Analysis 2/1

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Import datafile

```
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
serum.geneglobe = readxl::read_excel("./data/Serum_SerumEV_GeneGlobeRQ_CT35.xlsx", sheet = "Serum_GeneG
EV.geneglobe = readxl::read_excel("./data/Serum_SerumEV_GeneGlobeRQ_CT35.xlsx", sheet = "EV_GeneGlobeRQ
```

Tidy Data

```
# 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
```

Checking distribution for each microRNA

```r
# checking distribution for serum
normality.test.serum = data.frame(
  microRNA = colnames(serum.geneglobe.new[-1]),
  p.value = numeric(61)
)

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)
)

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

# Results display
normality.test.serum
```

```
##           microRNA      p.value
## 1     hsa-let-7a-5p 2.558331e-23
## 2     hsa-miR-100-5p 4.349041e-20
## 3    hsa-miR-103a-3p 7.231472e-26
## 4    hsa-miR-106a-5p 1.839331e-27
## 5        hsa-miR-107 5.340607e-26
## 6    hsa-miR-130b-3p 9.331356e-21
## 7    hsa-miR-146a-5p 3.147565e-28
## 8     hsa-miR-223-3p 1.595983e-22
## 9      hsa-miR-24-3p 5.127759e-24
## 10    hsa-miR-26b-5p 2.559564e-24
## 11    hsa-miR-30c-5p 1.217936e-21
## 12       hsa-miR-451a 6.542109e-28
## 13    hsa-miR-874-3p 8.232949e-19
## 14     hsa-miR-93-5p 1.834909e-26
## 15     hsa-let-7i-5p 1.266864e-25
## 16       hsa-miR-1246 2.250559e-20
## 17    hsa-miR-141-3p 6.773832e-24
## 18   hsa-miR-146b-3p 1.402517e-24
## 19    hsa-miR-18b-5p 2.615622e-27
## 20    hsa-miR-19b-3p 3.236080e-27
## 21   hsa-miR-193a-3p 8.266525e-30
## 22    hsa-miR-194-5p 8.092987e-25
## 23   hsa-miR-200a-3p 2.315388e-25
## 24   hsa-miR-200b-3p 3.059867e-24
## 25    hsa-miR-204-5p 4.326020e-24
## 26    hsa-miR-210-3p 3.686872e-26
## 27    hsa-miR-214-3p 4.321631e-22
```

```
## 28   hsa-miR-222-3p 8.520933e-24
## 29    hsa-miR-16-5p 4.532130e-27
## 30  hsa-miR-301a-3p 3.207730e-28
## 31      hsa-miR-320a 2.155441e-23
## 32   hsa-miR-27a-3p 9.763600e-26
## 33   hsa-miR-330-3p 1.859365e-23
## 34   hsa-miR-335-5p 1.996341e-25
## 35   hsa-miR-345-5p 7.519104e-23
## 36   hsa-miR-363-3p 1.760897e-28
## 37       hsa-miR-375 3.317770e-23
## 38  hsa-miR-518e-5p 2.656983e-30
## 39   hsa-miR-574-3p 6.279385e-26
## 40   hsa-miR-708-5p 1.145690e-30
## 41     hsa-miR-9-3p 1.475679e-29
## 42   hsa-miR-191-5p 6.756777e-25
## 43   hsa-miR-23a-3p 1.094593e-23
## 44  hsa-miR-199a-3p 8.601354e-27
## 45    hsa-miR-21-5p 3.270612e-23
## 46    hsa-let-7b-5p 3.270628e-26
## 47   hsa-miR-30a-5p 2.346560e-21
## 48  hsa-miR-199a-5p 1.951565e-27
## 49   hsa-miR-122-5p 1.433983e-24
## 50   hsa-miR-221-3p 1.202591e-27
## 51   hsa-miR-29a-3p 1.024645e-19
## 52    hsa-miR-31-5p 2.155509e-13
## 53   hsa-miR-34a-5p 1.061941e-23
## 54   hsa-miR-27b-3p 1.449977e-26
## 55    hsa-miR-25-3p 2.117583e-25
## 56   hsa-miR-218-5p 1.057341e-28
## 57   hsa-miR-155-5p 1.327326e-23
## 58  hsa-miR-125b-5p 3.079423e-21
## 59   hsa-miR-143-3p 2.480487e-18
## 60  hsa-miR-148a-3p 9.779177e-26
## 61  hsa-miR-374a-5p 5.177412e-27
```

`normality.test.EV`

```
##           microRNA      p.value
## 1    hsa-let-7a-5p 2.487931e-15
## 2    hsa-miR-100-5p 6.455385e-18
## 3   hsa-miR-103a-3p 8.158059e-15
## 4   hsa-miR-106a-5p 3.822017e-15
## 5       hsa-miR-107 4.537570e-15
## 6   hsa-miR-130b-3p 2.975883e-16
## 7   hsa-miR-146a-5p 1.061301e-17
## 8    hsa-miR-223-3p 6.300071e-18
## 9     hsa-miR-24-3p 1.176324e-16
## 10   hsa-miR-26b-5p 6.486458e-15
## 11   hsa-miR-30c-5p 9.137247e-15
## 12     hsa-miR-451a 1.891211e-14
## 13   hsa-miR-874-3p 8.530888e-13
## 14    hsa-miR-93-5p 1.805469e-14
## 15    hsa-let-7i-5p 7.718787e-14
## 16      hsa-miR-1246 5.276919e-14
```

```
## 17  hsa-miR-141-3p 3.465216e-17
## 18 hsa-miR-146b-3p 3.421526e-15
## 19  hsa-miR-18b-5p 7.006765e-16
## 20  hsa-miR-19b-3p 4.557650e-15
## 21 hsa-miR-193a-3p 7.513604e-19
## 22  hsa-miR-194-5p 1.476202e-14
## 23 hsa-miR-200a-3p 8.242175e-21
## 24 hsa-miR-200b-3p 3.805918e-19
## 25  hsa-miR-204-5p 1.684910e-12
## 26  hsa-miR-210-3p 3.145080e-12
## 27  hsa-miR-214-3p 3.147982e-19
## 28  hsa-miR-222-3p 1.242499e-13
## 29   hsa-miR-16-5p 6.154232e-15
## 30 hsa-miR-301a-3p 1.692750e-16
## 31     hsa-miR-320a 3.491095e-17
## 32  hsa-miR-27a-3p 5.376571e-18
## 33  hsa-miR-330-3p 4.789581e-16
## 34  hsa-miR-335-5p 3.068903e-19
## 35  hsa-miR-345-5p 8.008568e-15
## 36  hsa-miR-363-3p 1.173861e-14
## 37      hsa-miR-375 8.517595e-20
## 38 hsa-miR-518e-5p 4.395935e-21
## 39  hsa-miR-574-3p 3.804053e-14
## 40  hsa-miR-708-5p 4.885815e-22
## 41    hsa-miR-9-3p 4.167507e-19
## 42  hsa-miR-191-5p 2.983431e-15
## 43  hsa-miR-23a-3p 6.217886e-17
## 44 hsa-miR-199a-3p 1.714171e-18
## 45   hsa-miR-21-5p 1.341752e-15
## 46   hsa-let-7b-5p 1.425033e-12
## 47  hsa-miR-30a-5p 5.010794e-14
## 48 hsa-miR-199a-5p 1.697282e-18
## 49  hsa-miR-122-5p 1.314878e-17
## 50  hsa-miR-221-3p 1.259561e-16
## 51  hsa-miR-29a-3p 1.211786e-17
## 52   hsa-miR-31-5p 8.982345e-18
## 53  hsa-miR-34a-5p 4.125223e-17
## 54  hsa-miR-27b-3p 7.352681e-18
## 55   hsa-miR-25-3p 4.934957e-14
## 56  hsa-miR-218-5p 3.764179e-22
## 57  hsa-miR-155-5p 7.651754e-14
## 58 hsa-miR-125b-5p 2.502710e-15
## 59  hsa-miR-143-3p 5.167542e-19
## 60 hsa-miR-148a-3p 1.108249e-14
## 61 hsa-miR-374a-5p 4.976194e-16
```

Conclusion: None of the microRNA has the normal distribution.

Univariate GLM fitting

Biopsy Grade

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

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

```r
# univariate GLM
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$'Biopsy Grade Group'~serum.all[,i+1])
  result = summary(model)
  grade.serum.result$p.value[i] = result$coefficients[2,4]
}

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

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

# Display result
grade.serum.result
```

```
##            microRNA     p.value
## 1     hsa-let-7a-5p 0.082842694
## 2     hsa-miR-100-5p 0.089998706
## 3   hsa-miR-103a-3p 0.318997297
## 4   hsa-miR-106a-5p 0.120069799
## 5        hsa-miR-107 0.318915167
## 6   hsa-miR-130b-3p 0.577297707
## 7   hsa-miR-146a-5p 0.940900666
## 8    hsa-miR-223-3p 0.402763314
## 9     hsa-miR-24-3p 0.829278754
## 10   hsa-miR-26b-5p 0.348868212
## 11   hsa-miR-30c-5p 0.371258531
## 12     hsa-miR-451a 0.109854331
## 13   hsa-miR-874-3p 0.139060309
## 14    hsa-miR-93-5p 0.180248864
## 15    hsa-let-7i-5p 0.276539674
## 16     hsa-miR-1246 0.043973261
## 17   hsa-miR-141-3p 0.277801690
## 18 hsa-miR-146b-3p 0.602666448
```

```
## 19   hsa-miR-18b-5p 0.146509790
## 20   hsa-miR-19b-3p 0.167676066
## 21  hsa-miR-193a-3p 0.169680719
## 22   hsa-miR-194-5p 0.068161765
## 23  hsa-miR-200a-3p 0.369539700
## 24  hsa-miR-200b-3p 0.776076892
## 25   hsa-miR-204-5p 0.981549543
## 26   hsa-miR-210-3p 0.082736018
## 27   hsa-miR-214-3p 0.002936045
## 28   hsa-miR-222-3p 0.932503877
## 29    hsa-miR-16-5p 0.119822966
## 30  hsa-miR-301a-3p 0.049412355
## 31     hsa-miR-320a 0.635345297
## 32   hsa-miR-27a-3p 0.854689360
## 33   hsa-miR-330-3p 0.892187806
## 34   hsa-miR-335-5p 0.391761437
## 35   hsa-miR-345-5p 0.256175784
## 36   hsa-miR-363-3p 0.087591113
## 37      hsa-miR-375 0.126664097
## 38  hsa-miR-518e-5p 0.853600884
## 39   hsa-miR-574-3p 0.523611978
## 40   hsa-miR-708-5p 0.525351790
## 41     hsa-miR-9-3p 0.606717360
## 42   hsa-miR-191-5p 0.880724567
## 43   hsa-miR-23a-3p 0.635804388
## 44  hsa-miR-199a-3p 0.893287076
## 45    hsa-miR-21-5p 0.980086828
## 46    hsa-let-7b-5p 0.128201777
## 47   hsa-miR-30a-5p 0.810722053
## 48  hsa-miR-199a-5p 0.694082225
## 49   hsa-miR-122-5p 0.211327678
## 50   hsa-miR-221-3p 0.794005543
## 51   hsa-miR-29a-3p 0.375495718
## 52    hsa-miR-31-5p 0.170775812
## 53   hsa-miR-34a-5p 0.564256100
## 54   hsa-miR-27b-3p 0.951030144
## 55    hsa-miR-25-3p 0.491691646
## 56   hsa-miR-218-5p 0.924785927
## 57   hsa-miR-155-5p 0.992531437
## 58  hsa-miR-125b-5p 0.050866656
## 59   hsa-miR-143-3p 0.419155301
## 60  hsa-miR-148a-3p 0.273447660
## 61  hsa-miR-374a-5p 0.053369675
```

grade.EV.result

```
##          microRNA   p.value
## 1    hsa-let-7a-5p 0.12090800
## 2    hsa-miR-100-5p 0.58560126
## 3   hsa-miR-103a-3p 0.12826140
## 4   hsa-miR-106a-5p 0.24129429
## 5      hsa-miR-107 0.12150141
## 6   hsa-miR-130b-3p 0.17982463
## 7   hsa-miR-146a-5p 0.49946568
```

```
## 8    hsa-miR-223-3p 0.33273735
## 9     hsa-miR-24-3p 0.29214806
## 10  hsa-miR-26b-5p 0.10432205
## 11  hsa-miR-30c-5p 0.15570689
## 12     hsa-miR-451a 0.35267549
## 13  hsa-miR-874-3p 0.52850231
## 14   hsa-miR-93-5p 0.28841698
## 15   hsa-let-7i-5p 0.15519509
## 16     hsa-miR-1246 0.21364531
## 17  hsa-miR-141-3p 0.07836893
## 18 hsa-miR-146b-3p 0.77228699
## 19  hsa-miR-18b-5p 0.76662716
## 20  hsa-miR-19b-3p 0.49384653
## 21 hsa-miR-193a-3p 0.41113622
## 22  hsa-miR-194-5p 0.49780574
## 23 hsa-miR-200a-3p 0.56471034
## 24 hsa-miR-200b-3p 0.59434684
## 25  hsa-miR-204-5p 0.44598756
## 26  hsa-miR-210-3p 0.54771737
## 27  hsa-miR-214-3p 0.84976612
## 28  hsa-miR-222-3p 0.28553213
## 29   hsa-miR-16-5p 0.40915191
## 30 hsa-miR-301a-3p 0.39546234
## 31     hsa-miR-320a 0.23290856
## 32  hsa-miR-27a-3p 0.37650189
## 33  hsa-miR-330-3p 0.21628882
## 34  hsa-miR-335-5p 0.15685386
## 35  hsa-miR-345-5p 0.40437731
## 36  hsa-miR-363-3p 0.47761021
## 37      hsa-miR-375 0.44943671
## 38 hsa-miR-518e-5p 0.97687245
## 39  hsa-miR-574-3p 0.69375274
## 40  hsa-miR-708-5p 0.14125445
## 41     hsa-miR-9-3p 0.59813426
## 42  hsa-miR-191-5p 0.18868169
## 43  hsa-miR-23a-3p 0.32341625
## 44 hsa-miR-199a-3p 0.35462238
## 45   hsa-miR-21-5p 0.19991864
## 46   hsa-let-7b-5p 0.14439471
## 47  hsa-miR-30a-5p 0.63023075
## 48 hsa-miR-199a-5p 0.44186781
## 49  hsa-miR-122-5p 0.88327626
## 50  hsa-miR-221-3p 0.20046249
## 51  hsa-miR-29a-3p 0.29967678
## 52   hsa-miR-31-5p 0.04691240
## 53  hsa-miR-34a-5p 0.49264931
## 54  hsa-miR-27b-3p 0.39221086
## 55   hsa-miR-25-3p 0.33295063
## 56  hsa-miR-218-5p 0.05101086
## 57  hsa-miR-155-5p 0.33967156
## 58 hsa-miR-125b-5p 0.41277518
## 59  hsa-miR-143-3p 0.88358354
## 60 hsa-miR-148a-3p 0.56686671
## 61 hsa-miR-374a-5p 0.23829236
```

Now we want to focus on the significant predictors.

```
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
```

```
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
```

```
# backward selection for serum/grade model
library(MASS)
```

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

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

```
fullmodel1 = glm(data = serum.all, formula = `Biopsy Grade Group`~`hsa-miR-1246`+`hsa-miR-214-3p`+`hsa-r
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
```

Therefore the final model only contains hsa-miR-1246 and hsa-miR-214-3p for serum/biopsy grade. The final model only contains hsa-miR-31-5p for EV/biopsy grade.

Adverse Pathology

```r
# 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$'Adverse Pathology'~serum.all[,i+1], family = "binomial")
  result = summary(model)
  adverse.serum.result$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$'Adverse Pathology'~EV.all[,i+1], family = "binomial")
  result = summary(model)
  adverse.EV.result$p.value[i] = result$coefficients[2,4]
}

# Display result
adverse.serum.result
```

```
##          microRNA    p.value
## 1      hsa-let-7a-5p 0.57080781
## 2     hsa-miR-100-5p 0.29689036
## 3    hsa-miR-103a-3p 0.98918149
## 4    hsa-miR-106a-5p 0.65950349
## 5        hsa-miR-107 0.97624696
## 6    hsa-miR-130b-3p 0.50262130
## 7    hsa-miR-146a-5p 0.52642598
## 8     hsa-miR-223-3p 0.48067507
## 9      hsa-miR-24-3p 0.58295803
## 10    hsa-miR-26b-5p 0.81141350
## 11    hsa-miR-30c-5p 0.77895126
## 12      hsa-miR-451a 0.55299498
## 13    hsa-miR-874-3p 0.67735245
## 14     hsa-miR-93-5p 0.70841166
## 15     hsa-let-7i-5p 0.73690740
## 16      hsa-miR-1246 0.37524009
## 17    hsa-miR-141-3p 0.94517144
## 18   hsa-miR-146b-3p 0.32459308
## 19    hsa-miR-18b-5p 0.85908991
## 20    hsa-miR-19b-3p 0.56537327
## 21   hsa-miR-193a-3p 0.59880929
## 22    hsa-miR-194-5p 0.50057586
## 23   hsa-miR-200a-3p 0.17503682
## 24   hsa-miR-200b-3p 0.27385859
## 25    hsa-miR-204-5p 0.77199377
## 26    hsa-miR-210-3p 0.64502485
```

```
## 27   hsa-miR-214-3p 0.71675027
## 28   hsa-miR-222-3p 0.69630211
## 29    hsa-miR-16-5p 0.68194796
## 30 hsa-miR-301a-3p 0.42992295
## 31      hsa-miR-320a 0.89318818
## 32   hsa-miR-27a-3p 0.52306401
## 33   hsa-miR-330-3p 0.49006117
## 34   hsa-miR-335-5p 0.50280376
## 35   hsa-miR-345-5p 0.69204866
## 36   hsa-miR-363-3p 0.55208722
## 37       hsa-miR-375 0.19699114
## 38 hsa-miR-518e-5p 0.99137933
## 39   hsa-miR-574-3p 0.77832513
## 40   hsa-miR-708-5p 0.61614750
## 41     hsa-miR-9-3p 0.94098258
## 42   hsa-miR-191-5p 0.64059600
## 43   hsa-miR-23a-3p 0.47373667
## 44 hsa-miR-199a-3p 0.50463714
## 45    hsa-miR-21-5p 0.98863961
## 46    hsa-let-7b-5p 0.79185139
## 47   hsa-miR-30a-5p 0.37602531
## 48 hsa-miR-199a-5p 0.40718749
## 49   hsa-miR-122-5p 0.18761508
## 50   hsa-miR-221-3p 0.51611403
## 51   hsa-miR-29a-3p 0.87291282
## 52    hsa-miR-31-5p 0.05778742
## 53   hsa-miR-34a-5p 0.37053368
## 54   hsa-miR-27b-3p 0.53890753
## 55    hsa-miR-25-3p 0.71138473
## 56   hsa-miR-218-5p 0.85207664
## 57   hsa-miR-155-5p 0.56240089
## 58 hsa-miR-125b-5p 0.68651725
## 59   hsa-miR-143-3p 0.71383823
## 60 hsa-miR-148a-3p 0.41931984
## 61 hsa-miR-374a-5p 0.74983650
```

adverse.EV.result

```
##           microRNA    p.value
## 1    hsa-let-7a-5p 0.01557483
## 2    hsa-miR-100-5p 0.19649891
## 3  hsa-miR-103a-3p 0.09658261
## 4  hsa-miR-106a-5p 0.45016188
## 5       hsa-miR-107 0.08911622
## 6  hsa-miR-130b-3p 0.97098073
## 7  hsa-miR-146a-5p 0.82046344
## 8   hsa-miR-223-3p 0.81949879
## 9    hsa-miR-24-3p 0.68285169
## 10  hsa-miR-26b-5p 0.02204650
## 11  hsa-miR-30c-5p 0.08590173
## 12     hsa-miR-451a 0.61173352
## 13  hsa-miR-874-3p 0.69491322
## 14    hsa-miR-93-5p 0.97690413
## 15    hsa-let-7i-5p 0.11159985
```

```
## 16     hsa-miR-1246 0.95483533
## 17  hsa-miR-141-3p 0.06176250
## 18 hsa-miR-146b-3p 0.42257592
## 19  hsa-miR-18b-5p 0.86820434
## 20  hsa-miR-19b-3p 0.69007389
## 21 hsa-miR-193a-3p 0.70145054
## 22  hsa-miR-194-5p 0.32371449
## 23 hsa-miR-200a-3p 0.21122738
## 24 hsa-miR-200b-3p 0.46746923
## 25  hsa-miR-204-5p 0.40594292
## 26  hsa-miR-210-3p 0.90154527
## 27  hsa-miR-214-3p 0.44356660
## 28  hsa-miR-222-3p 0.84534269
## 29   hsa-miR-16-5p 0.71846479
## 30 hsa-miR-301a-3p 0.04196488
## 31     hsa-miR-320a 0.61902861
## 32  hsa-miR-27a-3p 0.59460951
## 33  hsa-miR-330-3p 0.87704016
## 34  hsa-miR-335-5p 0.35131496
## 35  hsa-miR-345-5p 0.62188241
## 36  hsa-miR-363-3p 0.61651719
## 37     hsa-miR-375 0.11669013
## 38 hsa-miR-518e-5p 0.79247611
## 39  hsa-miR-574-3p 0.67124261
## 40  hsa-miR-708-5p 0.36380639
## 41     hsa-miR-9-3p 0.32969878
## 42  hsa-miR-191-5p 0.27487859
## 43  hsa-miR-23a-3p 0.67434813
## 44 hsa-miR-199a-3p 0.45800364
## 45   hsa-miR-21-5p 0.31353650
## 46   hsa-let-7b-5p 0.35922295
## 47  hsa-miR-30a-5p 0.52272796
## 48 hsa-miR-199a-5p 0.31826004
## 49  hsa-miR-122-5p 0.06432088
## 50  hsa-miR-221-3p 0.47808069
## 51  hsa-miR-29a-3p 0.48789725
## 52   hsa-miR-31-5p 0.47781935
## 53  hsa-miR-34a-5p 0.11963438
## 54  hsa-miR-27b-3p 0.56252409
## 55   hsa-miR-25-3p 0.46593198
## 56  hsa-miR-218-5p 0.52702981
## 57  hsa-miR-155-5p 0.07211232
## 58 hsa-miR-125b-5p 0.21002176
## 59  hsa-miR-143-3p 0.81938582
## 60 hsa-miR-148a-3p 0.25184678
## 61 hsa-miR-374a-5p 0.05840589
```

Now we want to focus on the significant predictors.

```
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)
```

```
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
```

```
# backward selection for EV/adverse pathology model
library(MASS)
fullmodel2 = glm(data = EV.all, formula = `Adverse Pathology`~`hsa-let-7a-5p`+`hsa-miR-26b-5p`+`hsa-miR-
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
```

The final model only contains hsa-let-7a-5p for EV/adverse pathology.