* Analyze the results for running 1b model.  Understand the heatmap and graphs.
* Layout potential problems.
* Write a clear report of input-output.

Results:

* 1. Heatmap: too less tiles. By visualization, not very good results.
  2. ROC: AUC < 0.5
  3. Probability distribution: KRAS are not at high probability area.
  4. Only values on precision\_at\_1.txt ~= 80%; still don’t know what this file contains.

Overall, gene mutation prediction results fail to obtain the model performance the paper demonstrated.

After applying filters for LUAD tiles from model 1a, only 12 images used for testing.