

Total average binary classification accuracy across all datasets and models: 0.95536					
0.8 0.2 train test split					
Dataset Names + Tumor-Cancer Split	random forest (ntrees=8)	random forest (ntrees=200)	Xgboost (max. depth = 2, eta = 1, nthread = 2, nrounds = 2)	Xgboost (max.depth = 2, eta = 1, nthread = 2, nrounds = 4)	Average accuracy
Full BRCA miR data (breast) (86-86)	0.94118	0.97059	0.95329	0.9906	
BRCA (breast) (50-50)	0.95	1	0.94974	0.98817	
LIHC(liver) (49-49)	0.9	0.95	0.94953	0.98803	
THCA (thyroid) (50-50)	0.9	0.9	0.94974	0.98817	
HNSC (head + neck) (43-43)	0.88235	0.94118	0.94842	0.9873	
KIRC (kidney) (50-50)	1	1	0.94974	0.98817	
LUAD (lung) (39-39)	0.875	1	0.94734	0.9866	
					0.956255
0.7 0.3 train test split					
Dataset Names + Tumor-Cancer Split	random forest (ntrees=8)	random forest (ntrees=200)	Xgboost (max. depth = 2, eta = 1, nthread = 2, nrounds = 2)	Xgboost (max.depth = 2, eta = 1, nthread = 2, nrounds = 4)	
Full BRCA miR data (breast) (86-86)	0.98077	0.98077	0.95255	0.99008	
BRCA (breast) (50-50)	0.96667	0.9	0.94855	0.98739	
LIHC(liver) (49-49)	0.96552	0.93103	0.94842	0.9873	
THCA (thyroid) (50-50)	0.9	0.86666	0.94855	0.98739	
HNSC (head + neck) (43-43)	1	1	0.94698	0.98637	
KIRC (kidney) (50-50)	1	0.96666	0.94855	0.98739	
LUAD (lung) (39-39)	0.91304	0.91304	0.94599	0.98573	
					0.9584071429
0.75 0.25 train test split					
Dataset Names + Tumor-Cancer Split	random forest (ntrees=8)	random forest (ntrees=200)	Xgboost (max. depth = 2, eta = 1, nthread = 2, nrounds = 2)	Xgboost (max.depth = 2, eta = 1, nthread = 2, nrounds = 4)	
Full BRCA miR data (breast) (86-86)	0.93023	0.97674	0.95294	0.99036	
BRCA (breast) (50-50)	0.88	0.96	0.94919	0.9878	
LIHC(liver) (49-49)	0.95833	0.95833	0.94907	0.98772	
THCA (thyroid) (50-50)	0.88	0.92	0.94919	0.9878	
HNSC (head + neck) (43-43)	0.86364	0.95454	0.94767	0.98681	
KIRC (kidney) (50-50)	1	1	0.94919	0.9878	
LUAD (lung) (39-39)	0.9	0.9	0.94661	0.98613	
					0.9514317857