Model #	outcome	hsa.let.7b.5p	hsa.miR.184	hsa.miR.22.3p	loocv - classification output	loocv - classification binary	Agreement: outcome vs LOOCV	intercept	hsa.let.7b.5p_coeff	hsa.miR.184_coeff	hsa.miR.22.3p_coeff
	Dependent variable	Predictor	Predictor	Predictor	Predicted outcome	Predicted outcome	Agreement		Model parameter		
1	0	127305	5319	758	0.334	0	1	0.313	-9.98E-07	1.16E-05	1.15E-04
2	0	82749	1911	546	0.333	0	1	0.380	-1.54E-06	1.07E-05	1.08E-04
3	0	25157	4717	3137	0.805	1	0	0.502	-2.60E-06	9.04E-06	1.04E-04
4	0	107626	4283	2114	0.503	1	0	0.310	-9.64E-07	1.12E-05	1.18E-04
5	0	131115	2986	3283	0.656	1	0	0.209	-1.49E-07	1.17E-05	1.32E-04
6	0	141532	3180	1419	0.385	0	1	0.282	-7.27E-07	1.16E-05	1.19E-04
7	0	108456	3342	924	0.350	0	1	0.338	-1.20E-06	1.11E-05	1.13E-04
8	0	129569	8772	778	0.380	0	1	0.301	-8.87E-07	1.19E-05	1.15E-04
9	0	85214	5498	407	0.353	0	1	0.376	-1.50E-06	1.10E-05	1.08E-04
10	0	80505	7630	874	0.436	0	1	0.380	-1.52E-06	1.11E-05	1.08E-04
11	0	96798	3448	318	0.298	0	1	0.359	-1.38E-06	1.10E-05	1.10E-04
12	1	43127	8764	3132	0.713	1	1	0.274	-9.77E-07	1.20E-05	1.20E-04
13	1	82362	15669	2239	0.640	1	1	0.312	-1.33E-06	1.10E-05	1.19E-04
14	1	33742	9202	4866	0.946	1	1	0.311	-1.22E-06	1.17E-05	1.17E-04
15	1	27027	20885	4365	1.038	1	1	0.316	-1.28E-06	1.17E-05	1.17E-04
16	1	35250	24119	4699	1.112	1	1	0.311	-1.27E-06	1.19E-05	1.19E-04
17	1	35957	12890	4614	0.958	1	1	0.312	-1.23E-06	1.16E-05	1.17E-04
18	1	27112	23983	2843	0.879	1	1	0.299	-1.13E-06	1.13E-05	1.19E-04
19	1	82557	5504	980	0.342	0	0	0.216	-8.74E-07	1.26E-05	1.31E-04
20	1	52805	23762	3691	0.953	1	1	0.315	-1.26E-06	1.14E-05	1.17E-04
21	1	47405	998	9406	1.628	1	1	0.176	-5.65E-07	1.07E-05	1.56E-04
22	1	25157	19415	6642	1.337	1	1	0.287	-1.23E-06	1.23E-05	1.27E-04
23	1	22758	15395	4554	0.999	1	1	0.314	-1.25E-06	1.16E-05	1.17E-04
24	1	45776	5191	4232	0.802	1	1	0.297	-1.13E-06	1.20E-05	1.17E-04
25	1	82298	4274	3017	0.600	1	1	0.302	-1.29E-06	1.21E-05	1.17E-04
26	1	62430	1839	2647	0.539	1	1	0.248	-9.01E-07	1.29E-05	1.22E-04
27	1	116371	4893	1448	0.354	0	0	0.316	-1.67E-06	1.19E-05	1.20E-04
28	1	32350	9734	3374	0.765	1	1	0.277	-9.75E-07	1.19E-05	1.20E-04
29	1	111065	4519	5398	0.828	1	1	0.353	-1.57E-06	1.15E-05	1.11E-04
30	1	114855	3444	1934	0.400	0	0	0.325	-1.68E-06	1.20E-05	1.17E-04
31	1	102374	6342	2819	0.569	1	1	0.334	-1.57E-06	1.16E-05	1.14E-04
32	1	148442	330	2661	0.332	0	0	0.428	-2.54E-06	1.17E-05	1.04E-04
33	1	35230	16260	4413	0.975	1	1	0.313	-1.24E-06	1.16E-05	1.17E-04
34	1	80649	59723	1039	1.097	1	1	0.296	-1.13E-06	1.29E-05	1.17E-04
35	1	20148	5302	3884	0.781	1	1	0.270	-9.13E-07	1.22E-05	1.19E-04
							80.00%				

Result

R-code:

```
library(boot)
library(ROCR)
library(LUR)
data <- read.delim(file.choose("211008-P71-Input-data.txt"))
#check the data
summary(data)
str(data)
typeof(data)
hist(data$hsa.let.7b.5p)
hist(data$hsa.miR.184)
hist(data$hsa.miR.22.3p)
##LOOCV using the LUR package
loocv.data <-
loocv(data,dependent="outcome",c("hsa.let.7b.5p","hsa.miR.184","hsa.miR.22.3p"),export_coefficients=TRUE)
write.table(loocv.data,"211012-P71-LOOCV-output.txt",sep=" ")
```

Supplemental table 4. Leave-one-out cross validation analysis

The three predictors three predictor microRNAs (*let-7b-5p, miR-184, miR-22-3p)* were examined for the binary outcome cancer-free versus confirmed cases. 35 regression models were generated, and each time one sample was left out to build the model. The sample that was left out was classified using the model generated from the remaining 34 samples. We then compared in how many instances the prediction agreed with the actual outcome and observed an 80% match between the prediction and the outcome. The related R-code is shown below the table