Total average binary c models: 0.95536	lassification acc	curacy across all d	atasets and						
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			average for random forest	average for xgboost	
BRCA (breast) (50-50)	0.95	1	0.94974	0.98817		0.8 0.2	0.9435928571	0.9689171429	0.956255
LIHC(liver) (49-49)	0.9	0.95	0.94953	0.98803		0.7 0.3	0.9488685714	0.9679457143	0.9584071429
THCA (thyroid) (50-50)	0.9	0.9	0.94974	0.98817		0.75 0.25	0.934415	0.9684485714	0.9514317857
HNSC (head + neck) (43- 43)	0.88235	0.94118	0.94842	0.9873		overall	0.9422921429	0.9684371429	0.9553646429
KIRC (kidney) (50-50)	1	1	0.94974	0.98817					
LUAD (lung) (39-39)	0.875	1	0.94734	0.9866			conclusion: XGBoost has	a higher overall perfo	rmance.
average	0.9212185714	0.9659671429	0.9496857143	0.9881485714					
0.7.0.0 4 1 1 1 111					0.956255				
0.7 0.3 train test split			Xgboost (max. depth = 2, eta = 1,	Xgboost (max.depth					
Dataset Names + Tumor- Cancer Split	random forest (ntrees=8)	random forest (ntrees=200)	nthread = 2, nrounds = 2)	nthread = 2, nrounds = 4)			average accuracy	cancer name	
Full BRCA miR data (breast) (86-86)	0.98077	0.98077	0.95255	0.99008			0.9675083333	Full Breast Data	
BRCA (breast) (50-50)	0.96667	0.9	0.94855	0.98739			0.9556258333		
LIHC(liver) (49-49)	0.96552	0.93103	0.94842	0.9873			0.9561066667		
THCA (thyroid) (50-50)	0.9	0.86666	0.94855	0.98739			0.9314583333		
HNSC (head + neck) (43- 43)	1	1	0.94698	0.98637			0.9537716667	Head + Neck HNSC	
KIRC (kidney) (50-50)	1	0.96666	0.94855	0.98739			0.9814583333	Kidney KIRC	
LUAD (lung) (39-39)	0.91304	0.91304	0.94599	0.98573			0.9416233333	Lung LUAD	
average	0.9608571429	0.93688	0.9485128571	0.9873785714	0.9584071429		0.9553646429	Average Total	
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					
average	0.9160285714	0.9528014286	0.9491228571	0.9877742857	0.9514317857				
Full BRCA miR data (breast) (86-86)									
BRCA (breast) (50-50)									
LIHC(liver) (49-49)	+								
THCA (thyroid) (50-50) HNSC (head + neck) (43-	1								
43) KIRC (kidney) (50-50)									
LUAD (lung) (39-39)									