re-run the model 1a, model 1b on larger dataset to be sure.

* Model 1a: use Feb21 rerun workflows
* Model 1b: use March gene mutation workflows.

LUAD\_test 297 --> Number of images.

Model 1a

297 images used.

ROC - < AUC < 50

Gene mutation probability distribution - OK ; LUAD are at high %.

Heatmaps- looks fine.

* Various factors will influence:
  + Image processing artifacts
  + Different cancer stage patients