

# Univariate GLM for Biopsy Grade

Jieqi Tu

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## Method

Biopsy grade groups were dichotomized as “Low” (if  $\leq 2$ ) and “High” (if  $> 2$ ). Univariate generalized linear models were used to detect association between dichotomous biopsy grades and all the serum and serum microRNAs. The logit link function was used when modeling. All the significance level was set as 0.05.

## Results for Univariate Generalized Linear Models

Since hsa-miR-130b-3p only have value 0, here we excluded this variable.

```
EV.new = EV.new[, -7]

serum.result = data.frame(
  microRNA = colnames(serum.new)[-c(1,63)],
  coefficient.estimates = numeric(61),
  standard.deviation = numeric(61),
  p.value = numeric(61)
)

for (i in 1:61) {
  model = glm(formula = serum.new$'grades'~serum.new[,i+1], family = "binomial")
  result = summary(model)
  serum.result$coefficient.estimates[i] = result$coefficients[2,1]
  serum.result$standard.deviation[i] = result$coefficients[2,2]
  serum.result$p.value[i] = result$coefficients[2,4]
}

EV.result = data.frame(
  microRNA = colnames(EV.new)[-c(1,62)],
  coefficient.estimates = numeric(60),
  standard.deviation = numeric(60),
  p.value = numeric(60)
)

for (i in 1:60) {
  model = glm(formula = EV.new$'grades'~EV.new[,i+1], family = "binomial")
  result = summary(model)
  EV.result$coefficient.estimates[i] = result$coefficients[2,1]
  EV.result$standard.deviation[i] = result$coefficients[2,2]
```

```
EV.result$p.value[i] = result$coefficients[2,4]
}

# Show the results
serum.result = serum.result[order(serum.result$p.value),]; serum.result
```

##	microRNA	coefficient.estimate	standard.deviation	p.value
## 19	hsa-miR-18b-5p	-0.743187040	2.946448e-01	0.01165852
## 16	hsa-miR-1246	1.164413776	4.896201e-01	0.01739746
## 36	hsa-miR-363-3p	-0.523952383	2.358564e-01	0.02631784
## 29	hsa-miR-16-5p	-0.668757665	3.135823e-01	0.03295439
## 31	hsa-miR-320a	1.782631859	8.422667e-01	0.03430489
## 30	hsa-miR-301a-3p	-0.342657733	1.632699e-01	0.03584160
## 32	hsa-miR-27a-3p	1.625053770	8.248484e-01	0.04882413
## 7	hsa-miR-146a-5p	1.239661369	6.323519e-01	0.04994930
## 54	hsa-miR-27b-3p	1.664006933	8.811097e-01	0.05895410
## 4	hsa-miR-106a-5p	-0.857775542	4.582776e-01	0.06124289
## 58	hsa-miR-125b-5p	-0.353638711	1.898046e-01	0.06243794
## 45	hsa-miR-21-5p	1.750634404	9.586487e-01	0.06782799
## 9	hsa-miR-24-3p	1.674304345	9.325431e-01	0.07258718
## 20	hsa-miR-19b-3p	-0.745864120	4.228828e-01	0.07777228
## 51	hsa-miR-29a-3p	0.962971932	5.758440e-01	0.09446926
## 14	hsa-miR-93-5p	-0.607140267	3.690363e-01	0.09992762
## 12	hsa-miR-451a	-0.393945112	2.620444e-01	0.13274814
## 43	hsa-miR-23a-3p	1.118422073	7.652213e-01	0.14385993
## 27	hsa-miR-214-3p	-0.193633878	1.380117e-01	0.16060937
## 46	hsa-let-7b-5p	-0.695662311	5.004360e-01	0.16449472
## 28	hsa-miR-222-3p	1.015007623	7.477631e-01	0.17465668
## 23	hsa-miR-200a-3p	0.575123279	4.399963e-01	0.19117560
## 57	hsa-miR-155-5p	0.360163425	2.783148e-01	0.19563561
## 8	hsa-miR-223-3p	0.476563111	3.753316e-01	0.20418720
## 48	hsa-miR-199a-5p	0.368463317	2.957037e-01	0.21274391
## 44	hsa-miR-199a-3p	0.648562388	5.579343e-01	0.24505883
## 17	hsa-miR-141-3p	-0.107133289	9.365951e-02	0.25268205
## 61	hsa-miR-374a-5p	-0.376044128	3.514204e-01	0.28458818
## 13	hsa-miR-874-3p	0.321643060	3.288292e-01	0.32800200
## 59	hsa-miR-143-3p	0.357019124	3.654390e-01	0.32858913
## 33	hsa-miR-330-3p	0.176435151	2.214524e-01	0.42561465
## 50	hsa-miR-221-3p	0.402844952	5.071711e-01	0.42702198
## 56	hsa-miR-218-5p	1.240960086	1.590100e+00	0.43513853
## 11	hsa-miR-30c-5p	0.527796040	8.451236e-01	0.53228657
## 42	hsa-miR-191-5p	0.336821144	5.765956e-01	0.55911612
## 47	hsa-miR-30a-5p	-0.132833085	2.390571e-01	0.57844725
## 18	hsa-miR-146b-3p	0.183732054	3.551028e-01	0.60487331
## 6	hsa-miR-130b-3p	0.175632254	3.405577e-01	0.60605035
## 24	hsa-miR-200b-3p	-0.069684097	1.397646e-01	0.61807399
## 10	hsa-miR-26b-5p	-0.234301811	4.736369e-01	0.62082140
## 3	hsa-miR-103a-3p	0.325687207	7.028567e-01	0.64309457
## 55	hsa-miR-25-3p	-0.149970651	3.934311e-01	0.70306484
## 39	hsa-miR-574-3p	-0.104580973	3.250763e-01	0.74767079
## 52	hsa-miR-31-5p	0.047084773	1.595557e-01	0.76791797
## 60	hsa-miR-148a-3p	0.107852717	3.857307e-01	0.77977958
## 2	hsa-miR-100-5p	-0.024455140	9.180508e-02	0.78994571

## 37	hsa-miR-375	-0.025844608	1.040902e-01	0.80390969
## 49	hsa-miR-122-5p	0.029825238	1.333384e-01	0.82300568
## 21	hsa-miR-193a-3p	-0.282071482	1.664136e+00	0.86540316
## 35	hsa-miR-345-5p	-0.046445575	2.955317e-01	0.87511923
## 34	hsa-miR-335-5p	-0.026836436	2.048747e-01	0.89578360
## 53	hsa-miR-34a-5p	0.012816830	1.036752e-01	0.90161236
## 5	hsa-miR-107	-0.071034248	6.430917e-01	0.91204662
## 1	hsa-let-7a-5p	-0.055073631	5.855560e-01	0.92506660
## 25	hsa-miR-204-5p	-0.016512645	1.799139e-01	0.92687220
## 15	hsa-let-7i-5p	-0.036205532	7.370944e-01	0.96082425
## 26	hsa-miR-210-3p	-0.008391044	2.587651e-01	0.97413132
## 22	hsa-miR-194-5p	-0.004335452	2.200093e-01	0.98427809
## 41	hsa-miR-9-3p	235.748620009	2.043333e+04	0.99079465
## 40	hsa-miR-708-5p	22.617915828	2.046807e+03	0.99118328
## 38	hsa-miR-518e-5p	200.732076161	2.177872e+04	0.99264609

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

##	microRNA	coefficient.estimate	standard.deviation	p.value
## 19	hsa-miR-19b-3p	-1.3446683118	0.51248235	0.00869463
## 11	hsa-miR-451a	-0.6917863605	0.27588175	0.01215725
## 58	hsa-miR-143-3p	-0.8285107920	0.35040051	0.01805599
## 54	hsa-miR-25-3p	-0.9929845337	0.43103198	0.02123738
## 25	hsa-miR-210-3p	-0.9217085990	0.41096326	0.02490968
## 12	hsa-miR-874-3p	-0.9177562684	0.42491013	0.03078171
## 35	hsa-miR-363-3p	-0.6468596945	0.30472009	0.03377065
## 18	hsa-miR-18b-5p	-1.0580510876	0.50614942	0.03658253
## 27	hsa-miR-222-3p	-1.6823935172	0.85244993	0.04842747
## 46	hsa-miR-30a-5p	-0.7416624679	0.37668677	0.04896339
## 26	hsa-miR-214-3p	-0.3210337402	0.16763551	0.05548358
## 28	hsa-miR-16-5p	-0.7113027526	0.38996602	0.06815024
## 59	hsa-miR-148a-3p	-0.6433251987	0.38108178	0.09138144
## 6	hsa-miR-146a-5p	-0.9608522408	0.60274397	0.11090692
## 44	hsa-miR-21-5p	-1.1030510386	0.69406263	0.11200006
## 13	hsa-miR-93-5p	-0.7857653879	0.54790378	0.15153510
## 30	hsa-miR-320a	-0.8572540300	0.60619016	0.15731292
## 38	hsa-miR-574-3p	-0.6510438869	0.47970075	0.17472162
## 31	hsa-miR-27a-3p	-0.9538082763	0.70681386	0.17719323
## 20	hsa-miR-193a-3p	0.9200392667	0.68844025	0.18141490
## 8	hsa-miR-24-3p	-0.9804501017	0.73973104	0.18503378
## 50	hsa-miR-29a-3p	-0.6073548412	0.49729673	0.22196763
## 4	hsa-miR-106a-5p	-0.5900103419	0.49733702	0.23548842
## 14	hsa-let-7i-5p	-0.4985639445	0.42199371	0.23742450
## 56	hsa-miR-155-5p	-0.2681919273	0.23205677	0.24779698
## 33	hsa-miR-335-5p	0.6294082609	0.56631855	0.26639483
## 49	hsa-miR-221-3p	0.7563504475	0.69813522	0.27863679
## 17	hsa-miR-146b-3p	0.3271998226	0.30436703	0.28236699
## 55	hsa-miR-218-5p	-0.2874970101	0.27372875	0.29358070
## 57	hsa-miR-125b-5p	-0.2970464661	0.28315405	0.29414908
## 45	hsa-let-7b-5p	-0.3859335628	0.38727924	0.31899498
## 15	hsa-miR-1246	-0.2746506951	0.30071140	0.36106560
## 2	hsa-miR-100-5p	-0.2551259478	0.28574012	0.37193211
## 53	hsa-miR-27b-3p	-0.5600459664	0.69325374	0.41917617
## 42	hsa-miR-23a-3p	-0.5405247508	0.71296819	0.44837133

```
## 1 hsa-let-7a-5p 0.3408351675 0.46170940 0.46039123
## 16 hsa-miR-141-3p 0.2328645710 0.32635999 0.47552368
## 52 hsa-miR-34a-5p -0.1185725166 0.16791741 0.48010360
## 21 hsa-miR-194-5p -0.1775678821 0.25460693 0.48554019
## 60 hsa-miR-374a-5p -0.2573769508 0.37456480 0.49199704
## 5 hsa-miR-107 0.3330761235 0.58642514 0.57005044
## 51 hsa-miR-31-5p 0.0958339241 0.18163856 0.59777157
## 39 hsa-miR-708-5p 0.3122312868 0.59888594 0.60212053
## 3 hsa-miR-103a-3p 0.2745885420 0.53777107 0.60962775
## 34 hsa-miR-345-5p -0.3010963169 0.59573854 0.61326606
## 29 hsa-miR-301a-3p 0.2087809846 0.42176708 0.62058961
## 36 hsa-miR-375 -0.0560210123 0.11616070 0.62961298
## 24 hsa-miR-204-5p 0.0926256474 0.20749771 0.65531296
## 40 hsa-miR-9-3p -0.1507514128 0.34322940 0.66050594
## 9 hsa-miR-26b-5p 0.2019807298 0.46000878 0.66060345
## 41 hsa-miR-191-5p 0.2114557460 0.62418933 0.73478406
## 32 hsa-miR-330-3p 0.1092165159 0.37699083 0.77204115
## 37 hsa-miR-518e-5p 0.0843606885 0.52453668 0.87222812
## 48 hsa-miR-122-5p 0.0155028662 0.09872006 0.87521438
## 7 hsa-miR-223-3p 0.0528107861 0.40992539 0.89749198
## 47 hsa-miR-199a-5p -0.0480477346 0.42083624 0.90910141
## 43 hsa-miR-199a-3p 0.0423888818 0.56599483 0.94030008
## 10 hsa-miR-30c-5p -0.0431059318 0.62563398 0.94506954
## 22 hsa-miR-200a-3p -0.0012793952 0.05331124 0.98085372
## 23 hsa-miR-200b-3p 0.0002637405 0.05295898 0.99602648
```

```
# Print significant variables
serum.result %>%
  filter(p.value <= 0.05)
```

```
## microRNA coefficient.estimates standard.deviation p.value
## 1 hsa-miR-18b-5p -0.7431870 0.2946448 0.01165852
## 2 hsa-miR-1246 1.1644138 0.4896201 0.01739746
## 3 hsa-miR-363-3p -0.5239524 0.2358564 0.02631784
## 4 hsa-miR-16-5p -0.6687577 0.3135823 0.03295439
## 5 hsa-miR-320a 1.7826319 0.8422667 0.03430489
## 6 hsa-miR-301a-3p -0.3426577 0.1632699 0.03584160
## 7 hsa-miR-27a-3p 1.6250538 0.8248484 0.04882413
## 8 hsa-miR-146a-5p 1.2396614 0.6323519 0.04994930
```

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

```
## microRNA coefficient.estimates standard.deviation p.value
## 1 hsa-miR-19b-3p -1.3446683 0.5124824 0.00869463
## 2 hsa-miR-451a -0.6917864 0.2758818 0.01215725
## 3 hsa-miR-143-3p -0.8285108 0.3504005 0.01805599
## 4 hsa-miR-25-3p -0.9929845 0.4310320 0.02123738
## 5 hsa-miR-210-3p -0.9217086 0.4109633 0.02490968
## 6 hsa-miR-874-3p -0.9177563 0.4249101 0.03078171
## 7 hsa-miR-363-3p -0.6468597 0.3047201 0.03377065
## 8 hsa-miR-18b-5p -1.0580511 0.5061494 0.03658253
## 9 hsa-miR-222-3p -1.6823935 0.8524499 0.04842747
## 10 hsa-miR-30a-5p -0.7416625 0.3766868 0.04896339
```

## Variable selection

We now first look into the model fitting

```
# Variable selection for serum miRNAs
library(MASS)
```

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

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

```
##
## select
```

```
fullmodel.serum = glm(grades~'hsa-miR-18b-5p'+'hsa-miR-1246' +'hsa-miR-363-3p' + 'hsa-miR-16-5p' + 'hsa-
serum.step = stepAIC(object = fullmodel.serum, direction = "backward")
```

```
## Start: AIC=131.91
## grades ~ 'hsa-miR-18b-5p' + 'hsa-miR-1246' + 'hsa-miR-363-3p' +
## 'hsa-miR-16-5p' + 'hsa-miR-320a' + 'hsa-miR-301a-3p' + 'hsa-miR-27a-3p' +
## 'hsa-miR-146a-5p'
```

```
##
##           Df Deviance    AIC
## - 'hsa-miR-27a-3p'    1   113.92 129.91
## - 'hsa-miR-16-5p'     1   114.12 130.12
## - 'hsa-miR-146a-5p'   1   114.39 130.39
## - 'hsa-miR-363-3p'    1   114.77 130.77
## - 'hsa-miR-1246'      1   114.81 130.81
## - 'hsa-miR-18b-5p'    1   115.61 131.61
## <none>                113.91 131.91
## - 'hsa-miR-301a-3p'    1   117.08 133.08
## - 'hsa-miR-320a'      1   117.38 133.38
```

```
##
## Step: AIC=129.92
## grades ~ 'hsa-miR-18b-5p' + 'hsa-miR-1246' + 'hsa-miR-363-3p' +
## 'hsa-miR-16-5p' + 'hsa-miR-320a' + 'hsa-miR-301a-3p' + 'hsa-miR-146a-5p'
```

```
##
##           Df Deviance    AIC
## - 'hsa-miR-16-5p'     1   114.12 128.12
## - 'hsa-miR-146a-5p'   1   114.52 128.52
## - 'hsa-miR-363-3p'    1   114.84 128.84
## - 'hsa-miR-1246'      1   114.92 128.92
## - 'hsa-miR-18b-5p'    1   115.61 129.61
## <none>                113.92 129.91
## - 'hsa-miR-301a-3p'    1   117.08 131.08
## - 'hsa-miR-320a'      1   117.41 131.41
```

```
##
## Step: AIC=128.12
## grades ~ 'hsa-miR-18b-5p' + 'hsa-miR-1246' + 'hsa-miR-363-3p' +
## 'hsa-miR-320a' + 'hsa-miR-301a-3p' + 'hsa-miR-146a-5p'
```

```
##
##           Df Deviance    AIC
```

```

## - 'hsa-miR-146a-5p' 1 114.56 126.56
## - 'hsa-miR-363-3p' 1 114.87 126.87
## - 'hsa-miR-1246' 1 114.96 126.96
## - 'hsa-miR-18b-5p' 1 115.61 127.61
## <none> 114.12 128.12
## - 'hsa-miR-301a-3p' 1 117.48 129.49
## - 'hsa-miR-320a' 1 118.20 130.20
##
## Step: AIC=126.57
## grades ~ 'hsa-miR-18b-5p' + 'hsa-miR-1246' + 'hsa-miR-363-3p' +
## 'hsa-miR-320a' + 'hsa-miR-301a-3p'
##
## Df Deviance AIC
## - 'hsa-miR-1246' 1 115.40 125.40
## - 'hsa-miR-18b-5p' 1 115.99 125.99
## - 'hsa-miR-363-3p' 1 116.08 126.08
## <none> 114.56 126.56
## - 'hsa-miR-301a-3p' 1 117.97 127.97
## - 'hsa-miR-320a' 1 119.71 129.71
##
## Step: AIC=125.4
## grades ~ 'hsa-miR-18b-5p' + 'hsa-miR-363-3p' + 'hsa-miR-320a' +
## 'hsa-miR-301a-3p'
##
## Df Deviance AIC
## <none> 115.40 125.40
## - 'hsa-miR-363-3p' 1 117.58 125.58
## - 'hsa-miR-18b-5p' 1 117.60 125.60
## - 'hsa-miR-301a-3p' 1 119.07 127.07
## - 'hsa-miR-320a' 1 124.08 132.08

```

*# Variable selection for EM serum miRNAs*

```

fullmodel.EV = glm(grades~'hsa-miR-19b-3p' + 'hsa-miR-451a' + 'hsa-miR-143-3p' + 'hsa-miR-25-3p' + 'hsa-miR-363-3p' + 'hsa-miR-18b-5p' + 'hsa-miR-222-3p' + 'hsa-miR-30a-5p', family = "poisson")
EV.step = stepAIC(object = fullmodel.EV, direction = "backward")

```

```

## Start: AIC=142.45
## grades ~ 'hsa-miR-19b-3p' + 'hsa-miR-451a' + 'hsa-miR-143-3p' +
## 'hsa-miR-25-3p' + 'hsa-miR-210-3p' + 'hsa-miR-874-3p' + 'hsa-miR-363-3p' +
## 'hsa-miR-18b-5p' + 'hsa-miR-222-3p' + 'hsa-miR-30a-5p'
##
## Df Deviance AIC
## - 'hsa-miR-451a' 1 120.46 140.46
## - 'hsa-miR-19b-3p' 1 120.50 140.50
## - 'hsa-miR-143-3p' 1 120.57 140.57
## - 'hsa-miR-210-3p' 1 120.59 140.59
## - 'hsa-miR-874-3p' 1 120.66 140.66
## - 'hsa-miR-222-3p' 1 120.79 140.79
## - 'hsa-miR-30a-5p' 1 121.03 141.03
## <none> 120.45 142.45
## - 'hsa-miR-25-3p' 1 122.92 142.92
## - 'hsa-miR-18b-5p' 1 123.18 143.18
## - 'hsa-miR-363-3p' 1 124.14 144.14
##

```

```

## Step: AIC=140.46
## grades ~ 'hsa-miR-19b-3p' + 'hsa-miR-143-3p' + 'hsa-miR-25-3p' +
## 'hsa-miR-210-3p' + 'hsa-miR-874-3p' + 'hsa-miR-363-3p' +
## 'hsa-miR-18b-5p' + 'hsa-miR-222-3p' + 'hsa-miR-30a-5p'
##
##
##      Df Deviance    AIC
## - 'hsa-miR-19b-3p'  1  120.50 138.50
## - 'hsa-miR-143-3p'  1  120.58 138.58
## - 'hsa-miR-210-3p'  1  120.63 138.63
## - 'hsa-miR-874-3p'  1  120.69 138.69
## - 'hsa-miR-222-3p'  1  120.80 138.80
## - 'hsa-miR-30a-5p'  1  121.03 139.03
## <none>                120.46 140.46
## - 'hsa-miR-18b-5p'  1  123.19 141.19
## - 'hsa-miR-25-3p'   1  123.47 141.47
## - 'hsa-miR-363-3p'  1  124.55 142.55
##
## Step: AIC=138.5
## grades ~ 'hsa-miR-143-3p' + 'hsa-miR-25-3p' + 'hsa-miR-210-3p' +
## 'hsa-miR-874-3p' + 'hsa-miR-363-3p' + 'hsa-miR-18b-5p' +
## 'hsa-miR-222-3p' + 'hsa-miR-30a-5p'
##
##
##      Df Deviance    AIC
## - 'hsa-miR-143-3p'  1  120.62 136.62
## - 'hsa-miR-210-3p'  1  120.67 136.67
## - 'hsa-miR-874-3p'  1  120.82 136.82
## - 'hsa-miR-222-3p'  1  120.84 136.84
## - 'hsa-miR-30a-5p'  1  121.17 137.16
## <none>                120.50 138.50
## - 'hsa-miR-18b-5p'  1  123.58 139.57
## - 'hsa-miR-25-3p'   1  123.92 139.92
## - 'hsa-miR-363-3p'  1  125.70 141.70
##
## Step: AIC=136.62
## grades ~ 'hsa-miR-25-3p' + 'hsa-miR-210-3p' + 'hsa-miR-874-3p' +
## 'hsa-miR-363-3p' + 'hsa-miR-18b-5p' + 'hsa-miR-222-3p' +
## 'hsa-miR-30a-5p'
##
##
##      Df Deviance    AIC
## - 'hsa-miR-210-3p'  1  120.75 134.75
## - 'hsa-miR-874-3p'  1  120.93 134.93
## - 'hsa-miR-222-3p'  1  121.01 135.01
## - 'hsa-miR-30a-5p'  1  121.34 135.34
## <none>                120.62 136.62
## - 'hsa-miR-25-3p'   1  124.08 138.08
## - 'hsa-miR-18b-5p'  1  124.22 138.22
## - 'hsa-miR-363-3p'  1  125.78 139.78
##
## Step: AIC=134.75
## grades ~ 'hsa-miR-25-3p' + 'hsa-miR-874-3p' + 'hsa-miR-363-3p' +
## 'hsa-miR-18b-5p' + 'hsa-miR-222-3p' + 'hsa-miR-30a-5p'
##
##
##      Df Deviance    AIC
## - 'hsa-miR-874-3p'  1  121.06 133.06

```

```

## - 'hsa-miR-222-3p' 1 121.18 133.18
## - 'hsa-miR-30a-5p' 1 121.54 133.54
## <none> 120.75 134.75
## - 'hsa-miR-18b-5p' 1 124.31 136.31
## - 'hsa-miR-25-3p' 1 124.50 136.50
## - 'hsa-miR-363-3p' 1 125.78 137.78
##
## Step: AIC=133.06
## grades ~ 'hsa-miR-25-3p' + 'hsa-miR-363-3p' + 'hsa-miR-18b-5p' +
## 'hsa-miR-222-3p' + 'hsa-miR-30a-5p'
##
## Df Deviance AIC
## - 'hsa-miR-30a-5p' 1 121.65 131.65
## - 'hsa-miR-222-3p' 1 121.72 131.72
## <none> 121.06 133.06
## - 'hsa-miR-18b-5p' 1 124.67 134.67
## - 'hsa-miR-25-3p' 1 124.97 134.97
## - 'hsa-miR-363-3p' 1 126.40 136.40
##
## Step: AIC=131.65
## grades ~ 'hsa-miR-25-3p' + 'hsa-miR-363-3p' + 'hsa-miR-18b-5p' +
## 'hsa-miR-222-3p'
##
## Df Deviance AIC
## - 'hsa-miR-222-3p' 1 122.11 130.11
## <none> 121.65 131.65
## - 'hsa-miR-18b-5p' 1 125.15 133.15
## - 'hsa-miR-25-3p' 1 126.12 134.12
## - 'hsa-miR-363-3p' 1 127.17 135.17
##
## Step: AIC=130.11
## grades ~ 'hsa-miR-25-3p' + 'hsa-miR-363-3p' + 'hsa-miR-18b-5p'
##
## Df Deviance AIC
## <none> 122.11 130.11
## - 'hsa-miR-18b-5p' 1 126.17 132.17
## - 'hsa-miR-25-3p' 1 127.58 133.58
## - 'hsa-miR-363-3p' 1 128.23 134.23

```

## Classification

```
library(caret)
```

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

```
##
```

```
## Attaching package: 'caret'
```

```
## The following object is masked from 'package:purrr':
```

```
##
```

```
## lift
```



```
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
```

```
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##      cov, smooth, var
```

```
set.seed(1029)
```

```
rowTrain = createDataPartition(y = serum.new$grades,  
                                p = 0.75,  
                                list = FALSE)
```

```
ctrl = trainControl(method = "repeatedcv",  
                     repeats = 5,  
                     summaryFunction = twoClassSummary,  
                     classProbs = TRUE)
```

```
# Get column numbers for best predictors for serum miRNAs  
which(colnames(serum.new)=="hsa-miR-363-3p")
```

```
## [1] 37
```

```
which(colnames(serum.new)=="hsa-miR-18b-5p")
```

```
## [1] 20
```

```
which(colnames(serum.new)=="hsa-miR-301a-3p")
```

```
## [1] 31
```

```
which(colnames(serum.new)=="hsa-miR-320a")
```

```
## [1] 32
```

```
# Logistic regression
```

```
glm.serum = train(x = serum.new[rowTrain, c(37, 20, 31, 32)],  
                  y = serum.new$grades[rowTrain],  
                  method = "glm",  
                  metric = "ROC",  
                  trControl = ctrl)
```

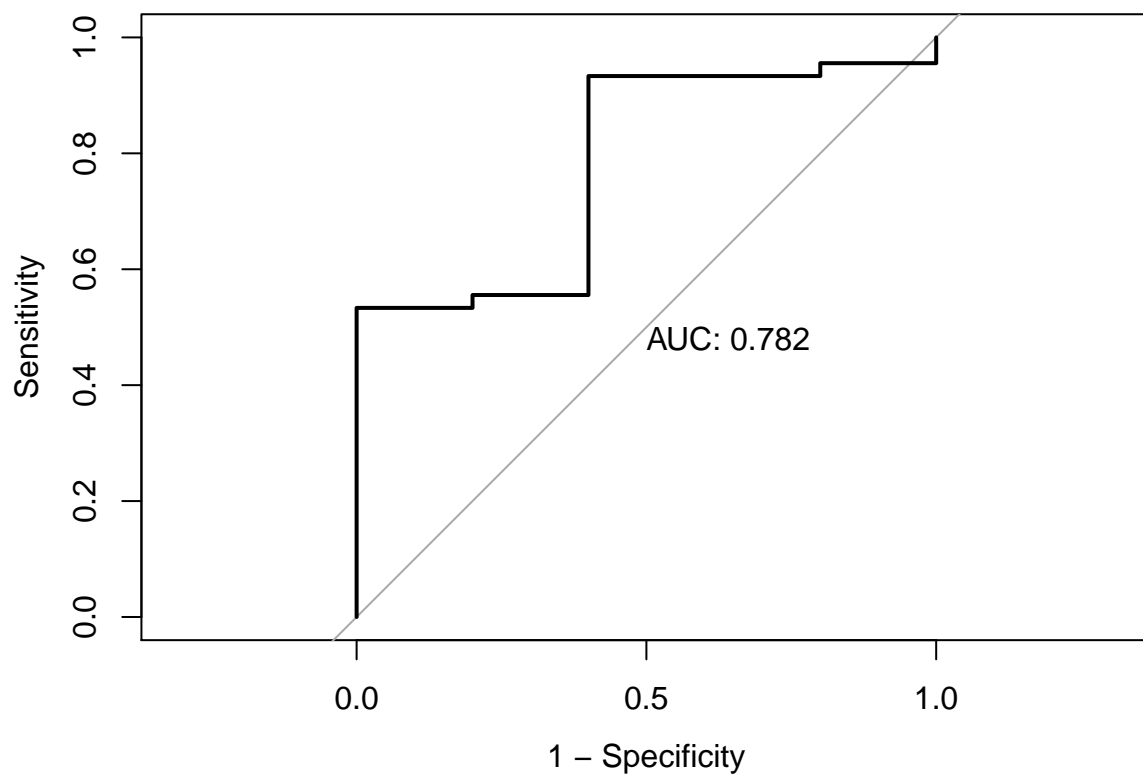
```
# See the prediction performance
```

```
glm.predict = predict(glm.serum, newdata = serum.new[-rowTrain,], type = "prob")[,2]  
roc.glm.serum = roc(serum.new$grades[-rowTrain], glm.predict)
```

```
## Setting levels: control = high, case = low
```

```
## Setting direction: controls < cases
```

```
plot(roc.glm.serum, legacy.axes = T, print.auc = T)
```



```
# Get column numbers for best predictors for EV serum miRNAs  
which(colnames(EV.new)=="hsa-miR-18b-5p")
```

```
## [1] 19
```

```
which(colnames(EV.new)=="hsa-miR-25-3p")
```

```
## [1] 55
```

```
which(colnames(EV.new)=="hsa-miR-363-3p")
```

```
## [1] 36
```

```
# Logistic regression  
rowTrain = createDataPartition(y = EV.new$grades,  
                                p = 0.75,
```

```

                                list = FALSE)
glm.EV = train(x = EV.new[rowTrain, c(19, 55, 36)],
               y = EV.new$grades[rowTrain],
               method = "glm",
               metric = "ROC",
               trControl = ctrl)

# See the prediction performance
glm.predict.EV = predict(glm.EV, newdata = EV.new[-rowTrain,], type = "prob")[,2]
roc.glm.EV = roc(EV.new$grades[-rowTrain], glm.predict.EV)

## Setting levels: control = high, case = low
## Setting direction: controls < cases

plot(roc.glm.EV, legacy.axes = T, print.auc = T)

```

