Analysis 2/6

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2/6/2021

Import data

```
biopsy.grade = readxl::read_excel("./data/GG_AP_ClinicalOutcomes_Biostats.xlsx", sheet = "Biopsy Grade (
adverse.pathology = readxl::read_excel("./data/GG_AP_ClinicalOutcomes_Biostats.xlsx", sheet = "Adverse I
serum.globalCTMean = readxl::read_excel("./data/Serum_AdjustedRQ_CT35_BioStats.xlsx", sheet = "GlobalCTI
serum.geNorm = readxl::read_excel("./data/Serum_AdjustedRQ_CT35_BioStats.xlsx", sheet = "geNorm RQ")
serum.NormFinder = readxl::read_excel("./data/Serum_AdjustedRQ_CT35_BioStats.xlsx", sheet = "geNorm Norr
EV.globalCTMean = readxl::read_excel("./data/SerumEV_AdjustedRQ_CT35_BioStats.xlsx", sheet = "GlobalCTM
EV.geNorm = readxl::read_excel("./data/SerumEV_AdjustedRQ_CT35_BioStats.xlsx", sheet = "geNorm RQ")
EV.NormFinder = readxl::read_excel("./data/SerumEV_AdjustedRQ_CT35_BioStats.xlsx", sheet = "geNorm Norml
serum.geneglobe = readxl::read_excel("./data/Serum_SerumEV_GeneGlobeRQ_CT35.xlsx", sheet = "Serum_GeneGl
EV.geneglobe = readxl::read_excel("./data/Serum_SerumEV_GeneGlobeRQ_CT35.xlsx", sheet = "EV_GeneGlobeRQ_
```

Tidy data

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.0      v purrr   0.3.4
## v tibble  3.0.4      v dplyr   1.0.2
## v tidyr   1.0.2      v stringr 1.4.0
## v readr   1.3.1      v forcats 0.5.0
```

```
## -- Conflicts ------------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
# Serum global CT mean
new = t(serum.globalCTMean)
name_tmp <- new[1,]
new <- new[-1,]
new <- apply(new,1,as.numeric) %>% t()
colnames(new) <- (name_tmp)
serum.globalCTMean.new = new %>% as.data.frame()
serum.globalCTMean.new = rownames_to_column(serum.globalCTMean.new)
```

```r
colnames(serum.globalCTMean.new)[1] = "Patient ID"

# Serum geNorm
new = t(serum.geNorm)
name_tmp <- new[1,]
new <- new[-1,]
new <- apply(new,1,as.numeric) %>% t()
colnames(new) <- (name_tmp)
serum.geNorm.new = new %>% as.data.frame()
serum.geNorm.new = rownames_to_column(serum.geNorm.new)
colnames(serum.globalCTMean.new)[1] = "Patient ID"

# Serum geNorm Finder
new = t(serum.NormFinder)
name_tmp <- new[1,]
new <- new[-1,]
new <- apply(new,1,as.numeric) %>% t()
colnames(new) <- (name_tmp)
serum.NormFinder.new = new %>% as.data.frame()
serum.NormFinder.new = rownames_to_column(serum.NormFinder.new)
colnames(serum.NormFinder.new)[1] = "Patient ID"

# EV global CT Mean
new = t(EV.globalCTMean)
name_tmp <- new[1,]
new <- new[-1,]
new <- apply(new,1,as.numeric) %>% t()
colnames(new) <- (name_tmp)
EV.globalCTMean.new = new %>% as.data.frame()
EV.globalCTMean.new = rownames_to_column(EV.globalCTMean.new)
colnames(EV.globalCTMean.new)[1] = "Patient ID"

# EV geNorm
new = t(EV.geNorm)
name_tmp <- new[1,]
new <- new[-1,]
new <- apply(new,1,as.numeric) %>% t()
colnames(new) <- (name_tmp)
EV.geNorm.new = new %>% as.data.frame()
EV.geNorm.new = rownames_to_column(EV.geNorm.new)
colnames(EV.geNorm.new)[1] = "Patient ID"

# EV geNorm NormFinder
new = t(EV.NormFinder)
name_tmp <- new[1,]
new <- new[-1,]
new <- apply(new,1,as.numeric) %>% t()
colnames(new) <- (name_tmp)
EV.NormFinder.new = new %>% as.data.frame()
EV.NormFinder.new = rownames_to_column(EV.NormFinder.new)
colnames(EV.NormFinder.new)[1] = "Patient ID"
```

```r
# Adverse pathology
adverse.pathology$`Adverse Pathology` = ifelse(adverse.pathology$`Adverse Pathology` == "99", NA, advers
```

```r
# change format from wide to long
# serum
new = t(serum.geneglobe)
name_tmp <- new[1,]
new <- new[-1,]
new <- apply(new,1,as.numeric) %>% t()
colnames(new) <- (name_tmp)
serum.geneglobe.new = new %>% as.data.frame()
serum.geneglobe.new = rownames_to_column(serum.geneglobe.new)
colnames(serum.geneglobe.new)[1] = "Patient ID"

# EV
new = t(EV.geneglobe)
name_tmp <- new[1,]
new <- new[-1,]
new <- apply(new,1,as.numeric) %>% t()
colnames(new) <- (name_tmp)
EV.geneglobe.new = new %>% as.data.frame()
EV.geneglobe.new = rownames_to_column(EV.geneglobe.new)
colnames(EV.geneglobe.new)[1] = "Patient ID"

# Adverse pathology
adverse.pathology$`Adverse Pathology` = ifelse(adverse.pathology$`Adverse Pathology` == "99", NA, advers
```

Distribution checking

```r
# serum global ct mean
normality.test.serum.CTMean = data.frame(
  microRNA = colnames(serum.globalCTMean.new[-1]),
  p.value = numeric(61),
  method = "Global CTMean"
)

for (i in 1:61) {
  test = shapiro.test(serum.globalCTMean.new[,i+1])
  normality.test.serum.CTMean$p.value[i] = test$p.value
}

# serum geNorm
normality.test.serum.geNorm = data.frame(
  microRNA = colnames(serum.geNorm.new[-1]),
  p.value = numeric(61),
  method = "geNorm"
)

for (i in 1:61) {
  test = shapiro.test(serum.geNorm.new[,i+1])
  normality.test.serum.geNorm$p.value[i] = test$p.value
```

```r
}

# serum geNorm NormFinder
normality.test.serum.NormFinder = data.frame(
  microRNA = colnames(serum.NormFinder.new[-1]),
  p.value = numeric(61),
  method = "NormFinder"
)

for (i in 1:61) {
  test = shapiro.test(serum.NormFinder.new[,i+1])
  normality.test.serum.NormFinder$p.value[i] = test$p.value
}

# EV global CT Mean
normality.test.EV.CTMean = data.frame(
  microRNA = colnames(EV.globalCTMean.new[-1]),
  p.value = numeric(61),
  method = "Global CTMean"
)

for (i in 1:61) {
  test = shapiro.test(EV.globalCTMean.new[,i+1])
  normality.test.EV.CTMean$p.value[i] = test$p.value
}

# EV geNorm
normality.test.EV.geNorm = data.frame(
  microRNA = colnames(EV.geNorm.new[-1]),
  p.value = numeric(61),
  method = "geNorm"
)

for (i in 1:61) {
  test = shapiro.test(EV.geNorm.new[,i+1])
  normality.test.EV.geNorm$p.value[i] = test$p.value
}

EV.NormFinder.new2 = EV.NormFinder.new[,-7]
# EV NormFinder
normality.test.EV.NormFinder = data.frame(
  microRNA = colnames(EV.NormFinder.new2[-1]),
  p.value = numeric(60),
  method = "NormFinder"
)

for (i in 1:60) {
  test = shapiro.test(EV.NormFinder.new2[,i+1])
  normality.test.EV.NormFinder$p.value[i] = test$p.value
}

normality.test.serum = data.frame(
  microRNA = colnames(serum.geneglobe.new[-1]),
```

```r
  p.value = numeric(61),
  method = "Gene Globe"
)

for (i in 1:61) {
  test = shapiro.test(serum.geneglobe.new[,i+1])
  normality.test.serum$p.value[i] = test$p.value
}

# checking distribution for EV
normality.test.EV = data.frame(
  microRNA = colnames(EV.geneglobe.new[-1]),
  p.value = numeric(61),
  method = "Gene Globe"
)

for (i in 1:61) {
  test = shapiro.test(EV.geneglobe.new[,i+1])
  normality.test.EV$p.value[i] = test$p.value
}

normality.result.serum = rbind(normality.test.serum, normality.test.serum.CTMean, normality.test.serum.
normality.result.EV = rbind(normality.test.EV, normality.test.EV.CTMean, normality.test.EV.geNorm, norm

library(openxlsx)
write.xlsx(list(normality.result.serum, normality.result.EV), file = "Normality test results.xlsx")
```

Univariate GLM fitting

```r
# datafile combine
# left join for grade groups
serum.grade.original = left_join(serum.geneglobe.new, biopsy.grade, by = "Patient ID")
EV.grade.original = left_join(EV.geneglobe.new, biopsy.grade, by = "Patient ID")

# left join for adverse pathology
serum.all.original = left_join(serum.grade.original, adverse.pathology, by = "Patient ID")
EV.all.original = left_join(EV.grade.original, adverse.pathology, by = "Patient ID")

grade.serum.result = data.frame(
  microRNA = colnames(serum.geneglobe.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = serum.all.original$`Biopsy Grade Group`~serum.all.original[,i+1])
  result = summary(model)
  grade.serum.result$p.value[i] = result$coefficients[2,4]
}

grade.EV.result = data.frame(
  microRNA = colnames(EV.geneglobe.new)[-1],
  p.value = numeric(61)
```

```r
)

for (i in 1:61) {
  model = glm(formula = EV.all.original$`Biopsy Grade Group`~EV.all.original[,i+1])
  result = summary(model)
  grade.EV.result$p.value[i] = result$coefficients[2,4]
}

# Display result
# univariate GLM
adverse.serum.result = data.frame(
  microRNA = colnames(serum.geneglobe.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = serum.all.original$`Adverse Pathology`~serum.all.original[,i+1], family = "binom
  result = summary(model)
  adverse.serum.result$p.value[i] = result$coefficients[2,4]
}

adverse.EV.result = data.frame(
  microRNA = colnames(EV.geneglobe.new)[-1],
  p.value = numeric(61)
)

for (i in 1:61) {
  model = glm(formula = EV.all.original$`Adverse Pathology`~EV.all.original[,i+1], family = "binomial")
  result = summary(model)
  adverse.EV.result$p.value[i] = result$coefficients[2,4]
}

# Display result
adverse.EV.result= grade.serum.result[order(grade.serum.result$p.value),]
grade.EV.result = grade.EV.result[order(grade.EV.result$p.value),]

# Serum global CTMean
grade.serum.CTMean.result = data.frame(
  microRNA = colnames(serum.globalCTMean.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = serum.all.original$`Biopsy Grade Group`~serum.globalCTMean.new[,i+1])
  result = summary(model)
  grade.serum.CTMean.result$p.value[i] = result$coefficients[2,4]
}

grade.serum.CTMean.result = grade.serum.CTMean.result[order(grade.serum.CTMean.result$p.value),]

# Serum geNorm
grade.serum.geNorm.result = data.frame(
  microRNA = colnames(serum.geNorm.new)[-1],
  p.value = numeric(61)
)
```

```r
for (i in 1:61) {
  model = glm(formula = serum.all.original$`Biopsy Grade Group`~serum.geNorm.new[,i+1])
  result = summary(model)
  grade.serum.geNorm.result$p.value[i] = result$coefficients[2,4]
}

grade.serum.geNorm.result = grade.serum.geNorm.result[order(grade.serum.geNorm.result$p.value),]

# Serum NormFinder
grade.serum.NormFinder.result = data.frame(
  microRNA = colnames(serum.NormFinder.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = serum.all.original$`Biopsy Grade Group`~serum.NormFinder.new[,i+1])
  result = summary(model)
  grade.serum.NormFinder.result$p.value[i] = result$coefficients[2,4]
}

grade.serum.NormFinder.result = grade.serum.geNorm.result[order(grade.serum.NormFinder.result$p.value),]

EV.grade.CTMean = left_join(EV.globalCTMean.new,biopsy.grade, by = "Patient ID")

# EV global CT Mean
grade.EV.CTMean.result = data.frame(
  microRNA = colnames(EV.globalCTMean.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = EV.grade.CTMean$`Biopsy Grade Group`~ EV.globalCTMean.new[,i+1])
  result = summary(model)
  grade.EV.CTMean.result$p.value[i] = result$coefficients[2,4]
}

grade.EV.CTMean.result = grade.EV.CTMean.result[order(grade.EV.CTMean.result$p.value),]

# EV geNorm
grade.EV.geNorm.result = data.frame(
  microRNA = colnames(EV.geNorm.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = EV.grade.CTMean$`Biopsy Grade Group`~ EV.geNorm.new[,i+1])
  result = summary(model)
  grade.EV.geNorm.result$p.value[i] = result$coefficients[2,4]
}

grade.EV.geNorm.result = grade.EV.geNorm.result[order(grade.EV.geNorm.result$p.value),]


# EV Norm Finder
grade.EV.NormFinder.result = data.frame(
  microRNA = colnames(EV.NormFinder.new2)[-1],
```

```r
    p.value = numeric(60)
)
for (i in 1:60) {
  model = glm(formula = EV.grade.CTMean$'Biopsy Grade Group'~ EV.NormFinder.new2[,i+1])
  result = summary(model)
  grade.EV.NormFinder.result$p.value[i] = result$coefficients[2,4]
}


grade.EV.NormFinder.result = grade.EV.NormFinder.result[order(grade.EV.NormFinder.result$p.value),]

# Collect the results
grade.serum.GLM.result = write.xlsx(list(grade.serum.result, grade.serum.CTMean.result, grade.serum.geN
grade.EV.GLM.result = write.xlsx(list(grade.EV.result, grade.EV.CTMean.result, grade.EV.geNorm.result,


# univariate GLM
adverse.serum.result = data.frame(
  microRNA = colnames(serum.geneglobe.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = serum.all.original$'Adverse Pathology'~serum.all.original[,i+1], family = "binom
  result = summary(model)
  adverse.serum.result$p.value[i] = result$coefficients[2,4]
}

adverse.EV.result = data.frame(
  microRNA = colnames(EV.geneglobe.new)[-1],
  p.value = numeric(61)
)

for (i in 1:61) {
  model = glm(formula = EV.all.original$'Adverse Pathology'~EV.all.original[,i+1], family = "binomial")
  result = summary(model)
  adverse.EV.result$p.value[i] = result$coefficients[2,4]
}

# Display result
adverse.serum.result = adverse.serum.result[order(adverse.serum.result$p.value),]
adverse.EV.result = adverse.EV.result[order(adverse.EV.result$p.value),]

# Serum global CTMean
adverse.serum.CTMean.result = data.frame(
  microRNA = colnames(serum.globalCTMean.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = serum.all.original$'Adverse Pathology'~serum.globalCTMean.new[,i+1], family = "
  result = summary(model)
  adverse.serum.CTMean.result$p.value[i] = result$coefficients[2,4]
}

adverse.serum.CTMean.result = adverse.serum.CTMean.result[order(adverse.serum.CTMean.result$p.value),]
```

```r
# Serum geNorm
adverse.serum.geNorm.result = data.frame(
  microRNA = colnames(serum.geNorm.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = serum.all.original$'Adverse Pathology'~serum.geNorm.new[,i+1], family = "binomia
  result = summary(model)
  adverse.serum.geNorm.result$p.value[i] = result$coefficients[2,4]
}

adverse.serum.geNorm.result = adverse.serum.geNorm.result[order(adverse.serum.geNorm.result$p.value),]

# Serum NormFinder
adverse.serum.NormFinder.result = data.frame(
  microRNA = colnames(serum.NormFinder.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = serum.all.original$'Adverse Pathology'~serum.NormFinder.new[,i+1], family = "bi
  result = summary(model)
  adverse.serum.NormFinder.result$p.value[i] = result$coefficients[2,4]
}

adverse.serum.NormFinder.result = adverse.serum.geNorm.result[order(adverse.serum.NormFinder.result$p.va

EV.adverse.CTMean = left_join(EV.globalCTMean.new, adverse.pathology, by = "Patient ID")

# EV global CT Mean
adverse.EV.CTMean.result = data.frame(
  microRNA = colnames(EV.globalCTMean.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = EV.adverse.CTMean$'Adverse Pathology'~ EV.globalCTMean.new[,i+1], family = "bin
  result = summary(model)
  adverse.EV.CTMean.result$p.value[i] = result$coefficients[2,4]
}

adverse.EV.CTMean.result = adverse.EV.CTMean.result[order(adverse.EV.CTMean.result$p.value),]

# EV geNorm
adverse.EV.geNorm.result = data.frame(
  microRNA = colnames(EV.geNorm.new)[-1],
  p.value = numeric(61)
)
for (i in 1:61) {
  model = glm(formula = EV.adverse.CTMean$'Adverse Pathology'~ EV.geNorm.new[,i+1], family = "binomial"]
  result = summary(model)
  adverse.EV.geNorm.result$p.value[i] = result$coefficients[2,4]
}

adverse.EV.geNorm.result = adverse.EV.geNorm.result[order(adverse.EV.geNorm.result$p.value),]
```

```r
# EV Norm Finder
adverse.EV.NormFinder.result = data.frame(
  microRNA = colnames(EV.NormFinder.new2)[-1],
  p.value = numeric(60)
)
for (i in 1:60) {
  model = glm(formula = EV.adverse.CTMean$`Adverse Pathology`~ EV.NormFinder.new2[,i+1], family = "binor
  result = summary(model)
  adverse.EV.NormFinder.result$p.value[i] = result$coefficients[2,4]
}

adverse.EV.NormFinder.result = adverse.EV.NormFinder.result[order(adverse.EV.NormFinder.result$p.value)

# Collect the results
adverse.serum.GLM.result = write.xlsx(list(adverse.serum.result, adverse.serum.CTMean.result, adverse.se
adverse.EV.GLM.result = write.xlsx(list(adverse.EV.result, adverse.EV.CTMean.result, adverse.EV.geNorm.
```

Variable selection

```r
# get the significant results
grade.serum.result.significant =
  grade.serum.result %>% filter(p.value <= 0.05)

grade.serum.result.significant
```

```
##         microRNA      p.value
## 1    hsa-miR-1246 0.043973261
## 2  hsa-miR-214-3p 0.002936045
## 3 hsa-miR-301a-3p 0.049412355
```

```r
grade.EV.result.significant =
  grade.EV.result %>% filter(p.value <= 0.05)

grade.EV.result.significant
```

```
##        microRNA   p.value
## 1 hsa-miR-31-5p 0.0469124
```

```r
# serum CT mean
grade.serum.CTMean.result.sigficant =
  grade.serum.CTMean.result %>% filter(p.value <= 0.05)

grade.serum.CTMean.result.sigficant
```

```
##         microRNA      p.value
## 1    hsa-miR-1246 0.001271339
## 2  hsa-miR-363-3p 0.007745707
## 3    hsa-miR-320a 0.009909141
```

```
## 4   hsa-miR-125b-5p 0.012125587
## 5    hsa-miR-27a-3p 0.016748086
## 6     hsa-miR-16-5p 0.022936940
## 7     hsa-let-7b-5p 0.029406367
## 8    hsa-miR-27b-3p 0.031226246
## 9    hsa-miR-29a-3p 0.031678110
## 10    hsa-miR-21-5p 0.034516917
## 11      hsa-miR-451a 0.043542910
## 12   hsa-miR-874-3p 0.049943956
```

```r
# serum geNorm
grade.serum.geNorm.result.sigficant =
  grade.serum.geNorm.result %>% filter(p.value <= 0.05)

grade.serum.geNorm.result.sigficant
```

```
##            microRNA      p.value
## 1    hsa-miR-27a-3p 0.000476291
## 2    hsa-miR-27b-3p 0.001216949
## 3    hsa-miR-363-3p 0.003297383
## 4      hsa-miR-1246 0.003664409
## 5    hsa-miR-23a-3p 0.007040136
## 6     hsa-miR-16-5p 0.007799315
## 7    hsa-miR-29a-3p 0.009050055
## 8     hsa-miR-24-3p 0.009811907
## 9   hsa-miR-199a-5p 0.011890831
## 10      hsa-miR-320a 0.016906740
## 11   hsa-miR-221-3p 0.018812295
## 12    hsa-let-7b-5p 0.024130465
## 13 hsa-miR-125b-5p 0.029336944
## 14   hsa-miR-19b-3p 0.031916099
## 15 hsa-miR-146a-5p 0.031997515
## 16    hsa-miR-21-5p 0.033266949
## 17      hsa-miR-451a 0.035029297
## 18    hsa-miR-93-5p 0.041290153
## 19 hsa-miR-199a-3p 0.048268150
```

```r
# serum Norm Finder
grade.serum.NormFinder.result.sigficant =
  grade.serum.NormFinder.result %>% filter(p.value <= 0.05)

grade.serum.NormFinder.result.sigficant
```

```
##            microRNA      p.value
## 1     hsa-miR-21-5p 0.033266949
## 2   hsa-miR-199a-5p 0.011890831
## 3   hsa-miR-199a-3p 0.048268150
## 4      hsa-miR-1246 0.003664409
## 5     hsa-let-7b-5p 0.024130465
## 6    hsa-miR-29a-3p 0.009050055
## 7     hsa-miR-24-3p 0.009811907
## 8    hsa-miR-19b-3p 0.031916099
## 9      hsa-miR-451a 0.035029297
```

```
## 10    hsa-miR-16-5p 0.007799315
## 11 hsa-miR-125b-5p 0.029336944
## 12     hsa-miR-320a 0.016906740
## 13    hsa-miR-93-5p 0.041290153
## 14   hsa-miR-27b-3p 0.001216949
## 15   hsa-miR-363-3p 0.003297383
## 16   hsa-miR-27a-3p 0.000476291
## 17   hsa-miR-221-3p 0.018812295
## 18   hsa-miR-23a-3p 0.007040136
## 19 hsa-miR-146a-5p 0.031997515
```

```r
# EV CT Mean
grade.EV.CTMean.result.sigficant =
  grade.EV.CTMean.result %>% filter(p.value <= 0.05)

grade.EV.CTMean.result.sigficant
```

```
##           microRNA    p.value
## 1    hsa-miR-335-5p 0.01159337
## 2    hsa-miR-191-5p 0.02341843
## 3       hsa-miR-107 0.02547737
## 4   hsa-miR-130b-3p 0.02717597
## 5    hsa-miR-221-3p 0.02823415
## 6    hsa-miR-214-3p 0.02859529
## 7   hsa-miR-103a-3p 0.03263166
## 8    hsa-miR-330-3p 0.03553350
## 9    hsa-miR-30a-5p 0.04297077
## 10    hsa-let-7a-5p 0.04594460
```

```r
# EV geNorm
grade.EV.geNorm.result.sigficant =
  grade.EV.geNorm.result %>% filter(p.value <= 0.05)

grade.EV.geNorm.result.sigficant
```

```
##           microRNA    p.value
## 1   hsa-miR-335-5p 0.01378420
## 2 hsa-miR-130b-3p 0.01469987
## 3   hsa-miR-191-5p 0.01956625
## 4   hsa-miR-221-3p 0.02120301
## 5   hsa-miR-214-3p 0.02457067
## 6       hsa-miR-107 0.03391916
## 7   hsa-miR-330-3p 0.04228921
## 8 hsa-miR-103a-3p 0.04673851
```

```r
# EV Norm Finder
grade.EV.NormFinder.result.sigficant =
  grade.EV.NormFinder.result %>% filter(p.value <= 0.05)

grade.EV.NormFinder.result.sigficant
```

```
##           microRNA    p.value
```

```
## 1    hsa-miR-19b-3p 0.001397571
## 2    hsa-miR-874-3p 0.001597862
## 3    hsa-miR-214-3p 0.001602595
## 4    hsa-miR-30a-5p 0.001882057
## 5    hsa-miR-143-3p 0.002017969
## 6    hsa-miR-363-3p 0.004718015
## 7      hsa-miR-451a 0.006681248
## 8   hsa-miR-148a-3p 0.007793501
## 9     hsa-miR-25-3p 0.009321136
## 10    hsa-miR-16-5p 0.013555541
## 11   hsa-miR-222-3p 0.013659194
## 12   hsa-miR-210-3p 0.017858613
## 13   hsa-miR-18b-5p 0.037341870
```

```r
# get the significant results
adverse.serum.result.significant =
  adverse.serum.result %>% filter(p.value <= 0.05)

adverse.serum.result.significant
```

```
## [1] microRNA p.value
## <0 rows> (or 0-length row.names)
```

```r
adverse.EV.result.significant =
  adverse.EV.result %>% filter(p.value <= 0.05)

adverse.EV.result.significant
```

```
##          microRNA    p.value
## 1   hsa-let-7a-5p 0.01557483
## 2   hsa-miR-26b-5p 0.02204650
## 3 hsa-miR-301a-3p 0.04196488
```

```r
# serum CT mean
adverse.serum.CTMean.result.sigficant =
  adverse.serum.CTMean.result %>% filter(p.value <= 0.05)

adverse.serum.CTMean.result.sigficant
```

```
##        microRNA    p.value
## 1 hsa-miR-1246 0.04570637
```

```r
# serum geNorm
adverse.serum.geNorm.result.sigficant =
  adverse.serum.geNorm.result %>% filter(p.value <= 0.05)

adverse.serum.geNorm.result.sigficant
```

```
##          microRNA    p.value
## 1 hsa-miR-574-3p 0.03365112
## 2 hsa-miR-100-5p 0.04422544
## 3   hsa-miR-1246 0.04512989
```

```r
# serum Norm Finder
adverse.serum.NormFinder.result.sigficant =
  adverse.serum.NormFinder.result %>% filter(p.value <= 0.05)

adverse.serum.NormFinder.result.sigficant
```

```
##          microRNA    p.value
## 1 hsa-miR-100-5p 0.04422544
## 2 hsa-miR-574-3p 0.03365112
## 3   hsa-miR-1246 0.04512989
```

```r
# EV CT Mean
adverse.EV.CTMean.result.sigficant =
  adverse.EV.CTMean.result %>% filter(p.value <= 0.05)

adverse.EV.CTMean.result.sigficant
```

```
##            microRNA     p.value
## 1    hsa-let-7a-5p 0.003771774
## 2    hsa-miR-30c-5p 0.005253809
## 3    hsa-miR-26b-5p 0.007504636
## 4     hsa-miR-25-3p 0.009131855
## 5       hsa-miR-107 0.011090428
## 6   hsa-miR-103a-3p 0.014519363
## 7   hsa-miR-199a-5p 0.016607385
## 8   hsa-miR-301a-3p 0.017798625
## 9    hsa-miR-363-3p 0.020035672
## 10   hsa-miR-191-5p 0.020135915
## 11   hsa-miR-19b-3p 0.020770834
## 12   hsa-miR-221-3p 0.024797302
## 13   hsa-miR-27b-3p 0.035392855
## 14     hsa-miR-451a 0.039403343
## 15 hsa-miR-374a-5p 0.039811432
## 16    hsa-miR-16-5p 0.039851686
```

```r
# EV geNorm
adverse.EV.geNorm.result.sigficant =
  adverse.EV.geNorm.result %>% filter(p.value <= 0.05)

adverse.EV.geNorm.result.sigficant
```

```
##            microRNA     p.value
## 1     hsa-miR-25-3p 0.001866174
## 2   hsa-miR-199a-5p 0.006152689
## 3    hsa-miR-30c-5p 0.006253693
## 4     hsa-let-7a-5p 0.007167119
## 5    hsa-miR-191-5p 0.007713078
## 6    hsa-miR-27b-3p 0.008710479
## 7    hsa-miR-363-3p 0.010365983
## 8    hsa-miR-26b-5p 0.011409933
## 9    hsa-miR-221-3p 0.012717792
## 10    hsa-miR-16-5p 0.012747414
```

```
## 11  hsa-miR-19b-3p 0.014234249
## 12     hsa-miR-107 0.016092505
## 13  hsa-miR-27a-3p 0.018368701
## 14 hsa-miR-301a-3p 0.019008830
## 15     hsa-miR-451a 0.019989595
## 16 hsa-miR-199a-3p 0.024240830
## 17 hsa-miR-103a-3p 0.024745420
## 18  hsa-miR-23a-3p 0.029135267
## 19   hsa-miR-24-3p 0.041222617
## 20  hsa-miR-141-3p 0.042960727
```

```r
# EV Norm Finder
adverse.EV.NormFinder.result.sigficant =
  adverse.EV.NormFinder.result %>% filter(p.value <= 0.05)

adverse.EV.NormFinder.result.sigficant
```

```
##           microRNA     p.value
## 1  hsa-miR-199a-5p 0.003628430
## 2   hsa-miR-30c-5p 0.005693966
## 3   hsa-miR-221-3p 0.008664604
## 4   hsa-miR-27b-3p 0.010925055
## 5    hsa-let-7a-5p 0.011559027
## 6    hsa-miR-25-3p 0.014727002
## 7   hsa-miR-191-5p 0.020005157
## 8   hsa-miR-363-3p 0.028273898
## 9   hsa-miR-19b-3p 0.030360856
## 10     hsa-miR-107 0.032202085
## 11    hsa-miR-451a 0.034692098
## 12    hsa-miR-16-5p 0.038086990
## 13 hsa-miR-199a-3p 0.044443907
## 14 hsa-miR-103a-3p 0.047507256
## 15  hsa-miR-27a-3p 0.048521467
```

Biopsy Grade selection

```r
library(MASS)
```

```
##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##     select
```

```r
fullmodel1 = glm(data = serum.all.original, formula = 'Biopsy Grade Group'~'hsa-miR-1246'+'hsa-miR-214-3
serum.grade.final = stepAIC(object = fullmodel1, direction = "backward")
```

```
## Start:  AIC=512.47
## 'Biopsy Grade Group' ~ 'hsa-miR-1246' + 'hsa-miR-214-3p' + 'hsa-miR-301a-3p'
```

```
##
##                       Df Deviance    AIC
## - `hsa-miR-301a-3p`  1    141.49 510.80
## <none>                   141.25 512.47
## - `hsa-miR-214-3p`   1    145.02 515.82
## - `hsa-miR-1246`     1    145.59 516.62
##
## Step:  AIC=510.8
## `Biopsy Grade Group` ~ `hsa-miR-1246` + `hsa-miR-214-3p`
##
##                      Df Deviance    AIC
## <none>                   141.49 510.80
## - `hsa-miR-1246`     1    145.64 514.68
## - `hsa-miR-214-3p`   1    149.16 519.52
```

```r
# serum CT Mean
fullmodel.serum.ctmean = glm(formula = serum.all.original$`Biopsy Grade Group`~ serum.globalCTMean.new$

step.serum.grade.CTMean = stepAIC(object = fullmodel.serum.ctmean, direction = "backward")
```

```
## Start:  AIC=505.63
## serum.all.original$`Biopsy Grade Group` ~ serum.globalCTMean.new$`hsa-miR-1246` +
##     serum.globalCTMean.new$`hsa-miR-363-3p` + serum.globalCTMean.new$`hsa-miR-320a` +
##     serum.globalCTMean.new$`hsa-miR-125b-5p` + serum.globalCTMean.new$`hsa-miR-27a-3p` +
##     serum.globalCTMean.new$`hsa-miR-16-5p` + serum.globalCTMean.new$`hsa-let-7b-5p` +
##     serum.globalCTMean.new$`hsa-miR-27b-3p` + serum.globalCTMean.new$`hsa-miR-29a-3p` +
##     serum.globalCTMean.new$`hsa-miR-21-5p` + serum.globalCTMean.new$`hsa-miR-451a` +
##     serum.globalCTMean.new$`hsa-miR-874-3p`
##
##                                              Df Deviance    AIC
## - serum.globalCTMean.new$`hsa-miR-27a-3p`    1    125.06 503.75
## - serum.globalCTMean.new$`hsa-let-7b-5p`     1    125.07 503.77
## - serum.globalCTMean.new$`hsa-miR-16-5p`     1    125.16 503.91
## - serum.globalCTMean.new$`hsa-miR-21-5p`     1    125.25 504.07
## - serum.globalCTMean.new$`hsa-miR-27b-3p`    1    125.47 504.42
## - serum.globalCTMean.new$`hsa-miR-29a-3p`    1    125.70 504.78
## - serum.globalCTMean.new$`hsa-miR-1246`      1    125.79 504.94
## - serum.globalCTMean.new$`hsa-miR-451a`      1    125.87 505.06
## <none>                                            124.99 505.63
## - serum.globalCTMean.new$`hsa-miR-320a`      1    126.28 505.73
## - serum.globalCTMean.new$`hsa-miR-874-3p`    1    126.63 506.29
## - serum.globalCTMean.new$`hsa-miR-363-3p`    1    129.18 510.33
## - serum.globalCTMean.new$`hsa-miR-125b-5p`   1    133.35 516.79
##
## Step:  AIC=503.75
## serum.all.original$`Biopsy Grade Group` ~ serum.globalCTMean.new$`hsa-miR-1246` +
##     serum.globalCTMean.new$`hsa-miR-363-3p` + serum.globalCTMean.new$`hsa-miR-320a` +
##     serum.globalCTMean.new$`hsa-miR-125b-5p` + serum.globalCTMean.new$`hsa-miR-16-5p` +
##     serum.globalCTMean.new$`hsa-let-7b-5p` + serum.globalCTMean.new$`hsa-miR-27b-3p` +
##     serum.globalCTMean.new$`hsa-miR-29a-3p` + serum.globalCTMean.new$`hsa-miR-21-5p` +
##     serum.globalCTMean.new$`hsa-miR-451a` + serum.globalCTMean.new$`hsa-miR-874-3p`
##
##                                            Df Deviance    AIC
## - serum.globalCTMean.new$`hsa-let-7b-5p`    1    125.14 501.89
```

```
## - serum.globalCTMean.new$`hsa-miR-16-5p`    1    125.28 502.12
## - serum.globalCTMean.new$`hsa-miR-21-5p`    1    125.40 502.31
## - serum.globalCTMean.new$`hsa-miR-29a-3p`   1    125.70 502.79
## - serum.globalCTMean.new$`hsa-miR-1246`     1    125.79 502.94
## - serum.globalCTMean.new$`hsa-miR-27b-3p`   1    125.96 503.20
## - serum.globalCTMean.new$`hsa-miR-451a`     1    126.04 503.34
## <none>                                           125.06 503.75
## - serum.globalCTMean.new$`hsa-miR-320a`     1    126.33 503.81
## - serum.globalCTMean.new$`hsa-miR-874-3p`   1    126.74 504.46
## - serum.globalCTMean.new$`hsa-miR-363-3p`   1    129.20 508.36
## - serum.globalCTMean.new$`hsa-miR-125b-5p`  1    133.39 514.84
##
## Step:  AIC=501.89
## serum.all.original$`Biopsy Grade Group` ~ serum.globalCTMean.new$`hsa-miR-1246` +
##     serum.globalCTMean.new$`hsa-miR-363-3p` + serum.globalCTMean.new$`hsa-miR-320a` +
##     serum.globalCTMean.new$`hsa-miR-125b-5p` + serum.globalCTMean.new$`hsa-miR-16-5p` +
##     serum.globalCTMean.new$`hsa-miR-27b-3p` + serum.globalCTMean.new$`hsa-miR-29a-3p` +
##     serum.globalCTMean.new$`hsa-miR-21-5p` + serum.globalCTMean.new$`hsa-miR-451a` +
##     serum.globalCTMean.new$`hsa-miR-874-3p`
##
##                                             Df Deviance    AIC
## - serum.globalCTMean.new$`hsa-miR-16-5p`    1    125.29 500.12
## - serum.globalCTMean.new$`hsa-miR-21-5p`    1    125.44 500.37
## - serum.globalCTMean.new$`hsa-miR-29a-3p`   1    125.85 501.04
## - serum.globalCTMean.new$`hsa-miR-1246`     1    125.90 501.12
## - serum.globalCTMean.new$`hsa-miR-27b-3p`   1    126.02 501.31
## - serum.globalCTMean.new$`hsa-miR-451a`     1    126.18 501.57
## - serum.globalCTMean.new$`hsa-miR-320a`     1    126.37 501.87
## <none>                                           125.14 501.89
## - serum.globalCTMean.new$`hsa-miR-874-3p`   1    126.80 502.56
## - serum.globalCTMean.new$`hsa-miR-363-3p`   1    129.21 506.38
## - serum.globalCTMean.new$`hsa-miR-125b-5p`  1    133.41 512.88
##
## Step:  AIC=500.12
## serum.all.original$`Biopsy Grade Group` ~ serum.globalCTMean.new$`hsa-miR-1246` +
##     serum.globalCTMean.new$`hsa-miR-363-3p` + serum.globalCTMean.new$`hsa-miR-320a` +
##     serum.globalCTMean.new$`hsa-miR-125b-5p` + serum.globalCTMean.new$`hsa-miR-27b-3p` +
##     serum.globalCTMean.new$`hsa-miR-29a-3p` + serum.globalCTMean.new$`hsa-miR-21-5p` +
##     serum.globalCTMean.new$`hsa-miR-451a` + serum.globalCTMean.new$`hsa-miR-874-3p`
##
##                                             Df Deviance    AIC
## - serum.globalCTMean.new$`hsa-miR-21-5p`    1    125.57 498.57
## - serum.globalCTMean.new$`hsa-miR-29a-3p`   1    125.95 499.19
## - serum.globalCTMean.new$`hsa-miR-27b-3p`   1    126.06 499.36
## - serum.globalCTMean.new$`hsa-miR-1246`     1    126.23 499.64
## - serum.globalCTMean.new$`hsa-miR-451a`     1    126.45 500.00
## <none>                                           125.29 500.12
## - serum.globalCTMean.new$`hsa-miR-320a`     1    126.63 500.28
## - serum.globalCTMean.new$`hsa-miR-874-3p`   1    127.18 501.17
## - serum.globalCTMean.new$`hsa-miR-363-3p`   1    129.63 505.04
## - serum.globalCTMean.new$`hsa-miR-125b-5p`  1    133.44 510.92
##
## Step:  AIC=498.57
## serum.all.original$`Biopsy Grade Group` ~ serum.globalCTMean.new$`hsa-miR-1246` +
```

```
##     serum.globalCTMean.new$'hsa-miR-363-3p' + serum.globalCTMean.new$'hsa-miR-320a' +
##     serum.globalCTMean.new$'hsa-miR-125b-5p' + serum.globalCTMean.new$'hsa-miR-27b-3p' +
##     serum.globalCTMean.new$'hsa-miR-29a-3p' + serum.globalCTMean.new$'hsa-miR-451a' +
##     serum.globalCTMean.new$'hsa-miR-874-3p'
##
##                                           Df Deviance    AIC
## - serum.globalCTMean.new$'hsa-miR-29a-3p'  1   126.36 497.86
## - serum.globalCTMean.new$'hsa-miR-1246'    1   126.44 497.97
## - serum.globalCTMean.new$'hsa-miR-27b-3p'  1   126.59 498.22
## - serum.globalCTMean.new$'hsa-miR-451a'    1   126.73 498.45
## <none>                                         125.57 498.57
## - serum.globalCTMean.new$'hsa-miR-320a'    1   127.21 499.21
## - serum.globalCTMean.new$'hsa-miR-874-3p'  1   127.54 499.73
## - serum.globalCTMean.new$'hsa-miR-363-3p'  1   130.06 503.71
## - serum.globalCTMean.new$'hsa-miR-125b-5p' 1   133.78 509.43
##
## Step:  AIC=497.86
## serum.all.original$'Biopsy Grade Group' ~ serum.globalCTMean.new$'hsa-miR-1246' +
##     serum.globalCTMean.new$'hsa-miR-363-3p' + serum.globalCTMean.new$'hsa-miR-320a' +
##     serum.globalCTMean.new$'hsa-miR-125b-5p' + serum.globalCTMean.new$'hsa-miR-27b-3p' +
##     serum.globalCTMean.new$'hsa-miR-451a' + serum.globalCTMean.new$'hsa-miR-874-3p'
##
##                                           Df Deviance    AIC
## - serum.globalCTMean.new$'hsa-miR-451a'    1   127.33 497.41
## <none>                                         126.36 497.86
## - serum.globalCTMean.new$'hsa-miR-27b-3p'  1   127.90 498.31
## - serum.globalCTMean.new$'hsa-miR-320a'    1   127.90 498.32
## - serum.globalCTMean.new$'hsa-miR-1246'    1   128.05 498.55
## - serum.globalCTMean.new$'hsa-miR-874-3p'  1   128.92 499.93
## - serum.globalCTMean.new$'hsa-miR-363-3p'  1   130.31 502.10
## - serum.globalCTMean.new$'hsa-miR-125b-5p' 1   134.44 508.43
##
## Step:  AIC=497.41
## serum.all.original$'Biopsy Grade Group' ~ serum.globalCTMean.new$'hsa-miR-1246' +
##     serum.globalCTMean.new$'hsa-miR-363-3p' + serum.globalCTMean.new$'hsa-miR-320a' +
##     serum.globalCTMean.new$'hsa-miR-125b-5p' + serum.globalCTMean.new$'hsa-miR-27b-3p' +
##     serum.globalCTMean.new$'hsa-miR-874-3p'
##
##                                           Df Deviance    AIC
## - serum.globalCTMean.new$'hsa-miR-27b-3p'  1   128.49 497.24
## <none>                                         127.33 497.41
## - serum.globalCTMean.new$'hsa-miR-1246'    1   128.69 497.57
## - serum.globalCTMean.new$'hsa-miR-874-3p'  1   129.31 498.54
## - serum.globalCTMean.new$'hsa-miR-320a'    1   130.02 499.65
## - serum.globalCTMean.new$'hsa-miR-363-3p'  1   132.12 502.90
## - serum.globalCTMean.new$'hsa-miR-125b-5p' 1   134.78 506.94
##
## Step:  AIC=497.24
## serum.all.original$'Biopsy Grade Group' ~ serum.globalCTMean.new$'hsa-miR-1246' +
##     serum.globalCTMean.new$'hsa-miR-363-3p' + serum.globalCTMean.new$'hsa-miR-320a' +
##     serum.globalCTMean.new$'hsa-miR-125b-5p' + serum.globalCTMean.new$'hsa-miR-874-3p'
##
##                                           Df Deviance    AIC
## <none>                                         128.49 497.24
```

```
## - serum.globalCTMean.new$`hsa-miR-874-3p`     1     129.98 497.59
## - serum.globalCTMean.new$`hsa-miR-1246`        1     130.28 498.06
## - serum.globalCTMean.new$`hsa-miR-320a`        1     132.07 500.83
## - serum.globalCTMean.new$`hsa-miR-363-3p`      1     133.82 503.50
## - serum.globalCTMean.new$`hsa-miR-125b-5p`     1     136.09 506.91
```

```r
# serum geNorm
fullmodel.serum.geNorm = glm(formula = serum.all.original$`Biopsy Grade Group`~ serum.geNorm.new$`hsa-m

step.serum.grade.geNorm = stepAIC(object = fullmodel.serum.geNorm, direction = "backward")
```

```
## Start:  AIC=510.17
## serum.all.original$`Biopsy Grade Group` ~ serum.geNorm.new$`hsa-miR-1246` +
##     serum.geNorm.new$`hsa-miR-363-3p` + serum.geNorm.new$`hsa-miR-320a` +
##     serum.geNorm.new$`hsa-miR-125b-5p` + serum.geNorm.new$`hsa-miR-27a-3p` +
##     serum.geNorm.new$`hsa-miR-16-5p` + serum.geNorm.new$`hsa-let-7b-5p` +
##     serum.geNorm.new$`hsa-miR-27b-3p` + serum.geNorm.new$`hsa-miR-29a-3p` +
##     serum.geNorm.new$`hsa-miR-21-5p` + serum.geNorm.new$`hsa-miR-451a` +
##     serum.geNorm.new$`hsa-miR-874-3p`
##
##                                      Df Deviance    AIC
## - serum.geNorm.new$`hsa-let-7b-5p`    1    127.81 508.17
## - serum.geNorm.new$`hsa-miR-27a-3p`   1    127.81 508.17
## - serum.geNorm.new$`hsa-miR-21-5p`    1    127.81 508.17
## - serum.geNorm.new$`hsa-miR-1246`     1    127.92 508.35
## - serum.geNorm.new$`hsa-miR-16-5p`    1    128.03 508.52
## - serum.geNorm.new$`hsa-miR-874-3p`   1    128.32 508.97
## - serum.geNorm.new$`hsa-miR-27b-3p`   1    128.46 509.19
## - serum.geNorm.new$`hsa-miR-320a`     1    128.76 509.68
## - serum.geNorm.new$`hsa-miR-451a`     1    128.82 509.77
## <none>                                     127.81 510.17
## - serum.geNorm.new$`hsa-miR-29a-3p`   1    129.66 511.08
## - serum.geNorm.new$`hsa-miR-363-3p`   1    130.13 511.83
## - serum.geNorm.new$`hsa-miR-125b-5p`  1    134.14 517.98
##
## Step:  AIC=508.17
## serum.all.original$`Biopsy Grade Group` ~ serum.geNorm.new$`hsa-miR-1246` +
##     serum.geNorm.new$`hsa-miR-363-3p` + serum.geNorm.new$`hsa-miR-320a` +
##     serum.geNorm.new$`hsa-miR-125b-5p` + serum.geNorm.new$`hsa-miR-27a-3p` +
##     serum.geNorm.new$`hsa-miR-16-5p` + serum.geNorm.new$`hsa-miR-27b-3p` +
##     serum.geNorm.new$`hsa-miR-29a-3p` + serum.geNorm.new$`hsa-miR-21-5p` +
##     serum.geNorm.new$`hsa-miR-451a` + serum.geNorm.new$`hsa-miR-874-3p`
##
##                                      Df Deviance    AIC
## - serum.geNorm.new$`hsa-miR-27a-3p`   1    127.81 506.17
## - serum.geNorm.new$`hsa-miR-21-5p`    1    127.81 506.17
## - serum.geNorm.new$`hsa-miR-1246`     1    127.92 506.35
## - serum.geNorm.new$`hsa-miR-16-5p`    1    128.09 506.61
## - serum.geNorm.new$`hsa-miR-874-3p`   1    128.32 506.97
## - serum.geNorm.new$`hsa-miR-27b-3p`   1    128.46 507.20
## - serum.geNorm.new$`hsa-miR-320a`     1    128.77 507.69
## - serum.geNorm.new$`hsa-miR-451a`     1    128.83 507.78
## <none>                                     127.81 508.17
## - serum.geNorm.new$`hsa-miR-29a-3p`   1    129.66 509.09
```

```
## - serum.geNorm.new$'hsa-miR-363-3p'   1   130.14 509.83
## - serum.geNorm.new$'hsa-miR-125b-5p'  1   134.16 516.01
##
## Step:  AIC=506.17
## serum.all.original$'Biopsy Grade Group' ~ serum.geNorm.new$'hsa-miR-1246' +
##     serum.geNorm.new$'hsa-miR-363-3p' + serum.geNorm.new$'hsa-miR-320a' +
##     serum.geNorm.new$'hsa-miR-125b-5p' + serum.geNorm.new$'hsa-miR-16-5p' +
##     serum.geNorm.new$'hsa-miR-27b-3p' + serum.geNorm.new$'hsa-miR-29a-3p' +
##     serum.geNorm.new$'hsa-miR-21-5p' + serum.geNorm.new$'hsa-miR-451a' +
##     serum.geNorm.new$'hsa-miR-874-3p'
##
##                                       Df Deviance    AIC
## - serum.geNorm.new$'hsa-miR-21-5p'     1   127.81 504.17
## - serum.geNorm.new$'hsa-miR-1246'      1   127.94 504.38
## - serum.geNorm.new$'hsa-miR-16-5p'     1   128.09 504.62
## - serum.geNorm.new$'hsa-miR-874-3p'    1   128.32 504.98
## - serum.geNorm.new$'hsa-miR-320a'      1   128.78 505.70
## - serum.geNorm.new$'hsa-miR-451a'      1   128.86 505.83
## <none>                                     127.81 506.17
## - serum.geNorm.new$'hsa-miR-27b-3p'    1   129.13 506.25
## - serum.geNorm.new$'hsa-miR-29a-3p'    1   129.77 507.26
## - serum.geNorm.new$'hsa-miR-363-3p'    1   130.19 507.92
## - serum.geNorm.new$'hsa-miR-125b-5p'   1   134.75 514.90
##
## Step:  AIC=504.17
## serum.all.original$'Biopsy Grade Group' ~ serum.geNorm.new$'hsa-miR-1246' +
##     serum.geNorm.new$'hsa-miR-363-3p' + serum.geNorm.new$'hsa-miR-320a' +
##     serum.geNorm.new$'hsa-miR-125b-5p' + serum.geNorm.new$'hsa-miR-16-5p' +
##     serum.geNorm.new$'hsa-miR-27b-3p' + serum.geNorm.new$'hsa-miR-29a-3p' +
##     serum.geNorm.new$'hsa-miR-451a' + serum.geNorm.new$'hsa-miR-874-3p'
##
##                                       Df Deviance    AIC
## - serum.geNorm.new$'hsa-miR-1246'      1   127.94 502.38
## - serum.geNorm.new$'hsa-miR-16-5p'     1   128.09 502.62
## - serum.geNorm.new$'hsa-miR-874-3p'    1   128.32 502.98
## - serum.geNorm.new$'hsa-miR-320a'      1   128.85 503.82
## - serum.geNorm.new$'hsa-miR-451a'      1   128.87 503.84
## <none>                                     127.81 504.17
## - serum.geNorm.new$'hsa-miR-27b-3p'    1   129.13 504.25
## - serum.geNorm.new$'hsa-miR-29a-3p'    1   129.84 505.37
## - serum.geNorm.new$'hsa-miR-363-3p'    1   130.25 506.00
## - serum.geNorm.new$'hsa-miR-125b-5p'   1   134.78 512.94
##
## Step:  AIC=502.38
## serum.all.original$'Biopsy Grade Group' ~ serum.geNorm.new$'hsa-miR-363-3p' +
##     serum.geNorm.new$'hsa-miR-320a' + serum.geNorm.new$'hsa-miR-125b-5p' +
##     serum.geNorm.new$'hsa-miR-16-5p' + serum.geNorm.new$'hsa-miR-27b-3p' +
##     serum.geNorm.new$'hsa-miR-29a-3p' + serum.geNorm.new$'hsa-miR-451a' +
##     serum.geNorm.new$'hsa-miR-874-3p'
##
##                                       Df Deviance    AIC
## - serum.geNorm.new$'hsa-miR-16-5p'     1   128.30 500.95
## - serum.geNorm.new$'hsa-miR-874-3p'    1   128.43 501.16
## - serum.geNorm.new$'hsa-miR-451a'      1   129.04 502.12
```

```
## <none>                                         127.94 502.38
## - serum.geNorm.new$'hsa-miR-320a'     1    129.38 502.65
## - serum.geNorm.new$'hsa-miR-27b-3p'   1    129.45 502.76
## - serum.geNorm.new$'hsa-miR-363-3p'   1    130.36 504.18
## - serum.geNorm.new$'hsa-miR-29a-3p'   1    130.54 504.46
## - serum.geNorm.new$'hsa-miR-125b-5p'  1    134.90 511.13
##
## Step:  AIC=500.95
## serum.all.original$'Biopsy Grade Group' ~ serum.geNorm.new$'hsa-miR-363-3p' +
##     serum.geNorm.new$'hsa-miR-320a' + serum.geNorm.new$'hsa-miR-125b-5p' +
##     serum.geNorm.new$'hsa-miR-27b-3p' + serum.geNorm.new$'hsa-miR-29a-3p' +
##     serum.geNorm.new$'hsa-miR-451a' + serum.geNorm.new$'hsa-miR-874-3p'
##
##                                       Df Deviance    AIC
## - serum.geNorm.new$'hsa-miR-874-3p'   1    128.97 500.00
## - serum.geNorm.new$'hsa-miR-451a'     1    129.05 500.13
## <none>                                     128.30 500.95
## - serum.geNorm.new$'hsa-miR-27b-3p'   1    129.89 501.45
## - serum.geNorm.new$'hsa-miR-320a'     1    130.05 501.70
## - serum.geNorm.new$'hsa-miR-29a-3p'   1    131.08 503.30
## - serum.geNorm.new$'hsa-miR-363-3p'   1    131.28 503.60
## - serum.geNorm.new$'hsa-miR-125b-5p'  1    134.94 509.19
##
## Step:  AIC=500
## serum.all.original$'Biopsy Grade Group' ~ serum.geNorm.new$'hsa-miR-363-3p' +
##     serum.geNorm.new$'hsa-miR-320a' + serum.geNorm.new$'hsa-miR-125b-5p' +
##     serum.geNorm.new$'hsa-miR-27b-3p' + serum.geNorm.new$'hsa-miR-29a-3p' +
##     serum.geNorm.new$'hsa-miR-451a'
##
##                                       Df Deviance    AIC
## - serum.geNorm.new$'hsa-miR-451a'     1    129.53 498.89
## - serum.geNorm.new$'hsa-miR-27b-3p'   1    130.18 499.89
## <none>                                     128.97 500.00
## - serum.geNorm.new$'hsa-miR-363-3p'   1    132.07 502.82
## - serum.geNorm.new$'hsa-miR-29a-3p'   1    132.29 503.16
## - serum.geNorm.new$'hsa-miR-320a'     1    133.50 505.01
## - serum.geNorm.new$'hsa-miR-125b-5p'  1    134.95 507.20
##
## Step:  AIC=498.89
## serum.all.original$'Biopsy Grade Group' ~ serum.geNorm.new$'hsa-miR-363-3p' +
##     serum.geNorm.new$'hsa-miR-320a' + serum.geNorm.new$'hsa-miR-125b-5p' +
##     serum.geNorm.new$'hsa-miR-27b-3p' + serum.geNorm.new$'hsa-miR-29a-3p'
##
##                                       Df Deviance    AIC
## - serum.geNorm.new$'hsa-miR-27b-3p'   1    130.37 498.19
## <none>                                     129.53 498.89
## - serum.geNorm.new$'hsa-miR-363-3p'   1    132.28 501.15
## - serum.geNorm.new$'hsa-miR-29a-3p'   1    132.36 501.26
## - serum.geNorm.new$'hsa-miR-320a'     1    134.96 505.21
## - serum.geNorm.new$'hsa-miR-125b-5p'  1    135.72 506.37
##
## Step:  AIC=498.19
## serum.all.original$'Biopsy Grade Group' ~ serum.geNorm.new$'hsa-miR-363-3p' +
##     serum.geNorm.new$'hsa-miR-320a' + serum.geNorm.new$'hsa-miR-125b-5p' +
```

```
##      serum.geNorm.new$`hsa-miR-29a-3p`
##
##                                    Df Deviance    AIC
## <none>                                  130.37 498.19
## - serum.geNorm.new$`hsa-miR-29a-3p`   1   132.88 500.06
## - serum.geNorm.new$`hsa-miR-320a`     1   136.31 505.24
## - serum.geNorm.new$`hsa-miR-363-3p`   1   137.52 507.03
## - serum.geNorm.new$`hsa-miR-125b-5p`  1   139.19 509.49
```

```r
# serum NormFinder
fullmodel.serum.NormFinder = glm(formula = serum.all.original$`Biopsy Grade Group`~ serum.NormFinder.ne

step.serum.grade.NormFinder = stepAIC(object = fullmodel.serum.NormFinder, direction = "backward")
```

```
## Start:  AIC=508.01
## serum.all.original$`Biopsy Grade Group` ~ serum.NormFinder.new$`hsa-miR-1246` +
##      serum.NormFinder.new$`hsa-miR-363-3p` + serum.NormFinder.new$`hsa-miR-320a` +
##      serum.NormFinder.new$`hsa-miR-125b-5p` + serum.NormFinder.new$`hsa-miR-27a-3p` +
##      serum.NormFinder.new$`hsa-miR-16-5p` + serum.NormFinder.new$`hsa-let-7b-5p` +
##      serum.NormFinder.new$`hsa-miR-27b-3p` + serum.NormFinder.new$`hsa-miR-29a-3p` +
##      serum.NormFinder.new$`hsa-miR-21-5p` + serum.NormFinder.new$`hsa-miR-451a` +
##      serum.NormFinder.new$`hsa-miR-874-3p`
##
##                                         Df Deviance    AIC
## - serum.NormFinder.new$`hsa-miR-27a-3p`  1   126.46 506.02
## - serum.NormFinder.new$`hsa-miR-16-5p`   1   126.47 506.03
## - serum.NormFinder.new$`hsa-let-7b-5p`   1   126.48 506.04
## - serum.NormFinder.new$`hsa-miR-21-5p`   1   126.53 506.12
## - serum.NormFinder.new$`hsa-miR-320a`    1   127.11 507.06
## - serum.NormFinder.new$`hsa-miR-1246`    1   127.13 507.08
## - serum.NormFinder.new$`hsa-miR-451a`    1   127.22 507.23
## - serum.NormFinder.new$`hsa-miR-874-3p`  1   127.50 507.68
## <none>                                       126.46 508.01
## - serum.NormFinder.new$`hsa-miR-27b-3p`  1   127.74 508.06
## - serum.NormFinder.new$`hsa-miR-29a-3p`  1   127.76 508.10
## - serum.NormFinder.new$`hsa-miR-363-3p`  1   128.85 509.81
## - serum.NormFinder.new$`hsa-miR-125b-5p` 1   136.73 521.86
##
## Step:  AIC=506.02
## serum.all.original$`Biopsy Grade Group` ~ serum.NormFinder.new$`hsa-miR-1246` +
##      serum.NormFinder.new$`hsa-miR-363-3p` + serum.NormFinder.new$`hsa-miR-320a` +
##      serum.NormFinder.new$`hsa-miR-125b-5p` + serum.NormFinder.new$`hsa-miR-16-5p` +
##      serum.NormFinder.new$`hsa-let-7b-5p` + serum.NormFinder.new$`hsa-miR-27b-3p` +
##      serum.NormFinder.new$`hsa-miR-29a-3p` + serum.NormFinder.new$`hsa-miR-21-5p` +
##      serum.NormFinder.new$`hsa-miR-451a` + serum.NormFinder.new$`hsa-miR-874-3p`
##
##                                         Df Deviance    AIC
## - serum.NormFinder.new$`hsa-miR-16-5p`   1   126.48 504.04
## - serum.NormFinder.new$`hsa-let-7b-5p`   1   126.48 504.05
## - serum.NormFinder.new$`hsa-miR-21-5p`   1   126.53 504.12
## - serum.NormFinder.new$`hsa-miR-320a`    1   127.11 505.06
## - serum.NormFinder.new$`hsa-miR-1246`    1   127.16 505.13
## - serum.NormFinder.new$`hsa-miR-451a`    1   127.24 505.27
## - serum.NormFinder.new$`hsa-miR-874-3p`  1   127.52 505.71
```

```
## <none>                                        126.46 506.02
## - serum.NormFinder.new$`hsa-miR-29a-3p`   1   127.92 506.35
## - serum.NormFinder.new$`hsa-miR-27b-3p`   1   128.75 507.65
## - serum.NormFinder.new$`hsa-miR-363-3p`   1   128.88 507.86
## - serum.NormFinder.new$`hsa-miR-125b-5p`  1   136.96 520.21
##
## Step:  AIC=504.04
## serum.all.original$`Biopsy Grade Group` ~ serum.NormFinder.new$`hsa-miR-1246` +
##     serum.NormFinder.new$`hsa-miR-363-3p` + serum.NormFinder.new$`hsa-miR-320a` +
##     serum.NormFinder.new$`hsa-miR-125b-5p` + serum.NormFinder.new$`hsa-let-7b-5p` +
##     serum.NormFinder.new$`hsa-miR-27b-3p` + serum.NormFinder.new$`hsa-miR-29a-3p` +
##     serum.NormFinder.new$`hsa-miR-21-5p` + serum.NormFinder.new$`hsa-miR-451a` +
##     serum.NormFinder.new$`hsa-miR-874-3p`
##
##                                           Df Deviance    AIC
## - serum.NormFinder.new$`hsa-let-7b-5p`     1   126.52 502.11
## - serum.NormFinder.new$`hsa-miR-21-5p`     1   126.55 502.16
## - serum.NormFinder.new$`hsa-miR-320a`      1   127.16 503.13
## - serum.NormFinder.new$`hsa-miR-1246`      1   127.28 503.33
## - serum.NormFinder.new$`hsa-miR-451a`      1   127.43 503.56
## - serum.NormFinder.new$`hsa-miR-874-3p`    1   127.61 503.86
## <none>                                        126.48 504.04
## - serum.NormFinder.new$`hsa-miR-29a-3p`    1   127.95 504.39
## - serum.NormFinder.new$`hsa-miR-27b-3p`    1   128.78 505.71
## - serum.NormFinder.new$`hsa-miR-363-3p`    1   129.11 506.23
## - serum.NormFinder.new$`hsa-miR-125b-5p`   1   137.04 518.32
##
## Step:  AIC=502.11
## serum.all.original$`Biopsy Grade Group` ~ serum.NormFinder.new$`hsa-miR-1246` +
##     serum.NormFinder.new$`hsa-miR-363-3p` + serum.NormFinder.new$`hsa-miR-320a` +
##     serum.NormFinder.new$`hsa-miR-125b-5p` + serum.NormFinder.new$`hsa-miR-27b-3p` +
##     serum.NormFinder.new$`hsa-miR-29a-3p` + serum.NormFinder.new$`hsa-miR-21-5p` +
##     serum.NormFinder.new$`hsa-miR-451a` + serum.NormFinder.new$`hsa-miR-874-3p`
##
##                                           Df Deviance    AIC
## - serum.NormFinder.new$`hsa-miR-21-5p`     1   126.60 500.23
## - serum.NormFinder.new$`hsa-miR-320a`      1   127.26 501.29
## - serum.NormFinder.new$`hsa-miR-1246`      1   127.31 501.38
## - serum.NormFinder.new$`hsa-miR-451a`      1   127.53 501.72
## - serum.NormFinder.new$`hsa-miR-874-3p`    1   127.68 501.96
## <none>                                        126.52 502.11
## - serum.NormFinder.new$`hsa-miR-29a-3p`    1   127.95 502.40
## - serum.NormFinder.new$`hsa-miR-27b-3p`    1   129.00 504.05
## - serum.NormFinder.new$`hsa-miR-363-3p`    1   129.30 504.53
## - serum.NormFinder.new$`hsa-miR-125b-5p`   1   137.44 516.92
##
## Step:  AIC=500.23
## serum.all.original$`Biopsy Grade Group` ~ serum.NormFinder.new$`hsa-miR-1246` +
##     serum.NormFinder.new$`hsa-miR-363-3p` + serum.NormFinder.new$`hsa-miR-320a` +
##     serum.NormFinder.new$`hsa-miR-125b-5p` + serum.NormFinder.new$`hsa-miR-27b-3p` +
##     serum.NormFinder.new$`hsa-miR-29a-3p` + serum.NormFinder.new$`hsa-miR-451a` +
##     serum.NormFinder.new$`hsa-miR-874-3p`
##
##                                           Df Deviance    AIC
```

```
## - serum.NormFinder.new$'hsa-miR-320a'     1   127.26 499.29
## - serum.NormFinder.new$'hsa-miR-1246'     1   127.41 499.53
## - serum.NormFinder.new$'hsa-miR-451a'     1   127.62 499.86
## - serum.NormFinder.new$'hsa-miR-874-3p'   1   127.73 500.04
## <none>                                        126.60 500.23
## - serum.NormFinder.new$'hsa-miR-29a-3p'   1   127.97 500.42
## - serum.NormFinder.new$'hsa-miR-27b-3p'   1   129.09 502.20
## - serum.NormFinder.new$'hsa-miR-363-3p'   1   129.31 502.54
## - serum.NormFinder.new$'hsa-miR-125b-5p'  1   137.51 515.02
##
## Step:  AIC=499.29
## serum.all.original$'Biopsy Grade Group' ~ serum.NormFinder.new$'hsa-miR-1246' +
##       serum.NormFinder.new$'hsa-miR-363-3p' + serum.NormFinder.new$'hsa-miR-125b-5p' +
##       serum.NormFinder.new$'hsa-miR-27b-3p' + serum.NormFinder.new$'hsa-miR-29a-3p' +
##       serum.NormFinder.new$'hsa-miR-451a' + serum.NormFinder.new$'hsa-miR-874-3p'
##
##                                           Df Deviance    AIC
## <none>                                        127.26 499.29
## - serum.NormFinder.new$'hsa-miR-29a-3p'   1   128.53 499.30
## - serum.NormFinder.new$'hsa-miR-1246'     1   128.70 499.57
## - serum.NormFinder.new$'hsa-miR-451a'     1   129.07 500.17
## - serum.NormFinder.new$'hsa-miR-363-3p'   1   130.09 501.76
## - serum.NormFinder.new$'hsa-miR-27b-3p'   1   130.33 502.13
## - serum.NormFinder.new$'hsa-miR-874-3p'   1   130.37 502.19
## - serum.NormFinder.new$'hsa-miR-125b-5p'  1   138.17 513.99
```

```r
# EV CT mean
fullmodel.EV.CTMean = glm(formula = EV.all.original$'Biopsy Grade Group'~ EV.globalCTMean.new$'hsa-miR-3

step.EV.grade.CTMean = stepAIC(object = fullmodel.EV.CTMean, direction = "backward")
```

```
## Start:  AIC=320.25
## EV.all.original$'Biopsy Grade Group' ~ EV.globalCTMean.new$'hsa-miR-335-5p' +
##       EV.globalCTMean.new$'hsa-miR-191-5p' + EV.globalCTMean.new$'hsa-miR-107' +
##       EV.globalCTMean.new$'hsa-miR-130b-3p' + EV.globalCTMean.new$'hsa-miR-221-3p' +
##       EV.globalCTMean.new$'hsa-miR-214-3p' + EV.globalCTMean.new$'hsa-miR-103a-3p' +
##       EV.globalCTMean.new$'hsa-miR-330-3p' + EV.globalCTMean.new$'hsa-miR-30a-5p' +
##       EV.globalCTMean.new$'hsa-let-7a-5p'
##
##                                           Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-191-5p'    1   85.192 318.43
## - EV.globalCTMean.new$'hsa-miR-107'       1   85.240 318.49
## - EV.globalCTMean.new$'hsa-miR-103a-3p'   1   85.353 318.65
## - EV.globalCTMean.new$'hsa-miR-30a-5p'    1   85.497 318.85
## - EV.globalCTMean.new$'hsa-miR-221-3p'    1   85.615 319.01
## - EV.globalCTMean.new$'hsa-miR-330-3p'    1   85.681 319.10
## - EV.globalCTMean.new$'hsa-let-7a-5p'     1   85.724 319.16
## - EV.globalCTMean.new$'hsa-miR-130b-3p'   1   86.016 319.56
## - EV.globalCTMean.new$'hsa-miR-214-3p'    1   86.096 319.67
## <none>                                        85.061 320.25
## - EV.globalCTMean.new$'hsa-miR-335-5p'    1   86.636 320.41
##
## Step:  AIC=318.43
## EV.all.original$'Biopsy Grade Group' ~ EV.globalCTMean.new$'hsa-miR-335-5p' +
```

```
##       EV.globalCTMean.new$'hsa-miR-107' + EV.globalCTMean.new$'hsa-miR-130b-3p' +
##       EV.globalCTMean.new$'hsa-miR-221-3p' + EV.globalCTMean.new$'hsa-miR-214-3p' +
##       EV.globalCTMean.new$'hsa-miR-103a-3p' + EV.globalCTMean.new$'hsa-miR-330-3p' +
##       EV.globalCTMean.new$'hsa-miR-30a-5p' + EV.globalCTMean.new$'hsa-let-7a-5p'
##
##                                        Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-107'     1   85.417 316.74
## - EV.globalCTMean.new$'hsa-miR-103a-3p' 1   85.436 316.76
## - EV.globalCTMean.new$'hsa-miR-221-3p'  1   85.617 317.01
## - EV.globalCTMean.new$'hsa-miR-30a-5p'  1   85.673 317.09
## - EV.globalCTMean.new$'hsa-let-7a-5p'   1   85.738 317.18
## - EV.globalCTMean.new$'hsa-miR-330-3p'  1   85.914 317.42
## - EV.globalCTMean.new$'hsa-miR-130b-3p' 1   86.034 317.59
## - EV.globalCTMean.new$'hsa-miR-214-3p'  1   86.358 318.03
## - EV.globalCTMean.new$'hsa-miR-335-5p'  1   86.644 318.42
## <none>                                      85.192 318.43
##
## Step:  AIC=316.74
## EV.all.original$'Biopsy Grade Group' ~ EV.globalCTMean.new$'hsa-miR-335-5p' +
##     EV.globalCTMean.new$'hsa-miR-130b-3p' + EV.globalCTMean.new$'hsa-miR-221-3p' +
##     EV.globalCTMean.new$'hsa-miR-214-3p' + EV.globalCTMean.new$'hsa-miR-103a-3p' +
##     EV.globalCTMean.new$'hsa-miR-330-3p' + EV.globalCTMean.new$'hsa-miR-30a-5p' +
##     EV.globalCTMean.new$'hsa-let-7a-5p'
##
##                                        Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-103a-3p' 1   85.437 314.77
## - EV.globalCTMean.new$'hsa-miR-221-3p'  1   85.902 315.41
## - EV.globalCTMean.new$'hsa-let-7a-5p'   1   85.911 315.42
## - EV.globalCTMean.new$'hsa-miR-30a-5p'  1   86.016 315.56
## - EV.globalCTMean.new$'hsa-miR-330-3p'  1   86.026 315.58
## - EV.globalCTMean.new$'hsa-miR-214-3p'  1   86.467 316.18
## - EV.globalCTMean.new$'hsa-miR-130b-3p' 1   86.639 316.41
## <none>                                      85.417 316.74
## - EV.globalCTMean.new$'hsa-miR-335-5p'  1   87.016 316.93
##
## Step:  AIC=314.77
## EV.all.original$'Biopsy Grade Group' ~ EV.globalCTMean.new$'hsa-miR-335-5p' +
##     EV.globalCTMean.new$'hsa-miR-130b-3p' + EV.globalCTMean.new$'hsa-miR-221-3p' +
##     EV.globalCTMean.new$'hsa-miR-214-3p' + EV.globalCTMean.new$'hsa-miR-330-3p' +
##     EV.globalCTMean.new$'hsa-miR-30a-5p' + EV.globalCTMean.new$'hsa-let-7a-5p'
##
##                                        Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-221-3p'  1   85.966 313.50
## - EV.globalCTMean.new$'hsa-miR-30a-5p'  1   86.021 313.57
## - EV.globalCTMean.new$'hsa-miR-330-3p'  1   86.036 313.59
## - EV.globalCTMean.new$'hsa-miR-214-3p'  1   86.498 314.22
## - EV.globalCTMean.new$'hsa-miR-130b-3p' 1   86.712 314.51
## <none>                                      85.437 314.77
## - EV.globalCTMean.new$'hsa-let-7a-5p'   1   87.154 315.12
## - EV.globalCTMean.new$'hsa-miR-335-5p'  1   87.158 315.12
##
## Step:  AIC=313.5
## EV.all.original$'Biopsy Grade Group' ~ EV.globalCTMean.new$'hsa-miR-335-5p' +
##     EV.globalCTMean.new$'hsa-miR-130b-3p' + EV.globalCTMean.new$'hsa-miR-214-3p' +
```

```
##     EV.globalCTMean.new$'hsa-miR-330-3p' + EV.globalCTMean.new$'hsa-miR-30a-5p' +
##     EV.globalCTMean.new$'hsa-let-7a-5p'
##
##                                        Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-330-3p'  1   86.303 311.96
## - EV.globalCTMean.new$'hsa-miR-30a-5p'  1   86.559 312.31
## - EV.globalCTMean.new$'hsa-miR-130b-3p' 1   86.712 312.51
## - EV.globalCTMean.new$'hsa-miR-214-3p'  1   86.966 312.86
## - EV.globalCTMean.new$'hsa-miR-335-5p'  1   87.269 313.27
## - EV.globalCTMean.new$'hsa-let-7a-5p'   1   87.301 313.31
## <none>                                      85.966 313.50
##
## Step:  AIC=311.96
## EV.all.original$'Biopsy Grade Group' ~ EV.globalCTMean.new$'hsa-miR-335-5p' +
##     EV.globalCTMean.new$'hsa-miR-130b-3p' + EV.globalCTMean.new$'hsa-miR-214-3p' +
##     EV.globalCTMean.new$'hsa-miR-30a-5p' + EV.globalCTMean.new$'hsa-let-7a-5p'
##
##                                        Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-30a-5p'  1   87.083 311.02
## - EV.globalCTMean.new$'hsa-miR-130b-3p' 1   87.144 311.10
## - EV.globalCTMean.new$'hsa-miR-214-3p'  1   87.209 311.19
## - EV.globalCTMean.new$'hsa-let-7a-5p'   1   87.645 311.78
## <none>                                      86.303 311.96
## - EV.globalCTMean.new$'hsa-miR-335-5p'  1   88.984 313.57
##
## Step:  AIC=311.02
## EV.all.original$'Biopsy Grade Group' ~ EV.globalCTMean.new$'hsa-miR-335-5p' +
##     EV.globalCTMean.new$'hsa-miR-130b-3p' + EV.globalCTMean.new$'hsa-miR-214-3p' +
##     EV.globalCTMean.new$'hsa-let-7a-5p'
##
##                                        Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-130b-3p' 1   88.081 310.36
## - EV.globalCTMean.new$'hsa-miR-214-3p'  1   88.412 310.81
## <none>                                      87.083 311.02
## - EV.globalCTMean.new$'hsa-let-7a-5p'   1   88.923 311.49
## - EV.globalCTMean.new$'hsa-miR-335-5p'  1   89.882 312.75
##
## Step: AIC=310.36
## EV.all.original$'Biopsy Grade Group' ~ EV.globalCTMean.new$'hsa-miR-335-5p' +
##     EV.globalCTMean.new$'hsa-miR-214-3p' + EV.globalCTMean.new$'hsa-let-7a-5p'
##
##                                        Df Deviance    AIC
## <none>                                      88.081 310.36
## - EV.globalCTMean.new$'hsa-miR-214-3p'  1   89.672 310.48
## - EV.globalCTMean.new$'hsa-let-7a-5p'   1   90.301 311.30
## - EV.globalCTMean.new$'hsa-miR-335-5p'  1   92.291 313.87
```

```r
# EV geNorm
fullmodel.EV.geNorm = glm(formula = EV.all.original$'Biopsy Grade Group'~ EV.geNorm.new$'hsa-miR-335-5p

step.EV.grade.geNorm = stepAIC(object = fullmodel.EV.geNorm, direction = "backward")
```

```
## Start:  AIC=317.08
## EV.all.original$'Biopsy Grade Group' ~ EV.geNorm.new$'hsa-miR-335-5p' +
```

```
##     EV.geNorm.new$'hsa-miR-130b-3p' + EV.geNorm.new$'hsa-miR-191-5p' +
##     EV.geNorm.new$'hsa-miR-221-3p' + EV.geNorm.new$'hsa-miR-214-3p' +
##     EV.geNorm.new$'hsa-miR-107' + EV.geNorm.new$'hsa-miR-330-3p' +
##     EV.geNorm.new$'hsa-miR-103a-3p'
##
##                                     Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-191-5p'     1   85.843 315.33
## - EV.geNorm.new$'hsa-miR-221-3p'     1   86.025 315.58
## - EV.geNorm.new$'hsa-miR-330-3p'     1   86.210 315.83
## - EV.geNorm.new$'hsa-miR-103a-3p'    1   86.211 315.83
## - EV.geNorm.new$'hsa-miR-107'        1   86.366 316.04
## - EV.geNorm.new$'hsa-miR-130b-3p'    1   86.588 316.35
## <none>                                  85.661 317.08
## - EV.geNorm.new$'hsa-miR-335-5p'     1   87.156 317.12
## - EV.geNorm.new$'hsa-miR-214-3p'     1   87.299 317.31
##
## Step:  AIC=315.33
## EV.all.original$'Biopsy Grade Group' ~ EV.geNorm.new$'hsa-miR-335-5p' +
##     EV.geNorm.new$'hsa-miR-130b-3p' + EV.geNorm.new$'hsa-miR-221-3p' +
##     EV.geNorm.new$'hsa-miR-214-3p' + EV.geNorm.new$'hsa-miR-107' +
##     EV.geNorm.new$'hsa-miR-330-3p' + EV.geNorm.new$'hsa-miR-103a-3p'
##
##                                     Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-221-3p'     1   86.036 313.59
## - EV.geNorm.new$'hsa-miR-103a-3p'    1   86.361 314.04
## - EV.geNorm.new$'hsa-miR-330-3p'     1   86.513 314.24
## - EV.geNorm.new$'hsa-miR-107'        1   86.653 314.43
## - EV.geNorm.new$'hsa-miR-130b-3p'    1   86.676 314.46
## - EV.geNorm.new$'hsa-miR-335-5p'     1   87.170 315.14
## <none>                                  85.843 315.33
## - EV.geNorm.new$'hsa-miR-214-3p'     1   87.670 315.81
##
## Step:  AIC=313.59
## EV.all.original$'Biopsy Grade Group' ~ EV.geNorm.new$'hsa-miR-335-5p' +
##     EV.geNorm.new$'hsa-miR-130b-3p' + EV.geNorm.new$'hsa-miR-214-3p' +
##     EV.geNorm.new$'hsa-miR-107' + EV.geNorm.new$'hsa-miR-330-3p' +
##     EV.geNorm.new$'hsa-miR-103a-3p'
##
##                                     Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-330-3p'     1   86.535 312.27
## - EV.geNorm.new$'hsa-miR-103a-3p'    1   86.645 312.42
## - EV.geNorm.new$'hsa-miR-130b-3p'    1   86.676 312.46
## - EV.geNorm.new$'hsa-miR-107'        1   86.899 312.77
## - EV.geNorm.new$'hsa-miR-335-5p'     1   87.182 313.15
## <none>                                  86.036 313.59
## - EV.geNorm.new$'hsa-miR-214-3p'     1   87.879 314.09
##
## Step:  AIC=312.27
## EV.all.original$'Biopsy Grade Group' ~ EV.geNorm.new$'hsa-miR-335-5p' +
##     EV.geNorm.new$'hsa-miR-130b-3p' + EV.geNorm.new$'hsa-miR-214-3p' +
##     EV.geNorm.new$'hsa-miR-107' + EV.geNorm.new$'hsa-miR-103a-3p'
##
##                                     Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-103a-3p'    1   86.933 310.81
```

```
## - EV.geNorm.new$'hsa-miR-107'      1   87.166 311.13
## - EV.geNorm.new$'hsa-miR-130b-3p'  1   87.353 311.38
## <none>                                 86.535 312.27
## - EV.geNorm.new$'hsa-miR-214-3p'   1   88.210 312.54
## - EV.geNorm.new$'hsa-miR-335-5p'   1   89.260 313.93
##
## Step:  AIC=310.82
## EV.all.original$'Biopsy Grade Group' ~ EV.geNorm.new$'hsa-miR-335-5p' +
##     EV.geNorm.new$'hsa-miR-130b-3p' + EV.geNorm.new$'hsa-miR-214-3p' +
##     EV.geNorm.new$'hsa-miR-107'
##
##                                    Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-130b-3p'  1   88.017 310.28
## - EV.geNorm.new$'hsa-miR-107'      1   88.237 310.57
## <none>                                 86.933 310.81
## - EV.geNorm.new$'hsa-miR-214-3p'   1   88.460 310.87
## - EV.geNorm.new$'hsa-miR-335-5p'   1   89.581 312.36
##
## Step:  AIC=310.28
## EV.all.original$'Biopsy Grade Group' ~ EV.geNorm.new$'hsa-miR-335-5p' +
##     EV.geNorm.new$'hsa-miR-214-3p' + EV.geNorm.new$'hsa-miR-107'
##
##                                    Df Deviance    AIC
## <none>                                 88.017 310.28
## - EV.geNorm.new$'hsa-miR-214-3p'   1   89.882 310.75
## - EV.geNorm.new$'hsa-miR-107'      1   90.303 311.30
## - EV.geNorm.new$'hsa-miR-335-5p'   1   91.708 313.12
```

```r
# EV NormFinder
fullmodel.EV.NormFinder = glm(formula = EV.all.original$'Biopsy Grade Group'~ EV.NormFinder.new$'hsa-mi

step.EV.grade.NormFinder = stepAIC(object = fullmodel.EV.NormFinder, direction = "backward")
```

```
## Start:  AIC=316.89
## EV.all.original$'Biopsy Grade Group' ~ EV.NormFinder.new$'hsa-miR-19b-3p' +
##     EV.NormFinder.new$'hsa-miR-874-3p' + EV.NormFinder.new$'hsa-miR-214-3p' +
##     EV.NormFinder.new$'hsa-miR-30a-5p' + EV.NormFinder.new$'hsa-miR-143-3p' +
##     EV.NormFinder.new$'hsa-miR-363-3p' + EV.NormFinder.new$'hsa-miR-451a' +
##     EV.NormFinder.new$'hsa-miR-148a-3p' + EV.NormFinder.new$'hsa-miR-25-3p' +
##     EV.NormFinder.new$'hsa-miR-16-5p' + EV.NormFinder.new$'hsa-miR-222-3p' +
##     EV.NormFinder.new$'hsa-miR-210-3p' + EV.NormFinder.new$'hsa-miR-18b-5p'
##
##                                     Df Deviance    AIC
## - EV.NormFinder.new$'hsa-miR-30a-5p'  1   78.591 314.91
## - EV.NormFinder.new$'hsa-miR-18b-5p'  1   78.598 314.92
## - EV.NormFinder.new$'hsa-miR-222-3p'  1   78.628 314.97
## - EV.NormFinder.new$'hsa-miR-25-3p'   1   78.653 315.00
## - EV.NormFinder.new$'hsa-miR-874-3p'  1   78.656 315.01
## - EV.NormFinder.new$'hsa-miR-451a'    1   78.793 315.21
## - EV.NormFinder.new$'hsa-miR-210-3p'  1   78.955 315.46
## - EV.NormFinder.new$'hsa-miR-148a-3p' 1   78.959 315.46
## - EV.NormFinder.new$'hsa-miR-214-3p'  1   79.421 316.15
## - EV.NormFinder.new$'hsa-miR-19b-3p'  1   79.723 316.60
## <none>                                    78.580 316.89
```

```
## - EV.NormFinder.new$'hsa-miR-143-3p'   1   80.408 317.61
## - EV.NormFinder.new$'hsa-miR-363-3p'   1   80.760 318.12
## - EV.NormFinder.new$'hsa-miR-16-5p'    1   80.979 318.44
##
## Step:   AIC=314.91
## EV.all.original$'Biopsy Grade Group' ~ EV.NormFinder.new$'hsa-miR-19b-3p' +
##     EV.NormFinder.new$'hsa-miR-874-3p' + EV.NormFinder.new$'hsa-miR-214-3p' +
##     EV.NormFinder.new$'hsa-miR-143-3p' + EV.NormFinder.new$'hsa-miR-363-3p' +
##     EV.NormFinder.new$'hsa-miR-451a' + EV.NormFinder.new$'hsa-miR-148a-3p' +
##     EV.NormFinder.new$'hsa-miR-25-3p' + EV.NormFinder.new$'hsa-miR-16-5p' +
##     EV.NormFinder.new$'hsa-miR-222-3p' + EV.NormFinder.new$'hsa-miR-210-3p' +
##     EV.NormFinder.new$'hsa-miR-18b-5p'
##
##                                     Df Deviance    AIC
## - EV.NormFinder.new$'hsa-miR-18b-5p'  1   78.611 312.94
## - EV.NormFinder.new$'hsa-miR-222-3p'  1   78.630 312.97
## - EV.NormFinder.new$'hsa-miR-25-3p'   1   78.681 313.05
## - EV.NormFinder.new$'hsa-miR-874-3p'  1   78.737 313.13
## - EV.NormFinder.new$'hsa-miR-451a'    1   78.805 313.23
## - EV.NormFinder.new$'hsa-miR-210-3p'  1   78.998 313.52
## - EV.NormFinder.new$'hsa-miR-148a-3p' 1   79.011 313.54
## - EV.NormFinder.new$'hsa-miR-214-3p'  1   79.468 314.22
## - EV.NormFinder.new$'hsa-miR-19b-3p'  1   79.859 314.80
## <none>                                    78.591 314.91
## - EV.NormFinder.new$'hsa-miR-143-3p'  1   80.435 315.65
## - EV.NormFinder.new$'hsa-miR-363-3p'  1   80.764 316.13
## - EV.NormFinder.new$'hsa-miR-16-5p'   1   81.003 316.48
##
## Step:   AIC=312.94
## EV.all.original$'Biopsy Grade Group' ~ EV.NormFinder.new$'hsa-miR-19b-3p' +
##     EV.NormFinder.new$'hsa-miR-874-3p' + EV.NormFinder.new$'hsa-miR-214-3p' +
##     EV.NormFinder.new$'hsa-miR-143-3p' + EV.NormFinder.new$'hsa-miR-363-3p' +
##     EV.NormFinder.new$'hsa-miR-451a' + EV.NormFinder.new$'hsa-miR-148a-3p' +
##     EV.NormFinder.new$'hsa-miR-25-3p' + EV.NormFinder.new$'hsa-miR-16-5p' +
##     EV.NormFinder.new$'hsa-miR-222-3p' + EV.NormFinder.new$'hsa-miR-210-3p'
##
##                                     Df Deviance    AIC
## - EV.NormFinder.new$'hsa-miR-222-3p'  1   78.635 310.98
## - EV.NormFinder.new$'hsa-miR-874-3p'  1   78.741 311.14
## - EV.NormFinder.new$'hsa-miR-25-3p'   1   78.752 311.15
## - EV.NormFinder.new$'hsa-miR-451a'    1   78.823 311.26
## - EV.NormFinder.new$'hsa-miR-148a-3p' 1   79.027 311.56
## - EV.NormFinder.new$'hsa-miR-210-3p'  1   79.035 311.58
## - EV.NormFinder.new$'hsa-miR-214-3p'  1   79.477 312.23
## <none>                                    78.611 312.94
## - EV.NormFinder.new$'hsa-miR-19b-3p'  1   80.038 313.06
## - EV.NormFinder.new$'hsa-miR-143-3p'  1   80.557 313.83
## - EV.NormFinder.new$'hsa-miR-363-3p'  1   80.946 314.39
## - EV.NormFinder.new$'hsa-miR-16-5p'   1   81.009 314.49
##
## Step:   AIC=310.98
## EV.all.original$'Biopsy Grade Group' ~ EV.NormFinder.new$'hsa-miR-19b-3p' +
##     EV.NormFinder.new$'hsa-miR-874-3p' + EV.NormFinder.new$'hsa-miR-214-3p' +
##     EV.NormFinder.new$'hsa-miR-143-3p' + EV.NormFinder.new$'hsa-miR-363-3p' +
```

```
##      EV.NormFinder.new$'hsa-miR-451a' + EV.NormFinder.new$'hsa-miR-148a-3p' +
##      EV.NormFinder.new$'hsa-miR-25-3p' + EV.NormFinder.new$'hsa-miR-16-5p' +
##      EV.NormFinder.new$'hsa-miR-210-3p'
##
##                                          Df Deviance    AIC
## - EV.NormFinder.new$'hsa-miR-874-3p'      1   78.742 309.14
## - EV.NormFinder.new$'hsa-miR-25-3p'       1   78.824 309.26
## - EV.NormFinder.new$'hsa-miR-451a'        1   78.869 309.33
## - EV.NormFinder.new$'hsa-miR-148a-3p'     1   79.027 309.56
## - EV.NormFinder.new$'hsa-miR-210-3p'      1   79.083 309.65
## - EV.NormFinder.new$'hsa-miR-214-3p'      1   79.501 310.27
## <none>                                        78.635 310.98
## - EV.NormFinder.new$'hsa-miR-19b-3p'      1   80.090 311.14
## - EV.NormFinder.new$'hsa-miR-143-3p'      1   80.591 311.88
## - EV.NormFinder.new$'hsa-miR-363-3p'      1   80.956 312.41
## - EV.NormFinder.new$'hsa-miR-16-5p'       1   81.024 312.51
##
## Step:  AIC=309.14
## EV.all.original$'Biopsy Grade Group' ~ EV.NormFinder.new$'hsa-miR-19b-3p' +
##      EV.NormFinder.new$'hsa-miR-214-3p' + EV.NormFinder.new$'hsa-miR-143-3p' +
##      EV.NormFinder.new$'hsa-miR-363-3p' + EV.NormFinder.new$'hsa-miR-451a' +
##      EV.NormFinder.new$'hsa-miR-148a-3p' + EV.NormFinder.new$'hsa-miR-25-3p' +
##      EV.NormFinder.new$'hsa-miR-16-5p' + EV.NormFinder.new$'hsa-miR-210-3p'
##
##                                          Df Deviance    AIC
## - EV.NormFinder.new$'hsa-miR-25-3p'       1   78.945 307.44
## - EV.NormFinder.new$'hsa-miR-451a'        1   79.021 307.56
## - EV.NormFinder.new$'hsa-miR-148a-3p'     1   79.280 307.94
## - EV.NormFinder.new$'hsa-miR-210-3p'      1   79.412 308.14
## <none>                                        78.742 309.14
## - EV.NormFinder.new$'hsa-miR-214-3p'      1   80.160 309.24
## - EV.NormFinder.new$'hsa-miR-19b-3p'      1   80.273 309.41
## - EV.NormFinder.new$'hsa-miR-143-3p'      1   80.736 310.09
## - EV.NormFinder.new$'hsa-miR-363-3p'      1   81.136 310.67
## - EV.NormFinder.new$'hsa-miR-16-5p'       1   81.387 311.04
##
## Step:  AIC=307.44
## EV.all.original$'Biopsy Grade Group' ~ EV.NormFinder.new$'hsa-miR-19b-3p' +
##      EV.NormFinder.new$'hsa-miR-214-3p' + EV.NormFinder.new$'hsa-miR-143-3p' +
##      EV.NormFinder.new$'hsa-miR-363-3p' + EV.NormFinder.new$'hsa-miR-451a' +
##      EV.NormFinder.new$'hsa-miR-148a-3p' + EV.NormFinder.new$'hsa-miR-16-5p' +
##      EV.NormFinder.new$'hsa-miR-210-3p'
##
##                                          Df Deviance    AIC
## - EV.NormFinder.new$'hsa-miR-451a'        1   79.110 305.69
## - EV.NormFinder.new$'hsa-miR-210-3p'      1   79.448 306.19
## - EV.NormFinder.new$'hsa-miR-148a-3p'     1   79.558 306.35
## <none>                                        78.945 307.44
## - EV.NormFinder.new$'hsa-miR-19b-3p'      1   80.429 307.64
## - EV.NormFinder.new$'hsa-miR-214-3p'      1   80.474 307.70
## - EV.NormFinder.new$'hsa-miR-143-3p'      1   80.763 308.13
## - EV.NormFinder.new$'hsa-miR-363-3p'      1   81.139 308.68
## - EV.NormFinder.new$'hsa-miR-16-5p'       1   81.810 309.65
##
```

```
## Step:  AIC=305.69
## EV.all.original$'Biopsy Grade Group' ~ EV.NormFinder.new$'hsa-miR-19b-3p' +
##     EV.NormFinder.new$'hsa-miR-214-3p' + EV.NormFinder.new$'hsa-miR-143-3p' +
##     EV.NormFinder.new$'hsa-miR-363-3p' + EV.NormFinder.new$'hsa-miR-148a-3p' +
##     EV.NormFinder.new$'hsa-miR-16-5p' + EV.NormFinder.new$'hsa-miR-210-3p'
##
##                                          Df Deviance    AIC
## - EV.NormFinder.new$'hsa-miR-148a-3p'    1   79.623 304.45
## - EV.NormFinder.new$'hsa-miR-210-3p'     1   79.656 304.50
## <none>                                       79.110 305.69
## - EV.NormFinder.new$'hsa-miR-214-3p'     1   80.851 306.26
## - EV.NormFinder.new$'hsa-miR-143-3p'     1   80.861 306.27
## - EV.NormFinder.new$'hsa-miR-19b-3p'     1   80.871 306.29
## - EV.NormFinder.new$'hsa-miR-16-5p'      1   81.842 307.69
## - EV.NormFinder.new$'hsa-miR-363-3p'     1   81.954 307.86
##
## Step:  AIC=304.45
## EV.all.original$'Biopsy Grade Group' ~ EV.NormFinder.new$'hsa-miR-19b-3p' +
##     EV.NormFinder.new$'hsa-miR-214-3p' + EV.NormFinder.new$'hsa-miR-143-3p' +
##     EV.NormFinder.new$'hsa-miR-363-3p' + EV.NormFinder.new$'hsa-miR-16-5p' +
##     EV.NormFinder.new$'hsa-miR-210-3p'
##
##                                          Df Deviance    AIC
## - EV.NormFinder.new$'hsa-miR-210-3p'     1   80.153 303.23
## <none>                                       79.623 304.45
## - EV.NormFinder.new$'hsa-miR-214-3p'     1   81.428 305.10
## - EV.NormFinder.new$'hsa-miR-143-3p'     1   82.064 306.01
## - EV.NormFinder.new$'hsa-miR-19b-3p'     1   82.208 306.22
## - EV.NormFinder.new$'hsa-miR-363-3p'     1   82.605 306.79
## - EV.NormFinder.new$'hsa-miR-16-5p'      1   82.788 307.05
##
## Step:  AIC=303.23
## EV.all.original$'Biopsy Grade Group' ~ EV.NormFinder.new$'hsa-miR-19b-3p' +
##     EV.NormFinder.new$'hsa-miR-214-3p' + EV.NormFinder.new$'hsa-miR-143-3p' +
##     EV.NormFinder.new$'hsa-miR-363-3p' + EV.NormFinder.new$'hsa-miR-16-5p'
##
##                                          Df Deviance    AIC
## <none>                                       80.153 303.23
## - EV.NormFinder.new$'hsa-miR-214-3p'     1   82.132 304.11
## - EV.NormFinder.new$'hsa-miR-143-3p'     1   82.586 304.76
## - EV.NormFinder.new$'hsa-miR-363-3p'     1   82.762 305.01
## - EV.NormFinder.new$'hsa-miR-16-5p'      1   82.849 305.14
## - EV.NormFinder.new$'hsa-miR-19b-3p'     1   83.188 305.62
```

Adverse pathology selection

```
fullmodel2 = glm(data = EV.all.original, formula = 'Adverse Pathology'~'hsa-let-7a-5p'+'hsa-miR-26b-5p'
step.EV.adverse.final = stepAIC(object = fullmodel2, direction = "backward")
```

```
## Start:  AIC=62.82
## 'Adverse Pathology' ~ 'hsa-let-7a-5p' + 'hsa-miR-26b-5p' + 'hsa-miR-301a-3p'
##
```

```
##                       Df Deviance    AIC
## - 'hsa-miR-26b-5p'    1    54.820 60.820
## - 'hsa-miR-301a-3p'   1    55.734 61.734
## <none>                     54.819 62.819
## - 'hsa-let-7a-5p'     1    57.179 63.179
##
## Step:  AIC=60.82
## 'Adverse Pathology' ~ 'hsa-let-7a-5p' + 'hsa-miR-301a-3p'
##
##                       Df Deviance    AIC
## - 'hsa-miR-301a-3p'   1    55.941 59.941
## <none>                     54.820 60.820
## - 'hsa-let-7a-5p'     1    59.299 63.299
##
## Step:  AIC=59.94
## 'Adverse Pathology' ~ 'hsa-let-7a-5p'
##
##                       Df Deviance    AIC
## <none>                     55.941 59.941
## - 'hsa-let-7a-5p'     1    64.443 66.443
```

EV CT Mean
```
fullmodel.EV.CTMean.AP = glm(data = EV.all.original, formula = 'Adverse Pathology'~ EV.globalCTMean.new

step.EV.adverse.CTMean = stepAIC(object = fullmodel.EV.CTMean.AP, direction = "backward")
```

```
## Start:  AIC=64.39
## 'Adverse Pathology' ~ EV.globalCTMean.new$'hsa-let-7a-5p' + EV.globalCTMean.new$'hsa-miR-26b-5p' +
##      EV.globalCTMean.new$'hsa-miR-25-3p' + EV.globalCTMean.new$'hsa-miR-107' +
##      EV.globalCTMean.new$'hsa-miR-103a-3p' + EV.globalCTMean.new$'hsa-miR-199a-5p' +
##      EV.globalCTMean.new$'hsa-miR-301a-3p' + EV.globalCTMean.new$'hsa-miR-363-3p' +
##      EV.globalCTMean.new$'hsa-miR-191-5p' + EV.globalCTMean.new$'hsa-miR-19b-3p' +
##      EV.globalCTMean.new$'hsa-miR-221-3p' + EV.globalCTMean.new$'hsa-miR-27b-3p' +
##      EV.globalCTMean.new$'hsa-miR-451a' + EV.globalCTMean.new$'hsa-miR-374a-5p' +
##      EV.globalCTMean.new$'hsa-miR-16-5p'
##
##                                             Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-107'         1    32.397 62.397
## - EV.globalCTMean.new$'hsa-miR-374a-5p'     1    32.493 62.493
## - EV.globalCTMean.new$'hsa-miR-191-5p'      1    32.529 62.529
## - EV.globalCTMean.new$'hsa-miR-27b-3p'      1    32.552 62.552
## - EV.globalCTMean.new$'hsa-miR-301a-3p'     1    32.573 62.573
## - EV.globalCTMean.new$'hsa-miR-363-3p'      1    32.575 62.575
## - EV.globalCTMean.new$'hsa-miR-16-5p'       1    32.618 62.618
## - EV.globalCTMean.new$'hsa-miR-25-3p'       1    32.854 62.854
## - EV.globalCTMean.new$'hsa-miR-26b-5p'      1    32.924 62.924
## - EV.globalCTMean.new$'hsa-miR-221-3p'      1    32.945 62.945
## - EV.globalCTMean.new$'hsa-miR-19b-3p'      1    33.054 63.054
## - EV.globalCTMean.new$'hsa-miR-103a-3p'     1    33.668 63.668
## - EV.globalCTMean.new$'hsa-miR-451a'        1    33.799 63.799
## - EV.globalCTMean.new$'hsa-miR-199a-5p'     1    33.876 63.876
## <none>                                           32.391 64.391
## - EV.globalCTMean.new$'hsa-let-7a-5p'       1    37.766 67.766
##
```

```
## Step:  AIC=62.4
## 'Adverse Pathology' ~ EV.globalCTMean.new$'hsa-let-7a-5p' + EV.globalCTMean.new$'hsa-miR-26b-5p' +
##     EV.globalCTMean.new$'hsa-miR-25-3p' + EV.globalCTMean.new$'hsa-miR-103a-3p' +
##     EV.globalCTMean.new$'hsa-miR-199a-5p' + EV.globalCTMean.new$'hsa-miR-301a-3p' +
##     EV.globalCTMean.new$'hsa-miR-363-3p' + EV.globalCTMean.new$'hsa-miR-191-5p' +
##     EV.globalCTMean.new$'hsa-miR-19b-3p' + EV.globalCTMean.new$'hsa-miR-221-3p' +
##     EV.globalCTMean.new$'hsa-miR-27b-3p' + EV.globalCTMean.new$'hsa-miR-451a' +
##     EV.globalCTMean.new$'hsa-miR-374a-5p' + EV.globalCTMean.new$'hsa-miR-16-5p'
##
##                                         Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-374a-5p'  1   32.516 60.516
## - EV.globalCTMean.new$'hsa-miR-27b-3p'   1   32.555 60.555
## - EV.globalCTMean.new$'hsa-miR-301a-3p'  1   32.578 60.578
## - EV.globalCTMean.new$'hsa-miR-363-3p'   1   32.590 60.590
## - EV.globalCTMean.new$'hsa-miR-16-5p'    1   32.624 60.624
## - EV.globalCTMean.new$'hsa-miR-191-5p'   1   32.640 60.640
## - EV.globalCTMean.new$'hsa-miR-25-3p'    1   32.883 60.883
## - EV.globalCTMean.new$'hsa-miR-26b-5p'   1   32.924 60.924
## - EV.globalCTMean.new$'hsa-miR-221-3p'   1   32.952 60.952
## - EV.globalCTMean.new$'hsa-miR-19b-3p'   1   33.140 61.140
## - EV.globalCTMean.new$'hsa-miR-199a-5p'  1   33.889 61.889
## - EV.globalCTMean.new$'hsa-miR-451a'     1   33.970 61.970
## <none>                                      32.397 62.397
## - EV.globalCTMean.new$'hsa-miR-103a-3p'  1   35.455 63.455
## - EV.globalCTMean.new$'hsa-let-7a-5p'    1   38.564 66.564
##
## Step:  AIC=60.52
## 'Adverse Pathology' ~ EV.globalCTMean.new$'hsa-let-7a-5p' + EV.globalCTMean.new$'hsa-miR-26b-5p' +
##     EV.globalCTMean.new$'hsa-miR-25-3p' + EV.globalCTMean.new$'hsa-miR-103a-3p' +
##     EV.globalCTMean.new$'hsa-miR-199a-5p' + EV.globalCTMean.new$'hsa-miR-301a-3p' +
##     EV.globalCTMean.new$'hsa-miR-363-3p' + EV.globalCTMean.new$'hsa-miR-191-5p' +
##     EV.globalCTMean.new$'hsa-miR-19b-3p' + EV.globalCTMean.new$'hsa-miR-221-3p' +
##     EV.globalCTMean.new$'hsa-miR-27b-3p' + EV.globalCTMean.new$'hsa-miR-451a' +
##     EV.globalCTMean.new$'hsa-miR-16-5p'
##
##                                         Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-27b-3p'   1   32.616 58.616
## - EV.globalCTMean.new$'hsa-miR-363-3p'   1   32.667 58.667
## - EV.globalCTMean.new$'hsa-miR-16-5p'    1   32.745 58.745
## - EV.globalCTMean.new$'hsa-miR-301a-3p'  1   32.792 58.792
## - EV.globalCTMean.new$'hsa-miR-191-5p'   1   32.875 58.875
## - EV.globalCTMean.new$'hsa-miR-25-3p'    1   32.925 58.925
## - EV.globalCTMean.new$'hsa-miR-221-3p'   1   33.015 59.015
## - EV.globalCTMean.new$'hsa-miR-26b-5p'   1   33.067 59.067
## - EV.globalCTMean.new$'hsa-miR-19b-3p'   1   33.267 59.267
## - EV.globalCTMean.new$'hsa-miR-451a'     1   33.981 59.981
## - EV.globalCTMean.new$'hsa-miR-199a-5p'  1   34.073 60.073
## <none>                                      32.516 60.516
## - EV.globalCTMean.new$'hsa-miR-103a-3p'  1   36.901 62.901
## - EV.globalCTMean.new$'hsa-let-7a-5p'    1   39.123 65.123
##
## Step:  AIC=58.62
## 'Adverse Pathology' ~ EV.globalCTMean.new$'hsa-let-7a-5p' + EV.globalCTMean.new$'hsa-miR-26b-5p' +
##     EV.globalCTMean.new$'hsa-miR-25-3p' + EV.globalCTMean.new$'hsa-miR-103a-3p' +
```

```
##      EV.globalCTMean.new$'hsa-miR-199a-5p' + EV.globalCTMean.new$'hsa-miR-301a-3p' +
##      EV.globalCTMean.new$'hsa-miR-363-3p' + EV.globalCTMean.new$'hsa-miR-191-5p' +
##      EV.globalCTMean.new$'hsa-miR-19b-3p' + EV.globalCTMean.new$'hsa-miR-221-3p' +
##      EV.globalCTMean.new$'hsa-miR-451a' + EV.globalCTMean.new$'hsa-miR-16-5p'
##
##                                          Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-363-3p'    1   32.784 56.784
## - EV.globalCTMean.new$'hsa-miR-16-5p'     1   32.826 56.826
## - EV.globalCTMean.new$'hsa-miR-301a-3p'   1   32.941 56.941
## - EV.globalCTMean.new$'hsa-miR-25-3p'     1   32.988 56.988
## - EV.globalCTMean.new$'hsa-miR-26b-5p'    1   33.197 57.197
## - EV.globalCTMean.new$'hsa-miR-191-5p'    1   33.262 57.262
## - EV.globalCTMean.new$'hsa-miR-19b-3p'    1   33.270 57.270
## - EV.globalCTMean.new$'hsa-miR-221-3p'    1   33.425 57.425
## - EV.globalCTMean.new$'hsa-miR-451a'      1   34.038 58.038
## - EV.globalCTMean.new$'hsa-miR-199a-5p'   1   34.548 58.548
## <none>                                        32.616 58.616
## - EV.globalCTMean.new$'hsa-miR-103a-3p'   1   38.090 62.090
## - EV.globalCTMean.new$'hsa-let-7a-5p'     1   40.113 64.113
##
## Step:  AIC=56.78
## 'Adverse Pathology' ~ EV.globalCTMean.new$'hsa-let-7a-5p' + EV.globalCTMean.new$'hsa-miR-26b-5p' +
##      EV.globalCTMean.new$'hsa-miR-25-3p' + EV.globalCTMean.new$'hsa-miR-103a-3p' +
##      EV.globalCTMean.new$'hsa-miR-199a-5p' + EV.globalCTMean.new$'hsa-miR-301a-3p' +
##      EV.globalCTMean.new$'hsa-miR-191-5p' + EV.globalCTMean.new$'hsa-miR-19b-3p' +
##      EV.globalCTMean.new$'hsa-miR-221-3p' + EV.globalCTMean.new$'hsa-miR-451a' +
##      EV.globalCTMean.new$'hsa-miR-16-5p'
##
##                                          Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-16-5p'     1   32.895 54.895
## - EV.globalCTMean.new$'hsa-miR-301a-3p'   1   32.993 54.993
## - EV.globalCTMean.new$'hsa-miR-25-3p'     1   33.144 55.144
## - EV.globalCTMean.new$'hsa-miR-26b-5p'    1   33.447 55.447
## - EV.globalCTMean.new$'hsa-miR-191-5p'    1   33.496 55.496
## - EV.globalCTMean.new$'hsa-miR-19b-3p'    1   33.537 55.537
## - EV.globalCTMean.new$'hsa-miR-221-3p'    1   33.649 55.649
## - EV.globalCTMean.new$'hsa-miR-451a'      1   34.071 56.071
## - EV.globalCTMean.new$'hsa-miR-199a-5p'   1   34.587 56.587
## <none>                                        32.784 56.784
## - EV.globalCTMean.new$'hsa-miR-103a-3p'   1   40.474 62.474
## - EV.globalCTMean.new$'hsa-let-7a-5p'     1   41.628 63.628
##
## Step:  AIC=54.89
## 'Adverse Pathology' ~ EV.globalCTMean.new$'hsa-let-7a-5p' + EV.globalCTMean.new$'hsa-miR-26b-5p' +
##      EV.globalCTMean.new$'hsa-miR-25-3p' + EV.globalCTMean.new$'hsa-miR-103a-3p' +
##      EV.globalCTMean.new$'hsa-miR-199a-5p' + EV.globalCTMean.new$'hsa-miR-301a-3p' +
##      EV.globalCTMean.new$'hsa-miR-191-5p' + EV.globalCTMean.new$'hsa-miR-19b-3p' +
##      EV.globalCTMean.new$'hsa-miR-221-3p' + EV.globalCTMean.new$'hsa-miR-451a'
##
##                                          Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-25-3p'     1   33.153 53.153
## - EV.globalCTMean.new$'hsa-miR-301a-3p'   1   33.163 53.163
## - EV.globalCTMean.new$'hsa-miR-19b-3p'    1   33.577 53.577
## - EV.globalCTMean.new$'hsa-miR-191-5p'    1   33.598 53.598
```

```
## - EV.globalCTMean.new$‘hsa-miR-221-3p‘   1   33.706 53.706
## - EV.globalCTMean.new$‘hsa-miR-26b-5p‘    1   33.712 53.712
## - EV.globalCTMean.new$‘hsa-miR-199a-5p‘   1   34.669 54.669
## - EV.globalCTMean.new$‘hsa-miR-451a‘      1   34.866 54.866
## <none>                                       32.895 54.895
## - EV.globalCTMean.new$‘hsa-miR-103a-3p‘   1   40.594 60.594
## - EV.globalCTMean.new$‘hsa-let-7a-5p‘     1   41.979 61.979
##
## Step:  AIC=53.15
## ‘Adverse Pathology‘ ~ EV.globalCTMean.new$‘hsa-let-7a-5p‘ + EV.globalCTMean.new$‘hsa-miR-26b-5p‘ +
##     EV.globalCTMean.new$‘hsa-miR-103a-3p‘ + EV.globalCTMean.new$‘hsa-miR-199a-5p‘ +
##     EV.globalCTMean.new$‘hsa-miR-301a-3p‘ + EV.globalCTMean.new$‘hsa-miR-191-5p‘ +
##     EV.globalCTMean.new$‘hsa-miR-19b-3p‘ + EV.globalCTMean.new$‘hsa-miR-221-3p‘ +
##     EV.globalCTMean.new$‘hsa-miR-451a‘
##
##                                         Df Deviance    AIC
## - EV.globalCTMean.new$‘hsa-miR-301a-3p‘   1   33.342 51.342
## - EV.globalCTMean.new$‘hsa-miR-191-5p‘    1   33.660 51.660
## - EV.globalCTMean.new$‘hsa-miR-221-3p‘    1   33.894 51.894
## - EV.globalCTMean.new$‘hsa-miR-19b-3p‘    1   34.042 52.042
## - EV.globalCTMean.new$‘hsa-miR-26b-5p‘    1   34.272 52.272
## - EV.globalCTMean.new$‘hsa-miR-199a-5p‘   1   35.118 53.118
## <none>                                       33.153 53.153
## - EV.globalCTMean.new$‘hsa-miR-451a‘      1   35.253 53.253
## - EV.globalCTMean.new$‘hsa-miR-103a-3p‘   1   43.067 61.067
## - EV.globalCTMean.new$‘hsa-let-7a-5p‘     1   44.301 62.301
##
## Step:  AIC=51.34
## ‘Adverse Pathology‘ ~ EV.globalCTMean.new$‘hsa-let-7a-5p‘ + EV.globalCTMean.new$‘hsa-miR-26b-5p‘ +
##     EV.globalCTMean.new$‘hsa-miR-103a-3p‘ + EV.globalCTMean.new$‘hsa-miR-199a-5p‘ +
##     EV.globalCTMean.new$‘hsa-miR-191-5p‘ + EV.globalCTMean.new$‘hsa-miR-19b-3p‘ +
##     EV.globalCTMean.new$‘hsa-miR-221-3p‘ + EV.globalCTMean.new$‘hsa-miR-451a‘
##
##                                         Df Deviance    AIC
## - EV.globalCTMean.new$‘hsa-miR-191-5p‘    1   33.873 49.873
## - EV.globalCTMean.new$‘hsa-miR-221-3p‘    1   33.919 49.919
## - EV.globalCTMean.new$‘hsa-miR-26b-5p‘    1   34.273 50.273
## - EV.globalCTMean.new$‘hsa-miR-19b-3p‘    1   34.584 50.584
## - EV.globalCTMean.new$‘hsa-miR-199a-5p‘   1   35.216 51.216
## <none>                                       33.342 51.342
## - EV.globalCTMean.new$‘hsa-miR-451a‘      1   35.674 51.674
## - EV.globalCTMean.new$‘hsa-miR-103a-3p‘   1   43.453 59.453
## - EV.globalCTMean.new$‘hsa-let-7a-5p‘     1   44.301 60.301
##
## Step:  AIC=49.87
## ‘Adverse Pathology‘ ~ EV.globalCTMean.new$‘hsa-let-7a-5p‘ + EV.globalCTMean.new$‘hsa-miR-26b-5p‘ +
##     EV.globalCTMean.new$‘hsa-miR-103a-3p‘ + EV.globalCTMean.new$‘hsa-miR-199a-5p‘ +
##     EV.globalCTMean.new$‘hsa-miR-19b-3p‘ + EV.globalCTMean.new$‘hsa-miR-221-3p‘ +
##     EV.globalCTMean.new$‘hsa-miR-451a‘
##
##                                         Df Deviance    AIC
## - EV.globalCTMean.new$‘hsa-miR-221-3p‘    1   34.933 48.933
## - EV.globalCTMean.new$‘hsa-miR-19b-3p‘    1   35.204 49.204
## - EV.globalCTMean.new$‘hsa-miR-26b-5p‘    1   35.541 49.541
```

```
## <none>                                          33.873 49.873
## - EV.globalCTMean.new$'hsa-miR-451a'       1    36.073 50.073
## - EV.globalCTMean.new$'hsa-miR-199a-5p'    1    36.347 50.347
## - EV.globalCTMean.new$'hsa-let-7a-5p'      1    45.362 59.362
## - EV.globalCTMean.new$'hsa-miR-103a-3p'    1    45.755 59.755
##
## Step:  AIC=48.93
## 'Adverse Pathology' ~ EV.globalCTMean.new$'hsa-let-7a-5p' + EV.globalCTMean.new$'hsa-miR-26b-5p' +
##     EV.globalCTMean.new$'hsa-miR-103a-3p' + EV.globalCTMean.new$'hsa-miR-199a-5p' +
##     EV.globalCTMean.new$'hsa-miR-19b-3p' + EV.globalCTMean.new$'hsa-miR-451a'
##
##                                          Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-19b-3p'    1    35.745 47.745
## - EV.globalCTMean.new$'hsa-miR-26b-5p'    1    36.305 48.305
## - EV.globalCTMean.new$'hsa-miR-451a'      1    36.409 48.409
## <none>                                          34.933 48.933
## - EV.globalCTMean.new$'hsa-miR-199a-5p'   1    43.734 55.734
## - EV.globalCTMean.new$'hsa-miR-103a-3p'   1    46.222 58.222
## - EV.globalCTMean.new$'hsa-let-7a-5p'     1    46.774 58.774
##
## Step:  AIC=47.75
## 'Adverse Pathology' ~ EV.globalCTMean.new$'hsa-let-7a-5p' + EV.globalCTMean.new$'hsa-miR-26b-5p' +
##     EV.globalCTMean.new$'hsa-miR-103a-3p' + EV.globalCTMean.new$'hsa-miR-199a-5p' +
##     EV.globalCTMean.new$'hsa-miR-451a'
##
##                                          Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-451a'      1    36.410 46.410
## - EV.globalCTMean.new$'hsa-miR-26b-5p'    1    37.170 47.170
## <none>                                          35.745 47.745
## - EV.globalCTMean.new$'hsa-miR-199a-5p'   1    44.135 54.135
## - EV.globalCTMean.new$'hsa-miR-103a-3p'   1    46.976 56.976
## - EV.globalCTMean.new$'hsa-let-7a-5p'     1    48.133 58.133
##
## Step:  AIC=46.41
## 'Adverse Pathology' ~ EV.globalCTMean.new$'hsa-let-7a-5p' + EV.globalCTMean.new$'hsa-miR-26b-5p' +
##     EV.globalCTMean.new$'hsa-miR-103a-3p' + EV.globalCTMean.new$'hsa-miR-199a-5p'
##
##                                          Df Deviance    AIC
## - EV.globalCTMean.new$'hsa-miR-26b-5p'    1    37.892 45.892
## <none>                                          36.410 46.410
## - EV.globalCTMean.new$'hsa-miR-199a-5p'   1    44.541 52.541
## - EV.globalCTMean.new$'hsa-miR-103a-3p'   1    47.790 55.790
## - EV.globalCTMean.new$'hsa-let-7a-5p'     1    50.895 58.895
##
## Step:  AIC=45.89
## 'Adverse Pathology' ~ EV.globalCTMean.new$'hsa-let-7a-5p' + EV.globalCTMean.new$'hsa-miR-103a-3p' +
##     EV.globalCTMean.new$'hsa-miR-199a-5p'
##
##                                          Df Deviance    AIC
## <none>                                          37.892 45.892
## - EV.globalCTMean.new$'hsa-miR-199a-5p'   1    45.558 51.558
## - EV.globalCTMean.new$'hsa-miR-103a-3p'   1    47.792 53.792
## - EV.globalCTMean.new$'hsa-let-7a-5p'     1    55.034 61.034
```

```r
# EV geNorm
fullmodel.EV.geNorm.AP = glm(data = EV.all.original, formula = `Adverse Pathology`~ EV.geNorm.new$`hsa-

step.EV.adverse.geNorm = stepAIC(object = fullmodel.EV.geNorm.AP, direction = "backward")
```

```
## Start:  AIC=71.71
## `Adverse Pathology` ~ EV.geNorm.new$`hsa-miR-25-3p` + EV.geNorm.new$`hsa-miR-199a-5p` +
##     EV.geNorm.new$`hsa-miR-30c-5p` + EV.geNorm.new$`hsa-let-7a-5p` +
##     EV.geNorm.new$`hsa-miR-191-5p` + EV.geNorm.new$`hsa-miR-27b-3p` +
##     EV.geNorm.new$`hsa-miR-363-3p` + EV.geNorm.new$`hsa-miR-26b-5p` +
##     EV.geNorm.new$`hsa-miR-221-3p` + EV.geNorm.new$`hsa-miR-16-5p` +
##     EV.geNorm.new$`hsa-miR-19b-3p` + EV.geNorm.new$`hsa-miR-107` +
##     EV.geNorm.new$`hsa-miR-27a-3p` + EV.geNorm.new$`hsa-miR-301a-3p` +
##     EV.geNorm.new$`hsa-miR-451a` + EV.geNorm.new$`hsa-miR-199a-3p` +
##     EV.geNorm.new$`hsa-miR-103a-3p` + EV.geNorm.new$`hsa-miR-23a-3p` +
##     EV.geNorm.new$`hsa-miR-24-3p` + EV.geNorm.new$`hsa-miR-141-3`
##
##                                    Df Deviance    AIC
## - EV.geNorm.new$`hsa-miR-27b-3p`    1   29.728 69.728
## - EV.geNorm.new$`hsa-miR-16-5p`     1   29.729 69.729
## - EV.geNorm.new$`hsa-miR-199a-3p`   1   29.737 69.737
## - EV.geNorm.new$`hsa-miR-26b-5p`    1   29.749 69.749
## - EV.geNorm.new$`hsa-miR-30c-5p`    1   29.859 69.859
## - EV.geNorm.new$`hsa-miR-301a-3p`   1   29.889 69.889
## - EV.geNorm.new$`hsa-miR-107`       1   29.904 69.904
## - EV.geNorm.new$`hsa-let-7a-5p`     1   30.162 70.162
## - EV.geNorm.new$`hsa-miR-103a-3p`   1   30.281 70.281
## - EV.geNorm.new$`hsa-miR-23a-3p`    1   30.305 70.305
## - EV.geNorm.new$`hsa-miR-191-5p`    1   30.335 70.335
## - EV.geNorm.new$`hsa-miR-199a-5p`   1   30.352 70.352
## - EV.geNorm.new$`hsa-miR-363-3p`    1   30.395 70.395
## - EV.geNorm.new$`hsa-miR-27a-3p`    1   30.424 70.424
## - EV.geNorm.new$`hsa-miR-221-3p`    1   30.552 70.552
## - EV.geNorm.new$`hsa-miR-141-3`     1   31.305 71.305
## - EV.geNorm.new$`hsa-miR-24-3p`     1   31.503 71.503
## - EV.geNorm.new$`hsa-miR-25-3p`     1   31.627 71.627
## <none>                                 29.712 71.712
## - EV.geNorm.new$`hsa-miR-451a`      1   32.465 72.465
## - EV.geNorm.new$`hsa-miR-19b-3p`    1   33.006 73.006
##
## Step:  AIC=69.73
## `Adverse Pathology` ~ EV.geNorm.new$`hsa-miR-25-3p` + EV.geNorm.new$`hsa-miR-199a-5p` +
##     EV.geNorm.new$`hsa-miR-30c-5p` + EV.geNorm.new$`hsa-let-7a-5p` +
##     EV.geNorm.new$`hsa-miR-191-5p` + EV.geNorm.new$`hsa-miR-363-3p` +
##     EV.geNorm.new$`hsa-miR-26b-5p` + EV.geNorm.new$`hsa-miR-221-3p` +
##     EV.geNorm.new$`hsa-miR-16-5p` + EV.geNorm.new$`hsa-miR-19b-3p` +
##     EV.geNorm.new$`hsa-miR-107` + EV.geNorm.new$`hsa-miR-27a-3p` +
##     EV.geNorm.new$`hsa-miR-301a-3p` + EV.geNorm.new$`hsa-miR-451a` +
##     EV.geNorm.new$`hsa-miR-199a-3p` + EV.geNorm.new$`hsa-miR-103a-3p` +
##     EV.geNorm.new$`hsa-miR-23a-3p` + EV.geNorm.new$`hsa-miR-24-3p` +
##     EV.geNorm.new$`hsa-miR-141-3`
##
##                                    Df Deviance    AIC
```

```
## - EV.geNorm.new$'hsa-miR-199a-3p'   1    29.740 67.740
## - EV.geNorm.new$'hsa-miR-16-5p'      1    29.749 67.749
## - EV.geNorm.new$'hsa-miR-26b-5p'     1    29.763 67.763
## - EV.geNorm.new$'hsa-miR-301a-3p'    1    29.891 67.891
## - EV.geNorm.new$'hsa-miR-30c-5p'     1    29.938 67.938
## - EV.geNorm.new$'hsa-miR-107'        1    29.969 67.969
## - EV.geNorm.new$'hsa-let-7a-5p'      1    30.167 68.167
## - EV.geNorm.new$'hsa-miR-191-5p'     1    30.350 68.350
## - EV.geNorm.new$'hsa-miR-23a-3p'     1    30.354 68.354
## - EV.geNorm.new$'hsa-miR-103a-3p'    1    30.369 68.369
## - EV.geNorm.new$'hsa-miR-199a-5p'    1    30.401 68.401
## - EV.geNorm.new$'hsa-miR-27a-3p'     1    30.533 68.533
## - EV.geNorm.new$'hsa-miR-221-3p'     1    30.683 68.683
## - EV.geNorm.new$'hsa-miR-363-3p'     1    30.747 68.747
## - EV.geNorm.new$'hsa-miR-141-3'      1    31.333 69.333
## - EV.geNorm.new$'hsa-miR-24-3p'      1    31.540 69.540
## <none>                                   29.728 69.728
## - EV.geNorm.new$'hsa-miR-25-3p'      1    32.111 70.111
## - EV.geNorm.new$'hsa-miR-451a'       1    33.271 71.271
## - EV.geNorm.new$'hsa-miR-19b-3p'     1    33.321 71.321
##
## Step:  AIC=67.74
## 'Adverse Pathology' ~ EV.geNorm.new$'hsa-miR-25-3p' + EV.geNorm.new$'hsa-miR-199a-5p' +
##     EV.geNorm.new$'hsa-miR-30c-5p' + EV.geNorm.new$'hsa-let-7a-5p' +
##     EV.geNorm.new$'hsa-miR-191-5p' + EV.geNorm.new$'hsa-miR-363-3p' +
##     EV.geNorm.new$'hsa-miR-26b-5p' + EV.geNorm.new$'hsa-miR-221-3p' +
##     EV.geNorm.new$'hsa-miR-16-5p' + EV.geNorm.new$'hsa-miR-19b-3p' +
##     EV.geNorm.new$'hsa-miR-107' + EV.geNorm.new$'hsa-miR-27a-3p' +
##     EV.geNorm.new$'hsa-miR-301a-3p' + EV.geNorm.new$'hsa-miR-451a' +
##     EV.geNorm.new$'hsa-miR-103a-3p' + EV.geNorm.new$'hsa-miR-23a-3p' +
##     EV.geNorm.new$'hsa-miR-24-3p' + EV.geNorm.new$'hsa-miR-141-3'
##
##                                   Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-26b-5p'    1    29.764 65.764
## - EV.geNorm.new$'hsa-miR-16-5p'     1    29.764 65.764
## - EV.geNorm.new$'hsa-miR-301a-3p'   1    29.891 65.891
## - EV.geNorm.new$'hsa-miR-30c-5p'    1    29.938 65.938
## - EV.geNorm.new$'hsa-miR-107'       1    29.993 65.993
## - EV.geNorm.new$'hsa-let-7a-5p'     1    30.244 66.244
## - EV.geNorm.new$'hsa-miR-191-5p'    1    30.350 66.350
## - EV.geNorm.new$'hsa-miR-23a-3p'    1    30.404 66.404
## - EV.geNorm.new$'hsa-miR-103a-3p'   1    30.409 66.409
## - EV.geNorm.new$'hsa-miR-199a-5p'   1    30.437 66.437
## - EV.geNorm.new$'hsa-miR-27a-3p'    1    30.548 66.548
## - EV.geNorm.new$'hsa-miR-221-3p'    1    30.754 66.754
## - EV.geNorm.new$'hsa-miR-363-3p'    1    30.823 66.823
## - EV.geNorm.new$'hsa-miR-24-3p'     1    31.562 67.562
## - EV.geNorm.new$'hsa-miR-141-3'     1    31.663 67.663
## <none>                                   29.740 67.740
## - EV.geNorm.new$'hsa-miR-25-3p'     1    32.152 68.152
## - EV.geNorm.new$'hsa-miR-451a'      1    33.586 69.586
## - EV.geNorm.new$'hsa-miR-19b-3p'    1    33.749 69.749
##
## Step:  AIC=65.76
```

```
## 'Adverse Pathology' ~ EV.geNorm.new$'hsa-miR-25-3p' + EV.geNorm.new$'hsa-miR-199a-5p' +
##     EV.geNorm.new$'hsa-miR-30c-5p' + EV.geNorm.new$'hsa-let-7a-5p' +
##     EV.geNorm.new$'hsa-miR-191-5p' + EV.geNorm.new$'hsa-miR-363-3p' +
##     EV.geNorm.new$'hsa-miR-221-3p' + EV.geNorm.new$'hsa-miR-16-5p' +
##     EV.geNorm.new$'hsa-miR-19b-3p' + EV.geNorm.new$'hsa-miR-107' +
##     EV.geNorm.new$'hsa-miR-27a-3p' + EV.geNorm.new$'hsa-miR-301a-3p' +
##     EV.geNorm.new$'hsa-miR-451a' + EV.geNorm.new$'hsa-miR-103a-3p' +
##     EV.geNorm.new$'hsa-miR-23a-3p' + EV.geNorm.new$'hsa-miR-24-3p' +
##     EV.geNorm.new$'hsa-miR-141-3'
##
##                                   Df Deviance   AIC
## - EV.geNorm.new$'hsa-miR-16-5p'    1   29.792 63.792
## - EV.geNorm.new$'hsa-miR-30c-5p'   1   29.940 63.940
## - EV.geNorm.new$'hsa-miR-301a-3p'  1   30.035 64.035
## - EV.geNorm.new$'hsa-miR-107'      1   30.049 64.049
## - EV.geNorm.new$'hsa-miR-191-5p'   1   30.360 64.360
## - EV.geNorm.new$'hsa-let-7a-5p'    1   30.370 64.370
## - EV.geNorm.new$'hsa-miR-23a-3p'   1   30.406 64.406
## - EV.geNorm.new$'hsa-miR-199a-5p'  1   30.466 64.466
## - EV.geNorm.new$'hsa-miR-103a-3p'  1   30.476 64.476
## - EV.geNorm.new$'hsa-miR-27a-3p'   1   30.571 64.571
## - EV.geNorm.new$'hsa-miR-221-3p'   1   30.798 64.798
## - EV.geNorm.new$'hsa-miR-363-3p'   1   30.832 64.832
## - EV.geNorm.new$'hsa-miR-24-3p'    1   31.563 65.563
## - EV.geNorm.new$'hsa-miR-141-3'    1   31.673 65.673
## <none>                                29.764 65.764
## - EV.geNorm.new$'hsa-miR-25-3p'    1   32.481 66.481
## - EV.geNorm.new$'hsa-miR-451a'     1   33.799 67.799
## - EV.geNorm.new$'hsa-miR-19b-3p'   1   34.509 68.509
##
## Step:  AIC=63.79
## 'Adverse Pathology' ~ EV.geNorm.new$'hsa-miR-25-3p' + EV.geNorm.new$'hsa-miR-199a-5p' +
##     EV.geNorm.new$'hsa-miR-30c-5p' + EV.geNorm.new$'hsa-let-7a-5p' +
##     EV.geNorm.new$'hsa-miR-191-5p' + EV.geNorm.new$'hsa-miR-363-3p' +
##     EV.geNorm.new$'hsa-miR-221-3p' + EV.geNorm.new$'hsa-miR-19b-3p' +
##     EV.geNorm.new$'hsa-miR-107' + EV.geNorm.new$'hsa-miR-27a-3p' +
##     EV.geNorm.new$'hsa-miR-301a-3p' + EV.geNorm.new$'hsa-miR-451a' +
##     EV.geNorm.new$'hsa-miR-103a-3p' + EV.geNorm.new$'hsa-miR-23a-3p' +
##     EV.geNorm.new$'hsa-miR-24-3p' + EV.geNorm.new$'hsa-miR-141-3'
##
##                                   Df Deviance   AIC
## - EV.geNorm.new$'hsa-miR-30c-5p'   1   29.966 61.966
## - EV.geNorm.new$'hsa-miR-107'      1   30.073 62.073
## - EV.geNorm.new$'hsa-miR-301a-3p'  1   30.100 62.100
## - EV.geNorm.new$'hsa-miR-191-5p'   1   30.375 62.375
## - EV.geNorm.new$'hsa-miR-23a-3p'   1   30.406 62.406
## - EV.geNorm.new$'hsa-let-7a-5p'    1   30.421 62.421
## - EV.geNorm.new$'hsa-miR-199a-5p'  1   30.473 62.473
## - EV.geNorm.new$'hsa-miR-103a-3p'  1   30.495 62.495
## - EV.geNorm.new$'hsa-miR-27a-3p'   1   30.673 62.673
## - EV.geNorm.new$'hsa-miR-221-3p'   1   30.808 62.808
## - EV.geNorm.new$'hsa-miR-363-3p'   1   30.998 62.998
## - EV.geNorm.new$'hsa-miR-24-3p'    1   31.571 63.571
## <none>                                29.792 63.792
```

```
## - EV.geNorm.new$`hsa-miR-141-3`    1   32.268 64.268
## - EV.geNorm.new$`hsa-miR-25-3p`    1   32.663 64.663
## - EV.geNorm.new$`hsa-miR-451a`     1   34.344 66.344
## - EV.geNorm.new$`hsa-miR-19b-3p`   1   35.282 67.282
##
## Step:  AIC=61.97
## `Adverse Pathology` ~ EV.geNorm.new$`hsa-miR-25-3p` + EV.geNorm.new$`hsa-miR-199a-5p` +
##     EV.geNorm.new$`hsa-let-7a-5p` + EV.geNorm.new$`hsa-miR-191-5p` +
##     EV.geNorm.new$`hsa-miR-363-3p` + EV.geNorm.new$`hsa-miR-221-3p` +
##     EV.geNorm.new$`hsa-miR-19b-3p` + EV.geNorm.new$`hsa-miR-107` +
##     EV.geNorm.new$`hsa-miR-27a-3p` + EV.geNorm.new$`hsa-miR-301a-3p` +
##     EV.geNorm.new$`hsa-miR-451a` + EV.geNorm.new$`hsa-miR-103a-3p` +
##     EV.geNorm.new$`hsa-miR-23a-3p` + EV.geNorm.new$`hsa-miR-24-3p` +
##     EV.geNorm.new$`hsa-miR-141-3`
##
##                                    Df Deviance    AIC
## - EV.geNorm.new$`hsa-miR-301a-3p`  1   30.341 60.341
## - EV.geNorm.new$`hsa-miR-107`      1   30.376 60.376
## - EV.geNorm.new$`hsa-miR-191-5p`   1   30.455 60.455
## - EV.geNorm.new$`hsa-miR-23a-3p`   1   30.496 60.496
## - EV.geNorm.new$`hsa-miR-221-3p`   1   30.813 60.813
## - EV.geNorm.new$`hsa-miR-363-3p`   1   31.000 61.000
## - EV.geNorm.new$`hsa-miR-103a-3p`  1   31.120 61.120
## - EV.geNorm.new$`hsa-miR-199a-5p`  1   31.197 61.197
## - EV.geNorm.new$`hsa-miR-27a-3p`   1   31.247 61.247
## - EV.geNorm.new$`hsa-let-7a-5p`    1   31.674 61.674
## <none>                                 29.966 61.966
## - EV.geNorm.new$`hsa-miR-24-3p`    1   32.282 62.282
## - EV.geNorm.new$`hsa-miR-141-3`    1   32.376 62.376
## - EV.geNorm.new$`hsa-miR-25-3p`    1   32.767 62.767
## - EV.geNorm.new$`hsa-miR-451a`     1   34.641 64.641
## - EV.geNorm.new$`hsa-miR-19b-3p`   1   35.654 65.654
##
## Step:  AIC=60.34
## `Adverse Pathology` ~ EV.geNorm.new$`hsa-miR-25-3p` + EV.geNorm.new$`hsa-miR-199a-5p` +
##     EV.geNorm.new$`hsa-let-7a-5p` + EV.geNorm.new$`hsa-miR-191-5p` +
##     EV.geNorm.new$`hsa-miR-363-3p` + EV.geNorm.new$`hsa-miR-221-3p` +
##     EV.geNorm.new$`hsa-miR-19b-3p` + EV.geNorm.new$`hsa-miR-107` +
##     EV.geNorm.new$`hsa-miR-27a-3p` + EV.geNorm.new$`hsa-miR-451a` +
##     EV.geNorm.new$`hsa-miR-103a-3p` + EV.geNorm.new$`hsa-miR-23a-3p` +
##     EV.geNorm.new$`hsa-miR-24-3p` + EV.geNorm.new$`hsa-miR-141-3`
##
##                                    Df Deviance    AIC
## - EV.geNorm.new$`hsa-miR-107`      1   30.532 58.532
## - EV.geNorm.new$`hsa-miR-191-5p`   1   30.603 58.603
## - EV.geNorm.new$`hsa-miR-23a-3p`   1   31.023 59.023
## - EV.geNorm.new$`hsa-miR-103a-3p`  1   31.127 59.127
## - EV.geNorm.new$`hsa-miR-27a-3p`   1   31.285 59.285
## - EV.geNorm.new$`hsa-miR-221-3p`   1   31.358 59.358
## - EV.geNorm.new$`hsa-miR-363-3p`   1   31.538 59.538
## - EV.geNorm.new$`hsa-miR-199a-5p`  1   31.601 59.601
## - EV.geNorm.new$`hsa-let-7a-5p`    1   31.950 59.950
## <none>                                 30.341 60.341
## - EV.geNorm.new$`hsa-miR-24-3p`    1   32.433 60.433
```

```
## - EV.geNorm.new$'hsa-miR-141-3'     1    33.267 61.267
## - EV.geNorm.new$'hsa-miR-25-3p'     1    33.375 61.375
## - EV.geNorm.new$'hsa-miR-451a'      1    34.802 62.802
## - EV.geNorm.new$'hsa-miR-19b-3p'    1    36.390 64.390
##
## Step:  AIC=58.53
## 'Adverse Pathology' ~ EV.geNorm.new$'hsa-miR-25-3p' + EV.geNorm.new$'hsa-miR-199a-5p' +
##     EV.geNorm.new$'hsa-let-7a-5p' + EV.geNorm.new$'hsa-miR-191-5p' +
##     EV.geNorm.new$'hsa-miR-363-3p' + EV.geNorm.new$'hsa-miR-221-3p' +
##     EV.geNorm.new$'hsa-miR-19b-3p' + EV.geNorm.new$'hsa-miR-27a-3p' +
##     EV.geNorm.new$'hsa-miR-451a' + EV.geNorm.new$'hsa-miR-103a-3p' +
##     EV.geNorm.new$'hsa-miR-23a-3p' + EV.geNorm.new$'hsa-miR-24-3p' +
##     EV.geNorm.new$'hsa-miR-141-3'
##
##                                     Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-191-5p'     1    30.643 56.643
## - EV.geNorm.new$'hsa-miR-23a-3p'     1    31.308 57.308
## - EV.geNorm.new$'hsa-miR-103a-3p'    1    31.504 57.504
## - EV.geNorm.new$'hsa-miR-221-3p'     1    31.574 57.574
## - EV.geNorm.new$'hsa-miR-27a-3p'     1    31.608 57.608
## - EV.geNorm.new$'hsa-miR-363-3p'     1    31.750 57.750
## - EV.geNorm.new$'hsa-miR-199a-5p'    1    31.905 57.905
## - EV.geNorm.new$'hsa-let-7a-5p'      1    32.457 58.457
## <none>                                   30.532 58.532
## - EV.geNorm.new$'hsa-miR-24-3p'      1    32.769 58.769
## - EV.geNorm.new$'hsa-miR-141-3'      1    33.619 59.619
## - EV.geNorm.new$'hsa-miR-25-3p'      1    34.288 60.288
## - EV.geNorm.new$'hsa-miR-451a'       1    36.360 62.360
## - EV.geNorm.new$'hsa-miR-19b-3p'     1    36.391 62.391
##
## Step:  AIC=56.64
## 'Adverse Pathology' ~ EV.geNorm.new$'hsa-miR-25-3p' + EV.geNorm.new$'hsa-miR-199a-5p' +
##     EV.geNorm.new$'hsa-let-7a-5p' + EV.geNorm.new$'hsa-miR-363-3p' +
##     EV.geNorm.new$'hsa-miR-221-3p' + EV.geNorm.new$'hsa-miR-19b-3p' +
##     EV.geNorm.new$'hsa-miR-27a-3p' + EV.geNorm.new$'hsa-miR-451a' +
##     EV.geNorm.new$'hsa-miR-103a-3p' + EV.geNorm.new$'hsa-miR-23a-3p' +
##     EV.geNorm.new$'hsa-miR-24-3p' + EV.geNorm.new$'hsa-miR-141-3'
##
##                                     Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-23a-3p'     1    31.341 55.341
## - EV.geNorm.new$'hsa-miR-221-3p'     1    31.576 55.576
## - EV.geNorm.new$'hsa-miR-27a-3p'     1    31.664 55.664
## - EV.geNorm.new$'hsa-miR-363-3p'     1    31.751 55.751
## - EV.geNorm.new$'hsa-miR-199a-5p'    1    31.930 55.930
## <none>                                   30.643 56.643
## - EV.geNorm.new$'hsa-miR-24-3p'      1    32.791 56.791
## - EV.geNorm.new$'hsa-miR-103a-3p'    1    33.056 57.056
## - EV.geNorm.new$'hsa-let-7a-5p'      1    33.423 57.423
## - EV.geNorm.new$'hsa-miR-141-3'      1    33.625 57.625
## - EV.geNorm.new$'hsa-miR-25-3p'      1    34.424 58.424
## - EV.geNorm.new$'hsa-miR-451a'       1    36.361 60.361
## - EV.geNorm.new$'hsa-miR-19b-3p'     1    36.909 60.909
##
## Step:  AIC=55.34
```

```
## 'Adverse Pathology' ~ EV.geNorm.new$'hsa-miR-25-3p' + EV.geNorm.new$'hsa-miR-199a-5p' +
##     EV.geNorm.new$'hsa-let-7a-5p' + EV.geNorm.new$'hsa-miR-363-3p' +
##     EV.geNorm.new$'hsa-miR-221-3p' + EV.geNorm.new$'hsa-miR-19b-3p' +
##     EV.geNorm.new$'hsa-miR-27a-3p' + EV.geNorm.new$'hsa-miR-451a' +
##     EV.geNorm.new$'hsa-miR-103a-3p' + EV.geNorm.new$'hsa-miR-24-3p' +
##     EV.geNorm.new$'hsa-miR-141-3'
##
##                                   Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-221-3p'   1   32.276 54.276
## - EV.geNorm.new$'hsa-miR-24-3p'    1   32.791 54.791
## - EV.geNorm.new$'hsa-miR-363-3p'   1   32.809 54.809
## - EV.geNorm.new$'hsa-miR-199a-5p'  1   33.227 55.227
## <none>                                31.341 55.341
## - EV.geNorm.new$'hsa-miR-27a-3p'   1   33.405 55.405
## - EV.geNorm.new$'hsa-miR-103a-3p'  1   33.640 55.640
## - EV.geNorm.new$'hsa-miR-141-3'    1   33.795 55.795
## - EV.geNorm.new$'hsa-let-7a-5p'    1   33.981 55.981
## - EV.geNorm.new$'hsa-miR-25-3p'    1   35.889 57.889
## - EV.geNorm.new$'hsa-miR-19b-3p'   1   36.911 58.911
## - EV.geNorm.new$'hsa-miR-451a'     1   38.035 60.035
##
## Step:  AIC=54.28
## 'Adverse Pathology' ~ EV.geNorm.new$'hsa-miR-25-3p' + EV.geNorm.new$'hsa-miR-199a-5p' +
##     EV.geNorm.new$'hsa-let-7a-5p' + EV.geNorm.new$'hsa-miR-363-3p' +
##     EV.geNorm.new$'hsa-miR-19b-3p' + EV.geNorm.new$'hsa-miR-27a-3p' +
##     EV.geNorm.new$'hsa-miR-451a' + EV.geNorm.new$'hsa-miR-103a-3p' +
##     EV.geNorm.new$'hsa-miR-24-3p' + EV.geNorm.new$'hsa-miR-141-3'
##
##                                   Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-363-3p'   1   33.781 53.781
## - EV.geNorm.new$'hsa-miR-27a-3p'   1   34.053 54.053
## <none>                                32.276 54.276
## - EV.geNorm.new$'hsa-miR-24-3p'    1   34.555 54.555
## - EV.geNorm.new$'hsa-miR-141-3'    1   34.592 54.592
## - EV.geNorm.new$'hsa-miR-103a-3p'  1   35.144 55.144
## - EV.geNorm.new$'hsa-miR-199a-5p'  1   35.427 55.427
## - EV.geNorm.new$'hsa-let-7a-5p'    1   35.626 55.626
## - EV.geNorm.new$'hsa-miR-25-3p'    1   36.311 56.311
## - EV.geNorm.new$'hsa-miR-19b-3p'   1   36.988 56.988
## - EV.geNorm.new$'hsa-miR-451a'     1   38.359 58.359
##
## Step:  AIC=53.78
## 'Adverse Pathology' ~ EV.geNorm.new$'hsa-miR-25-3p' + EV.geNorm.new$'hsa-miR-199a-5p' +
##     EV.geNorm.new$'hsa-let-7a-5p' + EV.geNorm.new$'hsa-miR-19b-3p' +
##     EV.geNorm.new$'hsa-miR-27a-3p' + EV.geNorm.new$'hsa-miR-451a' +
##     EV.geNorm.new$'hsa-miR-103a-3p' + EV.geNorm.new$'hsa-miR-24-3p' +
##     EV.geNorm.new$'hsa-miR-141-3'
##
##                                   Df Deviance    AIC
## - EV.geNorm.new$'hsa-miR-27a-3p'   1   34.794 52.794
## - EV.geNorm.new$'hsa-miR-24-3p'    1   35.365 53.365
## <none>                                33.781 53.781
## - EV.geNorm.new$'hsa-miR-141-3'    1   36.385 54.385
## - EV.geNorm.new$'hsa-miR-199a-5p'  1   36.854 54.854
```

```
## - EV.geNorm.new$‘hsa-miR-25-3p‘      1   37.106 55.106
## - EV.geNorm.new$‘hsa-miR-103a-3p‘    1   37.412 55.412
## - EV.geNorm.new$‘hsa-let-7a-5p‘      1   37.686 55.686
## - EV.geNorm.new$‘hsa-miR-451a‘       1   38.361 56.361
## - EV.geNorm.new$‘hsa-miR-19b-3p‘     1   38.564 56.564
##
## Step:  AIC=52.79
## ‘Adverse Pathology‘ ~ EV.geNorm.new$‘hsa-miR-25-3p‘ + EV.geNorm.new$‘hsa-miR-199a-5p‘ +
##     EV.geNorm.new$‘hsa-let-7a-5p‘ + EV.geNorm.new$‘hsa-miR-19b-3p‘ +
##     EV.geNorm.new$‘hsa-miR-451a‘ + EV.geNorm.new$‘hsa-miR-103a-3p‘ +
##     EV.geNorm.new$‘hsa-miR-24-3p‘ + EV.geNorm.new$‘hsa-miR-141-3‘
##
##                                   Df Deviance    AIC
## - EV.geNorm.new$‘hsa-miR-24-3p‘    1   35.365 51.365
## - EV.geNorm.new$‘hsa-miR-141-3‘    1   36.751 52.751
## <none>                                34.794 52.794
## - EV.geNorm.new$‘hsa-miR-199a-5p‘  1   36.892 52.892
## - EV.geNorm.new$‘hsa-miR-103a-3p‘  1   37.524 53.524
## - EV.geNorm.new$‘hsa-let-7a-5p‘    1   37.819 53.819
## - EV.geNorm.new$‘hsa-miR-25-3p‘    1   38.092 54.092
## - EV.geNorm.new$‘hsa-miR-451a‘     1   39.175 55.175
## - EV.geNorm.new$‘hsa-miR-19b-3p‘   1   39.235 55.235
##
## Step:  AIC=51.36
## ‘Adverse Pathology‘ ~ EV.geNorm.new$‘hsa-miR-25-3p‘ + EV.geNorm.new$‘hsa-miR-199a-5p‘ +
##     EV.geNorm.new$‘hsa-let-7a-5p‘ + EV.geNorm.new$‘hsa-miR-19b-3p‘ +
##     EV.geNorm.new$‘hsa-miR-451a‘ + EV.geNorm.new$‘hsa-miR-103a-3p‘ +
##     EV.geNorm.new$‘hsa-miR-141-3‘
##
##                                   Df Deviance    AIC
## <none>                                35.365 51.365
## - EV.geNorm.new$‘hsa-miR-141-3‘    1   37.751 51.751
## - EV.geNorm.new$‘hsa-miR-103a-3p‘  1   38.008 52.008
## - EV.geNorm.new$‘hsa-miR-25-3p‘    1   38.125 52.125
## - EV.geNorm.new$‘hsa-let-7a-5p‘    1   38.458 52.458
## - EV.geNorm.new$‘hsa-miR-19b-3p‘   1   39.245 53.245
## - EV.geNorm.new$‘hsa-miR-451a‘     1   39.346 53.346
## - EV.geNorm.new$‘hsa-miR-199a-5p‘  1   40.082 54.082
```

```r
# EV NormFinder
fullmodel.EV.NormFinder.AP = glm(data = EV.all.original, formula = ‘Adverse Pathology‘~ EV.NormFinder.ne

step.EV.adverse.NormFinder = stepAIC(object = fullmodel.EV.NormFinder.AP, direction = "backward")
```

```
## Start:  AIC=65.57
## ‘Adverse Pathology‘ ~ EV.NormFinder.new$‘hsa-miR-199a-5p‘ + EV.NormFinder.new$‘hsa-miR-30c-5p‘ +
##     EV.NormFinder.new$‘hsa-miR-221-3p‘ + EV.NormFinder.new$‘hsa-miR-27b-3p‘ +
##     EV.NormFinder.new$‘hsa-let-7a-5p‘ + EV.NormFinder.new$‘hsa-miR-25-3p‘ +
##     EV.NormFinder.new$‘hsa-miR-191-5p‘ + EV.NormFinder.new$‘hsa-miR-363-3p‘ +
##     EV.NormFinder.new$‘hsa-miR-19b-3p‘ + EV.NormFinder.new$‘hsa-miR-107‘ +
##     EV.NormFinder.new$‘hsa-miR-451a‘ + EV.NormFinder.new$‘hsa-miR-16-5p‘ +
##     EV.NormFinder.new$‘hsa-miR-199a-3p‘ + EV.NormFinder.new$‘hsa-miR-103a-3p‘ +
##     EV.NormFinder.new$‘hsa-miR-27a-3p‘
##
```

```
##                                        Df Deviance     AIC
## - EV.NormFinder.new$`hsa-miR-107`        1    33.572 63.572
## - EV.NormFinder.new$`hsa-miR-363-3p`     1    33.594 63.594
## - EV.NormFinder.new$`hsa-miR-27b-3p`     1    33.713 63.713
## - EV.NormFinder.new$`hsa-miR-27a-3p`     1    33.757 63.757
## - EV.NormFinder.new$`hsa-miR-191-5p`     1    33.765 63.765
## - EV.NormFinder.new$`hsa-miR-16-5p`      1    34.169 64.169
## - EV.NormFinder.new$`hsa-miR-103a-3p`    1    34.251 64.251
## - EV.NormFinder.new$`hsa-miR-19b-3p`     1    34.392 64.392
## - EV.NormFinder.new$`hsa-miR-451a`       1    34.402 64.402
## - EV.NormFinder.new$`hsa-miR-30c-5p`     1    34.803 64.803
## - EV.NormFinder.new$`hsa-miR-199a-5p`    1    35.104 65.104
## - EV.NormFinder.new$`hsa-miR-199a-3p`    1    35.248 65.248
## - EV.NormFinder.new$`hsa-miR-221-3p`     1    35.326 65.326
## - EV.NormFinder.new$`hsa-miR-25-3p`      1    35.534 65.534
## <none>                                        33.571 65.571
## - EV.NormFinder.new$`hsa-let-7a-5p`      1    35.734 65.734
##
## Step:  AIC=63.57
## `Adverse Pathology` ~ EV.NormFinder.new$`hsa-miR-199a-5p` + EV.NormFinder.new$`hsa-miR-30c-5p` +
##     EV.NormFinder.new$`hsa-miR-221-3p` + EV.NormFinder.new$`hsa-miR-27b-3p` +
##     EV.NormFinder.new$`hsa-let-7a-5p` + EV.NormFinder.new$`hsa-miR-25-3p` +
##     EV.NormFinder.new$`hsa-miR-191-5p` + EV.NormFinder.new$`hsa-miR-363-3p` +
##     EV.NormFinder.new$`hsa-miR-19b-3p` + EV.NormFinder.new$`hsa-miR-451a` +
##     EV.NormFinder.new$`hsa-miR-16-5p` + EV.NormFinder.new$`hsa-miR-199a-3p` +
##     EV.NormFinder.new$`hsa-miR-103a-3p` + EV.NormFinder.new$`hsa-miR-27a-3p`
##
##                                        Df Deviance     AIC
## - EV.NormFinder.new$`hsa-miR-363-3p`     1    33.595 61.595
## - EV.NormFinder.new$`hsa-miR-27b-3p`     1    33.713 61.713
## - EV.NormFinder.new$`hsa-miR-27a-3p`     1    33.762 61.762
## - EV.NormFinder.new$`hsa-miR-191-5p`     1    33.793 61.793
## - EV.NormFinder.new$`hsa-miR-16-5p`      1    34.169 62.169
## - EV.NormFinder.new$`hsa-miR-19b-3p`     1    34.422 62.422
## - EV.NormFinder.new$`hsa-miR-451a`       1    34.571 62.571
## - EV.NormFinder.new$`hsa-miR-30c-5p`     1    34.817 62.817
## - EV.NormFinder.new$`hsa-miR-199a-5p`    1    35.275 63.275
## - EV.NormFinder.new$`hsa-miR-199a-3p`    1    35.371 63.371
## - EV.NormFinder.new$`hsa-miR-221-3p`     1    35.449 63.449
## <none>                                        33.572 63.572
## - EV.NormFinder.new$`hsa-let-7a-5p`      1    35.762 63.762
## - EV.NormFinder.new$`hsa-miR-25-3p`      1    36.074 64.074
## - EV.NormFinder.new$`hsa-miR-103a-3p`    1    36.367 64.367
##
## Step:  AIC=61.59
## `Adverse Pathology` ~ EV.NormFinder.new$`hsa-miR-199a-5p` + EV.NormFinder.new$`hsa-miR-30c-5p` +
##     EV.NormFinder.new$`hsa-miR-221-3p` + EV.NormFinder.new$`hsa-miR-27b-3p` +
##     EV.NormFinder.new$`hsa-let-7a-5p` + EV.NormFinder.new$`hsa-miR-25-3p` +
##     EV.NormFinder.new$`hsa-miR-191-5p` + EV.NormFinder.new$`hsa-miR-19b-3p` +
##     EV.NormFinder.new$`hsa-miR-451a` + EV.NormFinder.new$`hsa-miR-16-5p` +
##     EV.NormFinder.new$`hsa-miR-199a-3p` + EV.NormFinder.new$`hsa-miR-103a-3p` +
##     EV.NormFinder.new$`hsa-miR-27a-3p`
##
##                                                 Df Deviance     AIC
```

```
## - EV.NormFinder.new$`hsa-miR-27b-3p`    1    33.715 59.715
## - EV.NormFinder.new$`hsa-miR-27a-3p`    1    33.763 59.763
## - EV.NormFinder.new$`hsa-miR-191-5p`    1    33.803 59.803
## - EV.NormFinder.new$`hsa-miR-16-5p`     1    34.443 60.443
## - EV.NormFinder.new$`hsa-miR-19b-3p`    1    34.533 60.533
## - EV.NormFinder.new$`hsa-miR-451a`      1    35.002 61.002
## - EV.NormFinder.new$`hsa-miR-30c-5p`    1    35.032 61.032
## - EV.NormFinder.new$`hsa-miR-199a-5p`   1    35.346 61.346
## - EV.NormFinder.new$`hsa-miR-221-3p`    1    35.537 61.537
## - EV.NormFinder.new$`hsa-miR-199a-3p`   1    35.567 61.567
## <none>                                       33.595 61.595
## - EV.NormFinder.new$`hsa-let-7a-5p`     1    35.874 61.874
## - EV.NormFinder.new$`hsa-miR-25-3p`     1    36.202 62.202
## - EV.NormFinder.new$`hsa-miR-103a-3p`   1    36.431 62.431
##
## Step:  AIC=59.71
## `Adverse Pathology` ~ EV.NormFinder.new$`hsa-miR-199a-5p` + EV.NormFinder.new$`hsa-miR-30c-5p` +
##     EV.NormFinder.new$`hsa-miR-221-3p` + EV.NormFinder.new$`hsa-let-7a-5p` +
##     EV.NormFinder.new$`hsa-miR-25-3p` + EV.NormFinder.new$`hsa-miR-191-5p` +
##     EV.NormFinder.new$`hsa-miR-19b-3p` + EV.NormFinder.new$`hsa-miR-451a` +
##     EV.NormFinder.new$`hsa-miR-16-5p` + EV.NormFinder.new$`hsa-miR-199a-3p` +
##     EV.NormFinder.new$`hsa-miR-103a-3p` + EV.NormFinder.new$`hsa-miR-27a-3p`
##
##                                        Df Deviance    AIC
## - EV.NormFinder.new$`hsa-miR-27a-3p`    1    33.774 57.774
## - EV.NormFinder.new$`hsa-miR-191-5p`    1    34.084 58.084
## - EV.NormFinder.new$`hsa-miR-16-5p`     1    34.589 58.589
## - EV.NormFinder.new$`hsa-miR-19b-3p`    1    34.749 58.749
## - EV.NormFinder.new$`hsa-miR-199a-5p`   1    35.348 59.348
## - EV.NormFinder.new$`hsa-miR-199a-3p`   1    35.572 59.572
## - EV.NormFinder.new$`hsa-miR-451a`      1    35.630 59.630
## - EV.NormFinder.new$`hsa-miR-30c-5p`    1    35.685 59.685
## <none>                                       33.715 59.715
## - EV.NormFinder.new$`hsa-let-7a-5p`     1    36.144 60.144
## - EV.NormFinder.new$`hsa-miR-221-3p`    1    36.348 60.348
## - EV.NormFinder.new$`hsa-miR-25-3p`     1    37.155 61.155
## - EV.NormFinder.new$`hsa-miR-103a-3p`   1    37.184 61.184
##
## Step:  AIC=57.77
## `Adverse Pathology` ~ EV.NormFinder.new$`hsa-miR-199a-5p` + EV.NormFinder.new$`hsa-miR-30c-5p` +
##     EV.NormFinder.new$`hsa-miR-221-3p` + EV.NormFinder.new$`hsa-let-7a-5p` +
##     EV.NormFinder.new$`hsa-miR-25-3p` + EV.NormFinder.new$`hsa-miR-191-5p` +
##     EV.NormFinder.new$`hsa-miR-19b-3p` + EV.NormFinder.new$`hsa-miR-451a` +
##     EV.NormFinder.new$`hsa-miR-16-5p` + EV.NormFinder.new$`hsa-miR-199a-3p` +
##     EV.NormFinder.new$`hsa-miR-103a-3p`
##
##                                        Df Deviance    AIC
## - EV.NormFinder.new$`hsa-miR-191-5p`    1    34.085 56.085
## - EV.NormFinder.new$`hsa-miR-16-5p`     1    34.928 56.928
## - EV.NormFinder.new$`hsa-miR-19b-3p`    1    35.064 57.064
## - EV.NormFinder.new$`hsa-miR-199a-5p`   1    35.397 57.397
## - EV.NormFinder.new$`hsa-miR-199a-3p`   1    35.618 57.618
## - EV.NormFinder.new$`hsa-miR-30c-5p`    1    35.688 57.688
## - EV.NormFinder.new$`hsa-miR-451a`      1    35.716 57.716
```

```
## <none>                                    33.774 57.774
## - EV.NormFinder.new$`hsa-let-7a-5p`    1   36.488 58.488
## - EV.NormFinder.new$`hsa-miR-221-3p`   1   36.524 58.524
## - EV.NormFinder.new$`hsa-miR-103a-3p`  1   37.776 59.776
## - EV.NormFinder.new$`hsa-miR-25-3p`    1   38.206 60.206
##
## Step:  AIC=56.09
## `Adverse Pathology` ~ EV.NormFinder.new$`hsa-miR-199a-5p` + EV.NormFinder.new$`hsa-miR-30c-5p` +
##     EV.NormFinder.new$`hsa-miR-221-3p` + EV.NormFinder.new$`hsa-let-7a-5p` +
##     EV.NormFinder.new$`hsa-miR-25-3p` + EV.NormFinder.new$`hsa-miR-19b-3p` +
##     EV.NormFinder.new$`hsa-miR-451a` + EV.NormFinder.new$`hsa-miR-16-5p` +
##     EV.NormFinder.new$`hsa-miR-199a-3p` + EV.NormFinder.new$`hsa-miR-103a-3p`
##
##                                         Df Deviance    AIC
## - EV.NormFinder.new$`hsa-miR-16-5p`    1   35.227 55.227
## - EV.NormFinder.new$`hsa-miR-19b-3p`   1   35.315 55.315
## - EV.NormFinder.new$`hsa-miR-451a`     1   35.837 55.837
## - EV.NormFinder.new$`hsa-miR-199a-3p`  1   36.058 56.058
## <none>                                    34.085 56.085
## - EV.NormFinder.new$`hsa-miR-199a-5p`  1   36.444 56.444
## - EV.NormFinder.new$`hsa-let-7a-5p`    1   36.491 56.491
## - EV.NormFinder.new$`hsa-miR-30c-5p`   1   36.508 56.508
## - EV.NormFinder.new$`hsa-miR-221-3p`   1   37.490 57.490
## - EV.NormFinder.new$`hsa-miR-103a-3p`  1   38.174 58.174
## - EV.NormFinder.new$`hsa-miR-25-3p`    1   38.297 58.297
##
## Step:  AIC=55.23
## `Adverse Pathology` ~ EV.NormFinder.new$`hsa-miR-199a-5p` + EV.NormFinder.new$`hsa-miR-30c-5p` +
##     EV.NormFinder.new$`hsa-miR-221-3p` + EV.NormFinder.new$`hsa-let-7a-5p` +
##     EV.NormFinder.new$`hsa-miR-25-3p` + EV.NormFinder.new$`hsa-miR-19b-3p` +
##     EV.NormFinder.new$`hsa-miR-451a` + EV.NormFinder.new$`hsa-miR-199a-3p` +
##     EV.NormFinder.new$`hsa-miR-103a-3p`
##
##                                         Df Deviance    AIC
## - EV.NormFinder.new$`hsa-miR-19b-3p`   1   35.680 53.680
## <none>                                    35.227 55.227
## - EV.NormFinder.new$`hsa-miR-199a-5p`  1   37.520 55.520
## - EV.NormFinder.new$`hsa-let-7a-5p`    1   37.563 55.563
## - EV.NormFinder.new$`hsa-miR-30c-5p`   1   37.571 55.571
## - EV.NormFinder.new$`hsa-miR-199a-3p`  1   37.637 55.637
## - EV.NormFinder.new$`hsa-miR-221-3p`   1   38.235 56.235
## - EV.NormFinder.new$`hsa-miR-25-3p`    1   38.633 56.633
## - EV.NormFinder.new$`hsa-miR-103a-3p`  1   38.771 56.771
## - EV.NormFinder.new$`hsa-miR-451a`     1   39.305 57.305
##
## Step:  AIC=53.68
## `Adverse Pathology` ~ EV.NormFinder.new$`hsa-miR-199a-5p` + EV.NormFinder.new$`hsa-miR-30c-5p` +
##     EV.NormFinder.new$`hsa-miR-221-3p` + EV.NormFinder.new$`hsa-let-7a-5p` +
##     EV.NormFinder.new$`hsa-miR-25-3p` + EV.NormFinder.new$`hsa-miR-451a` +
##     EV.NormFinder.new$`hsa-miR-199a-3p` + EV.NormFinder.new$`hsa-miR-103a-3p`
##
##                                         Df Deviance    AIC
## - EV.NormFinder.new$`hsa-let-7a-5p`    1   37.564 53.564
## <none>                                    35.680 53.680
```

```
## - EV.NormFinder.new$'hsa-miR-199a-5p'  1   38.384 54.384
## - EV.NormFinder.new$'hsa-miR-30c-5p'   1   38.461 54.461
## - EV.NormFinder.new$'hsa-miR-221-3p'   1   38.522 54.522
## - EV.NormFinder.new$'hsa-miR-103a-3p'  1   38.779 54.779
## - EV.NormFinder.new$'hsa-miR-451a'     1   39.341 55.341
## - EV.NormFinder.new$'hsa-miR-199a-3p'  1   39.343 55.343
## - EV.NormFinder.new$'hsa-miR-25-3p'    1   40.553 56.553
##
## Step:  AIC=53.56
## 'Adverse Pathology' ~ EV.NormFinder.new$'hsa-miR-199a-5p' + EV.NormFinder.new$'hsa-miR-30c-5p' +
##     EV.NormFinder.new$'hsa-miR-221-3p' + EV.NormFinder.new$'hsa-miR-25-3p' +
##     EV.NormFinder.new$'hsa-miR-451a' + EV.NormFinder.new$'hsa-miR-199a-3p' +
##     EV.NormFinder.new$'hsa-miR-103a-3p'
##
##                                        Df Deviance    AIC
## - EV.NormFinder.new$'hsa-miR-103a-3p'  1   38.823 52.823
## - EV.NormFinder.new$'hsa-miR-199a-5p'  1   39.309 53.309
## <none>                                     37.564 53.564
## - EV.NormFinder.new$'hsa-miR-221-3p'   1   41.045 55.045
## - EV.NormFinder.new$'hsa-miR-199a-3p'  1   41.357 55.357
## - EV.NormFinder.new$'hsa-miR-451a'     1   43.430 57.430
## - EV.NormFinder.new$'hsa-miR-30c-5p'   1   43.739 57.739
## - EV.NormFinder.new$'hsa-miR-25-3p'    1   46.031 60.031
##
## Step:  AIC=52.82
## 'Adverse Pathology' ~ EV.NormFinder.new$'hsa-miR-199a-5p' + EV.NormFinder.new$'hsa-miR-30c-5p' +
##     EV.NormFinder.new$'hsa-miR-221-3p' + EV.NormFinder.new$'hsa-miR-25-3p' +
##     EV.NormFinder.new$'hsa-miR-451a' + EV.NormFinder.new$'hsa-miR-199a-3p'
##
##                                        Df Deviance    AIC
## - EV.NormFinder.new$'hsa-miR-199a-5p'  1   40.591 52.591
## <none>                                     38.823 52.823
## - EV.NormFinder.new$'hsa-miR-221-3p'   1   42.586 54.586
## - EV.NormFinder.new$'hsa-miR-199a-3p'  1   43.200 55.200
## - EV.NormFinder.new$'hsa-miR-451a'     1   44.133 56.133
## - EV.NormFinder.new$'hsa-miR-30c-5p'   1   44.962 56.962
## - EV.NormFinder.new$'hsa-miR-25-3p'    1   46.676 58.676
##
## Step:  AIC=52.59
## 'Adverse Pathology' ~ EV.NormFinder.new$'hsa-miR-30c-5p' + EV.NormFinder.new$'hsa-miR-221-3p' +
##     EV.NormFinder.new$'hsa-miR-25-3p' + EV.NormFinder.new$'hsa-miR-451a' +
##     EV.NormFinder.new$'hsa-miR-199a-3p'
##
##                                        Df Deviance    AIC
## <none>                                     40.591 52.591
## - EV.NormFinder.new$'hsa-miR-199a-3p'  1   43.407 53.407
## - EV.NormFinder.new$'hsa-miR-221-3p'   1   44.731 54.731
## - EV.NormFinder.new$'hsa-miR-451a'     1   44.986 54.986
## - EV.NormFinder.new$'hsa-miR-25-3p'    1   48.093 58.093
## - EV.NormFinder.new$'hsa-miR-30c-5p'   1   48.459 58.459
```

```r
# serum CT Mean
fullmodel.serum.ctmean.ap = glm(data = serum.all.original, formula = 'Adverse Pathology'~ serum.globalCT
step.EV.adverse.final = stepAIC(object = fullmodel.serum.ctmean.ap, direction = "backward")
```

```
## Start:  AIC=110.88
## 'Adverse Pathology' ~ serum.globalCTMean.new$'hsa-miR-1246'
##
##                                           Df Deviance    AIC
## <none>                                       106.88 110.88
## - serum.globalCTMean.new$'hsa-miR-1246'   1   111.68 113.68
```

```r
# serum geNorm
fullmodel.serum.geNorm.ap = glm(data = serum.all.original, formula = 'Adverse Pathology'~ serum.geNorm.n
step.EV.adverse.final = stepAIC(object = fullmodel.serum.geNorm.ap, direction = "backward")
```

```
## Start:  AIC=108.34
## 'Adverse Pathology' ~ serum.geNorm.new$'hsa-miR-1246' + serum.geNorm.new$'hsa-miR-100-5p' +
##     serum.geNorm.new$'hsa-miR-574-3p'
##
##                                       Df Deviance    AIC
## - serum.geNorm.new$'hsa-miR-574-3p'   1   101.94 107.94
## <none>                                    100.34 108.34
## - serum.geNorm.new$'hsa-miR-1246'     1   103.10 109.10
## - serum.geNorm.new$'hsa-miR-100-5p'   1   103.75 109.75
##
## Step:  AIC=107.94
## 'Adverse Pathology' ~ serum.geNorm.new$'hsa-miR-1246' + serum.geNorm.new$'hsa-miR-100-5p'
##
##                                       Df Deviance    AIC
## <none>                                    101.94 107.94
## - serum.geNorm.new$'hsa-miR-1246'     1   105.82 109.82
## - serum.geNorm.new$'hsa-miR-100-5p'   1   106.84 110.84
```

```r
# serum NormFinder
fullmodel.serum.NormFinder.ap = glm(data = serum.all.original, formula = 'Adverse Pathology'~ serum.Norm
step.EV.adverse.final = stepAIC(object = fullmodel.serum.NormFinder.ap, direction = "backward")
```

```
## Start:  AIC=112.47
## 'Adverse Pathology' ~ serum.NormFinder.new$'hsa-miR-100-5p' +
##     serum.NormFinder.new$'hsa-miR-574-3p' + serum.NormFinder.new$'hsa-miR-221-3p' +
##     serum.NormFinder.new$'hsa-miR-1246'
##
##                                           Df Deviance    AIC
## - serum.NormFinder.new$'hsa-miR-221-3p'   1   102.49 110.49
## - serum.NormFinder.new$'hsa-miR-574-3p'   1   103.06 111.06
## <none>                                        102.47 112.47
## - serum.NormFinder.new$'hsa-miR-100-5p'   1   104.58 112.58
## - serum.NormFinder.new$'hsa-miR-1246'     1   105.30 113.30
##
## Step:  AIC=110.49
## 'Adverse Pathology' ~ serum.NormFinder.new$'hsa-miR-100-5p' +
##     serum.NormFinder.new$'hsa-miR-574-3p' + serum.NormFinder.new$'hsa-miR-1246'
##
##                                           Df Deviance    AIC
## - serum.NormFinder.new$'hsa-miR-574-3p'   1   103.18 109.18
## <none>                                        102.49 110.49
## - serum.NormFinder.new$'hsa-miR-100-5p'   1   104.71 110.71
```

```
## - serum.NormFinder.new$`hsa-miR-1246`    1    105.30 111.30
##
## Step:  AIC=109.18
## `Adverse Pathology` ~ serum.NormFinder.new$`hsa-miR-100-5p` +
##      serum.NormFinder.new$`hsa-miR-1246`
##
##                                     Df Deviance    AIC
## <none>                                 103.18 109.18
## - serum.NormFinder.new$`hsa-miR-100-5p`  1    106.46 110.46
## - serum.NormFinder.new$`hsa-miR-1246`    1    107.01 111.01
```