

Radiogenomics Analysis Report

04/08/2021 03:18:43

-----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'

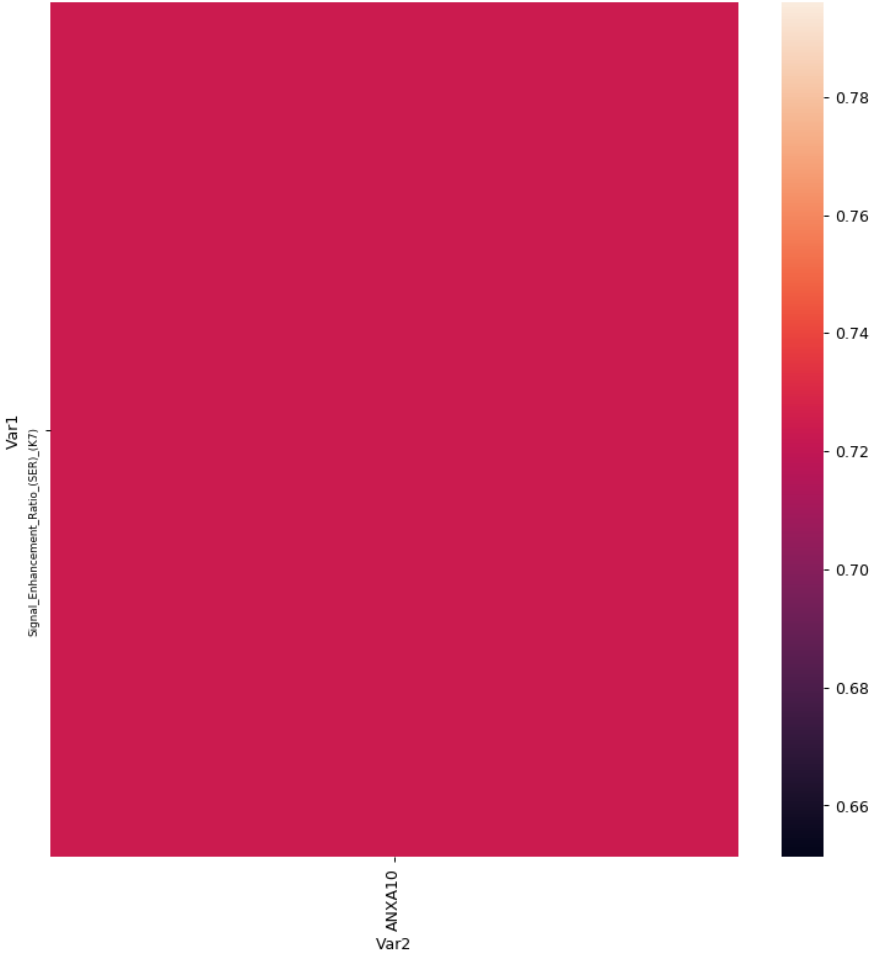
No. of samples: 89

performing Stand_scaler normalization for imaging features

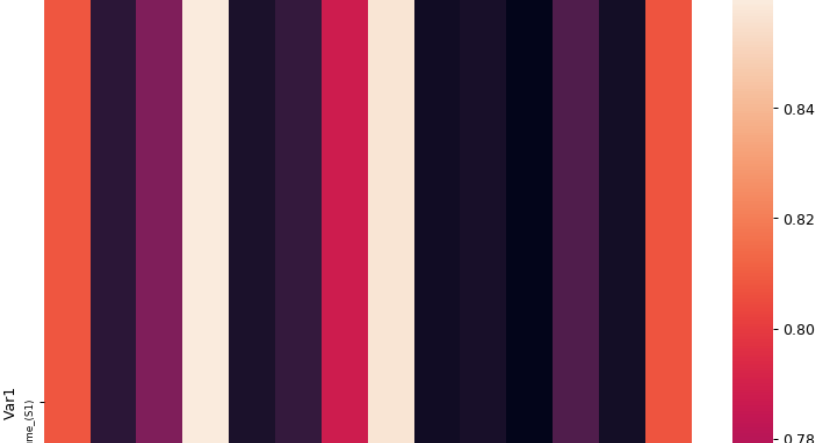
performing Stand_scaler for gene features

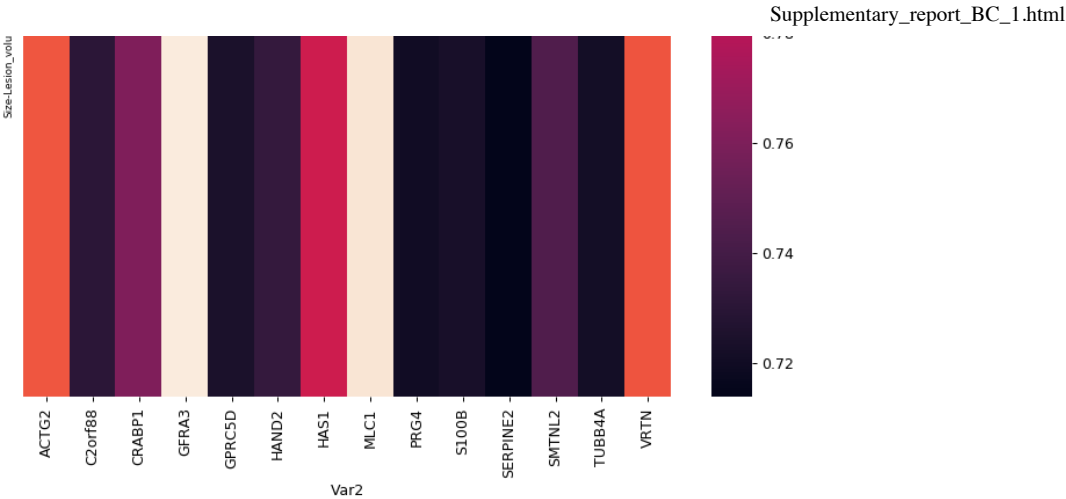
-----Multivariate Correlations (pearson based)-----

Top significant correlations (FDR_adjusted_pValue<0.05) for Signal features

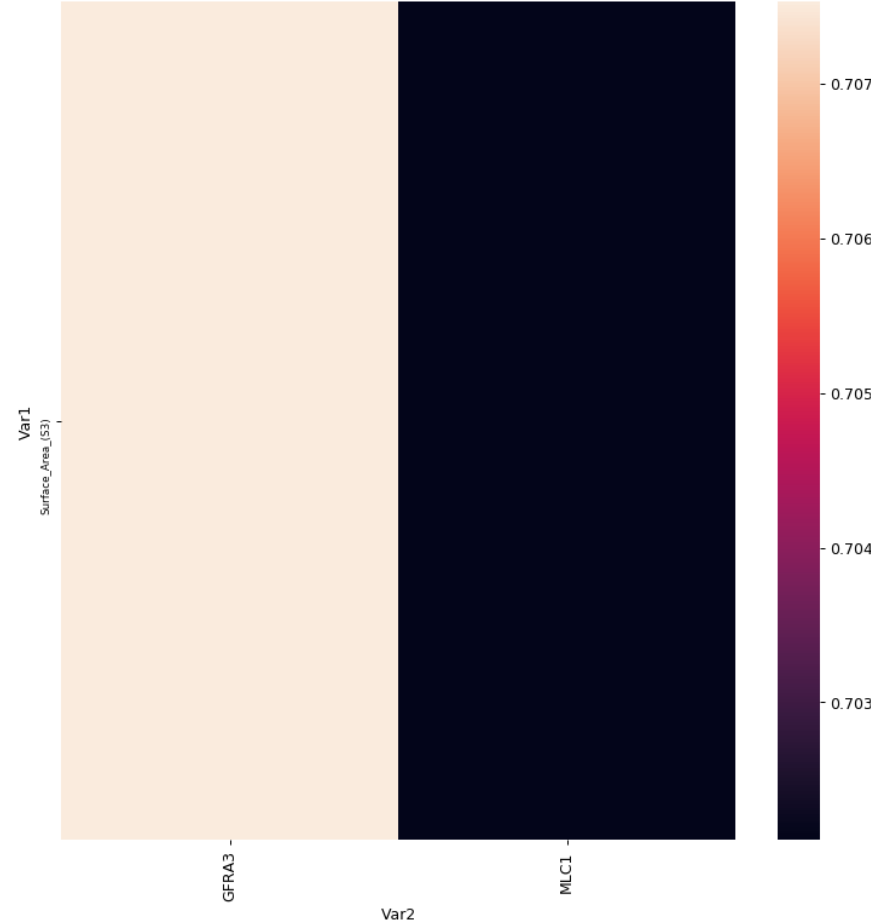


Top significant correlations (FDR_adjusted_pValue<0.05) for Size-Lesion features

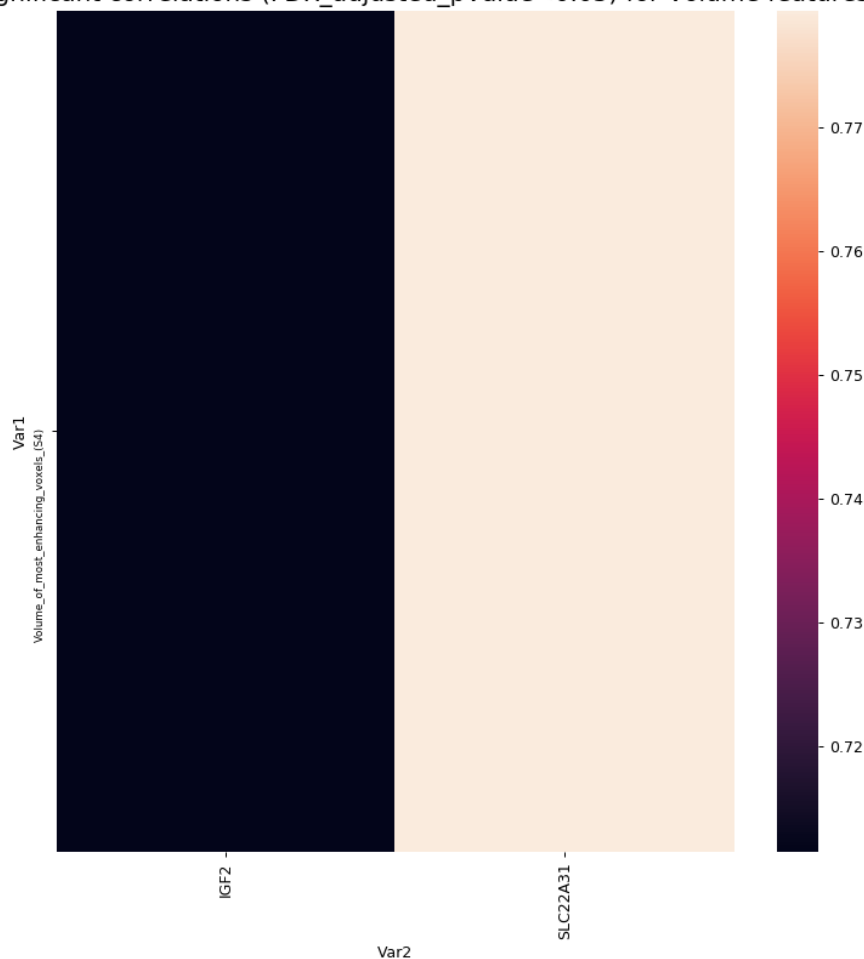




Top significant correlations (FDR_adjusted_pValue<0.05) for Surface features



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

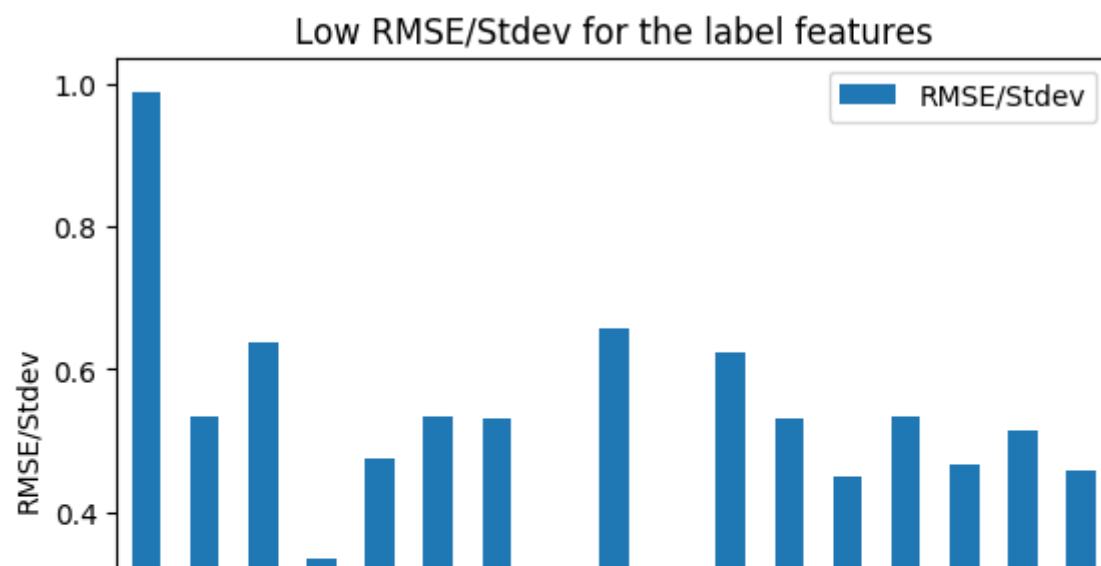
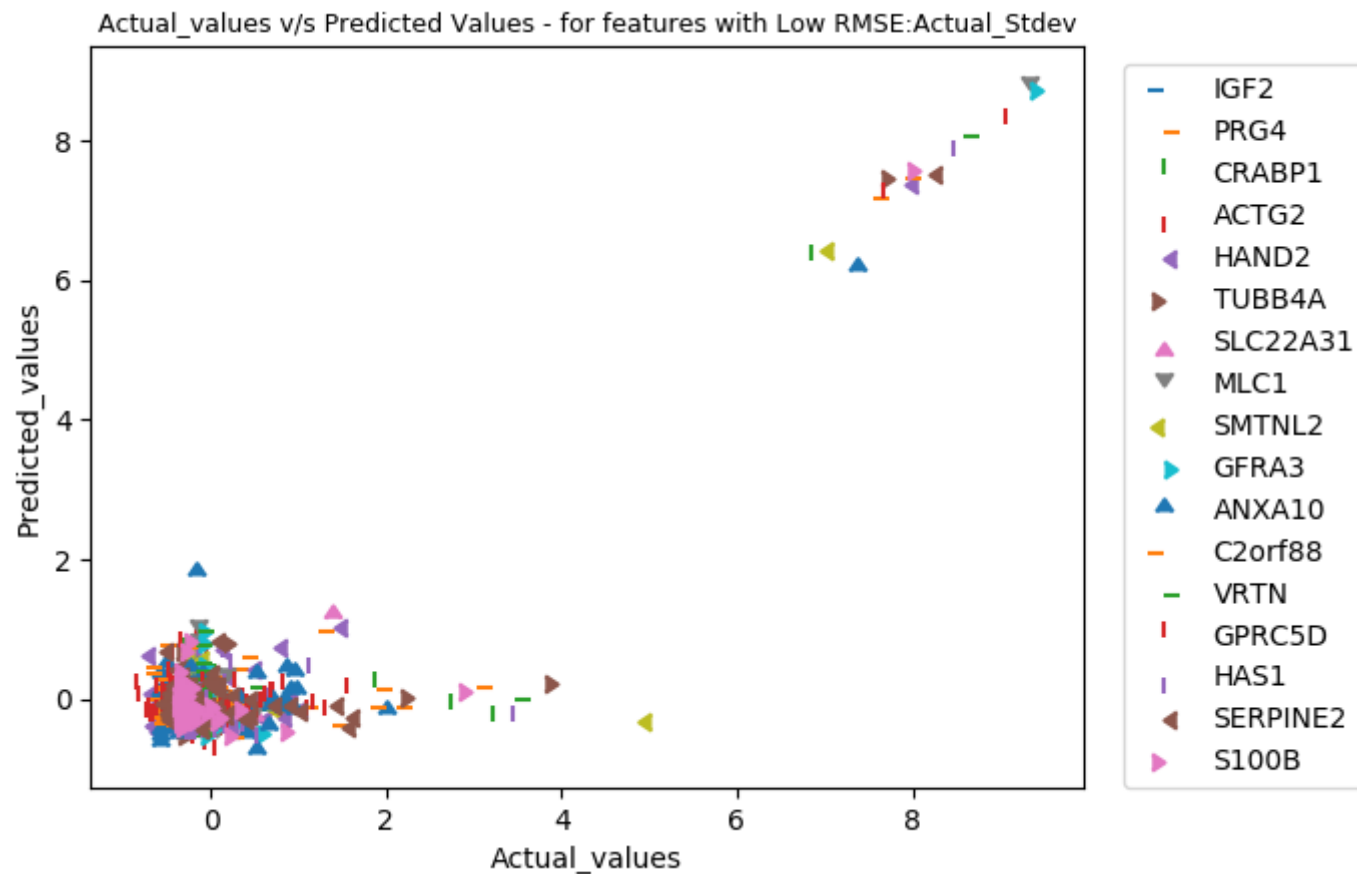
No. of features showing LOW 'RMSE/Stdev' (≤ 1.0): 17

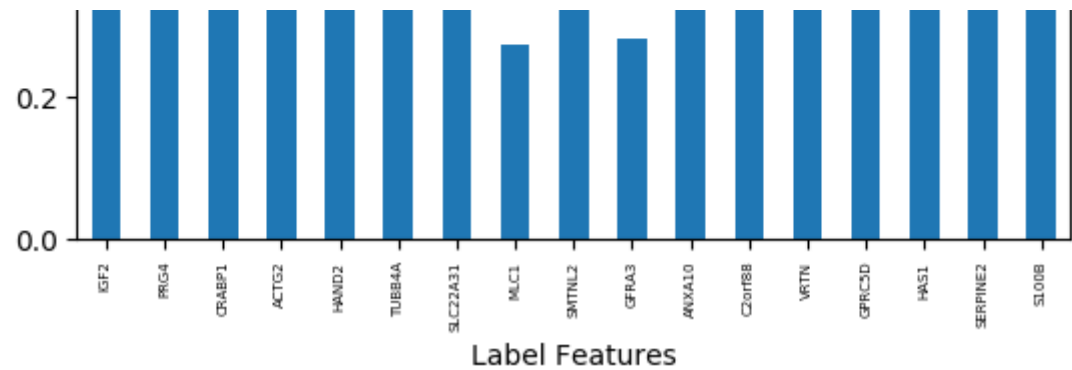
All such features with their Low 'RMSE/Stdev' values could be found in output file: train_eval_LinearRegression_Labels_with_Low_Ratio.csv

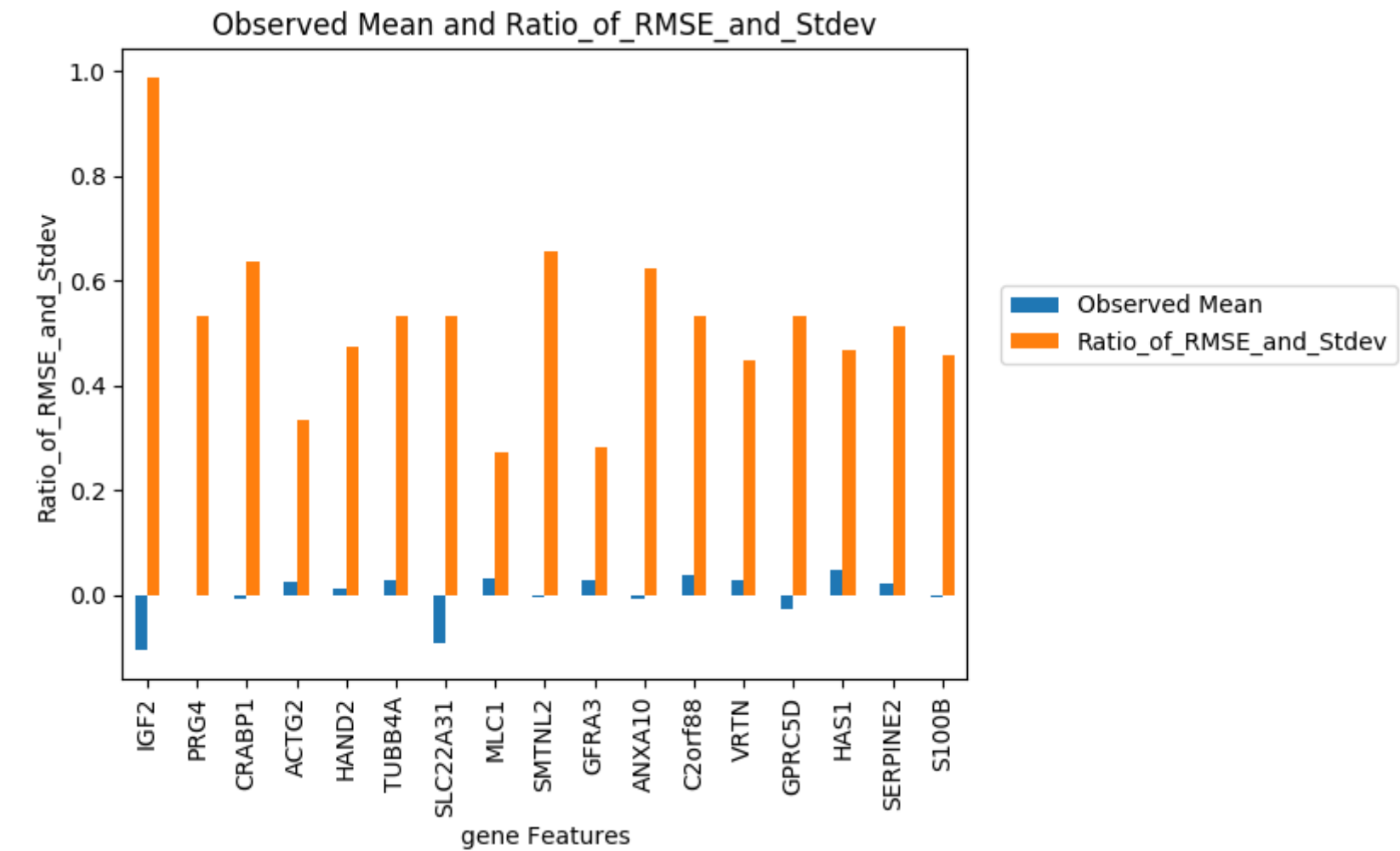
No. of features showing HIGH 'RMSE/Stdev' (> 1.0): 0

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

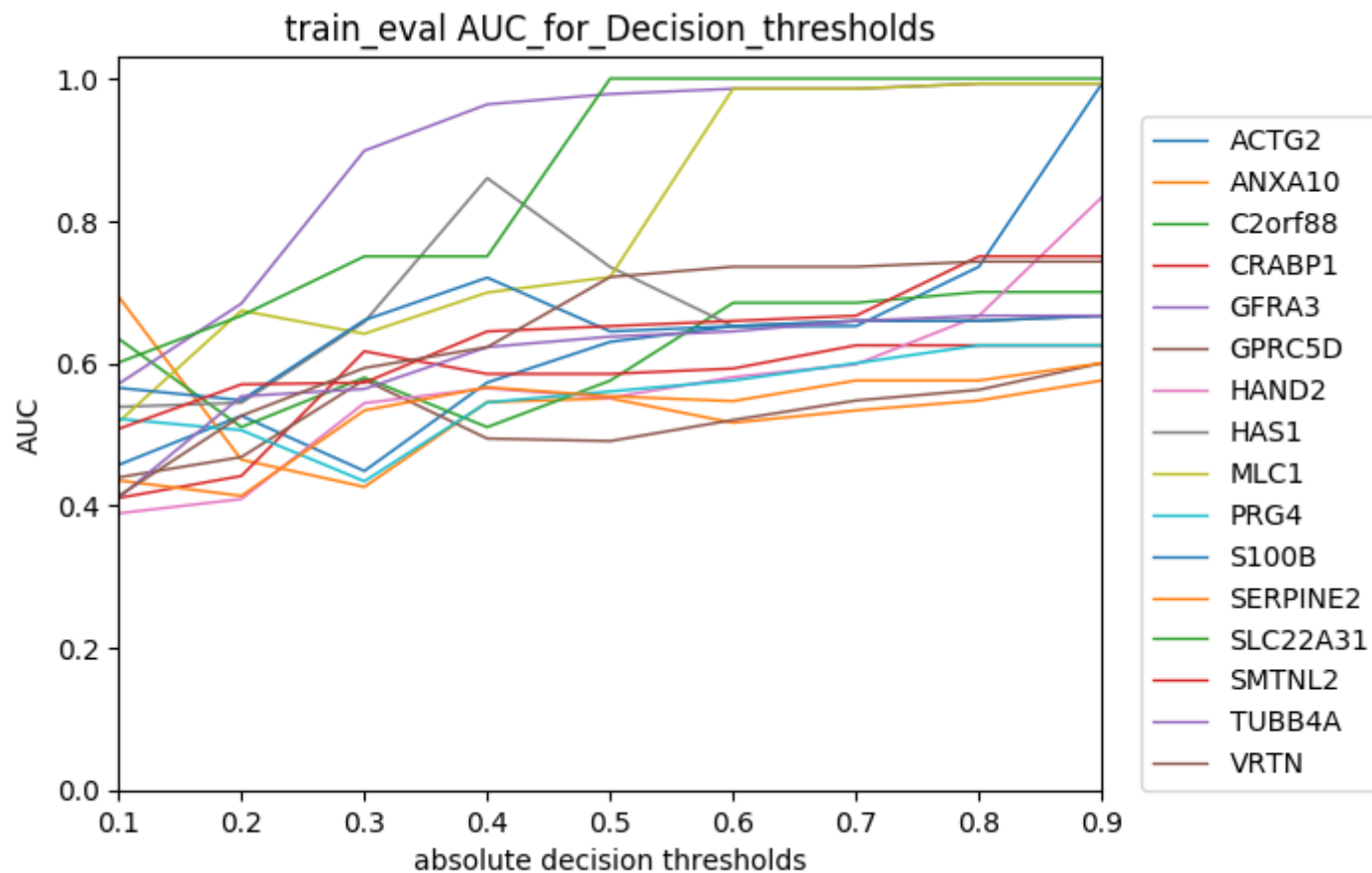
Model evaluation for Train data for label features showing Low 'RMSE/Stdev' (≤ 1.0)







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

Min Square Error for the Model

MSE of test_eval set: 1.04934720124

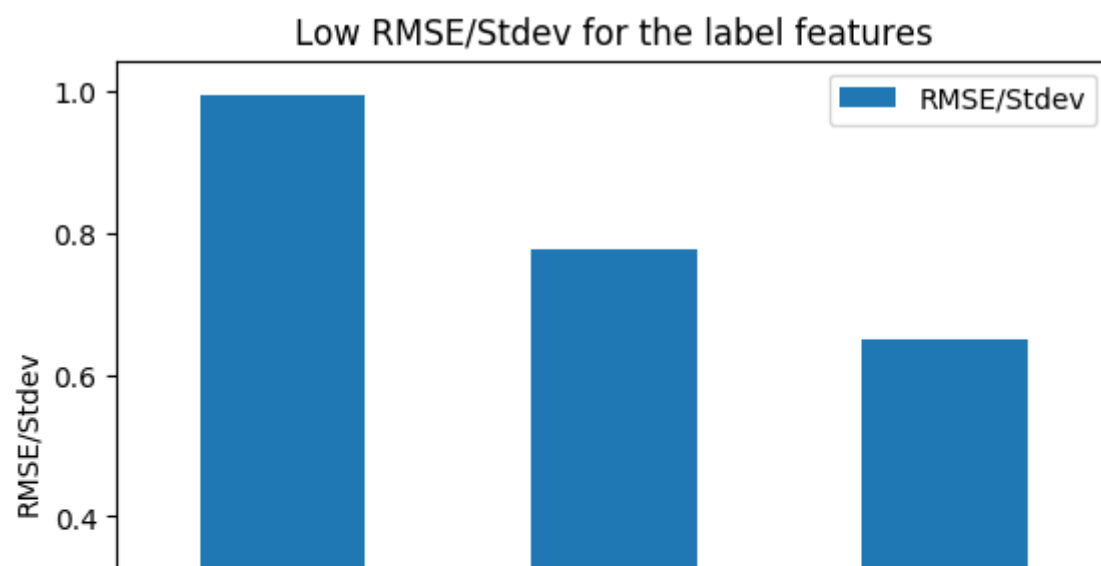
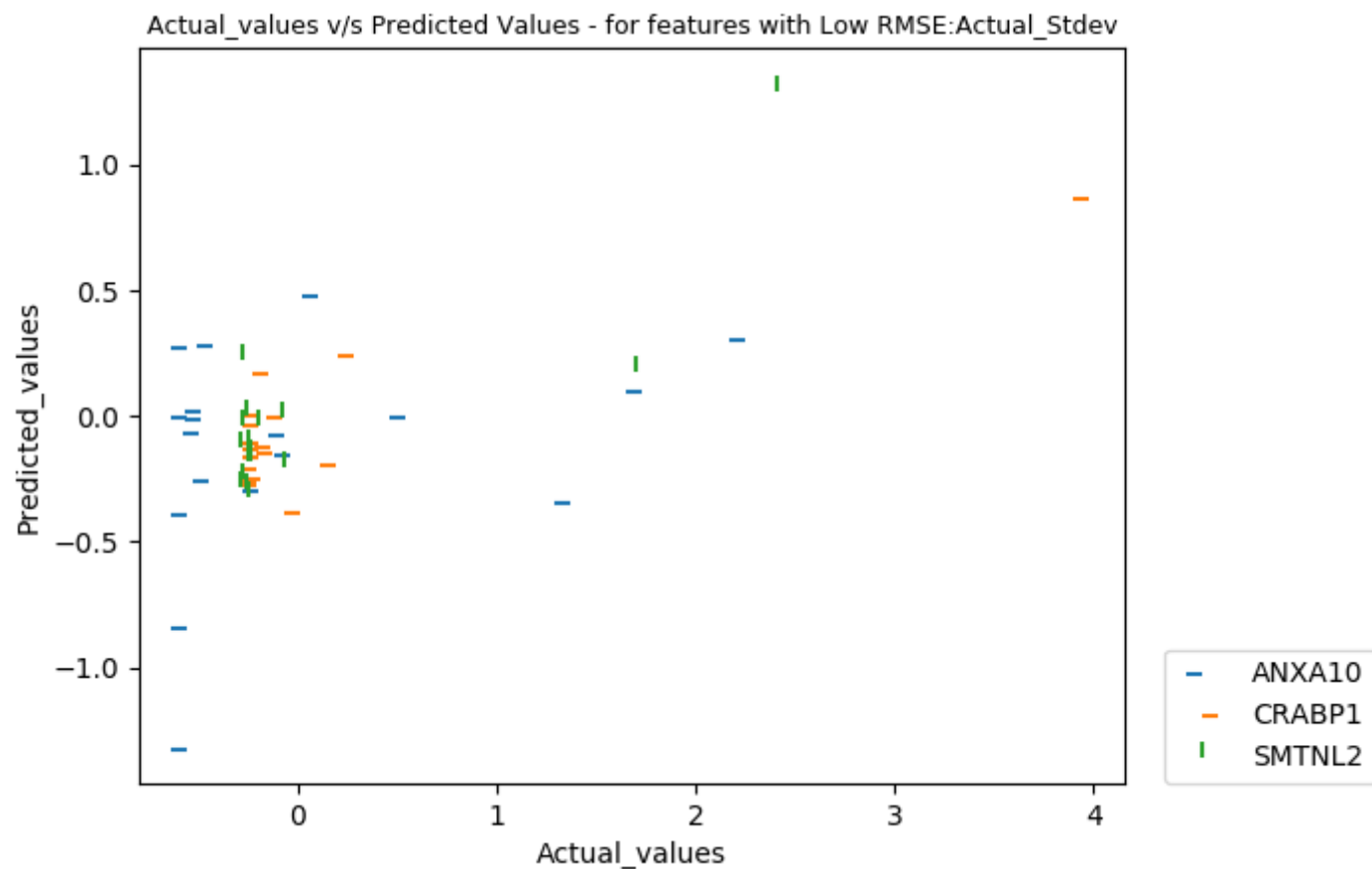
No. of features showing LOW 'RMSE/Stdev' (≤ 1.0): 3

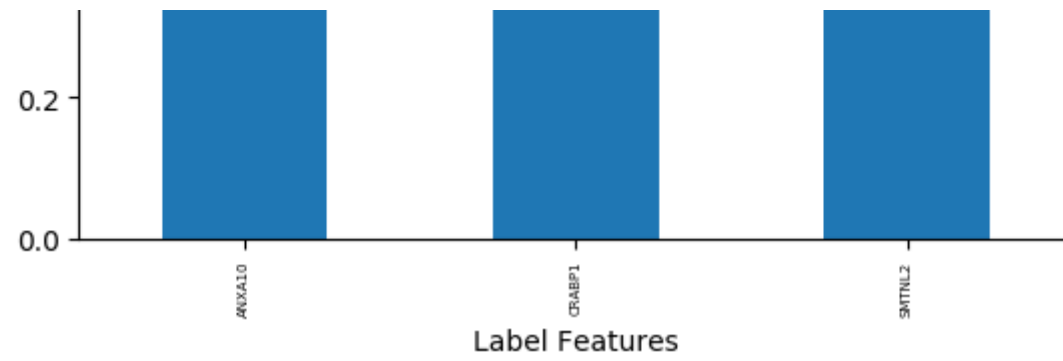
All such features with their Low 'RMSE/Stdev' values could be found in output file: test_eval_LinearRegression_Labels_with_Low_Ratio.csv

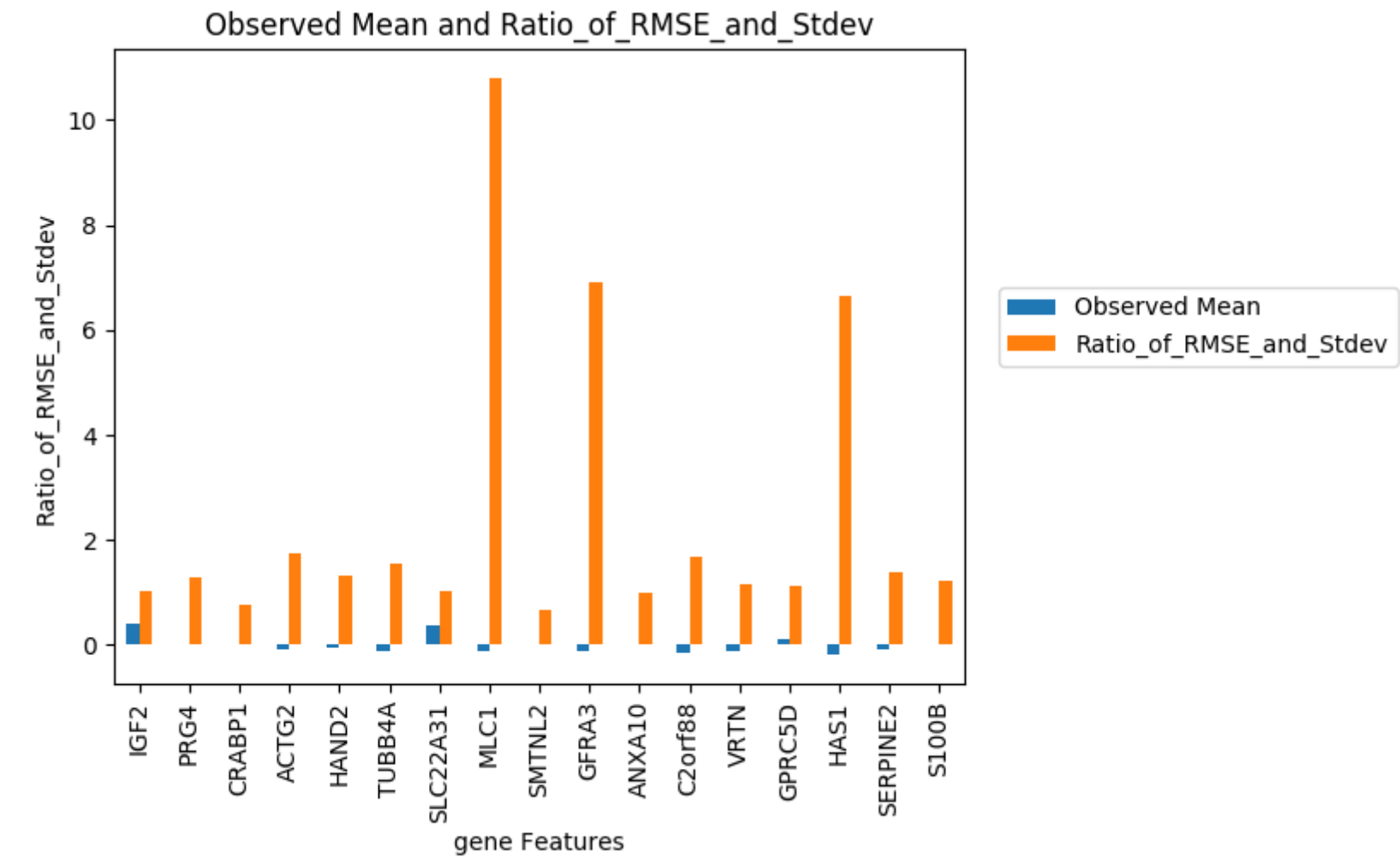
No. of features showing HIGH 'RMSE/Stdev' (> 1.0): 14

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

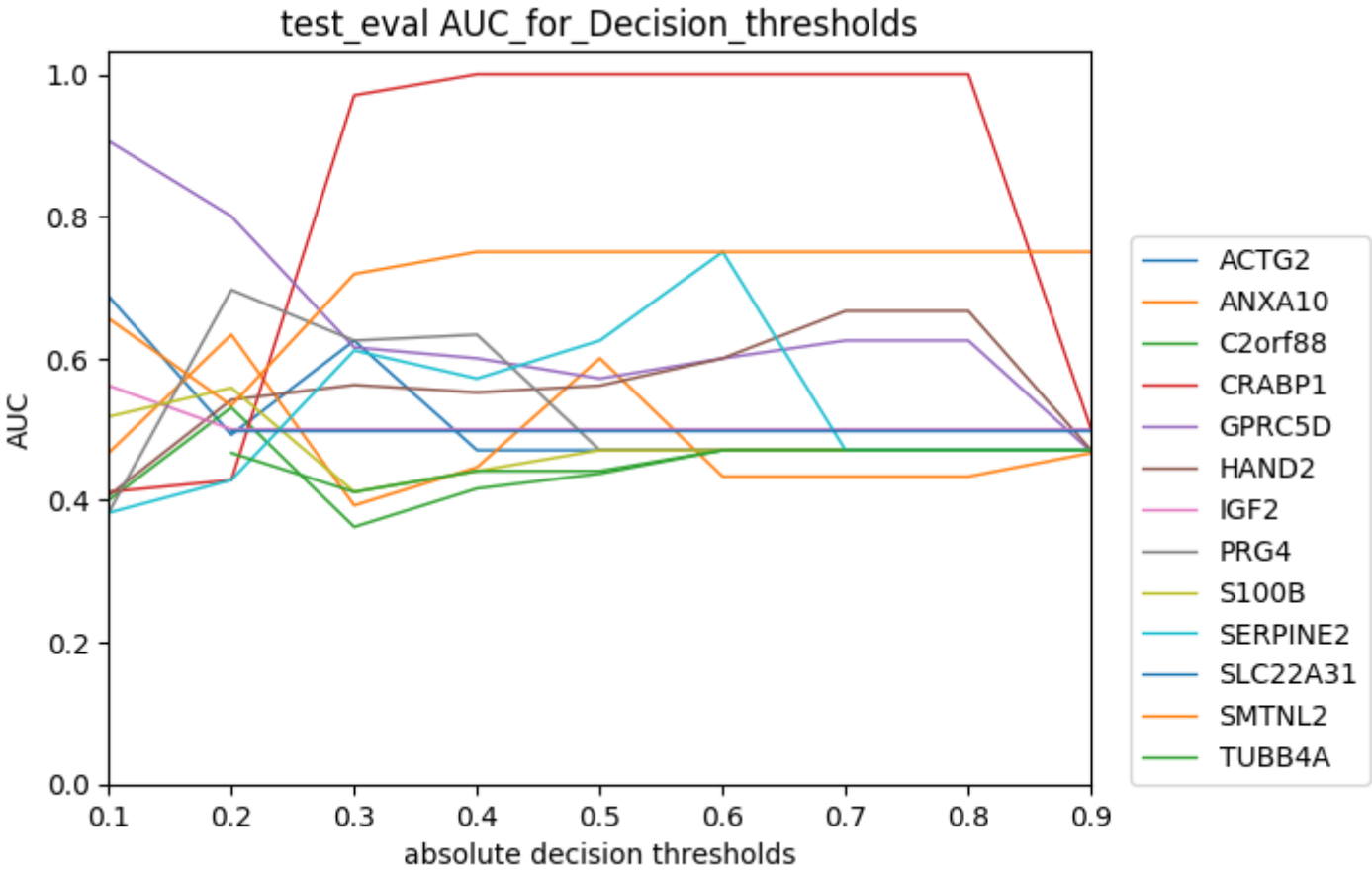
Model evaluation for Test data for label features showing Low 'RMSE/Stdev' (≤ 1.0)







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