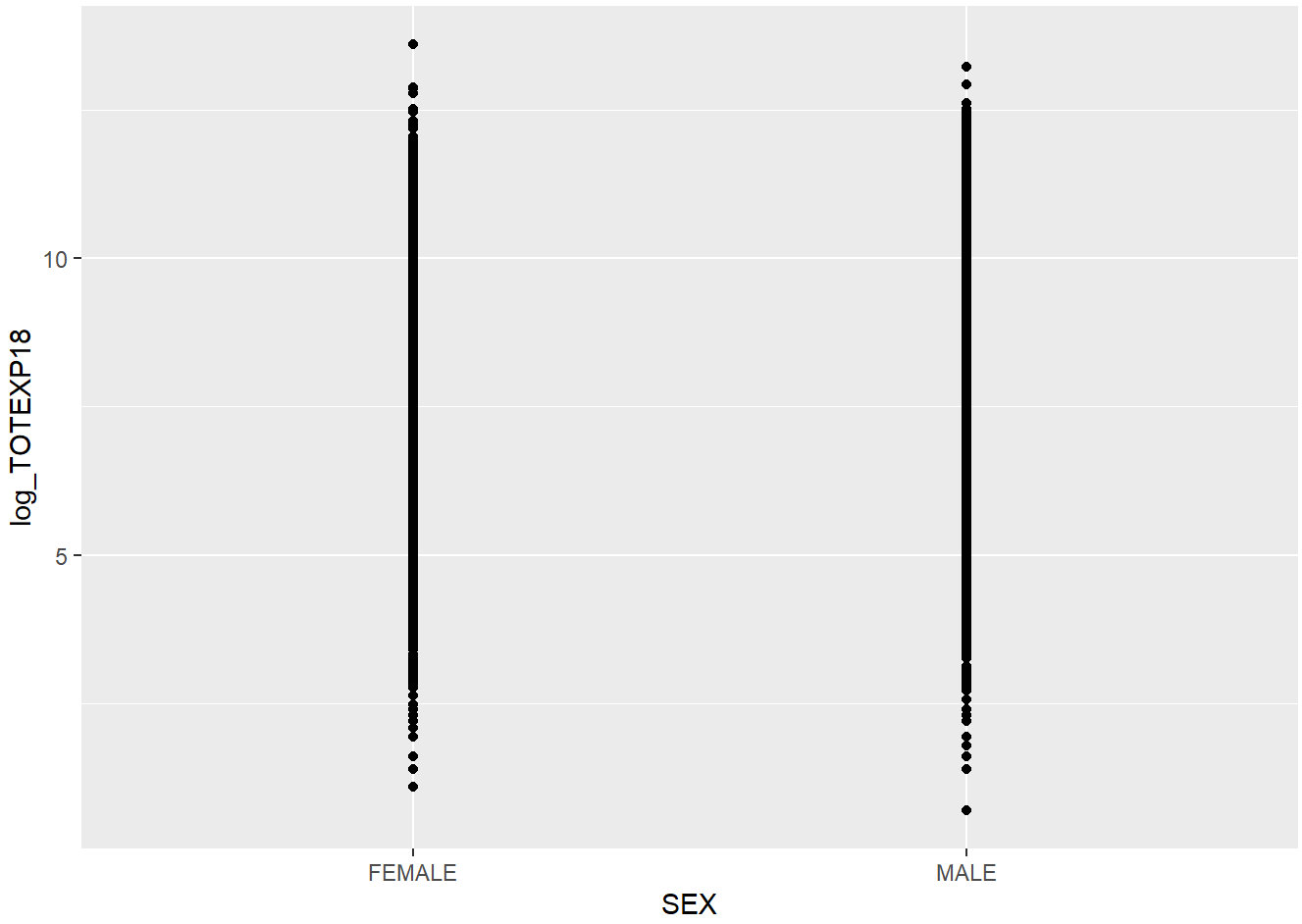

```
## `geom_smooth()` using formula = 'y ~ x'
```



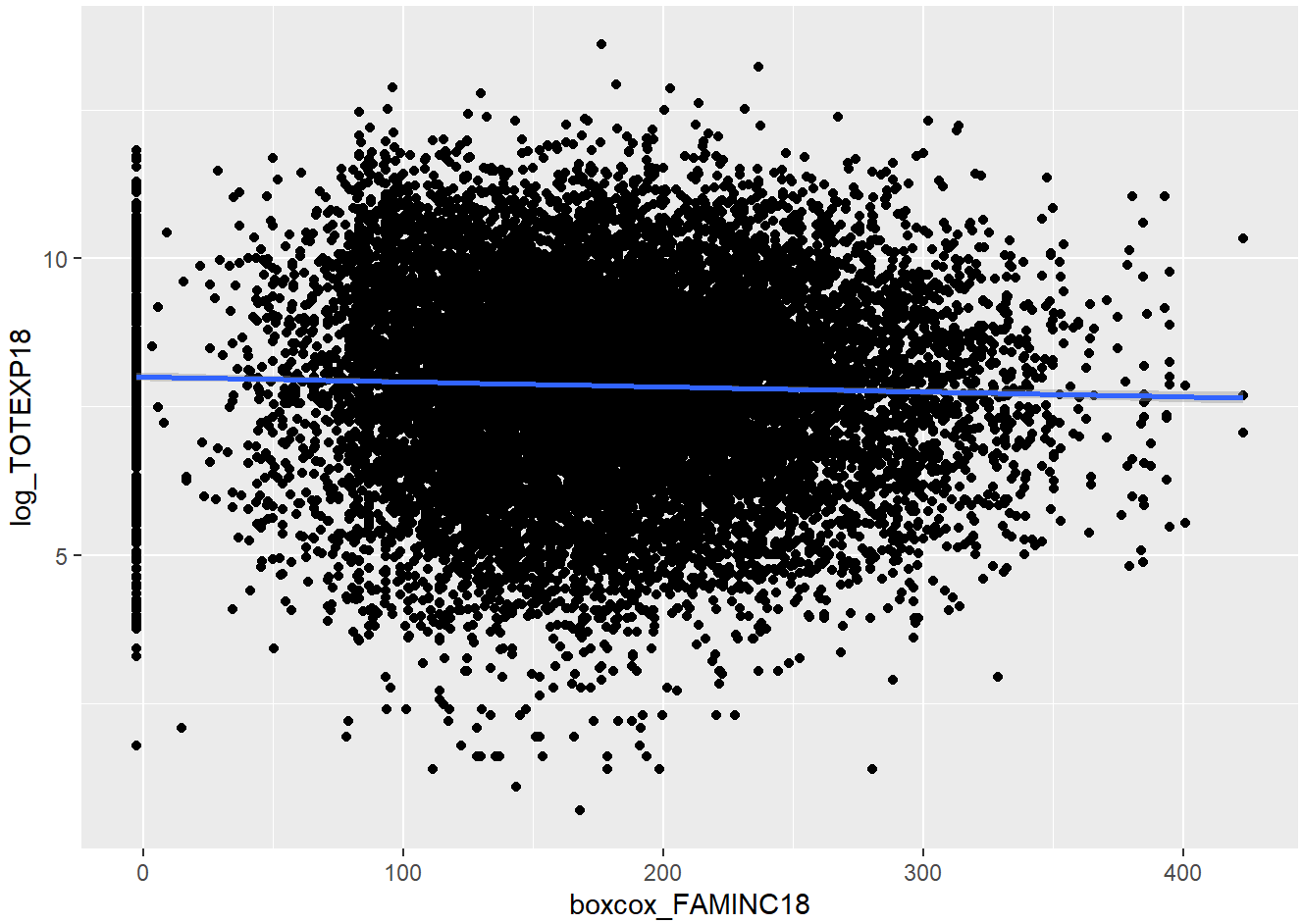

```
## `geom_smooth()` using formula = 'y ~ x'
```



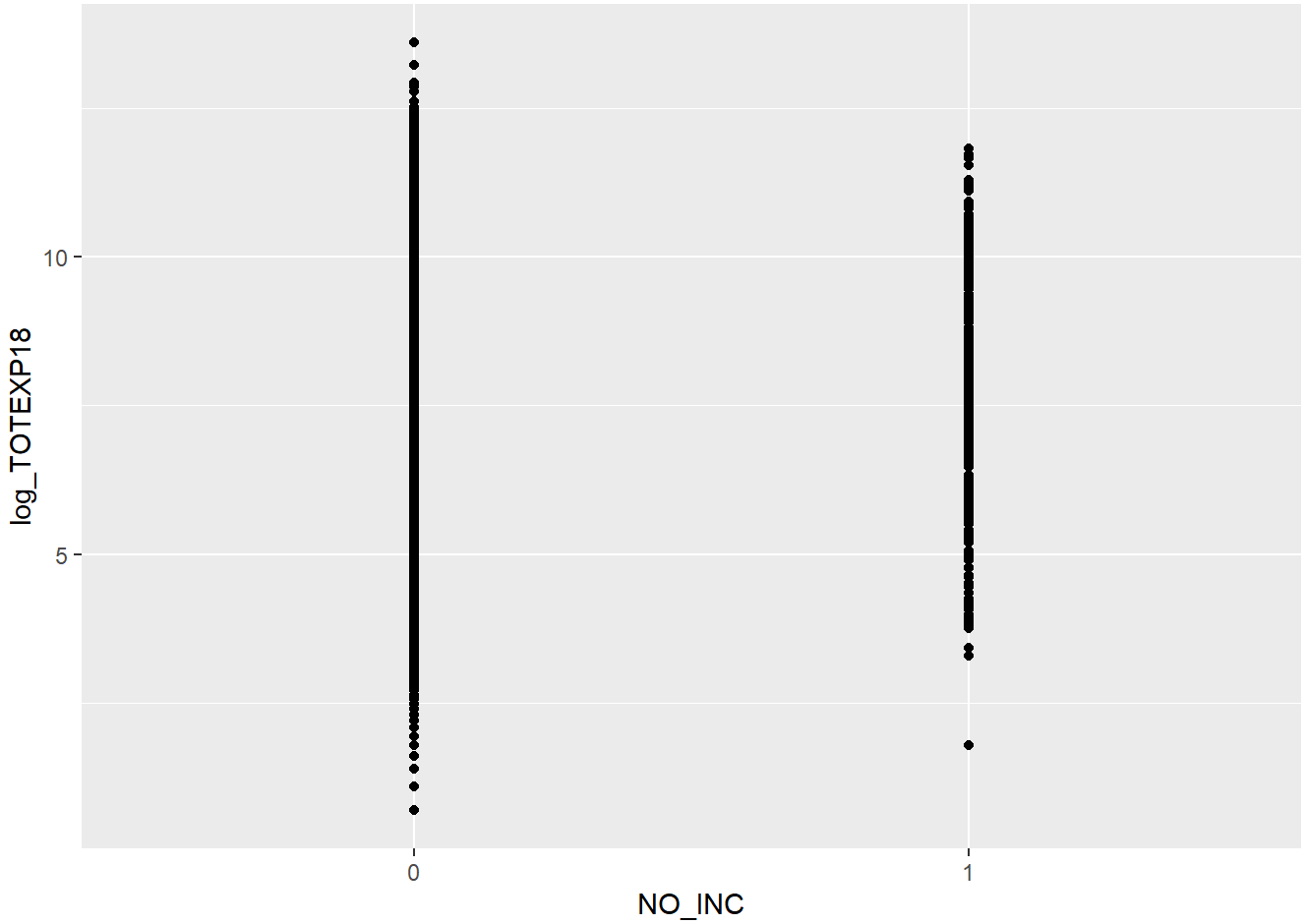

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
## `geom_smooth()` using formula = 'y ~ x'
```




```
## `geom_smooth()` using formula = 'y ~ x'
```




```
cat('\nObservations in orignal data = ', nrow(data_raw))
```

```
##
## Observations in orignal data =  18252
```

```
cat('\nObservations in cleaned data = ', nrow(data))
```

```
##
## Observations in cleaned data =  15724
```

```
cat('\nObservations in removed = ', nrow(data_raw)-nrow(data))
```

```
##
## Observations in removed =  2528
```

```
# I will use log transformed total expenditure
```

Time for model building and variable selection. I will create all first order terms, interaction terms, and b-spline transformed BMI to choose from.

```
response = "log_TOTEXP18"
first_order_terms = setdiff(colnames(data), c("log_TOTEXP18", "boxcox_TOTEXP18","TOTEXP18", "ADB
MI42", "AGE42X", "FAMINC18", "boxcox_FAMINC18"))
interaction_terms = combn(first_order_terms, 2, FUN = function(x) paste(x[1], x[2], sep = ":"))
b_spline_terms = "bs(ADBMI42, degree = 4) + bs(AGE42X, degree = 4) + bs(boxcox_FAMINC18, degree
= 3)"
quadratic_terms = "I(ADBMI42^2)"

# combine
all_terms = c(first_order_terms, interaction_terms, b_spline_terms)

# formula string
# formula_string = paste(all_terms, collapse = " + ")
formula_string <- paste(response," ~", paste(all_terms, collapse = " + "))
model_formula <- as.formula(formula_string)
print(model_formula)
```

```
## log_TOTEXP18 ~ MNHLTH42 + RACETHX + SEX + NO_INC + MNHLTH42:RACETHX +
##     MNHLTH42:SEX + MNHLTH42:NO_INC + RACETHX:SEX + RACETHX:NO_INC +
##     SEX:NO_INC + bs(ADBMI42, degree = 4) + bs(AGE42X, degree = 4) +
##     bs(boxcox_FAMINC18, degree = 3)
```

Full model

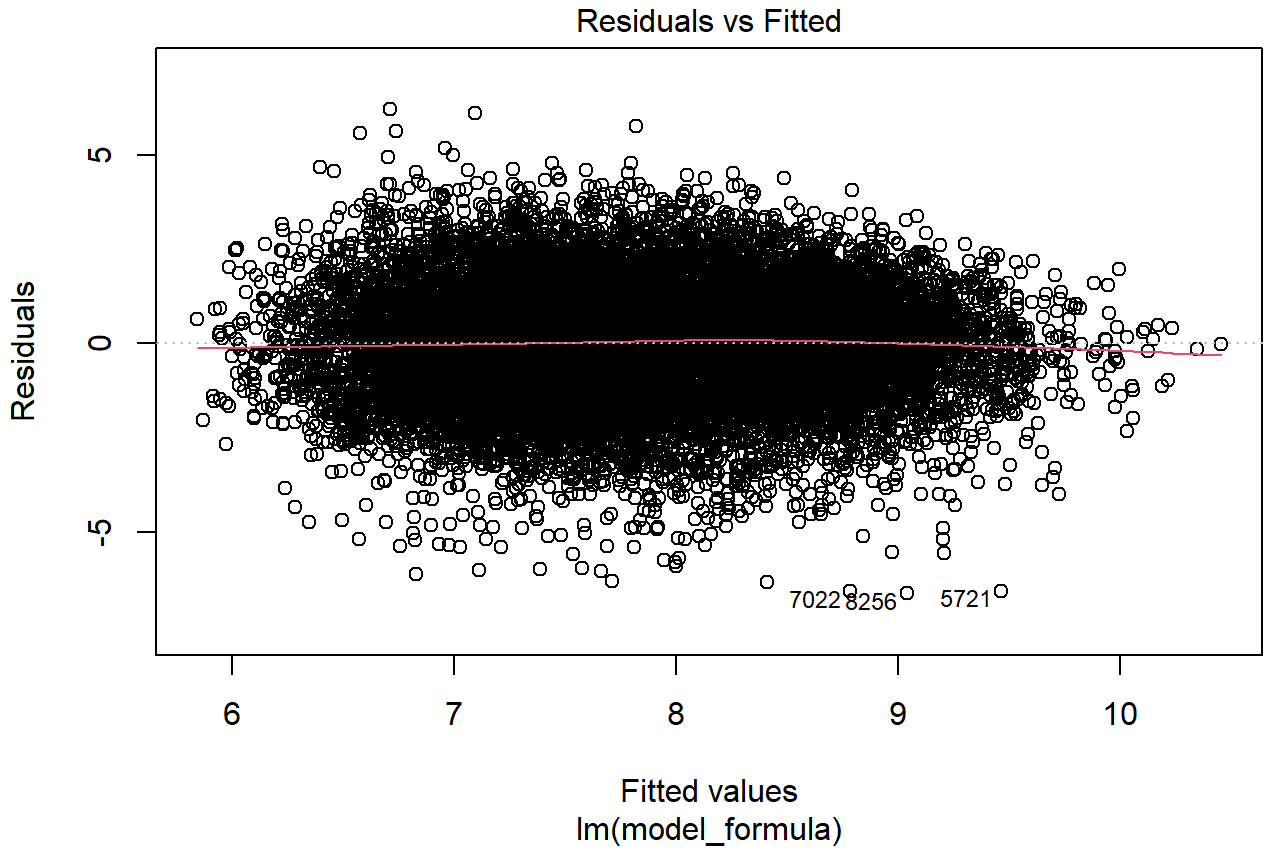
```
full_model = lm(model_formula, data = data)
summary(full_model)
```

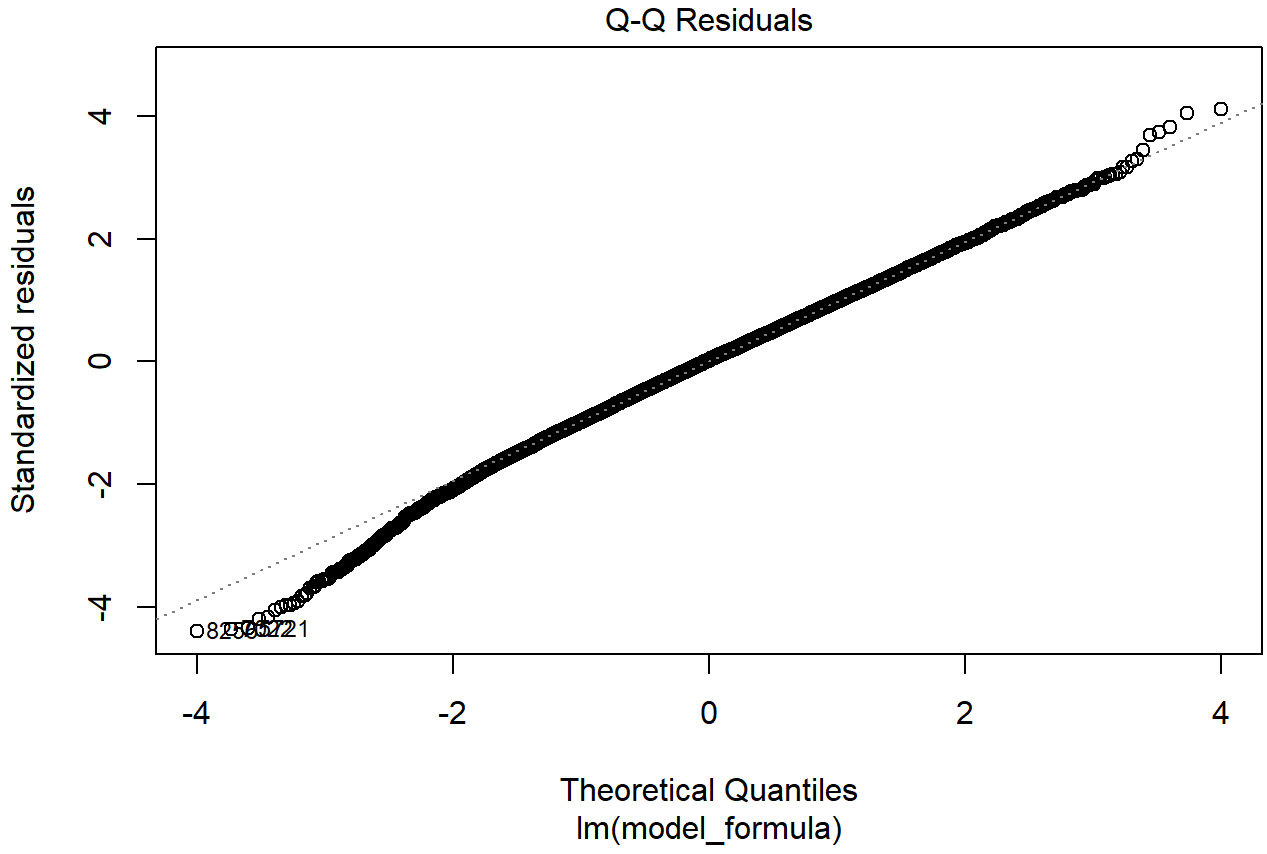
```
##
## Call:
## lm(formula = model_formula, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.6441 -0.9752  0.0374  1.0128  6.2243
##
## Coefficients:
##                                          Estimate Std. Error t value
## (Intercept)                              7.424503   0.449424  16.520
## MNHLTH42FAIR                             1.106175   0.270893   4.083
## MNHLTH42GOOD                             0.106991   0.149790   0.714
## MNHLTH42POOR                             1.448945   0.506252   2.862
## MNHLTH42VERY GOOD                        0.083000   0.136102   0.610
## RACETHXBLACK ONLY                        0.194320   0.126138   1.541
## RACETHXHISPANIC                          0.151690   0.123454   1.229
## RACETHXOTHER OR MULTIPLE                 0.749220   0.181473   4.129
## RACETHXWHITE ONLY                        0.590796   0.112044   5.273
## SEXMALE                                 -0.108379   0.117448  -0.923
## NO_INC1                                 -1.528080   0.502635  -3.040
## bs(ADBMI42, degree = 4)1                -1.385167   0.920936  -1.504
## bs(ADBMI42, degree = 4)2                -0.096251   0.465587  -0.207
## bs(ADBMI42, degree = 4)3                 0.547807   0.921680   0.594
## bs(ADBMI42, degree = 4)4                 0.158928   0.513603   0.309
## bs(AGE42X, degree = 4)1                  0.531884   0.203791   2.610
## bs(AGE42X, degree = 4)2                 -0.001142   0.184626  -0.006
## bs(AGE42X, degree = 4)3                  2.173903   0.178098  12.206
## bs(AGE42X, degree = 4)4                  1.769197   0.079462  22.265
## bs(boxcox_FAMINC18, degree = 3)1        -1.556297   0.409934  -3.796
## bs(boxcox_FAMINC18, degree = 3)2         0.258861   0.182317   1.420
## bs(boxcox_FAMINC18, degree = 3)3        -0.476589   0.371924  -1.281
## MNHLTH42FAIR:RACETHXBLACK ONLY          -0.212087   0.292241  -0.726
## MNHLTH42GOOD:RACETHXBLACK ONLY           0.326341   0.168951   1.932
## MNHLTH42POOR:RACETHXBLACK ONLY          -0.096960   0.561638  -0.173
## MNHLTH42VERY GOOD:RACETHXBLACK ONLY      0.145177   0.158738   0.915
## MNHLTH42FAIR:RACETHXHISPANIC            -0.234372   0.288709  -0.812
## MNHLTH42GOOD:RACETHXHISPANIC             0.133100   0.165514   0.804
## MNHLTH42POOR:RACETHXHISPANIC             0.234972   0.539383   0.436
## MNHLTH42VERY GOOD:RACETHXHISPANIC       -0.020070   0.155023  -0.129
## MNHLTH42FAIR:RACETHXOTHER OR MULTIPLE   -0.705688   0.361502  -1.952
## MNHLTH42GOOD:RACETHXOTHER OR MULTIPLE    0.150082   0.234402   0.640
## MNHLTH42POOR:RACETHXOTHER OR MULTIPLE   -0.331102   0.766448  -0.432
## MNHLTH42VERY GOOD:RACETHXOTHER OR MULTIPLE  0.067125   0.227216   0.295
## MNHLTH42FAIR:RACETHXWHITE ONLY          -0.297397   0.273400  -1.088
## MNHLTH42GOOD:RACETHXWHITE ONLY           0.297005   0.152649   1.946
## MNHLTH42POOR:RACETHXWHITE ONLY          -0.092467   0.505602  -0.183
## MNHLTH42VERY GOOD:RACETHXWHITE ONLY      0.008667   0.138745   0.062
## MNHLTH42FAIR:SEXMALE                     0.177868   0.096213   1.849
## MNHLTH42GOOD:SEXMALE                     0.029688   0.064592   0.460
## MNHLTH42POOR:SEXMALE                    -0.184738   0.190752  -0.968
## MNHLTH42VERY GOOD:SEXMALE                0.022143   0.061486   0.360
```

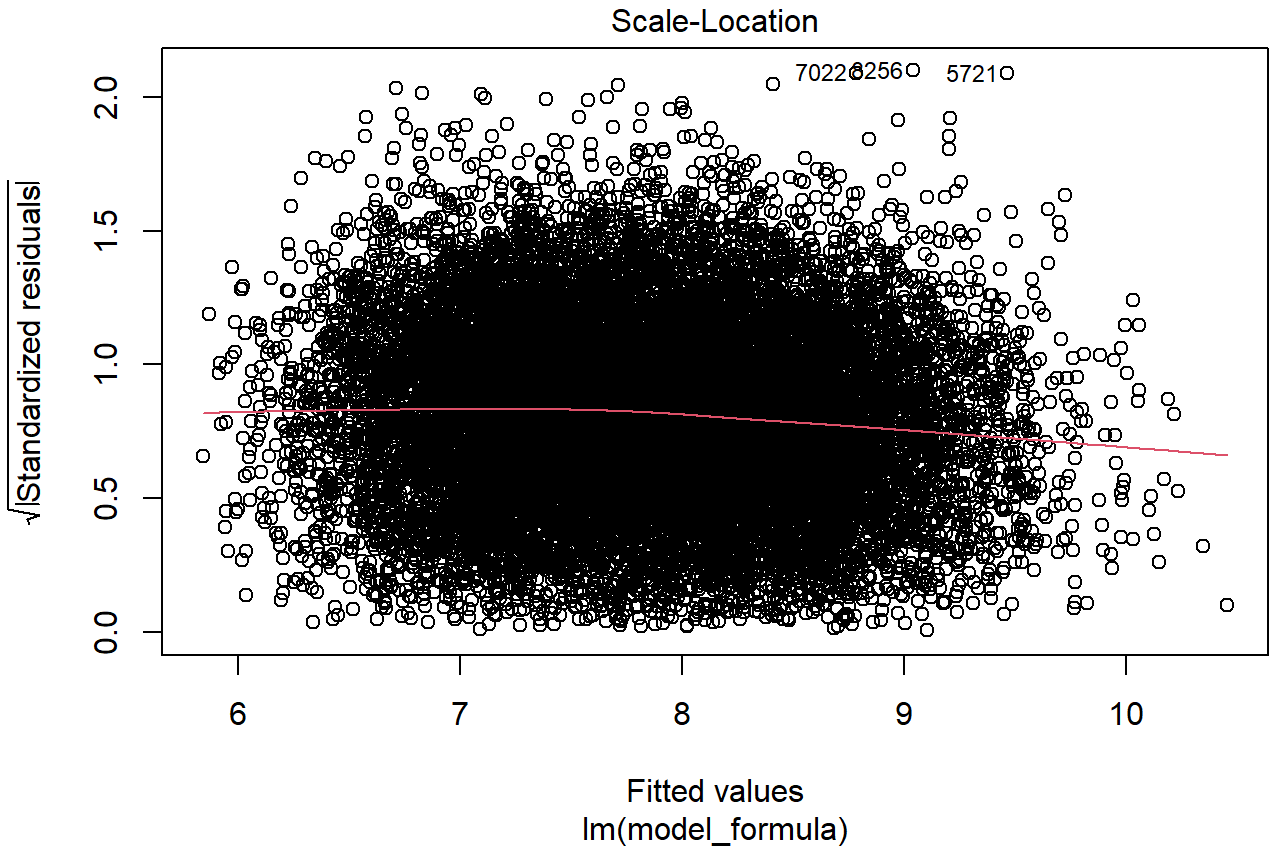
```
## MNHLTH42FAIR:NO_INC1                          0.065985   0.268993   0.245
## MNHLTH42GOOD:NO_INC1                          0.070205   0.230382   0.305
## MNHLTH42POOR:NO_INC1                         -0.169123   0.414535  -0.408
## MNHLTH42VERY GOOD:NO_INC1                     0.305629   0.252060   1.213
## RACETHXBLACK ONLY:SEXMALE                    -0.180018   0.131504  -1.369
## RACETHXHISPANIC:SEXMALE                      -0.337166   0.128102  -2.632
## RACETHXOTHER OR MULTIPLE:SEXMALE             -0.549151   0.179272  -3.063
## RACETHXWHITE ONLY:SEXMALE                    -0.225013   0.116643  -1.929
## RACETHXBLACK ONLY:NO_INC1                     0.783551   0.457895   1.711
## RACETHXHISPANIC:NO_INC1                       0.443921   0.462084   0.961
## RACETHXOTHER OR MULTIPLE:NO_INC1              0.168311   0.650042   0.259
## RACETHXWHITE ONLY:NO_INC1                     1.005707   0.451101   2.229
## SEXMALE:NO_INC1                               0.120962   0.179272   0.675
##                                              Pr(>|t|)
## (Intercept)                                   < 2e-16 ***
## MNHLTH42FAIR                                 4.46e-05 ***
## MNHLTH42GOOD                                 0.475068
## MNHLTH42POOR                                 0.004214 **
## MNHLTH42VERY GOOD                            0.541979
## RACETHXBLACK ONLY                            0.123451
## RACETHXHISPANIC                              0.219197
## RACETHXOTHER OR MULTIPLE                     3.67e-05 ***
## RACETHXWHITE ONLY                            1.36e-07 ***
## SEXMALE                                      0.356135
## NO_INC1                                      0.002369 **
## bs(ADBMI42, degree = 4)1                     0.132579
## bs(ADBMI42, degree = 4)2                     0.836224
## bs(ADBMI42, degree = 4)3                     0.552282
## bs(ADBMI42, degree = 4)4                     0.756994
## bs(AGE42X, degree = 4)1                      0.009064 **
## bs(AGE42X, degree = 4)2                      0.995063
## bs(AGE42X, degree = 4)3                       < 2e-16 ***
## bs(AGE42X, degree = 4)4                       < 2e-16 ***
## bs(boxcox_FAMINC18, degree = 3)1             0.000147 ***
## bs(boxcox_FAMINC18, degree = 3)2             0.155674
## bs(boxcox_FAMINC18, degree = 3)3             0.200067
## MNHLTH42FAIR:RACETHXBLACK ONLY               0.468017
## MNHLTH42GOOD:RACETHXBLACK ONLY               0.053430 .
## MNHLTH42POOR:RACETHXBLACK ONLY               0.862938
## MNHLTH42VERY GOOD:RACETHXBLACK ONLY          0.360433
## MNHLTH42FAIR:RACETHXHISPANIC                 0.416924
## MNHLTH42GOOD:RACETHXHISPANIC                 0.421317
## MNHLTH42POOR:RACETHXHISPANIC                 0.663111
## MNHLTH42VERY GOOD:RACETHXHISPANIC            0.896994
## MNHLTH42FAIR:RACETHXOTHER OR MULTIPLE        0.050944 .
## MNHLTH42GOOD:RACETHXOTHER OR MULTIPLE        0.522004
## MNHLTH42POOR:RACETHXOTHER OR MULTIPLE        0.665751
## MNHLTH42VERY GOOD:RACETHXOTHER OR MULTIPLE   0.767674
## MNHLTH42FAIR:RACETHXWHITE ONLY               0.276713
## MNHLTH42GOOD:RACETHXWHITE ONLY               0.051712 .
## MNHLTH42POOR:RACETHXWHITE ONLY               0.854890
## MNHLTH42VERY GOOD:RACETHXWHITE ONLY          0.950194
```

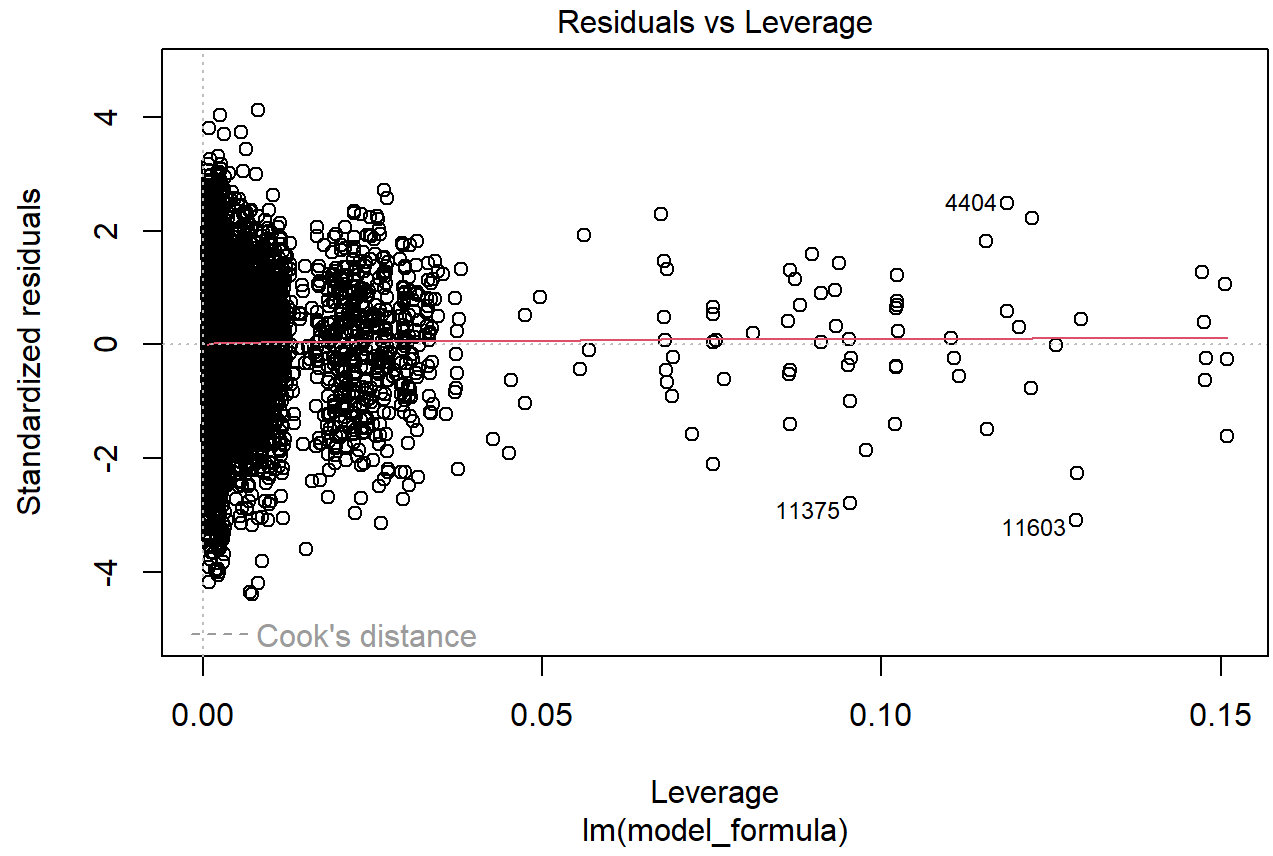
```
## MNHLTH42FAIR:SEXMALE                        0.064522 .
## MNHLTH42GOOD:SEXMALE                        0.645793
## MNHLTH42POOR:SEXMALE                        0.332825
## MNHLTH42VERY GOOD:SEXMALE                   0.718756
## MNHLTH42FAIR:NO_INC1                        0.806224
## MNHLTH42GOOD:NO_INC1                        0.760575
## MNHLTH42POOR:NO_INC1                        0.683293
## MNHLTH42VERY GOOD:NO_INC1                   0.225329
## RACETHXBLACK ONLY:SEXMALE                   0.171043
## RACETHXHISPANIC:SEXMALE                     0.008496 **
## RACETHXOTHER OR MULTIPLE:SEXMALE            0.002193 **
## RACETHXWHITE ONLY:SEXMALE                   0.053740 .
## RACETHXBLACK ONLY:NO_INC1                   0.087063 .
## RACETHXHISPANIC:NO_INC1                     0.336722
## RACETHXOTHER OR MULTIPLE:NO_INC1            0.795697
## RACETHXWHITE ONLY:NO_INC1                   0.025798 *
## SEXMALE:NO_INC1                             0.499852
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.515 on 15669 degrees of freedom
## Multiple R-squared:  0.196,  Adjusted R-squared:  0.1933
## F-statistic: 70.75 on 54 and 15669 DF,  p-value: < 2.2e-16
```

```
plot(full_model)
```


Residuals vs Fitted
Residuals
5
0
-5
7022
8256
5721
6
7
8
9
10
Fitted values
lm(model_formula)


Q-Q Residuals
Standardized residuals
4
2
0
-2
-4
-4
-2
0
2
4
Theoretical Quantiles
lm(model_formula)


Scale-Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
2.0
6
7
8
9
10
Fitted values
lm(model_formula)


Residuals vs Leverage
Standardized residuals
4
2
0
-2
-4
4404
11375
11603
Cook's distance
0.00
0.05
0.10
0.15
Leverage
lm(model_formula)

Stepwise variable selection (AIC)

```
null_model = lm(log_TOTEXP18~1, data=data)
stepwise = step(null_model, scope = list(lower = null_model, upper = full_model), direction = "b
oth", k = 2, trace = FALSE, test = "F", steps = 1000, add = 0.05 , drop = 0.05)
summary(stepwise)
```

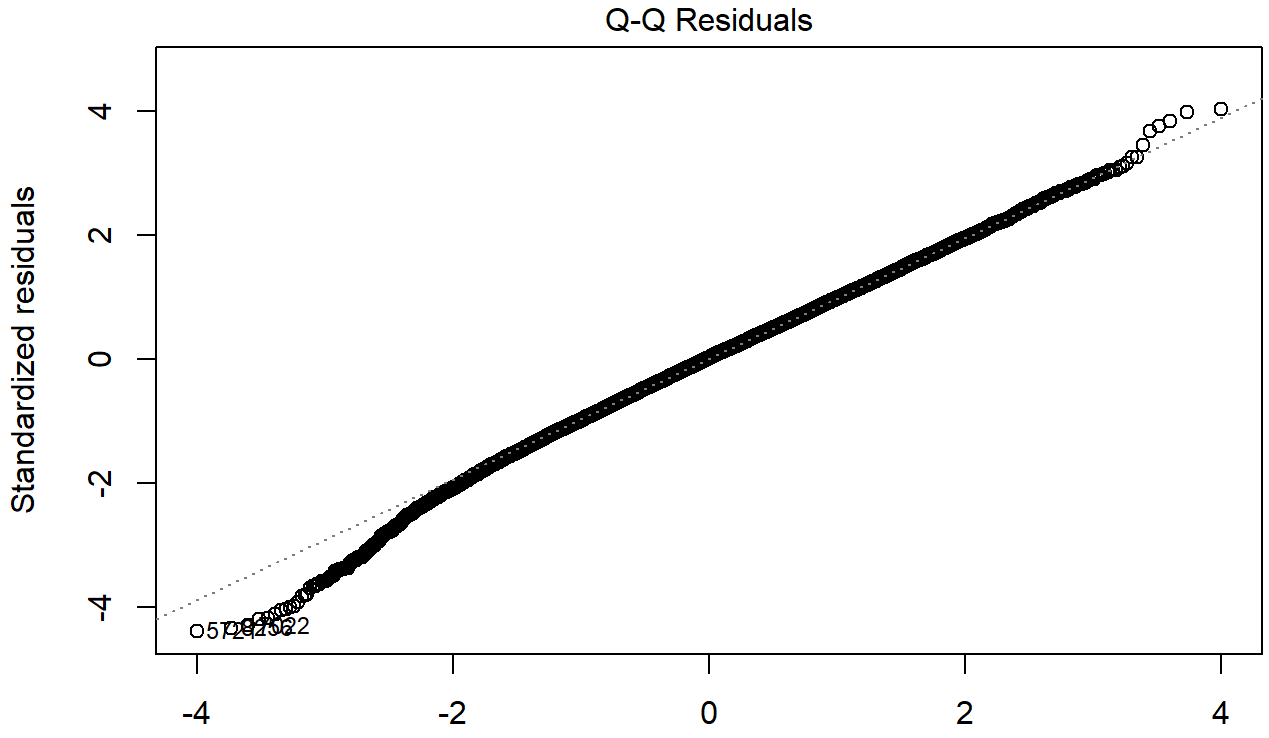
```
##
## Call:
## lm(formula = log_TOTEXP18 ~ bs(AGE42X, degree = 4) + MNHLTH42 +
##     RACETHX + SEX + bs(ADBMI42, degree = 4) + bs(boxcox_FAMINC18,
##     degree = 3) + NO_INC + RACETHX:SEX + RACETHX:NO_INC, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.6353 -0.9784  0.0346  1.0071  6.1133
##
## Coefficients:
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                       7.36057    0.44328  16.605  < 2e-16 ***
## bs(AGE42X, degree = 4)1           0.54598    0.20372   2.680 0.007368 **
## bs(AGE42X, degree = 4)2          -0.01287    0.18451  -0.070 0.944405
## bs(AGE42X, degree = 4)3           2.18346    0.17788  12.275  < 2e-16 ***
## bs(AGE42X, degree = 4)4           1.77610    0.07939  22.373  < 2e-16 ***
## MNHLTH42FAIR                      0.90514    0.04875  18.567  < 2e-16 ***
## MNHLTH42GOOD                      0.37487    0.03267  11.476  < 2e-16 ***
## MNHLTH42POOR                      1.32665    0.09390  14.129  < 2e-16 ***
## MNHLTH42VERY GOOD                 0.12009    0.03062   3.922 8.83e-05 ***
## RACETHXBLACK ONLY                 0.31155    0.08731   3.568 0.000361 ***
## RACETHXHISPANIC                   0.16812    0.08491   1.980 0.047738 *
## RACETHXOTHER OR MULTIPLE          0.73528    0.11749   6.258 4.00e-10 ***
## RACETHXWHITE ONLY                 0.65255    0.07784   8.384  < 2e-16 ***
## SEXMALE                          -0.07344    0.11198  -0.656 0.511972
## bs(ADBMI42, degree = 4)1         -1.41210    0.92067  -1.534 0.125103
## bs(ADBMI42, degree = 4)2         -0.09423    0.46521  -0.203 0.839489
## bs(ADBMI42, degree = 4)3          0.50761    0.92138   0.551 0.581692
## bs(ADBMI42, degree = 4)4          0.16976    0.51330   0.331 0.740863
## bs(boxcox_FAMINC18, degree = 3)1 -1.55115    0.40921  -3.791 0.000151 ***
## bs(boxcox_FAMINC18, degree = 3)2  0.26138    0.18219   1.435 0.151409
## bs(boxcox_FAMINC18, degree = 3)3 -0.47465    0.37160  -1.277 0.201509
## NO_INC1                          -1.36304    0.45830  -2.974 0.002943 **
## RACETHXBLACK ONLY:SEXMALE        -0.18516    0.13078  -1.416 0.156832
## RACETHXHISPANIC:SEXMALE          -0.34240    0.12747  -2.686 0.007238 **
## RACETHXOTHER OR MULTIPLE:SEXMALE -0.55270    0.17861  -3.095 0.001975 **
## RACETHXWHITE ONLY:SEXMALE        -0.23362    0.11609  -2.012 0.044186 *
## RACETHXBLACK ONLY:NO_INC1         0.75310    0.45230   1.665 0.095927 .
## RACETHXHISPANIC:NO_INC1           0.41835    0.45409   0.921 0.356916
## RACETHXOTHER OR MULTIPLE:NO_INC1  0.15877    0.64410   0.247 0.805296
## RACETHXWHITE ONLY:NO_INC1         0.99382    0.44541   2.231 0.025678 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.515 on 15694 degrees of freedom
## Multiple R-squared:  0.1946, Adjusted R-squared:  0.1931
## F-statistic: 130.7 on 29 and 15694 DF,  p-value: < 2.2e-16
```

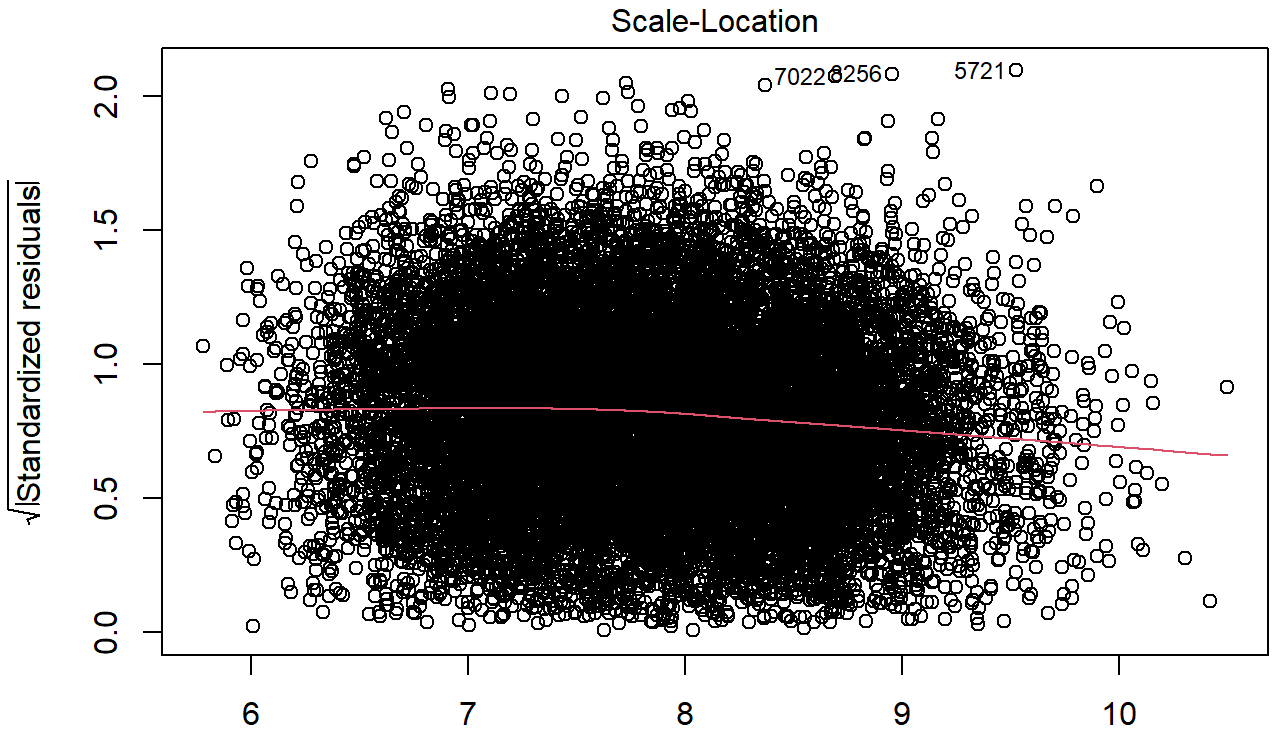
```
cat('\nNumber of terms = ',length(coef(stepwise))-1)
```

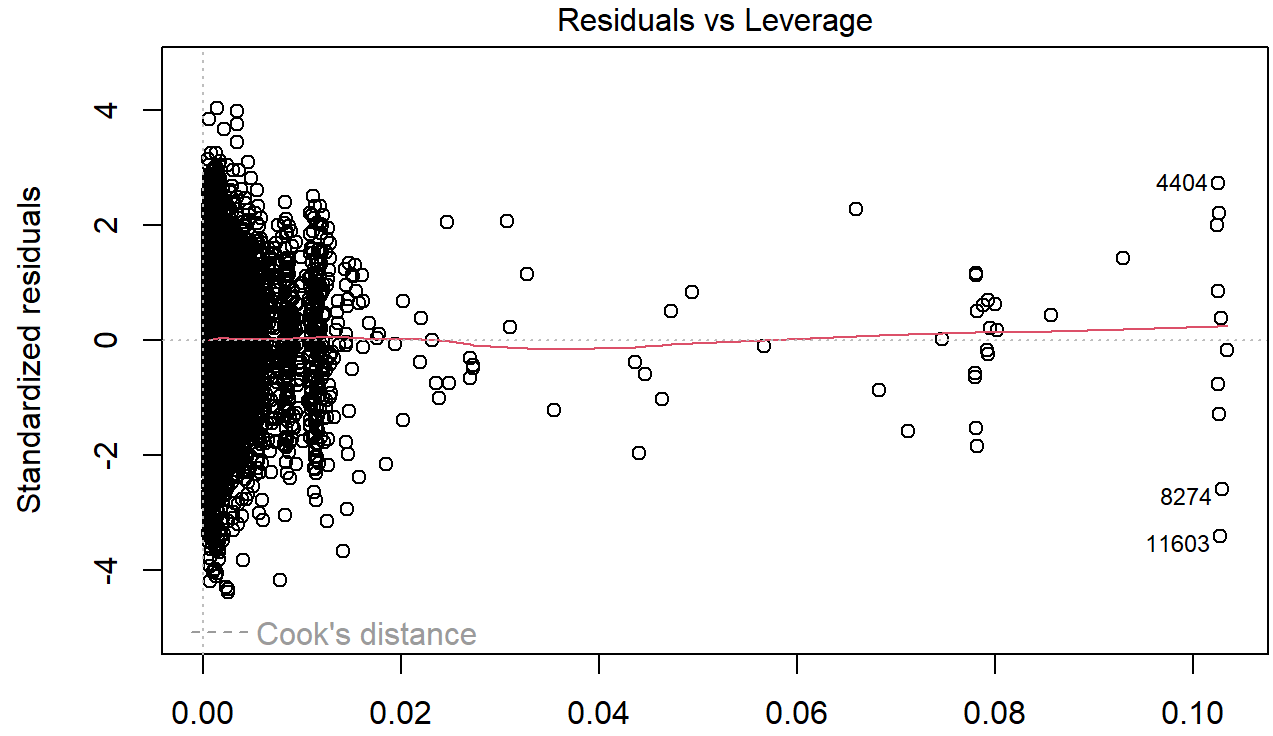
```
##
## Number of terms =  29
```

```
plot(stepwise)
```


Residuals vs Fitted
Residuals
5
0
-5
7022
8256
5721
6
7
8
9
10
Fitted values
lm(log_TOTEXP18 ~ bs(AGE42X, degree = 4) + MNHLTH42 + RACETHX + SEX + bs(AD .


Q-Q Residuals
Standardized residuals
4
2
0
-2
-4
-4
-2
0
2
4
Theoretical Quantiles
lm(log_TOTEXP18 ~ bs(AGE42X, degree = 4) + MNHLTH42 + RACETHX + SEX + bs(AD .


Scale-Location
70226
6256
5721
√|Standardized residuals|
0.0
0.5
1.0
1.5
2.0
6
7
8
9
10
Fitted values
lm(log_TOTEXP18 ~ bs(AGE42X, degree = 4) + MNHLTH42 + RACETHX + SEX + bs(AD .


Residuals vs Leverage
4404
8274
11603
Cook's distance
Standardized residuals
-4
-2
0
2
4
0.00
0.02
0.04
0.06
0.08
0.10
Leverage
lm(log_TOTEXP18 ~ bs(AGE42X, degree = 4) + MNHLTH42 + RACETHX + SEX + bs(AD .

Lasso variable selection

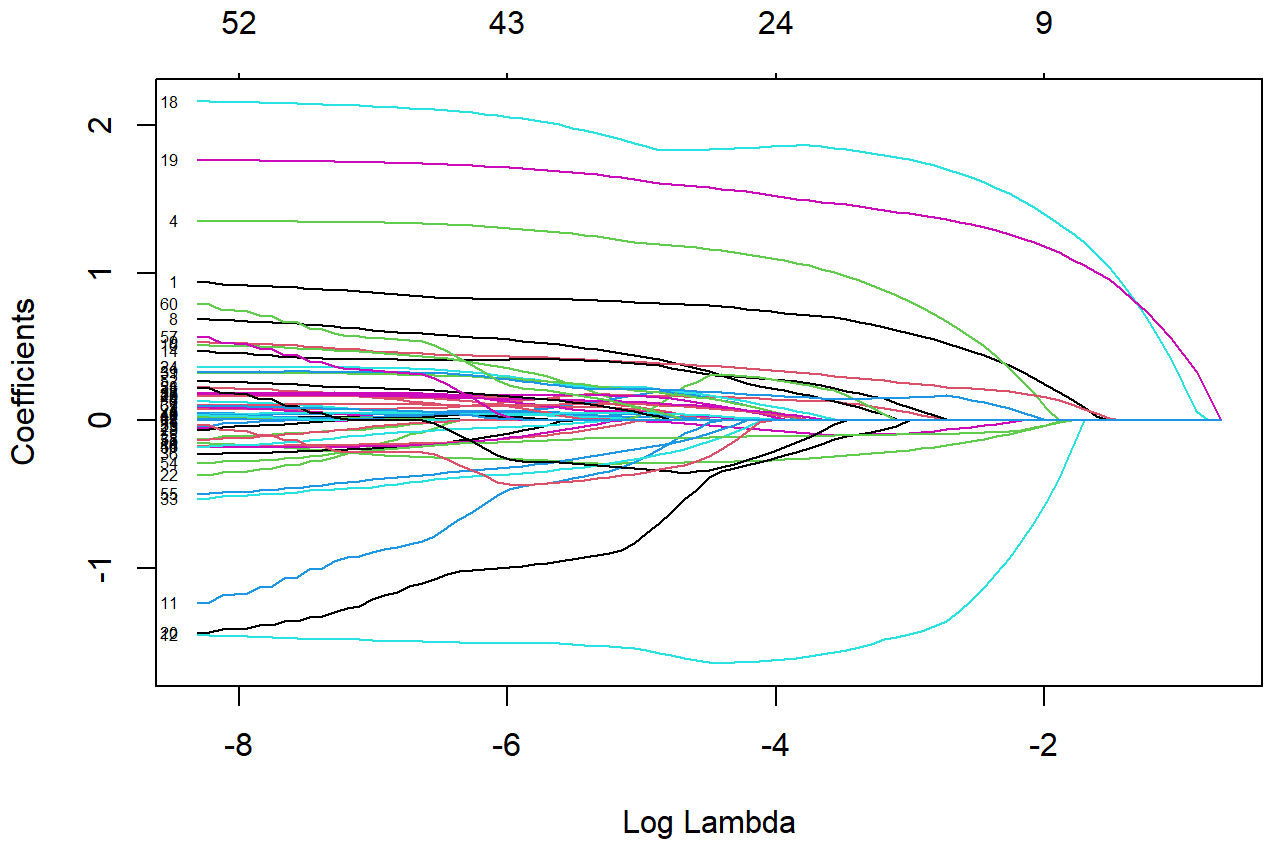
```
library(glmnet)
```

```
## Warning: package 'glmnet' was built under R version 4.4.2
```

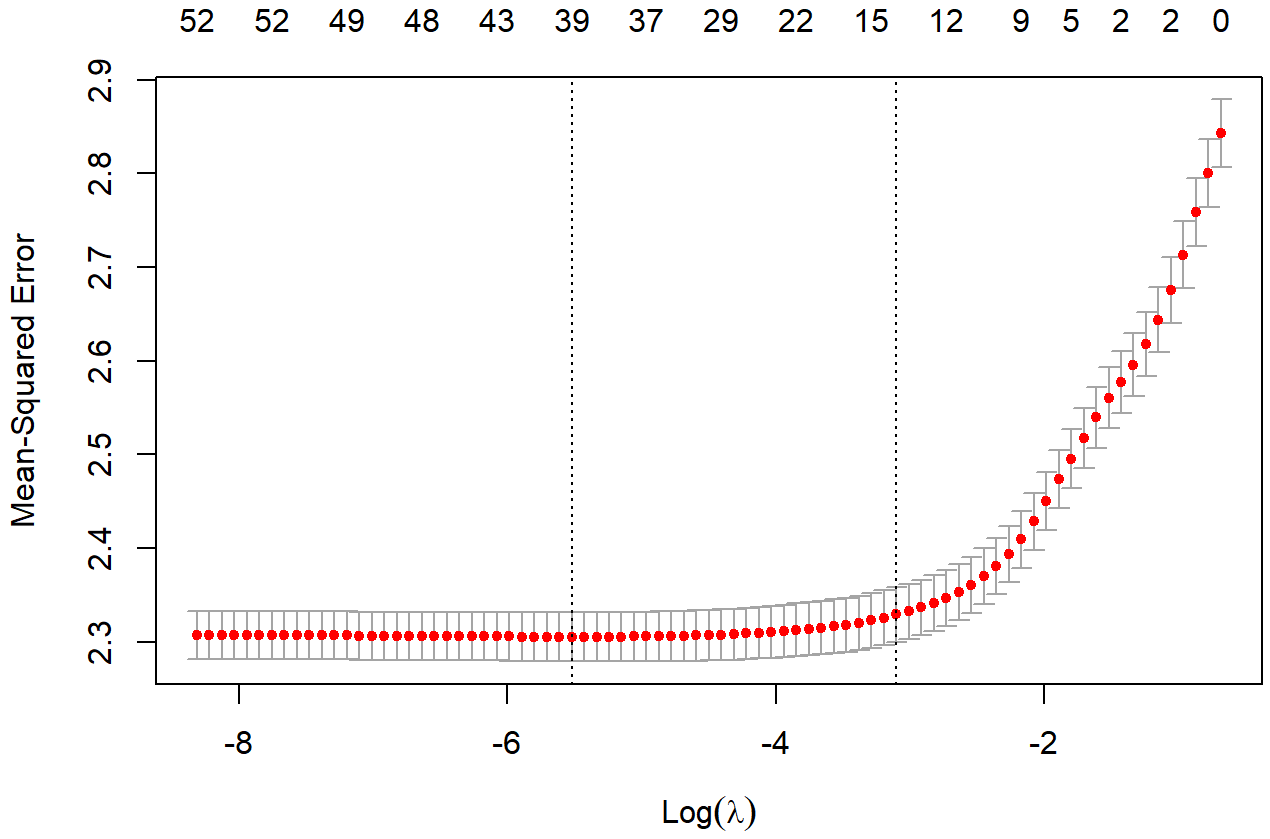
```
## Loading required package: Matrix
```

```
## Loaded glmnet 4.1-8
```

```
X = model.matrix(model_formula, data = data)[, -1]

# lasso model
lasso = glmnet(x = X, y = data$log_TOTEXP18, alpha = 1)
plot(lasso, xvar = "lambda", label = TRUE)
```




```
# cv to find optimal lambda
cv_lasso = cv.glmnet(x = X, y = data$log_TOTEXP18, alpha = 1, nfolds = 10)
plot(cv_lasso)
```




```
best_lambda = cv_lasso$lambda.min
cat("Best lambda from cross-validation:", best_lambda, "\n")
```

```
## Best lambda from cross-validation: 0.00400272
```

```
# use optimal lambda to fit best model
best_lasso = glmnet(x = X, y = data$log_TOTEXP18, alpha = 1, lambda = best_lambda)
coefficients_best_lasso = coef(best_lasso)
print(coefficients_best_lasso)
```

```
## 62 x 1 sparse Matrix of class "dgCMatrix"
##                                                      s0
## (Intercept)                                  7.5194231528
## MNHLTH42FAIR                                 0.8197911964
## MNHLTH42GOOD                                 0.1725829549
## MNHLTH42INVALID                              .
## MNHLTH42POOR                                 1.2667233038
## MNHLTH42VERY GOOD                            0.0403719872
## RACETHXBLACK ONLY                            0.0307027836
## RACETHXHISPANIC                              .
## RACETHXOTHER OR MULTIPLE                     0.5068335078
## RACETHXWHITE ONLY                            0.4199159745
## SEXMALE                                     -0.2765963034
## NO_INC1                                     -0.3921935415
## bs(ADBMI42, degree = 4)1                    -1.6029960736
## bs(ADBMI42, degree = 4)2                     .
## bs(ADBMI42, degree = 4)3                     0.3460983496
## bs(ADBMI42, degree = 4)4                     0.0993183580
## bs(AGE42X, degree = 4)1                      0.2552658983
## bs(AGE42X, degree = 4)2                      0.1014457386
## bs(AGE42X, degree = 4)3                      1.9942629548
## bs(AGE42X, degree = 4)4                      1.6837310491
## bs(boxcox_FAMINC18, degree = 3)1            -0.9418546330
## bs(boxcox_FAMINC18, degree = 3)2             0.0912136047
## bs(boxcox_FAMINC18, degree = 3)3             .
## MNHLTH42FAIR:RACETHXBLACK ONLY               0.0507873675
## MNHLTH42GOOD:RACETHXBLACK ONLY               0.2409113824
## MNHLTH42INVALID:RACETHXBLACK ONLY            .
## MNHLTH42POOR:RACETHXBLACK ONLY               .
## MNHLTH42VERY GOOD:RACETHXBLACK ONLY          0.1684019325
## MNHLTH42FAIR:RACETHXHISPANIC                 0.0005834217
## MNHLTH42GOOD:RACETHXHISPANIC                 0.0239758147
## MNHLTH42INVALID:RACETHXHISPANIC              .
## MNHLTH42POOR:RACETHXHISPANIC                 0.2544373459
## MNHLTH42VERY GOOD:RACETHXHISPANIC            .
## MNHLTH42FAIR:RACETHXOTHER OR MULTIPLE       -0.3250564148
## MNHLTH42GOOD:RACETHXOTHER OR MULTIPLE        0.0752525446
## MNHLTH42INVALID:RACETHXOTHER OR MULTIPLE     .
## MNHLTH42POOR:RACETHXOTHER OR MULTIPLE        .
## MNHLTH42VERY GOOD:RACETHXOTHER OR MULTIPLE   0.1072200695
## MNHLTH42FAIR:RACETHXWHITE ONLY               .
## MNHLTH42GOOD:RACETHXWHITE ONLY               0.2264406047
## MNHLTH42INVALID:RACETHXWHITE ONLY            .
## MNHLTH42POOR:RACETHXWHITE ONLY               .
## MNHLTH42VERY GOOD:RACETHXWHITE ONLY          0.0482764569
## MNHLTH42FAIR:SEXMALE                         0.1380564852
## MNHLTH42GOOD:SEXMALE                         .
## MNHLTH42INVALID:SEXMALE                      .
## MNHLTH42POOR:SEXMALE                        -0.0764411182
## MNHLTH42VERY GOOD:SEXMALE                    .
## MNHLTH42FAIR:NO_INC1                         .
## MNHLTH42GOOD:NO_INC1                         .
```

```
## MNHLTH42INVALID:NO_INC1                    .
## MNHLTH42POOR:NO_INC1                      -0.0543075334
## MNHLTH42VERY GOOD:NO_INC1                  0.1269345588
## RACETHXBLACK ONLY:SEXMALE                  .
## RACETHXHISPANIC:SEXMALE                   -0.1282326266
## RACETHXOTHER OR MULTIPLE:SEXMALE          -0.2657238557
## RACETHXWHITE ONLY:SEXMALE                 -0.0220612748
## RACETHXBLACK ONLY:NO_INC1                  .
## RACETHXHISPANIC:NO_INC1                   -0.2906400232
## RACETHXOTHER OR MULTIPLE:NO_INC1          -0.4104835460
## RACETHXWHITE ONLY:NO_INC1                  0.1777055987
## SEXMALE:NO_INC1                            .
```

```
summary(best_lasso)
```

```
##           Length Class     Mode
## a0         1     -none-    numeric
## beta      61     dgCMatrix S4
## df         1     -none-    numeric
## dim        2     -none-    numeric
## lambda     1     -none-    numeric
## dev.ratio  1     -none-    numeric
## nulldev    1     -none-    numeric
## npasses    1     -none-    numeric
## jerr       1     -none-    numeric
## offset     1     -none-    logical
## call       5     -none-    call
## nobs       1     -none-    numeric
```

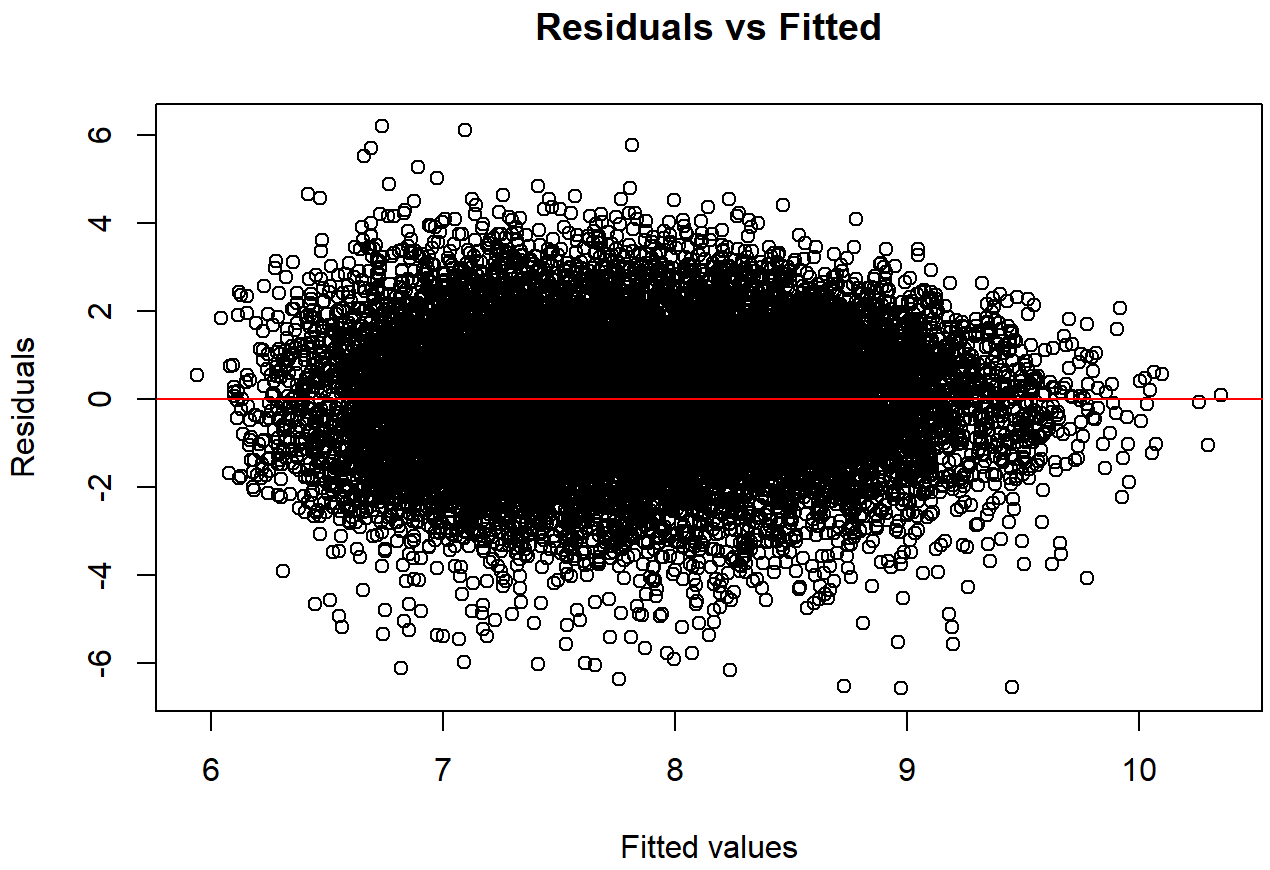
```
# num non zero coeff
non_zero_coeffs = sum(coefficients_best_lasso != 0)
cat("\nNumber of non-zero coefficients:", non_zero_coeffs, "\n")
```

```
##
## Number of non-zero coefficients: 40
```

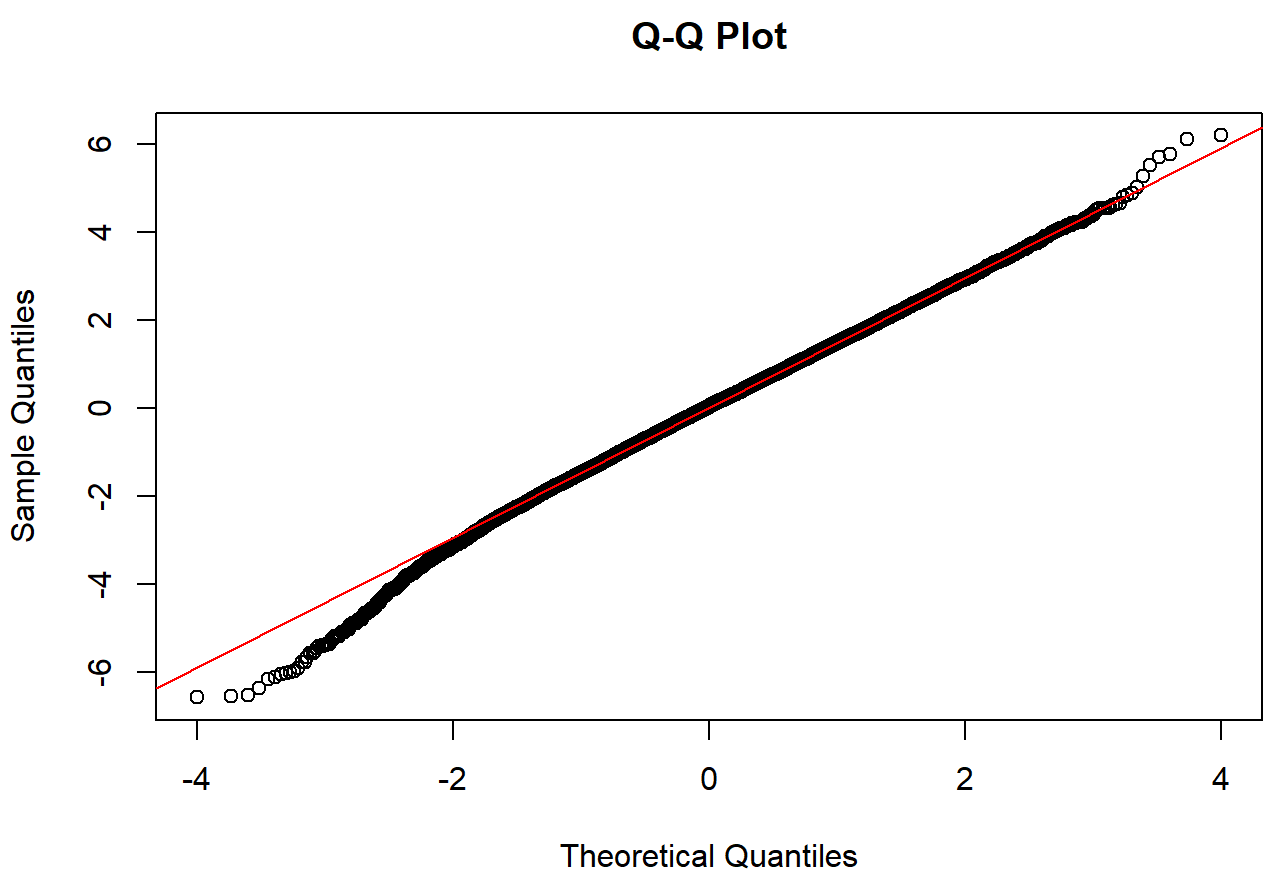
```
# DIAGNOSTICS:
# Predict using the best Lasso model
y_pred = predict(best_lasso, X)

# Compute residuals
residuals = data$log_TOTEXP18 - y_pred

# Compute R-squared (1 - RSS/TSS)
rss = sum(residuals^2)
tss = sum((data$log_TOTEXP18 - mean(data$log_TOTEXP18))^2)
r_squared = 1 - rss / tss
cat("\nR-squared:", r_squared, "\n")
```

```
##
## R-squared: 0.1950217
```

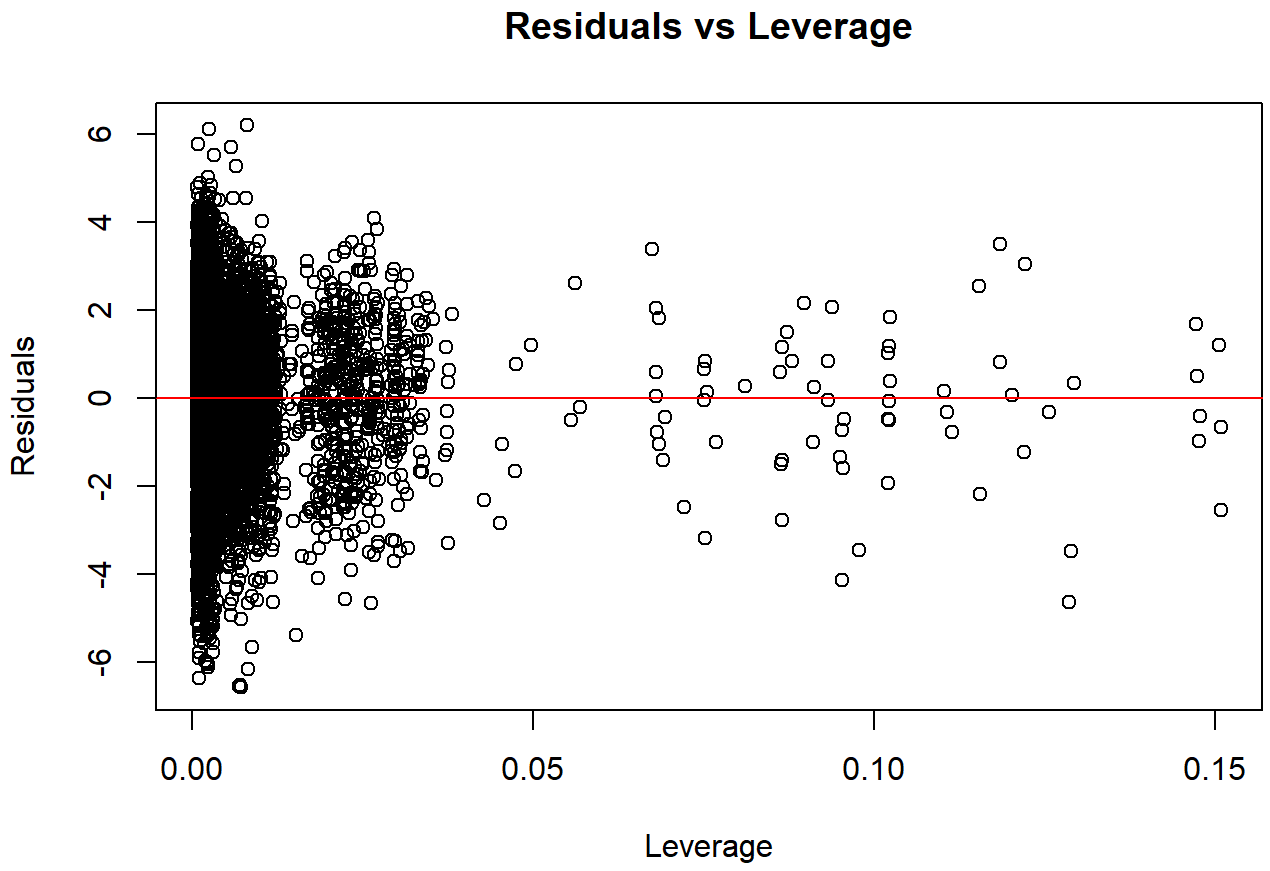
```
# Plot 1: Residuals vs Fitted Values
plot(y_pred, residuals, xlab = "Fitted values", ylab = "Residuals", main = "Residuals vs Fitte
d")
abline(h = 0, col = "red")
```




```
# Plot 2: Q-Q plot of residuals
qqnorm(residuals, main = "Q-Q Plot")
qqline(residuals, col = "red")
```




```
# Plot 3: Residuals vs Leverage plot
leverage = hatvalues(lm(data$log_TOTEXP18 ~ X))

plot(leverage, residuals, xlab = "Leverage", ylab = "Residuals", main = "Residuals vs Leverage")
abline(h = 0, col = "red")
```



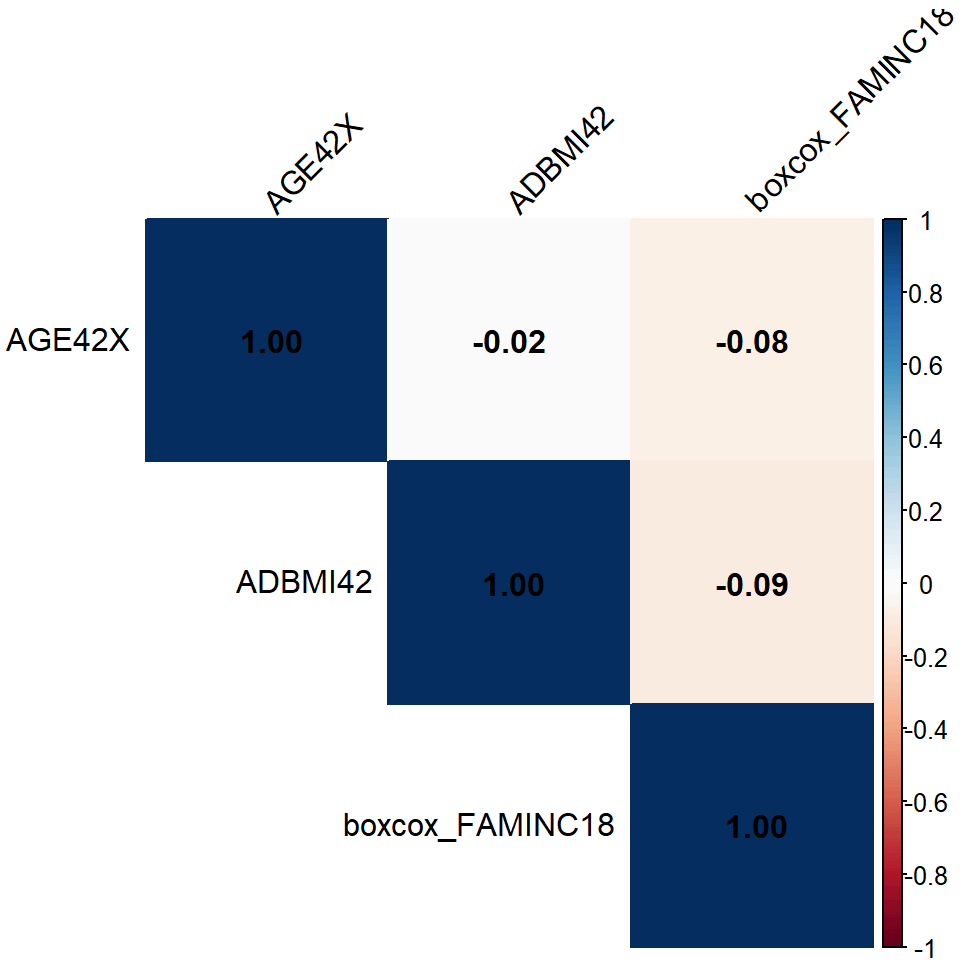
Problem 3:

The forward-backward stepwise (AIC) selected model explains almost the exact same amount of variance as the LASSO selected model but with only 29 predictors instead of 41. For this reason, I will choose the stepwise model and perform diagnostics on it.

Independence assumption:

Satisfied. The 3 continuous variables are not correlated.

```
# correlation matrix
cor_matrix = cor(data[, c("AGE42X", "ADBMI42", "boxcox_FAMINC18")], use = "complete.obs")
corrplot(cor_matrix, method = "color", type = "upper", tl.col = "black", tl.srt = 45, addCoef.co
l = "black")
```

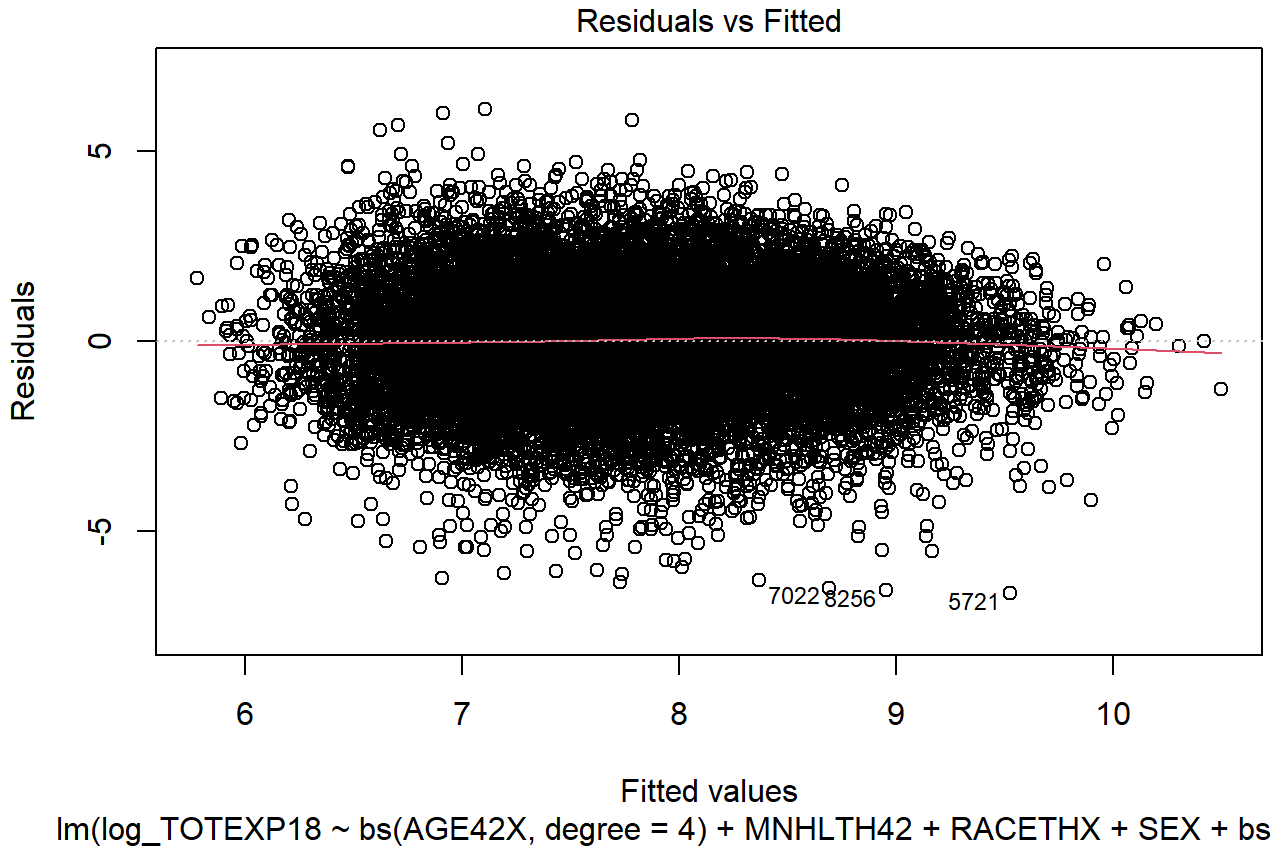


Linearity and constant variance of residuals assumptions:

Linearity is satisfied. The resdiuals vs fitted plot does not show any non-linear pattern.

The residuals also have mostly constant variance but there is a slight football shape. Also a trend of decreasing variance as fitted value increases.

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



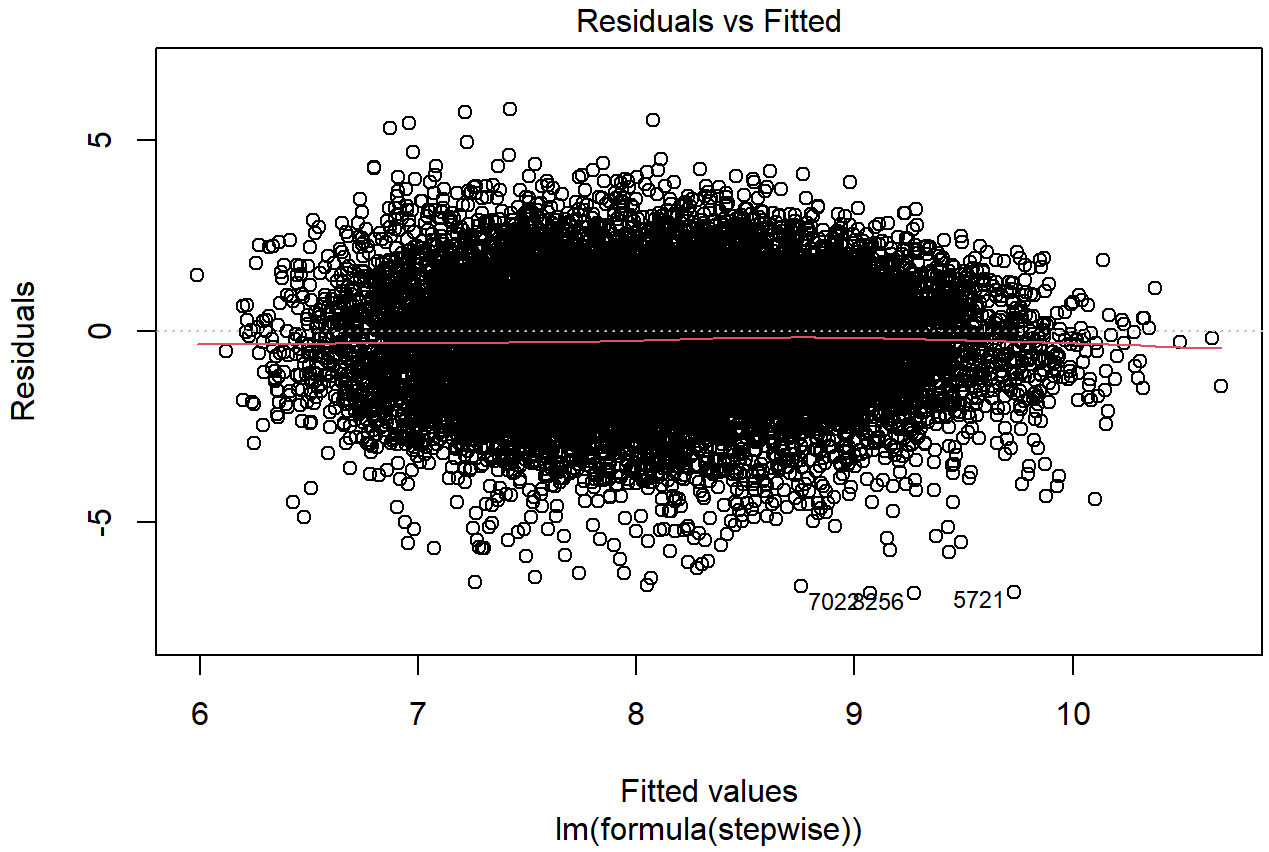
I will try a weighted least squares model to resolve the slight heteroscedasticity.

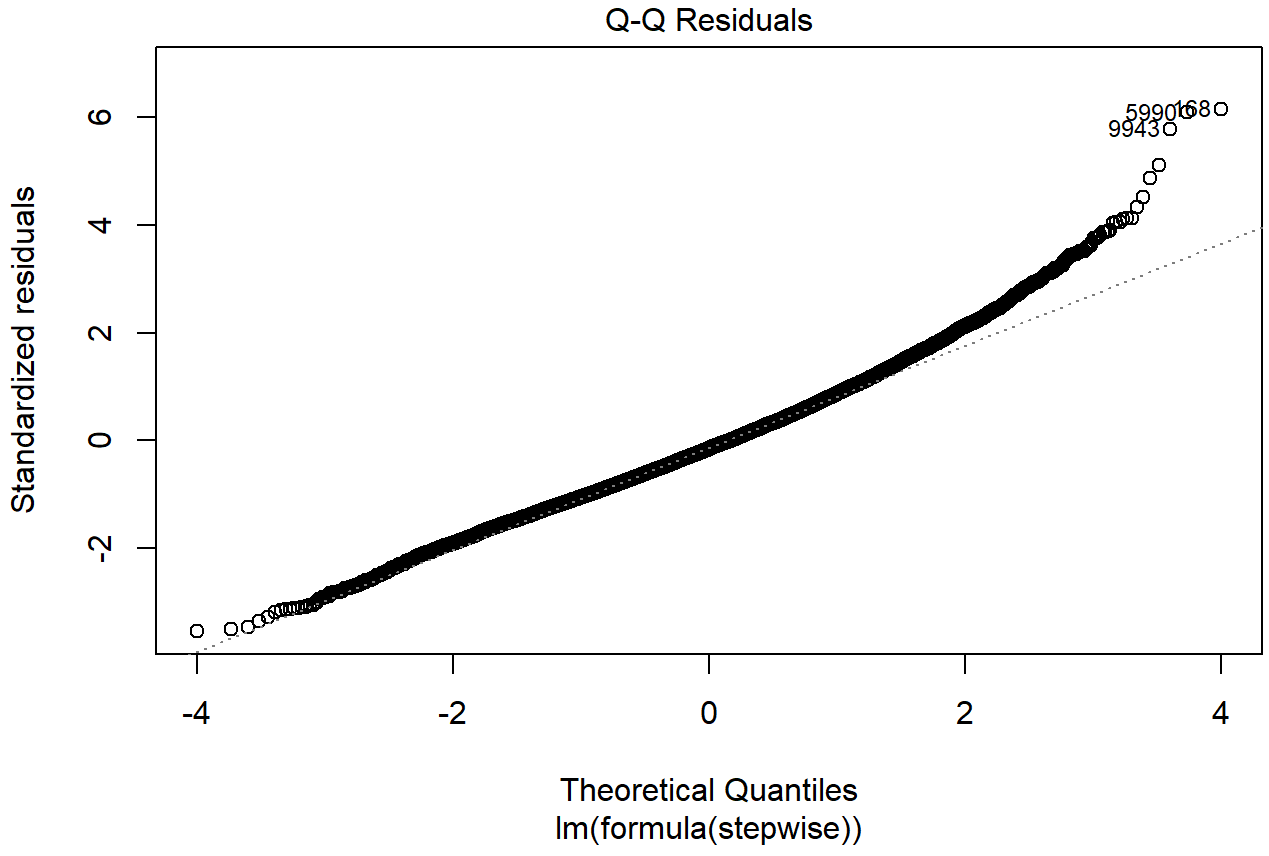
I tried several methods and neither improved the heteroscedasticity. They seemed to make everything else worse though.

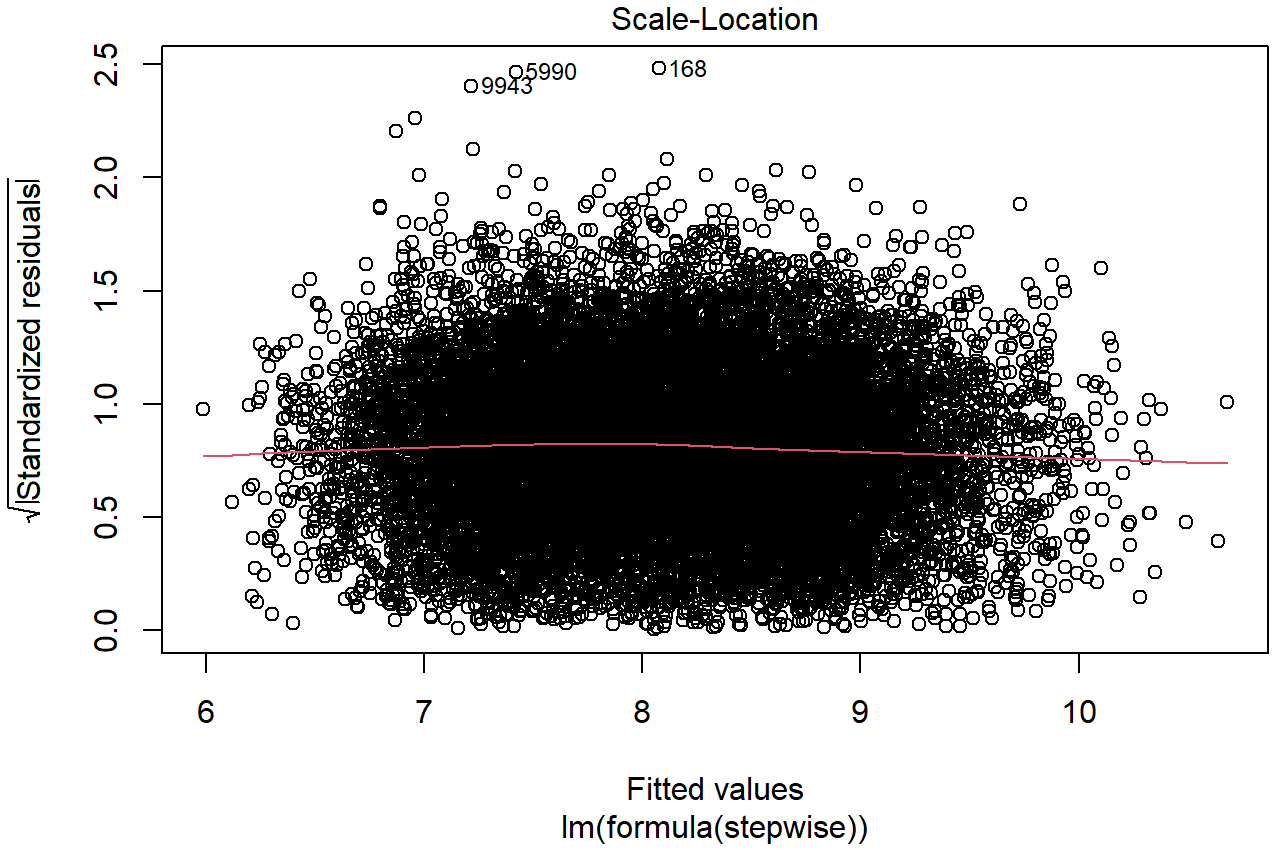
```
residuals = resid(stepwise)
variance_model = lm(I(residuals^2) ~ data$log_TOTEXP18)
fitted_variance = predict(variance_model)
weights = 1 / fitted_variance

# weights = 1 / fitted(stepwise)^2

wls_model = lm(formula(stepwise), data = data, weights = weights)
summary(wls_model)
```

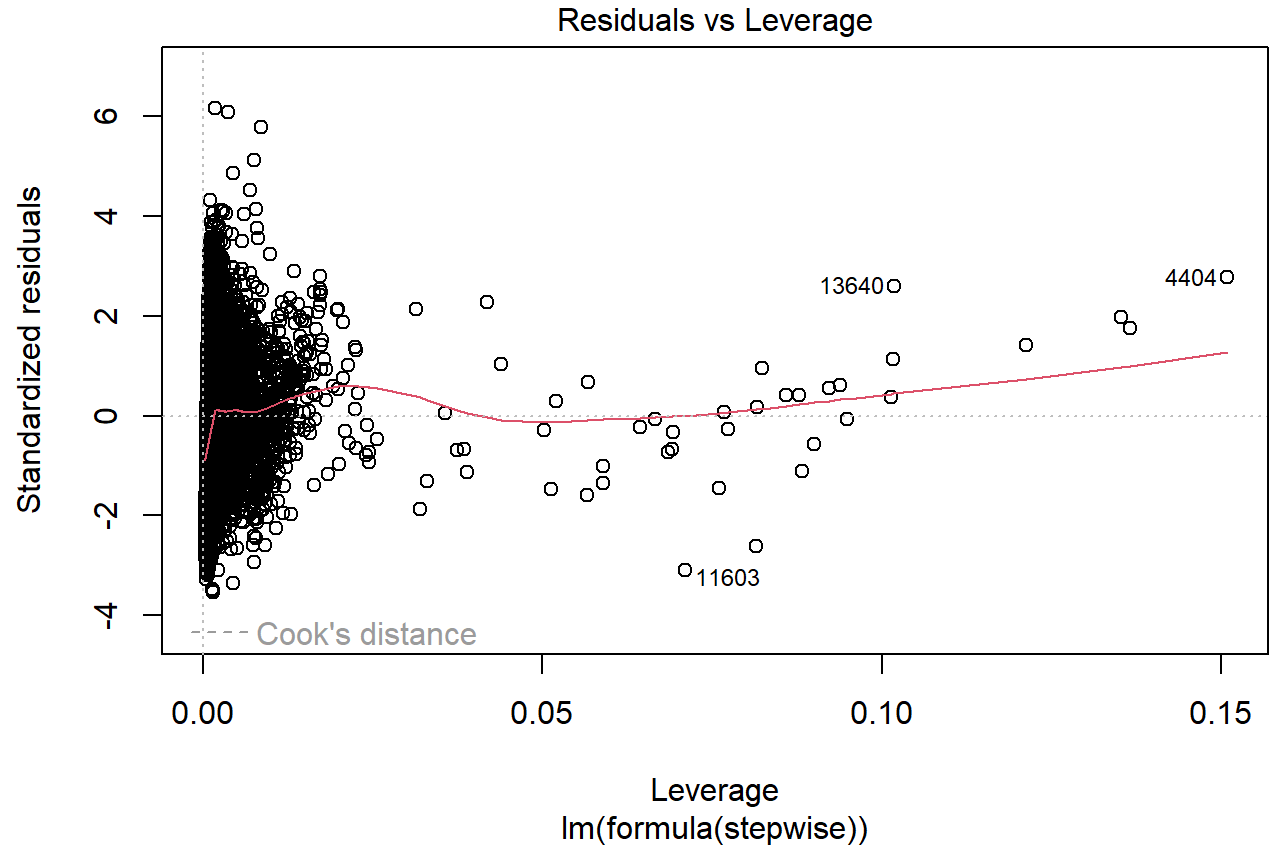
```
##
## Call:
## lm(formula = formula(stepwise), data = data, weights = weights)
##
## Weighted Residuals:
##     Min      1Q  Median      3Q     Max
## -3.6068 -0.7845 -0.1526  0.5189  6.2711
##
## Coefficients:
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                       7.69940    0.45233  17.022  < 2e-16 ***
## bs(AGE42X, degree = 4)1           0.47624    0.20990   2.269 0.023285 *
## bs(AGE42X, degree = 4)2           0.28899    0.18340   1.576 0.115103
## bs(AGE42X, degree = 4)3           2.01852    0.17622  11.455  < 2e-16 ***
## bs(AGE42X, degree = 4)4           1.74308    0.07976  21.853  < 2e-16 ***
## MNHLTH42FAIR                      0.90703    0.04722  19.207  < 2e-16 ***
## MNHLTH42GOOD                      0.39262    0.03271  12.003  < 2e-16 ***
## MNHLTH42POOR                      1.29946    0.08818  14.736  < 2e-16 ***
## MNHLTH42VERY GOOD                 0.11402    0.03097   3.681 0.000233 ***
## RACETHXBLACK ONLY                 0.36759    0.08967   4.099 4.16e-05 ***
## RACETHXHISPANIC                   0.23649    0.08763   2.699 0.006967 **
## RACETHXOTHER OR MULTIPLE          0.78202    0.11792   6.632 3.42e-11 ***
## RACETHXWHITE ONLY                 0.67418    0.08034   8.392  < 2e-16 ***
## SEXMALE                          -0.02627    0.11599  -0.227 0.820803
## bs(ADBMI42, degree = 4)1         -1.42523    0.93734  -1.521 0.128403
## bs(ADBMI42, degree = 4)2         -0.18771    0.45368  -0.414 0.679070
## bs(ADBMI42, degree = 4)3          0.50017    0.91665   0.546 0.585313
## bs(ADBMI42, degree = 4)4          0.19636    0.50423   0.389 0.696973
## bs(boxcox_FAMINC18, degree = 3)1 -1.66603    0.40825  -4.081 4.51e-05 ***
## bs(boxcox_FAMINC18, degree = 3)2  0.10235    0.18214   0.562 0.574190
## bs(boxcox_FAMINC18, degree = 3)3 -0.57693    0.37173  -1.552 0.120679
## NO_INC1                          -1.50957    0.48564  -3.108 0.001884 **
## RACETHXBLACK ONLY:SEXMALE        -0.16338    0.13450  -1.215 0.224495
## RACETHXHISPANIC:SEXMALE          -0.37048    0.13193  -2.808 0.004989 **
## RACETHXOTHER OR MULTIPLE:SEXMALE -0.61475    0.18169  -3.384 0.000717 ***
## RACETHXWHITE ONLY:SEXMALE        -0.23112    0.11987  -1.928 0.053871 .
## RACETHXBLACK ONLY:NO_INC1         0.88810    0.47956   1.852 0.064061 .
## RACETHXHISPANIC:NO_INC1           0.55156    0.48279   1.142 0.253281
## RACETHXOTHER OR MULTIPLE:NO_INC1  0.62457    0.67018   0.932 0.351376
## RACETHXWHITE ONLY:NO_INC1         1.08176    0.47244   2.290 0.022051 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.019 on 15694 degrees of freedom
## Multiple R-squared:  0.1868, Adjusted R-squared:  0.1853
## F-statistic: 124.3 on 29 and 15694 DF,  p-value: < 2.2e-16
```

```
plot(wls_model)
```


Residuals vs Fitted
Residuals
5
0
-5
6
7
8
9
10
5721
Fitted values
lm(formula(stepwise))


Q-Q Residuals
Standardized residuals
6
4
2
0
-2
-4
-2
0
2
4
99430
Theoretical Quantiles
lm(formula(stepwise))





I

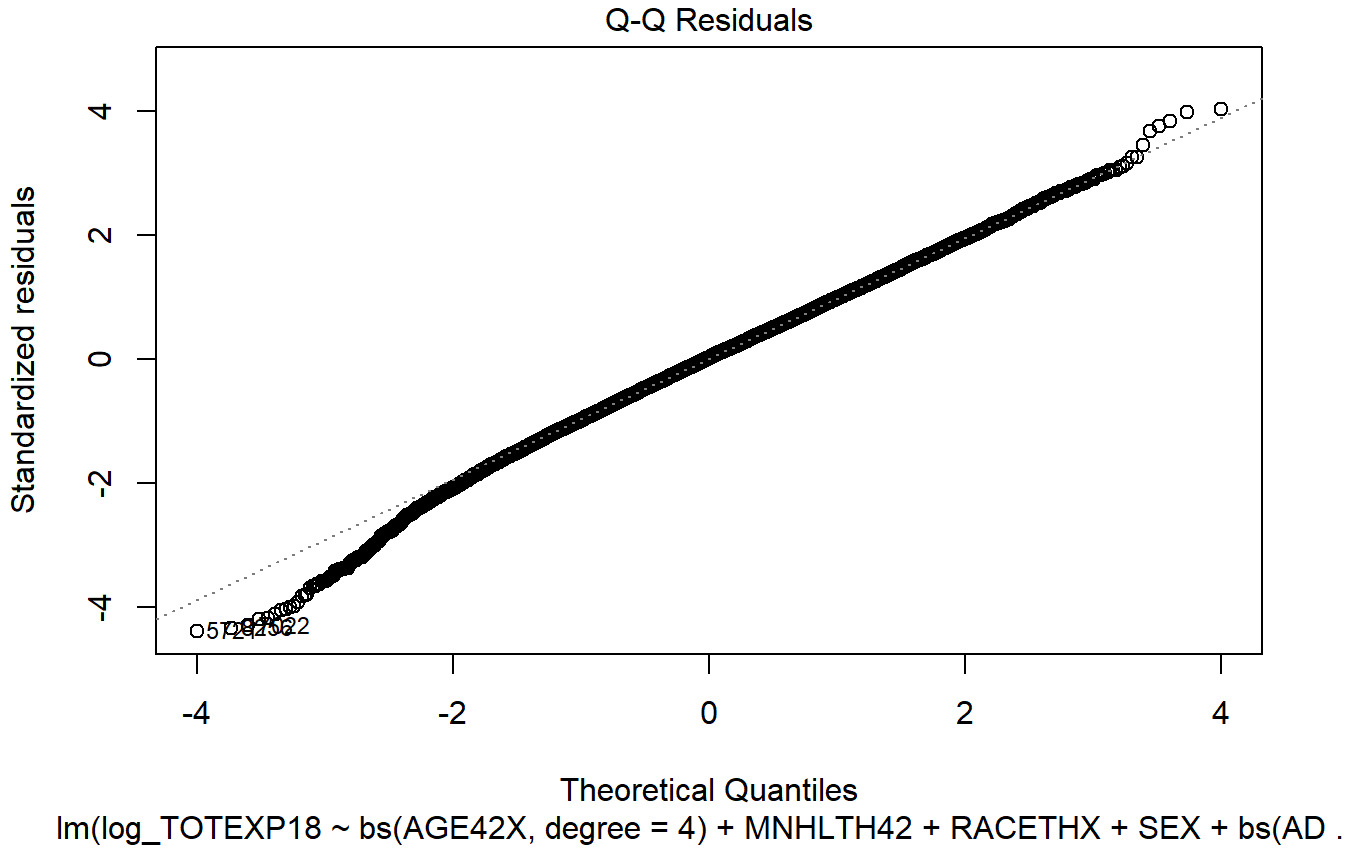
am willing to accept the level of heteroscedasticity in the stepwise model. It does not seem extreme enough to me

to be a problem.

Normality of residuals assumption:

Satisfied.

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



Multicollinearity:

I got rid of the b-spline transformations and interaction terms. The variance inflation factors (VIFs) are all close to 1 which means no collinearity.

```
library(car)
```

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

```
# stepwise formula: log_TOTEXP18 ~ bs(AGE42X, degree = 4) + MNHLTH42 + RACETHX + SEX + bs(ADBMI4
2, degree = 4) + bs(boxcox_FAMINC18, degree = 3) + NO_INC + RACETHX:SEX + RACETHX:NO_INC

linear_model = lm(log_TOTEXP18 ~ AGE42X + MNHLTH42 + RACETHX + SEX + ADBMI42 + boxcox_FAMINC18 +
NO_INC, data=data)
vif(linear_model)
```

```
##                     GVIF Df GVIF^(1/(2*Df))
## AGE42X          1.042501  1        1.021030
## MNHLTH42        1.105761  4        1.012646
## RACETHX         1.131593  4        1.015573
## SEX             1.012918  1        1.006438
## ADBMI42         1.046438  1        1.022955
## boxcox_FAMINC18 1.362076  1        1.167080
## NO_INC          1.192080  1        1.091824
```

Problem 4:

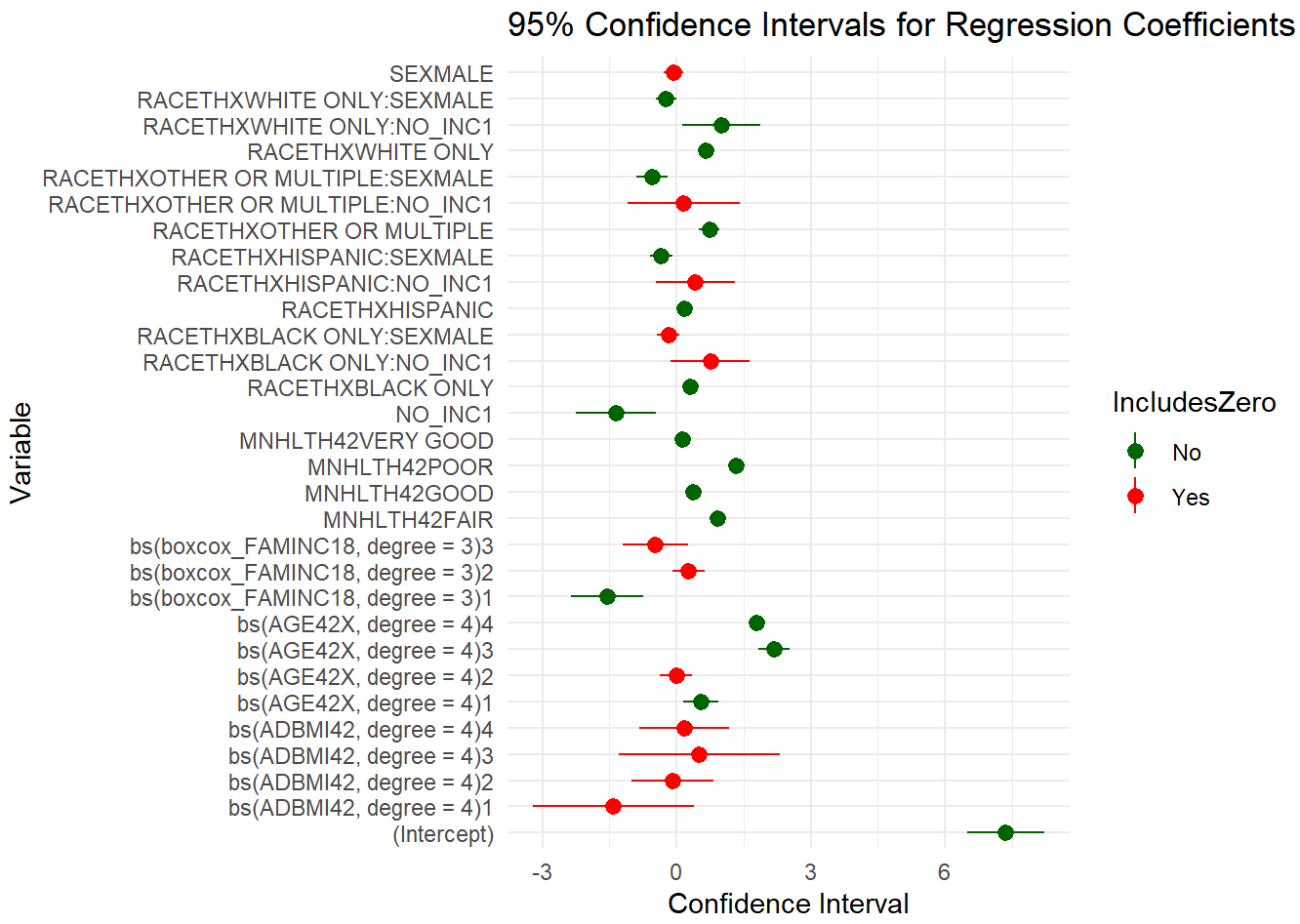
95% confidence intervals for coefficients.

Looks like a good chuck of the confidence intervals include 0.

```
conf_intervals = confint(stepwise, level = 0.95)
print(conf_intervals)
```

```
##                                       2.5 %       97.5 %
## (Intercept)                        6.491689857  8.229443464
## bs(AGE42X, degree = 4)1            0.146668481  0.945296092
## bs(AGE42X, degree = 4)2           -0.374536073  0.348801792
## bs(AGE42X, degree = 4)3            1.834782365  2.532129379
## bs(AGE42X, degree = 4)4            1.620493765  1.931710871
## MNHLTH42FAIR                       0.809582836  1.000698195
## MNHLTH42GOOD                       0.310838975  0.438894666
## MNHLTH42POOR                       1.142607206  1.510701410
## MNHLTH42VERY GOOD                  0.060064235  0.180107234
## RACETHXBLACK ONLY                  0.140405538  0.482696662
## RACETHXHISPANIC                    0.001675799  0.334561157
## RACETHXOTHER OR MULTIPLE           0.504978921  0.965580226
## RACETHXWHITE ONLY                  0.499979154  0.805117477
## SEXMALE                           -0.292938649  0.146063810
## bs(ADBMI42, degree = 4)1          -3.216720595  0.392511205
## bs(ADBMI42, degree = 4)2          -1.006092692  0.817635734
## bs(ADBMI42, degree = 4)3          -1.298404263  2.313632098
## bs(ADBMI42, degree = 4)4          -0.836368260  1.175881409
## bs(boxcox_FAMINC18, degree = 3)1 -2.353244129 -0.749061011
## bs(boxcox_FAMINC18, degree = 3)2 -0.095735491  0.618488232
## bs(boxcox_FAMINC18, degree = 3)3 -1.203024455  0.253726553
## NO_INC1                          -2.261346928 -0.464723373
## RACETHXBLACK ONLY:SEXMALE        -0.441495518  0.071172956
## RACETHXHISPANIC:SEXMALE          -0.592269009 -0.092538335
## RACETHXOTHER OR MULTIPLE:SEXMALE -0.902787329 -0.202612313
## RACETHXWHITE ONLY:SEXMALE        -0.461162421 -0.006079689
## RACETHXBLACK ONLY:NO_INC1        -0.133468569  1.639667986
## RACETHXHISPANIC:NO_INC1          -0.471723640  1.308416768
## RACETHXOTHER OR MULTIPLE:NO_INC1 -1.103731506  1.421276062
## RACETHXWHITE ONLY:NO_INC1         0.120770538  1.866869191
```

```
# Convert to data frame for plotting
conf_intervals_df <- as.data.frame(conf_intervals)
conf_intervals_df$Variable <- rownames(conf_intervals_df)  # Add variable names as a column

# Create a new column to indicate if the confidence interval includes 0
conf_intervals_df$IncludesZero <- ifelse(conf_intervals_df$`2.5 %` > 0 | conf_intervals_df$`97.5
%` < 0, "No", "Yes")

# Plot the confidence intervals
ggplot(conf_intervals_df, aes(x = Variable, ymin = `2.5 %`, ymax = `97.5 %`, color = IncludesZer
o)) +
  geom_pointrange(aes(y = ( `2.5 %` + `97.5 %` ) / 2)) +  # Use midpoint for 'y'
  coord_flip() +  # Flip coordinates to make the plot horizontal
  theme_minimal() +
  labs(
    title = "95% Confidence Intervals for Regression Coefficients",
    x = "Variable",
    y = "Confidence Interval"
  ) +
  scale_color_manual(values = c("Yes" = "red", "No" = "darkgreen"))
```



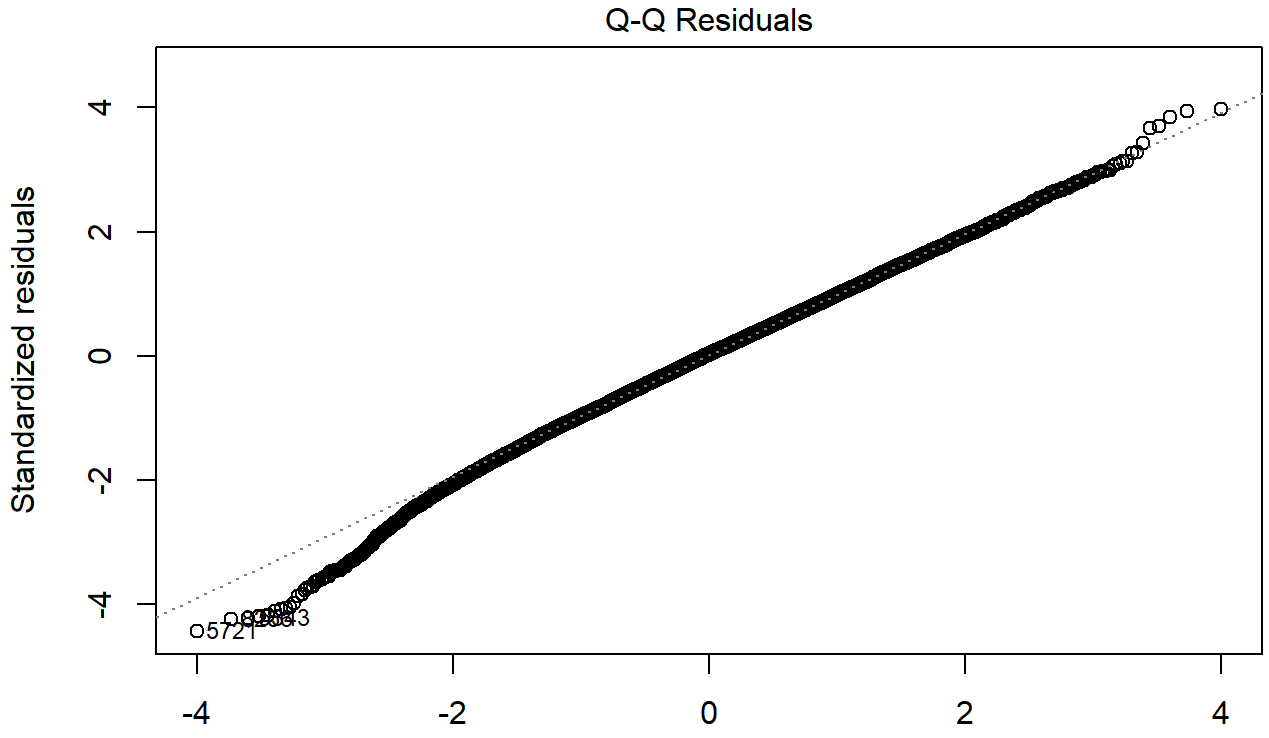
I will also fit a simple model just to see how it performs.

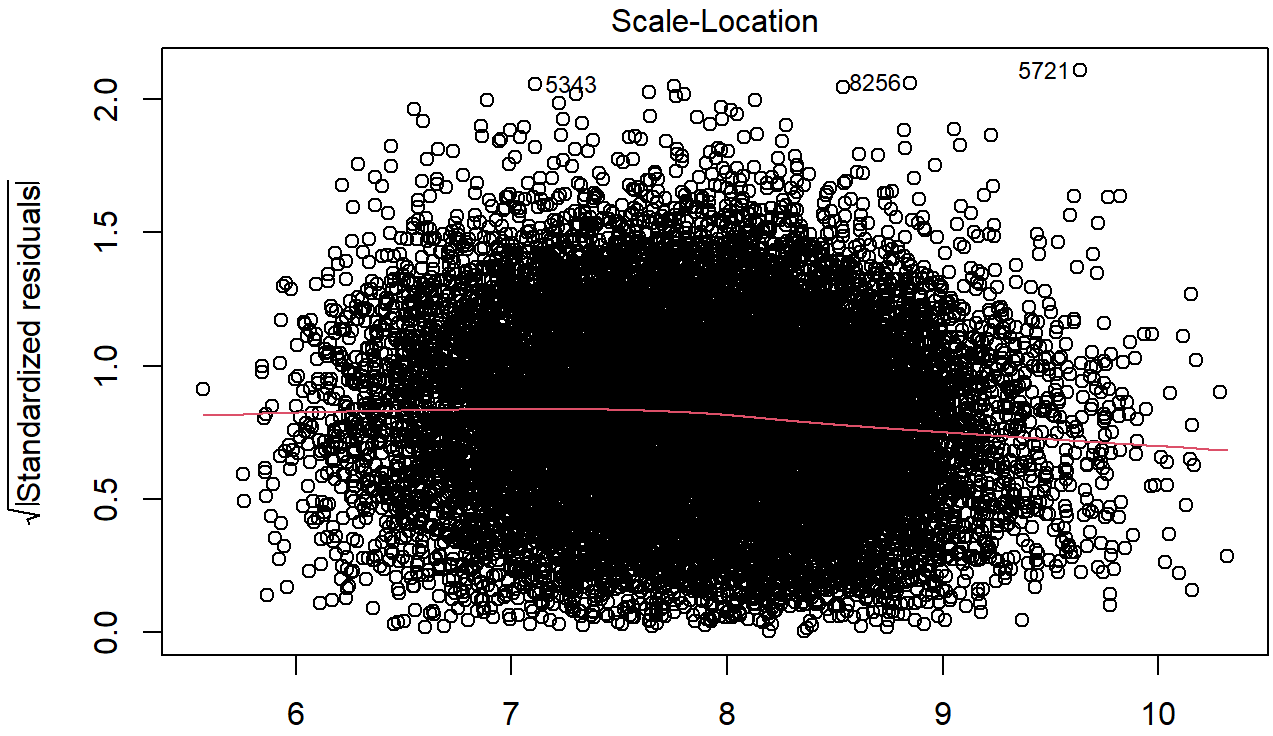
```
simple_model = lm(log_TOTEXP18 ~ AGE42X + ADBMI42 + MNHLTH42 + RACETHX + SEX + boxcox_FAMINC18 +
NO_INC, data=data)
summary(simple_model)
```

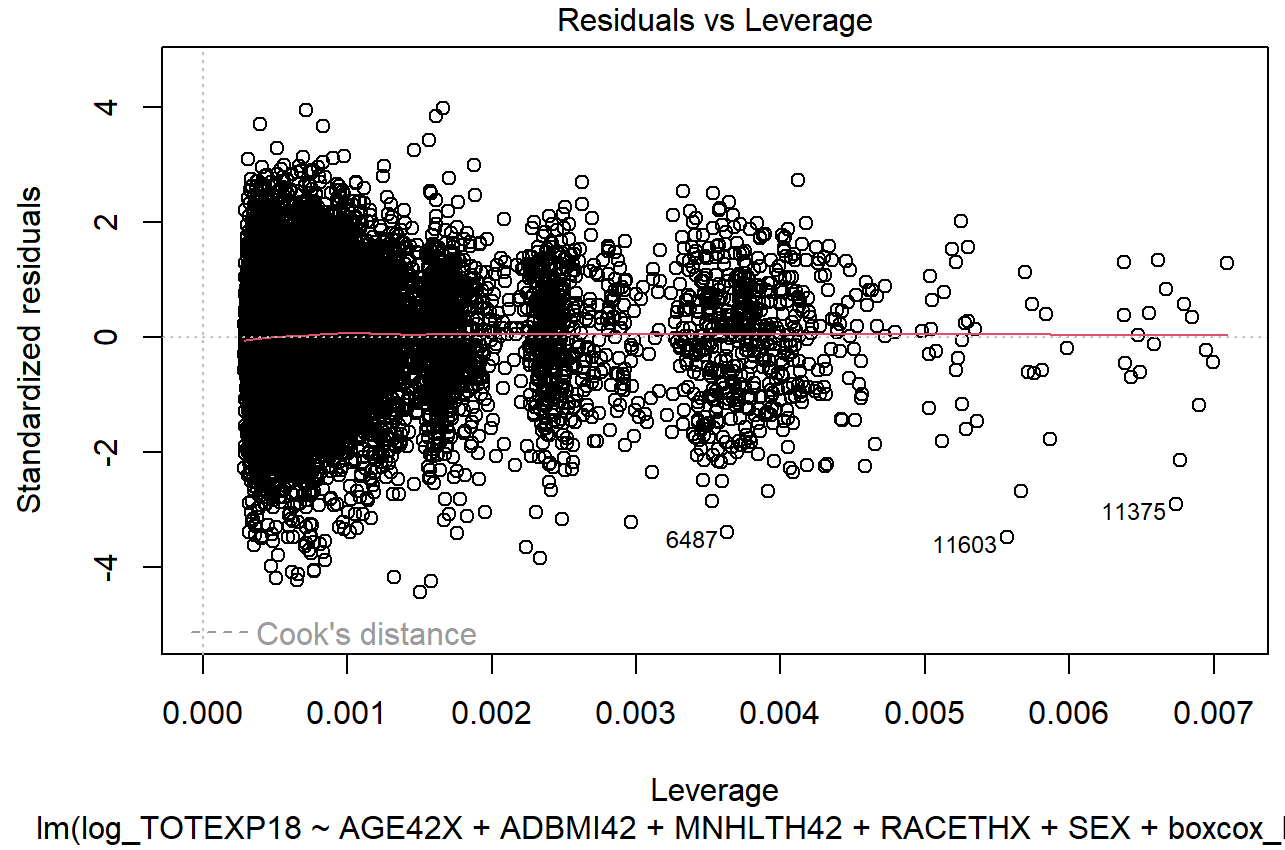
```
##
## Call:
## lm(formula = log_TOTEXP18 ~ AGE42X + ADBMI42 + MNHLTH42 + RACETHX +
##     SEX + boxcox_FAMINC18 + NO_INC, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.7450 -0.9841  0.0423  1.0168  6.0460
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                5.0269769  0.0934662  53.784  < 2e-16 ***
## AGE42X                     0.0305724  0.0006848  44.647  < 2e-16 ***
## ADBMI42                    0.0206268  0.0017402  11.853  < 2e-16 ***
## MNHLTH42FAIR               0.9107021  0.0487434  18.684  < 2e-16 ***
## MNHLTH42GOOD               0.3582367  0.0327063  10.953  < 2e-16 ***
## MNHLTH42POOR               1.3140116  0.0939775  13.982  < 2e-16 ***
## MNHLTH42VERY GOOD          0.1082867  0.0306654   3.531 0.000415 ***
## RACETHXBLACK ONLY          0.2429771  0.0662492   3.668 0.000246 ***
## RACETHXHISPANIC            0.0149461  0.0640367   0.233 0.815455
## RACETHXOTHER OR MULTIPLE   0.5121827  0.0892229   5.740 9.61e-09 ***
## RACETHXWHITE ONLY          0.5723745  0.0582530   9.826  < 2e-16 ***
## SEXMALE                   -0.3249948  0.0245677 -13.229  < 2e-16 ***
## boxcox_FAMINC18            0.0009672  0.0002110   4.585 4.58e-06 ***
## NO_INC1                    0.1072883  0.0907089   1.183 0.236916
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.52 on 15710 degrees of freedom
## Multiple R-squared:  0.1887, Adjusted R-squared:  0.188
## F-statistic:   281 on 13 and 15710 DF,  p-value: < 2.2e-16
```

```
plot(simple_model)
```


Residuals vs Fitted
Residuals
5
0
-5
5343
8256
5721
6
7
8
9
10
Fitted values
lm(log_TOTEXP18 ~ AGE42X + ADBMI42 + MNHLTH42 + RACETHX + SEX + boxcox_FAM


Q-Q Residuals
Standardized residuals
4
2
0
-2
-4
5721
-4
-2
0
2
4
Theoretical Quantiles
lm(log_TOTEXP18 ~ AGE42X + ADBMI42 + MNHLTH42 + RACETHX + SEX + boxcox_FAM

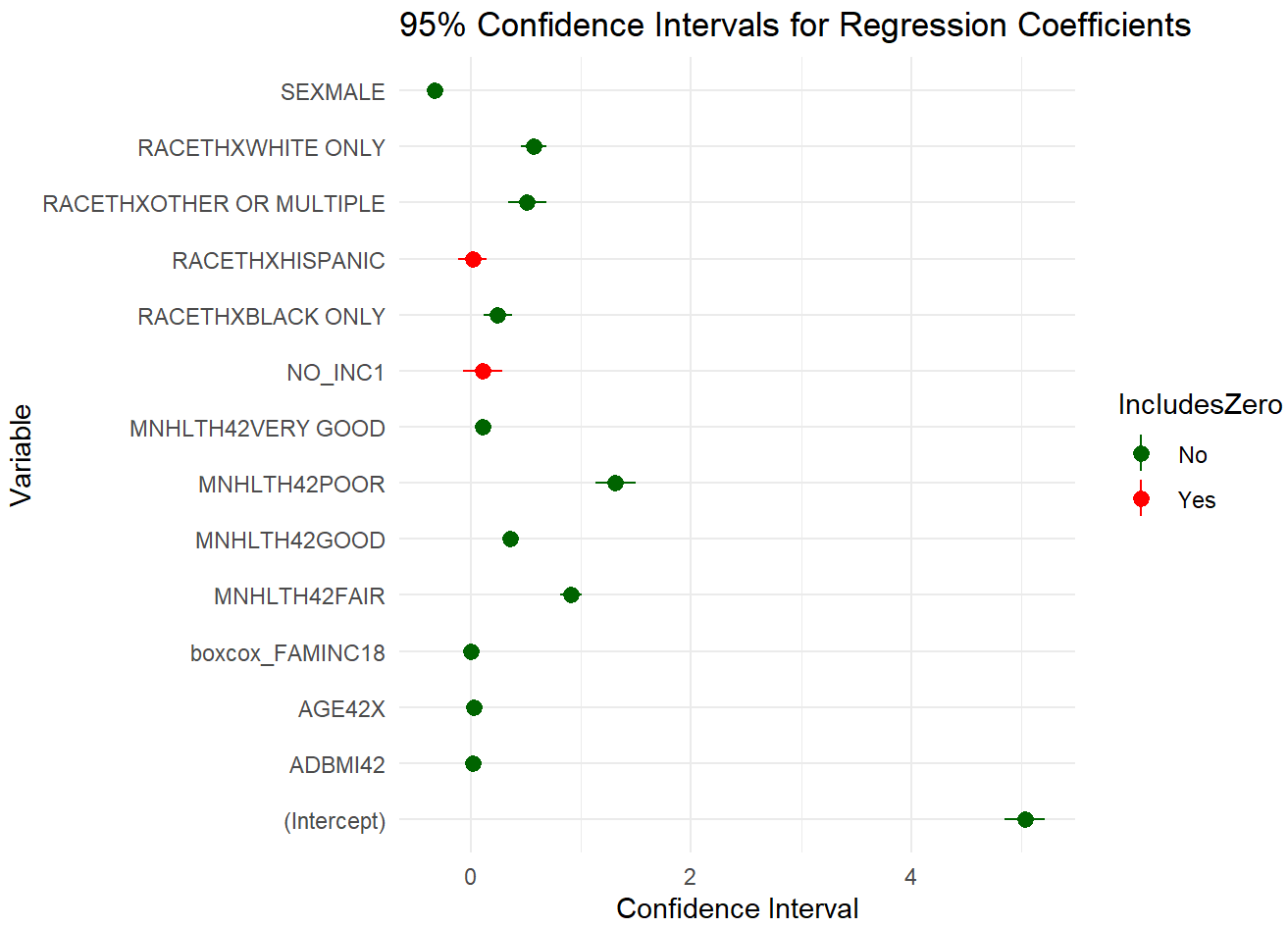

Scale-Location
5343
8256
5721
√|Standardized residuals|
0.0
0.5
1.0
1.5
2.0
6
7
8
9
10
Fitted values
lm(log_TOTEXP18 ~ AGE42X + ADBMI42 + MNHLTH42 + RACETHX + SEX + boxcox_FAM


Residuals vs Leverage
Standardized residuals
4
2
0
-2
-4
6487
11603
11375
Cook's distance
0.000
0.001
0.002
0.003
0.004
0.005
0.006
0.007
Leverage
lm(log_TOTEXP18 ~ AGE42X + ADBMI42 + MNHLTH42 + RACETHX + SEX + boxcox_FAM

```r
# conf intervals
conf_intervals = confint(simple_model, level = 0.95)
print(conf_intervals)
```

```
##                                2.5 %       97.5 %
## (Intercept)                4.843772354  5.210181466
## AGE42X                     0.029230181  0.031914593
## ADBMI42                    0.017215715  0.024037802
## MNHLTH42FAIR               0.815159298  1.006244823
## MNHLTH42GOOD               0.294128575  0.422344887
## MNHLTH42POOR               1.129804960  1.498218253
## MNHLTH42VERY GOOD          0.048178958  0.168394346
## RACETHXBLACK ONLY          0.113121051  0.372833154
## RACETHXHISPANIC           -0.110573285  0.140465430
## RACETHXOTHER OR MULTIPLE   0.337295623  0.687069788
## RACETHXWHITE ONLY          0.458191984  0.686557096
## SEXMALE                   -0.373150181 -0.276839323
## boxcox_FAMINC18            0.000553698  0.001380761
## NO_INC1                   -0.070511489  0.285088115
```

```r
# Convert to data frame for plotting
conf_intervals_df <- as.data.frame(conf_intervals)
conf_intervals_df$Variable <- rownames(conf_intervals_df)  # Add variable names as a column

# Create a new column to indicate if the confidence interval includes 0
conf_intervals_df$IncludesZero <- ifelse(conf_intervals_df$`2.5 %` > 0 | conf_intervals_df$`97.5
%` < 0, "No", "Yes")

# Plot the confidence intervals
ggplot(conf_intervals_df, aes(x = Variable, ymin = `2.5 %`, ymax = `97.5 %`, color = IncludesZer
o)) +
  geom_pointrange(aes(y = ( `2.5 %` + `97.5 %` ) / 2)) +  # Use midpoint for 'y'
  coord_flip() +  # Flip coordinates to make the plot horizontal
  theme_minimal() +
  labs(
    title = "95% Confidence Intervals for Regression Coefficients",
    x = "Variable",
    y = "Confidence Interval"
  ) +
  scale_color_manual(values = c("Yes" = "red", "No" = "darkgreen"))
```



Train/test split:

```
train_size = nrow(data) - 2000
train_data = data[1:train_size, ]
test_data = data[(train_size + 1):nrow(data), ]
```

Train/test prediction error for simple model:

```
simple_model_ = lm(log_TOTEXP18 ~ AGE42X + ADBMI42 + MNHLTH42 + RACETHX + SEX + boxcox_FAMINC18
+ NO_INC, data=train_data)
simple_model_pred = predict(simple_model_, newdata = test_data)
simple_model_pred = exp(simple_model_pred) - 1 # undo log transformation
simple_model_mse = mean((test_data$TOTEXP18 - simple_model_pred)^2)
print(paste("MSE for simple model = ", simple_model_mse))
```

```
## [1] "MSE for simple model =  337167774.117127"
```

```
print(paste("RMSE for simple model = ", sqrt(simple_model_mse)))
```

```
## [1] "RMSE for simple model =  18362.1288013434"
```

Train/test prediction error for full model:

```
full_model_ = lm(model_formula, data=train_data)
full_model_pred = predict(full_model_, newdata = test_data)
```

```
## Warning in bs(boxcox_FAMINC18, degree = 3L, knots = numeric(0), Boundary.knots
## = c(-2.60526315789473, : some 'x' values beyond boundary knots may cause
## ill-conditioned bases
```

```
full_model_pred = exp(full_model_pred) - 1 # undo log transformation
full_model_mse = mean((test_data$TOTEXP18 - full_model_pred)^2)
print(paste("MSE for full model = ", full_model_mse))
```

```
## [1] "MSE for full model =  336947320.599903"
```

```
print(paste("RMSE for full model = ", sqrt(full_model_mse)))
```

```
## [1] "RMSE for full model =  18356.1248797207"
```

Train/test prediction error for stepwise model:

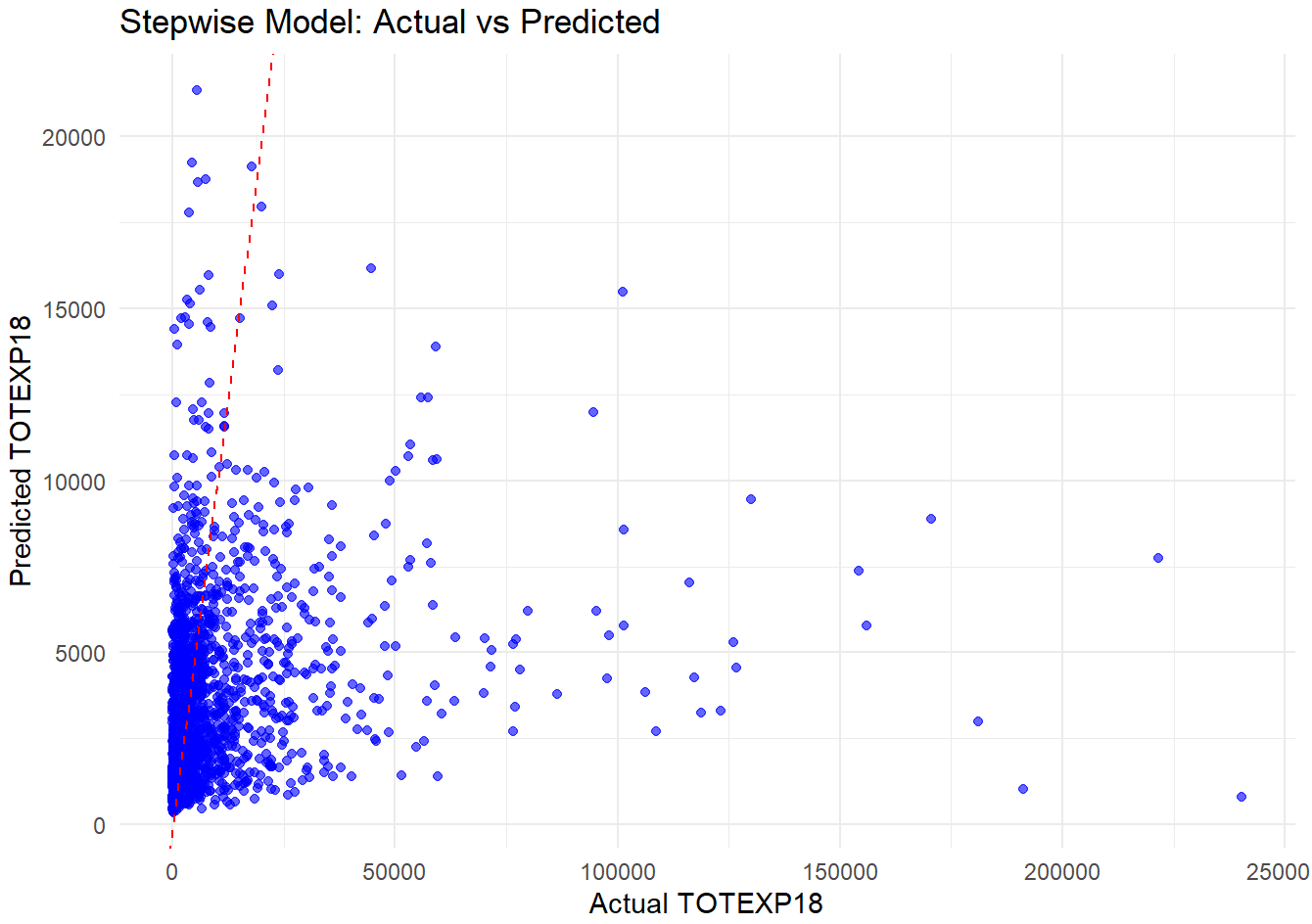
```
null_model_ = lm(log_TOTEXP18~1, data=train_data)
stepwise_model_ = step(null_model, scope = list(lower = null_model, upper = full_model_), direct
ion = "both", k = 2, trace = FALSE, test = "F", steps = 1000, add = 0.05 , drop = 0.05)

stepwise_model_pred = predict(stepwise_model_, newdata = test_data)
stepwise_model_pred = exp(stepwise_model_pred) - 1 # undo log transformation
stepwise_model_mse = mean((test_data$TOTEXP18 - stepwise_model_pred)^2)
print(paste("MSE for stepwise model = ", stepwise_model_mse))
```

```
## [1] "MSE for stepwise model =  336966631.013725"
```

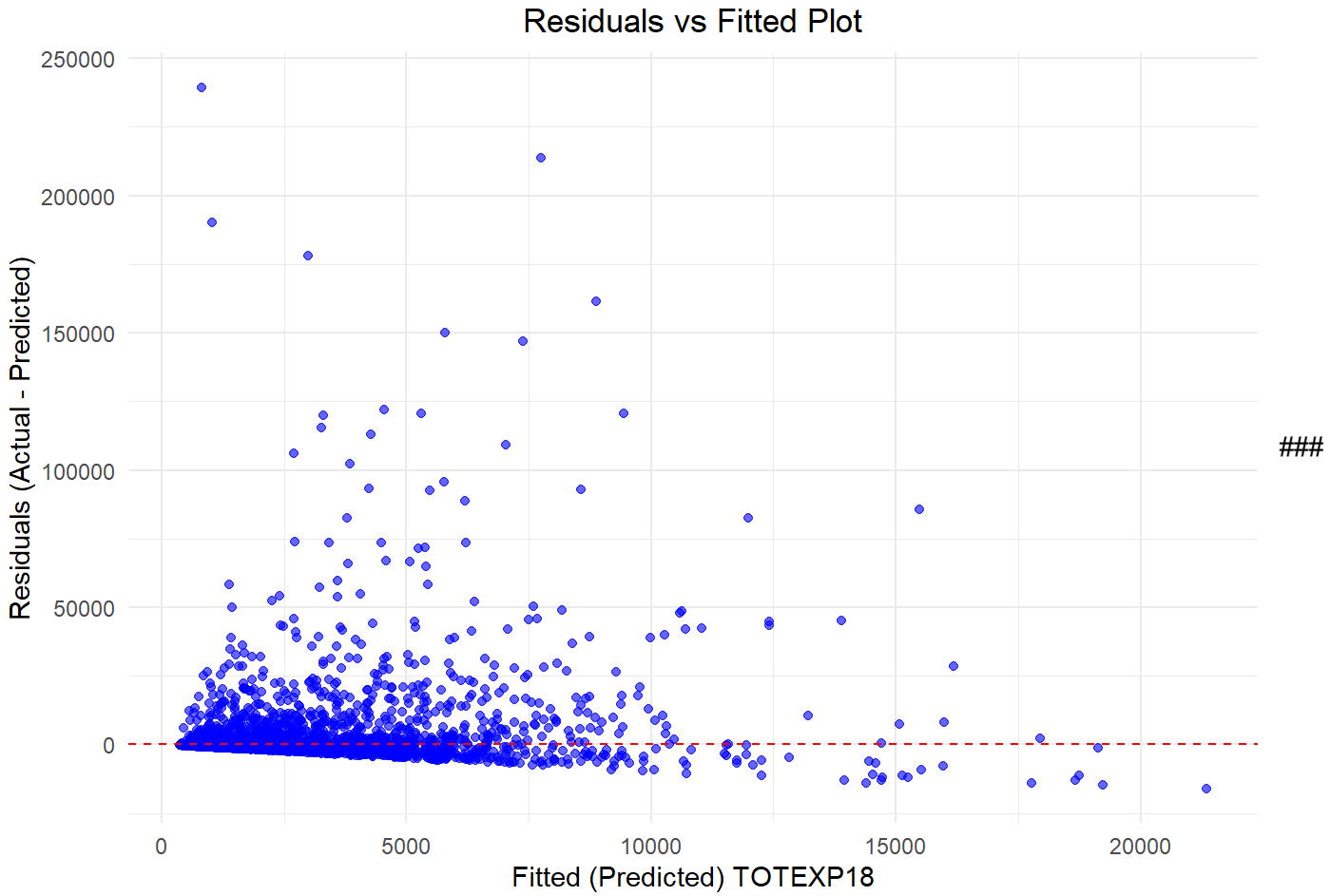
```
print(paste("RMSE for stepwise model = ", sqrt(stepwise_model_mse)))
```

```
## [1] "RMSE for stepwise model =  18356.6508659321"
```

```
test = test_data
test = cbind(stepwise_model_pred, test)
test$diff = (test$stepwise_model_pred - test$TOTEXP18)^2


# Plot actual vs predicted
plot_data = data.frame(
  Actual = test_data$TOTEXP18,
  Predicted = stepwise_model_pred
)

ggplot(plot_data, aes(x = Actual, y = Predicted)) +
  geom_point(alpha = 0.6, color = 'blue') +  # scatter plot of actual vs predicted
  geom_abline(slope = 1, intercept = 0, color = "red", linetype = "dashed") + # diagonal line fo
r reference
  labs(
    title = "Stepwise Model: Actual vs Predicted",
    x = "Actual TOTEXP18",
    y = "Predicted TOTEXP18"
  ) +
  theme_minimal()
```



```
# Plot residuals vs fitted for test data
residuals = test_data$TOTEXP18 - stepwise_model_pred

residuals_data = data.frame(
  Fitted = stepwise_model_pred,  # Predicted values (fitted)
  Residuals = residuals          # Residuals (errors)
)

ggplot(residuals_data, aes(x = Fitted, y = Residuals)) +
  geom_point(alpha = 0.6, color = 'blue') + # Scatter plot of residuals vs fitted
  geom_hline(yintercept = 0, color = "red", linetype = "dashed") + # Horizontal line at 0
  labs(
    title = "Residuals vs Fitted Plot",
    x = "Fitted (Predicted) TOTEXP18",
    y = "Residuals (Actual - Predicted)"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(hjust = 0.5)  # Center the title
  )
```



###

From the QC plots I made, it looks like a lot of my error comes from under estimating total expenditure for observations with some relatively high expenditures.

Train/test prediction error for lasso model:

```
X = model.matrix(model_formula, data = train_data)[, -1]
X_test = model.matrix(model_formula, data = test_data)[, -1]

# lasso model
lasso_ = glmnet(x = X, y = train_data$log_TOTEXP18, alpha = 1)

# cv to find optimal lambda
cv_lasso_ = cv.glmnet(x = X, y = train_data$log_TOTEXP18, alpha = 1, nfolds = 10)
best_lambda_ = cv_lasso_$lambda.min
best_lasso_ = glmnet(x = X, y = train_data$log_TOTEXP18, alpha = 1, lambda = best_lambda_)
coefficients_best_lasso_ = coef(best_lasso_)

# Make predictions using the best_lasso model
best_lasso_pred <- predict(best_lasso_, newx = X_test, s = best_lambda_)

# Inverse transform the predictions (since the target was log-transformed)
best_lasso_pred <- exp(best_lasso_pred) - 1

# Calculate MSE (Mean Squared Error)
best_lasso_mse <- mean((test_data$TOTEXP18 - best_lasso_pred)^2)

# Calculate RMSE (Root Mean Squared Error)
best_lasso_rmse <- sqrt(best_lasso_mse)

# Print the results
print(paste("MSE for Lasso model = ", best_lasso_mse))
```

```
## [1] "MSE for Lasso model =  339513246.296453"
```

```
print(paste("RMSE for Lasso model = ", best_lasso_rmse))
```

```
## [1] "RMSE for Lasso model =  18425.8852242288"
```

So it looks like all 4 models I fit don’t perform amazingly well. RMSE error is about $18,000 for all models. Lowest error is full model, then stepwise model, then simple model, then lasso model.

This doesn’t totally make sense to me because the full model should be more prone to overfitting. But I’ve already spent 10hrs on this and I have other classes.

Problem 5:

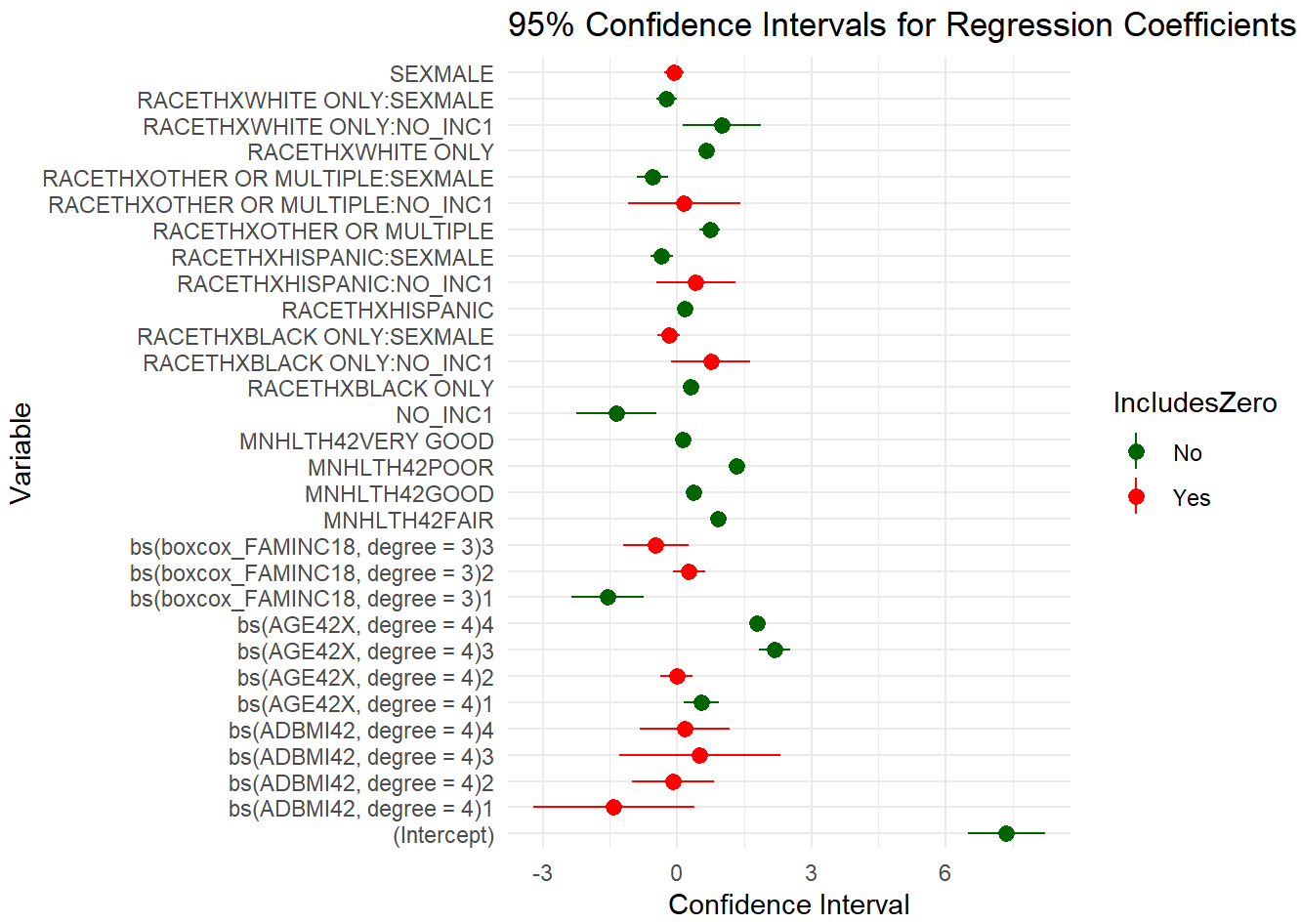
I found that mental health was a good indicator of how total medical expenditure. People with poor mental health spend the most, followed by those with fair, followed by those with good, then very good.

I found that older people have higher total expenditure.

I found that the “black only” ethnicity had higher expenditure. “Hispanic” also had higher expenditure but not as high as “black only”.

I found that people with no income have less expenditure.

```
conf_intervals = confint(stepwise, level = 0.95)

# Convert to data frame for plotting
conf_intervals_df <- as.data.frame(conf_intervals)
conf_intervals_df$Variable <- rownames(conf_intervals_df)  # Add variable names as a column

# Create a new column to indicate if the confidence interval includes 0
conf_intervals_df$IncludesZero <- ifelse(conf_intervals_df$`2.5 %` > 0 | conf_intervals_df$`97.5
%` < 0, "No", "Yes")

# Plot the confidence intervals
ggplot(conf_intervals_df, aes(x = Variable, ymin = `2.5 %`, ymax = `97.5 %`, color = IncludesZer
o)) +
  geom_pointrange(aes(y = ( `2.5 %` + `97.5 %` ) / 2)) +  # Use midpoint for 'y'
  coord_flip() +  # Flip coordinates to make the plot horizontal
  theme_minimal() +
  labs(
    title = "95% Confidence Intervals for Regression Coefficients",
    x = "Variable",
    y = "Confidence Interval"
  ) +
  scale_color_manual(values = c("Yes" = "red", "No" = "darkgreen"))
```



The paper “Racial and Ethnic Disparities in Health Care Use and Expenditures: Evidence from the MEPS” by R. E. Schoen, B. M. Stokes, & A. P. Ko (Health Affairs, 2013) also found that black and hispanic populations had higher total expenditure.

The paper “The Relationship Between Age and Health Care Expenditures in the United States” by H. A. Skinner, J. M. Staiger, & E. F. P. Rosenthal (The Journal of Health Economics, 2010) found that healthcare expenditure increases with age.

These support my findings.

Good job!
Very clear and organized work!