Radiogenomics Analysis Report

------------------------Model inputs------------------------

Mode:Train

Model:LinearRegression

Params:default

No. of imaging features provided: 36

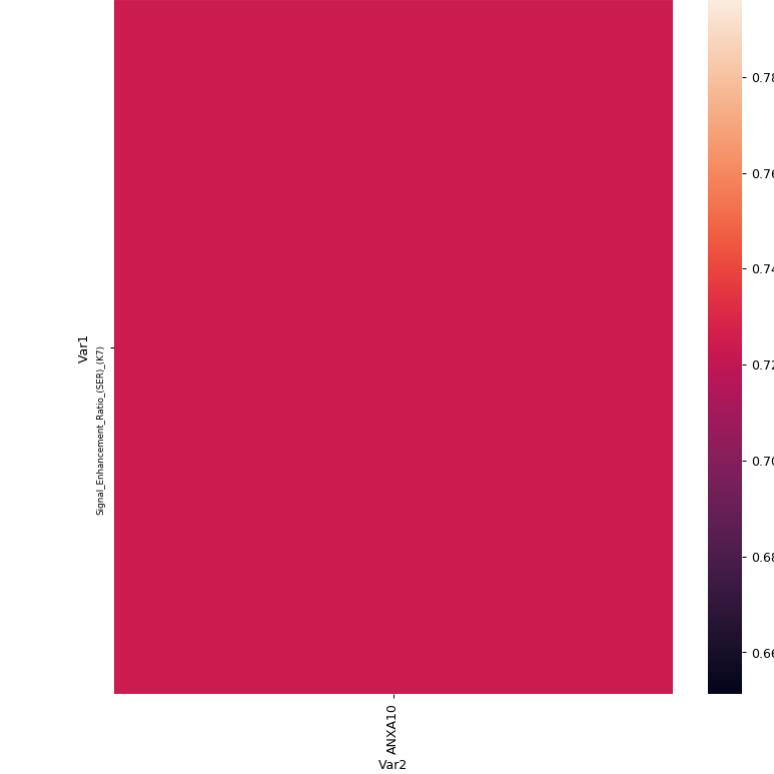**No. of gene features provided:976**

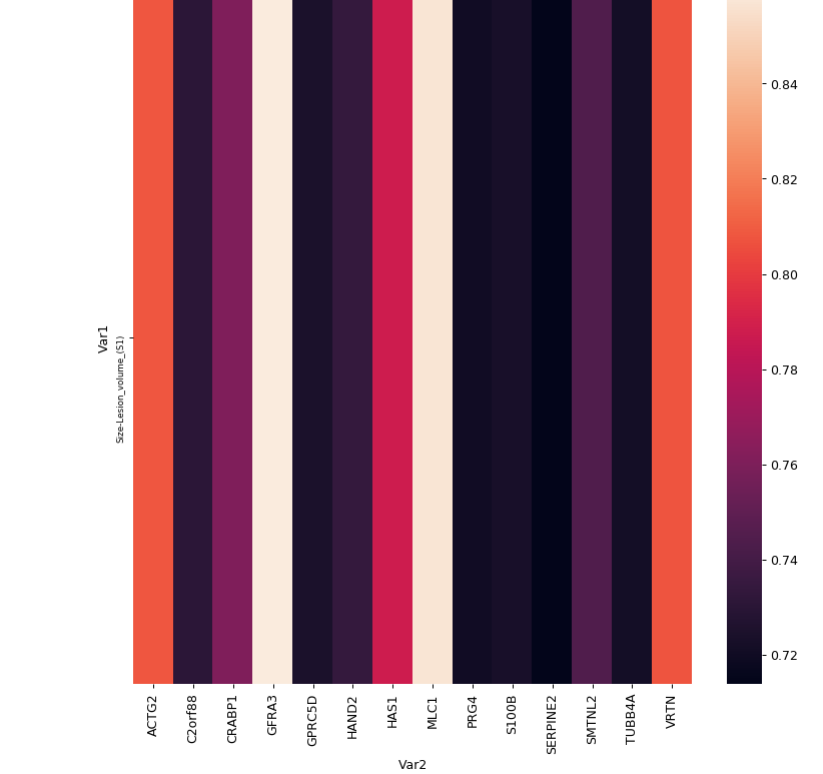**SampleID check results: 'The SampleIDs match for imaging and gene features'**

No. of samples: 89

performing Stand_scaler normalization for imaging features
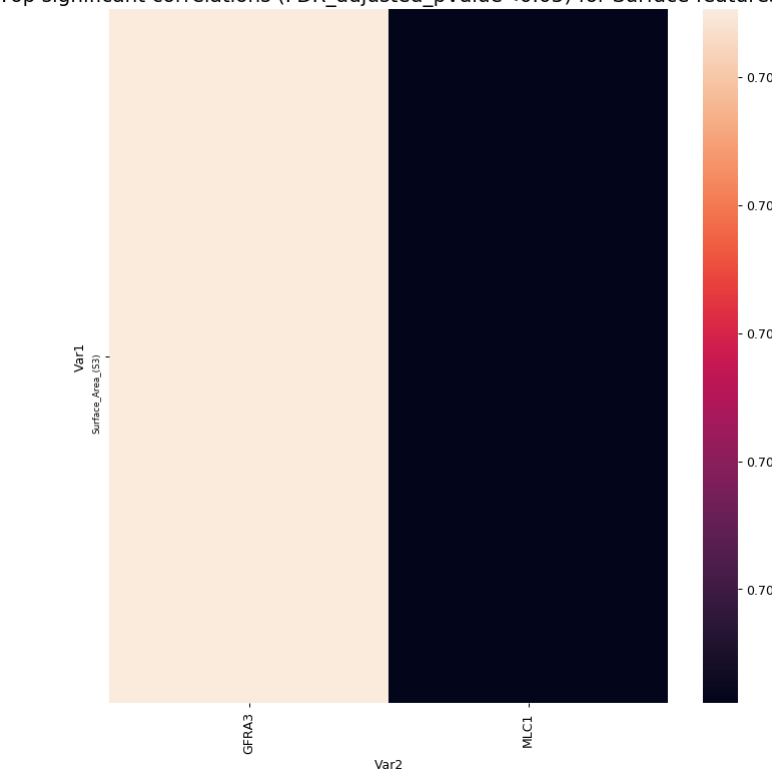
performing Stand_scaler for gene features

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

Top significant correlations (FDR_adjusted_pValue<0.05) for Signal features
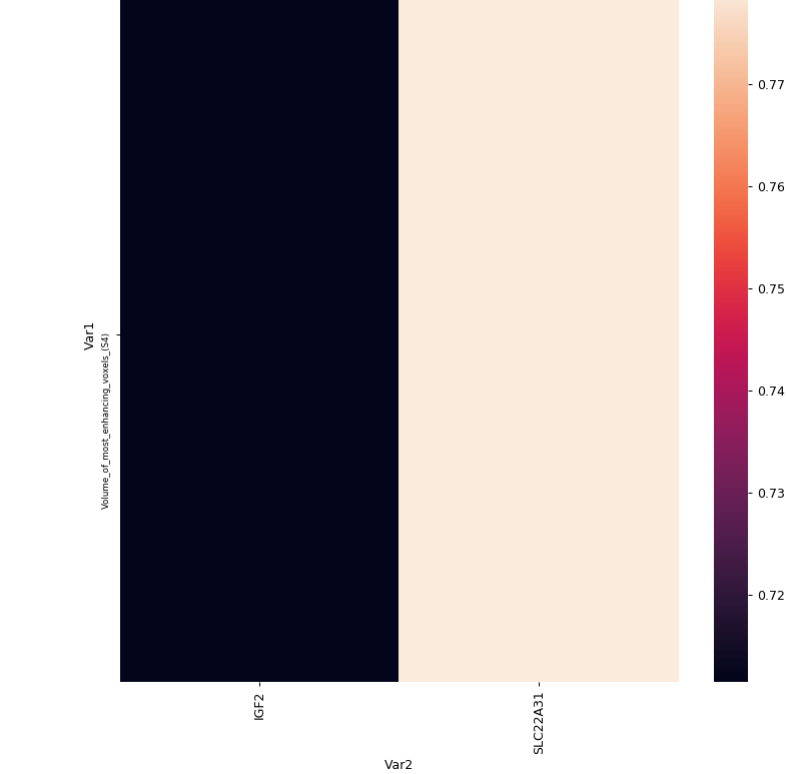

Top significant correlations (FDR_adjusted_pValue<0.05) for Size-Lesion features

Top significant correlations (FDR_adjusted_pValue<0.05) for Surface features

Top significant correlations (FDR_adjusted_pValue<0.05) for Volume features

----------------------------------**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)']

Below is the list of gene features

['ACTG2', 'ANXA10', 'C2orf88', 'CRABP1', 'GFRA3', 'GPRC5D', 'HAND2', 'HAS1', 'IGF2', 'MLC1', 'PRG4', 'S100B', 'SERPINE2', 'SLC22A31', 'SMTNL2', 'TUBB4A', 'VRTN']

Number of imaging features

4

Number of gene features

17

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

No. of samples for training:71

No. of samples for test:18

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

Model Type : LinearRegression

Cross Validation Metrics:

Parameters: cv=2 scoring:neg_mean_squared_error

Cross validation score:1.58662239033

Model Parameters:

copy_X:True

normalize:False

n_jobs:None

fit_intercept:True

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

Min Square Error for the Model

MSE of train_eval set:0.251854599778

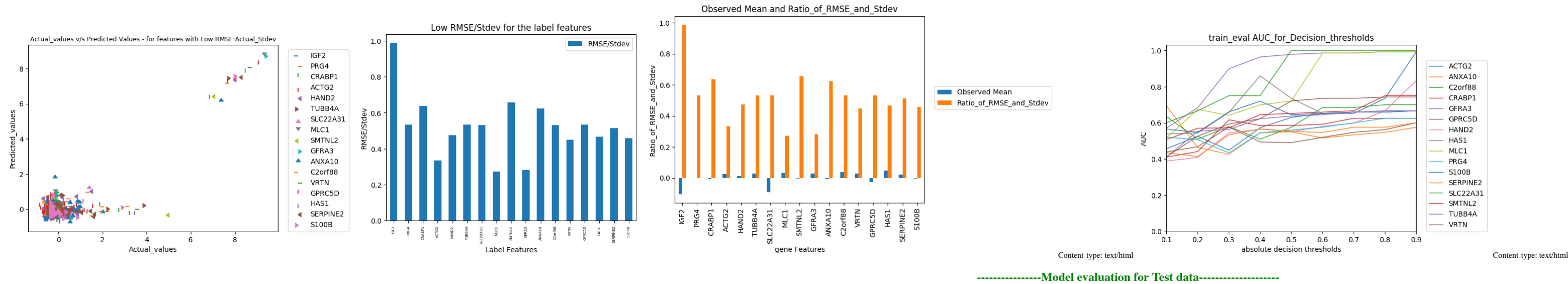**No. of features showing LOW 'RMSE/Stdev' (<=1.0): 17**

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

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

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

Min Square Error for the Model
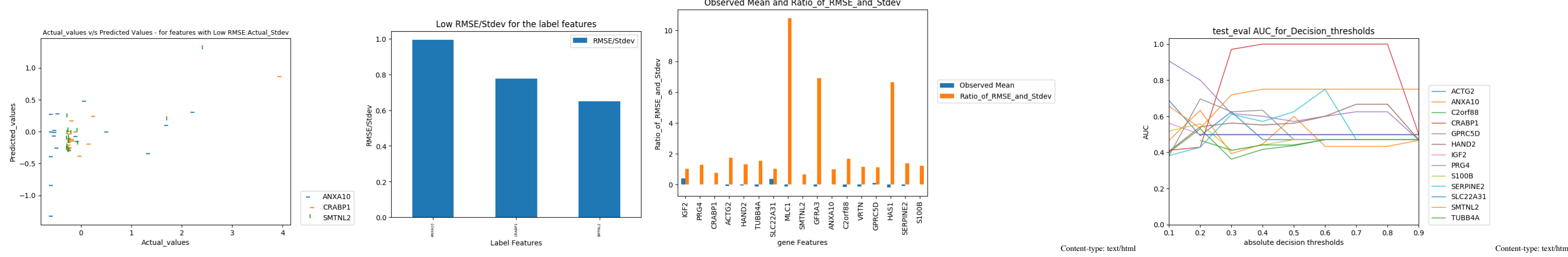
MSE of test_eval set:1.04934720124

No. of features showing LOW 'RMSE/Stdev' (<=1.0): 3

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

No. of features showing HIGH 'RMSE/Stdev' (>1.0): 14

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

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

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