Radiogenomics Analysis Report

-------------------------------**Model inputs**------------------------------

Mode:Train

Model:DecisionTree

Params:default

No. of imaging features provided: 36

No. of gene features provided:976

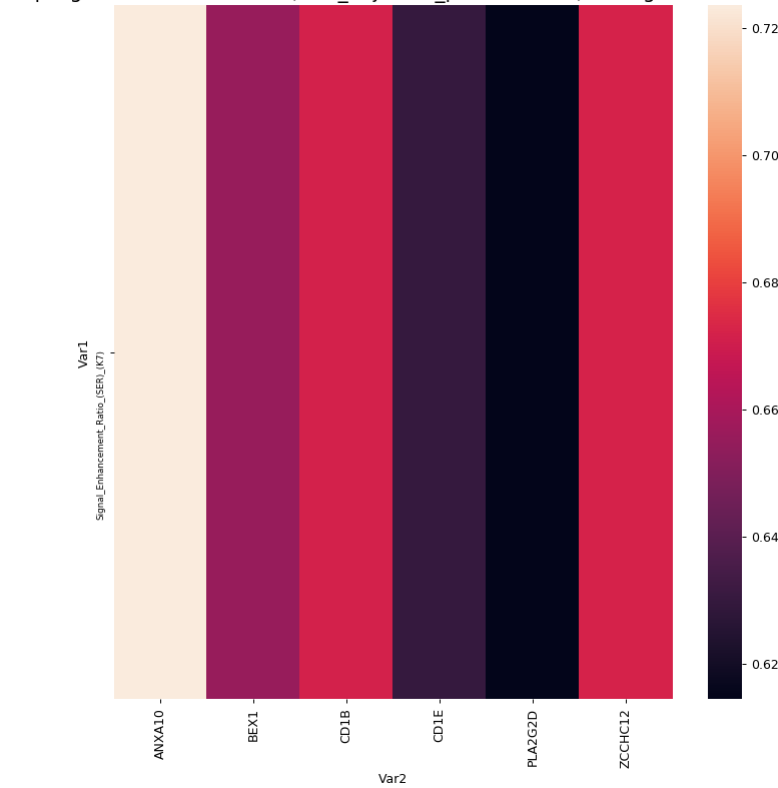**SampleID check results: 'The SampleIDs match for imaging and gene features'**

No. of samples: 89

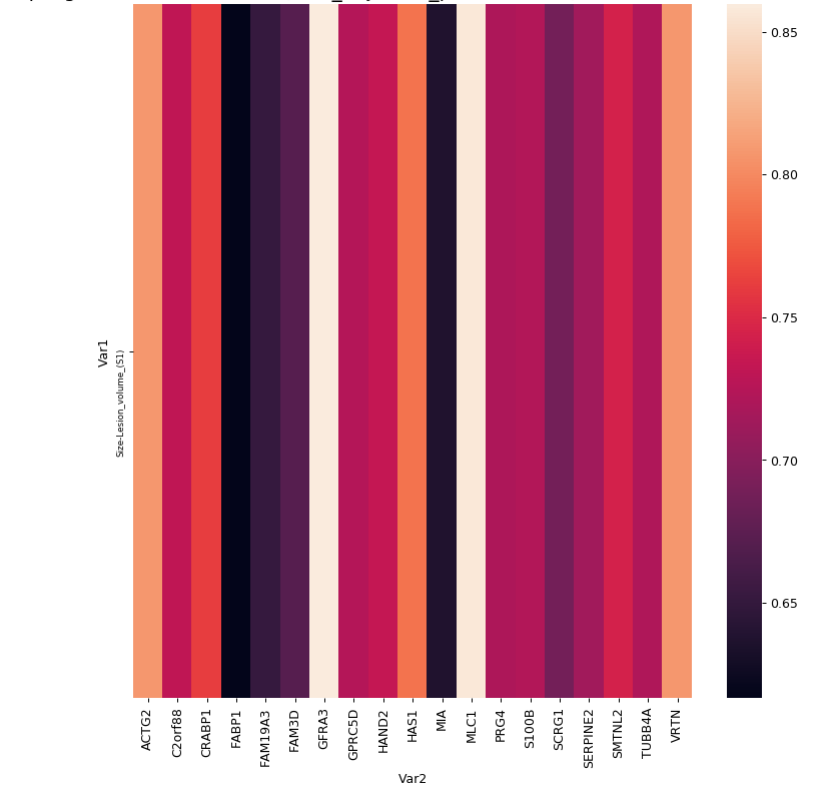**performing Stand_scaler normalization for imaging features**

performing Stand_scaler for gene features

---------------------------**Multivariate Correlations (pearson based)**----------------------

| Top significant correlations (FDR_adjusted_pValue<0.05) for Signal features | Top significant correlations (FDR_adjusted_pValue<0.05) for Size-Lesion features | Top significant correlations (FDR_adjusted_pValue<0.05) for Surface features | Top significant correlations (FDR_adjusted_pValue<0.05) for Volume features | Top significant correlations (FDR_adjusted_pValue<0.05) for Washout features |
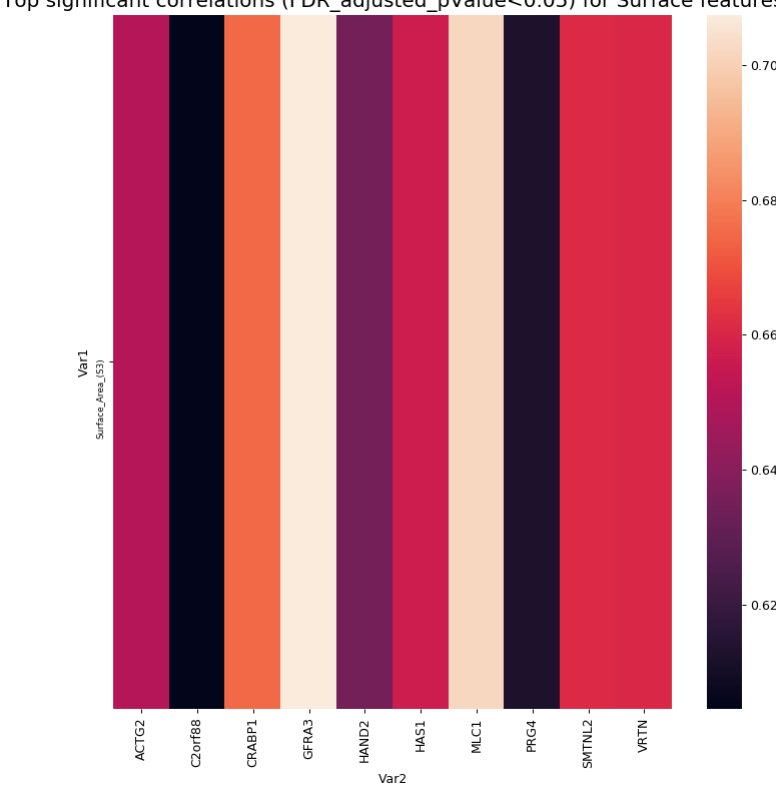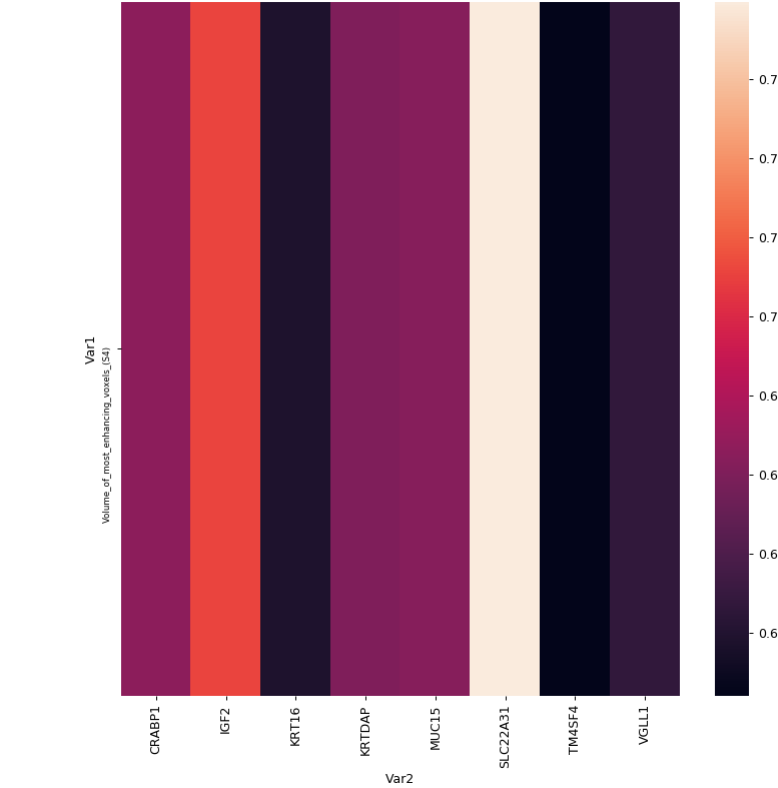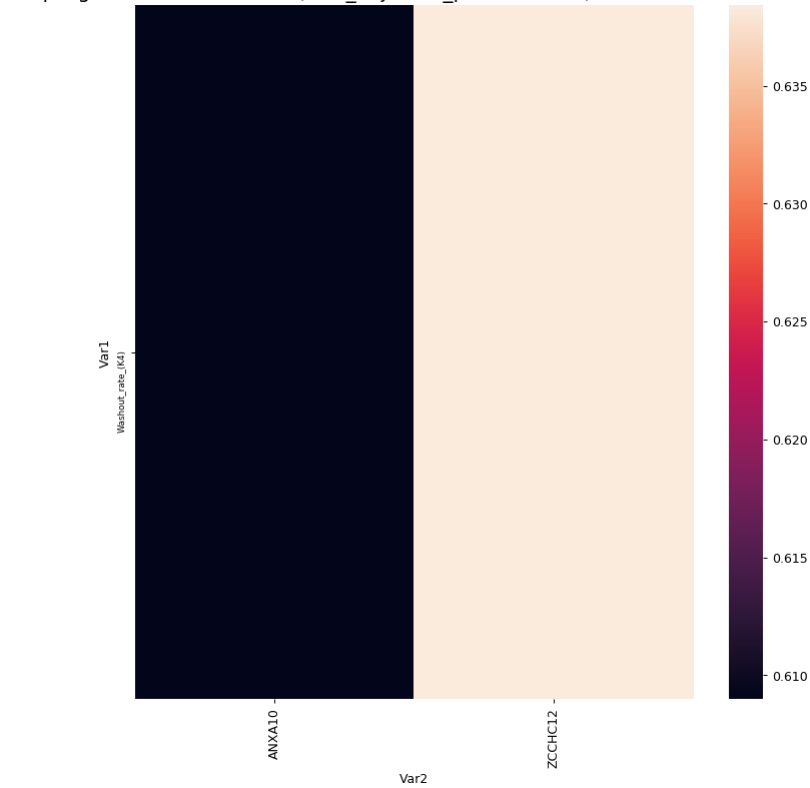
-----------------------------**Features with highly significant correlations**------------------------------------

Below is the list of imaging features

['Signal_Enhancement_Ratio_(SER)_(K7)', 'Size-Lesion_volume_(S1)', 'Surface_Area_(S3)', 'Volume_of_most_enhancing_voxels_(S4)', 'Washout_rate_(K4)']

Below is the list of gene features

['ACTG2', 'ANXA10', 'BEX1', 'C2orf88', 'CD1B', 'CD1E', 'CRABP1', 'FABP1', 'FAM19A3', 'FAM3D', 'GFRA3', 'GPRC5D', 'HAND2', 'HAS1', 'IGF2', 'KRT16', 'KRTDAP', 'MIA', 'MLC1', 'MUC15', 'PLA2G2D', 'PRG4', 'S100B', 'SCRG1', 'SERPINE2', 'SLC22A31', 'SMTNL2', 'TM4SF4', 'TUBB4A', 'VGLL1', 'VRTN', 'ZCCHC12']

Number of imaging features

5

Number of gene features

32

-------------------------------**Number of Samples for Training and Testing**-------------------------------

No. of samples for training:71

No. of samples for test:18

--------------------------**Model Summary**----------------------

Model Type : DecisionTree

Cross Validation Metrics:

Parameters: cv=2 scoring=neg_mean_squared_error

Cross validation score:0.966723821808

Model Parameters:

presort:False

splitter:best

min_impurity_decrease:0.0

max_leaf_nodes:None

min_samples_leaf:1

min_samples_split:2

min_weight_fraction_leaf:0.0

criterion:mse

random_state:None

min_impurity_split:None

max_features:None

max_depth:None

----------------**Model evaluation for Train data**-------------------

Min Square Error for the Model

MSE of train_eval set:0.0

No. of features showing LOW 'RMSE/Stdev' (<=1.0): 32

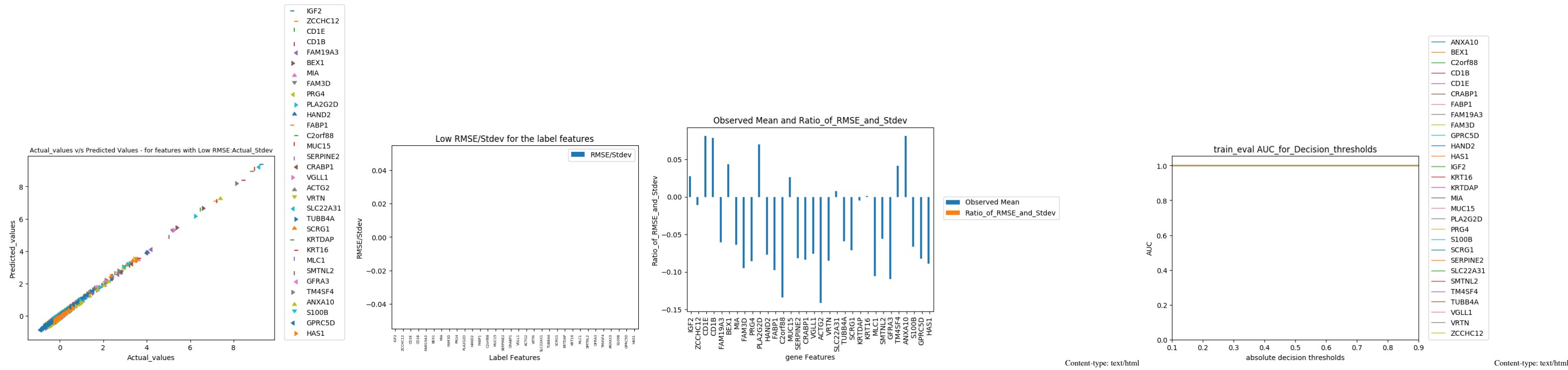**All such features with their Low 'RMSE/Stdev' values could be found in output file: train_eval_DecisionTree_Labels_with_Low_Ratio.csv**

No. of features showing HIGH 'RMSE/Stdev' (>1.0): 0

All such features with their High 'RMSE/Stdev' values could be found in output file: train_eval_DecisionTree_Labels_with_High_Ratio.csv

Model evaluation for Train data for label features showing Low 'RMSE/Stdev' (<=1.0)

----------------Model evaluation for Test data-------------------

Min Square Error for the Model

MSE of test_eval set:3.18905381756

No. of features showing LOW 'RMSE/Stdev' (<=1.0): 5

All such features with their Low 'RMSE/Stdev' values could be found in output file: test_eval_DecisionTree_Labels_with_Low_Ratio.csv

No. of features showing HIGH 'RMSE/Stdev' (>1.0): 27

All such features with their High 'RMSE/Stdev' values could be found in output file: test_eval_DecisionTree_Labels_with_High_Ratio.csv

Model evaluation for Test data for label features showing Low 'RMSE/Stdev' (<=1.0)