

An Exploration of the Use of Trastuzumab and Bevacizumab to treat additional types of Cancers

A Project completed under the Figure One Lab Internship Emulator

Key Scientific Question

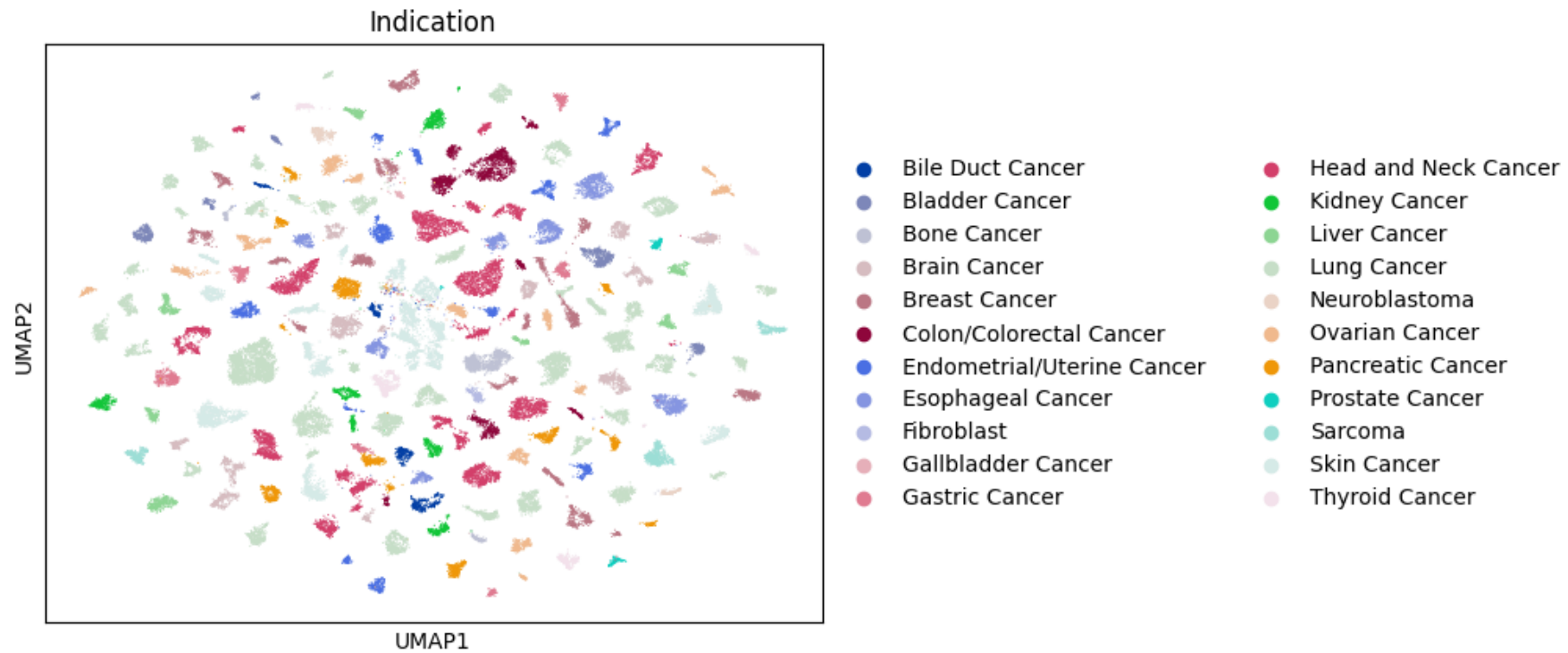
Using scRNA-seq data from available cancer cell lines, how will you explore the use of the FDA-approved antibody therapies Trastuzumab and Bevacizumab in the treatment of additional cancers?

Methods

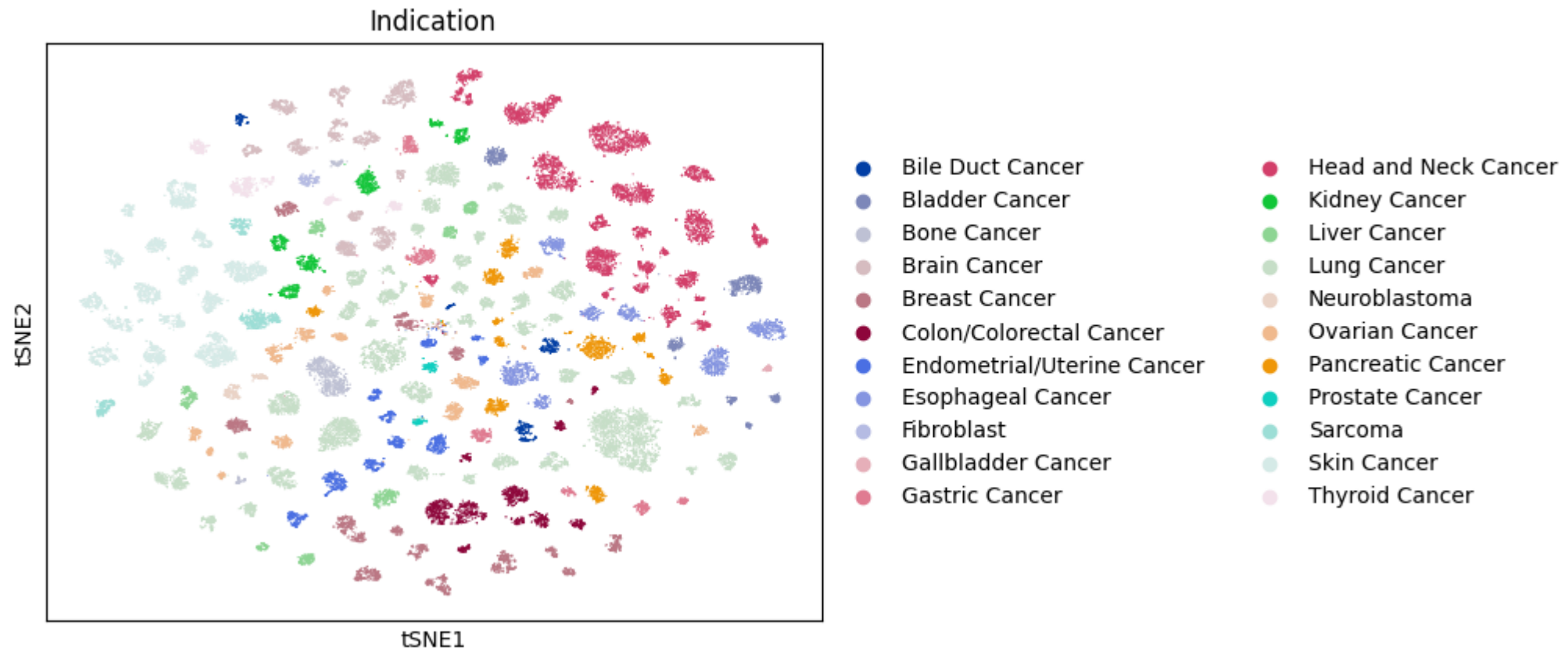
- Preprocessing, annotation and initial exploration of the data was done using code provided in *240701_kinker_anndata.ipynb* and *240702_kinker_scanpy.ipynb*, two Jupyter notebooks created by Mr. Dean Lee.
- The data was further analysed using differential gene expression analysis, t-tests, one-way ANOVA tests and Tukey's HSD tests.
- The analysis was conducted in Python, using the *scanpy* and *anndata* packages.

Plots

UMAP clustering

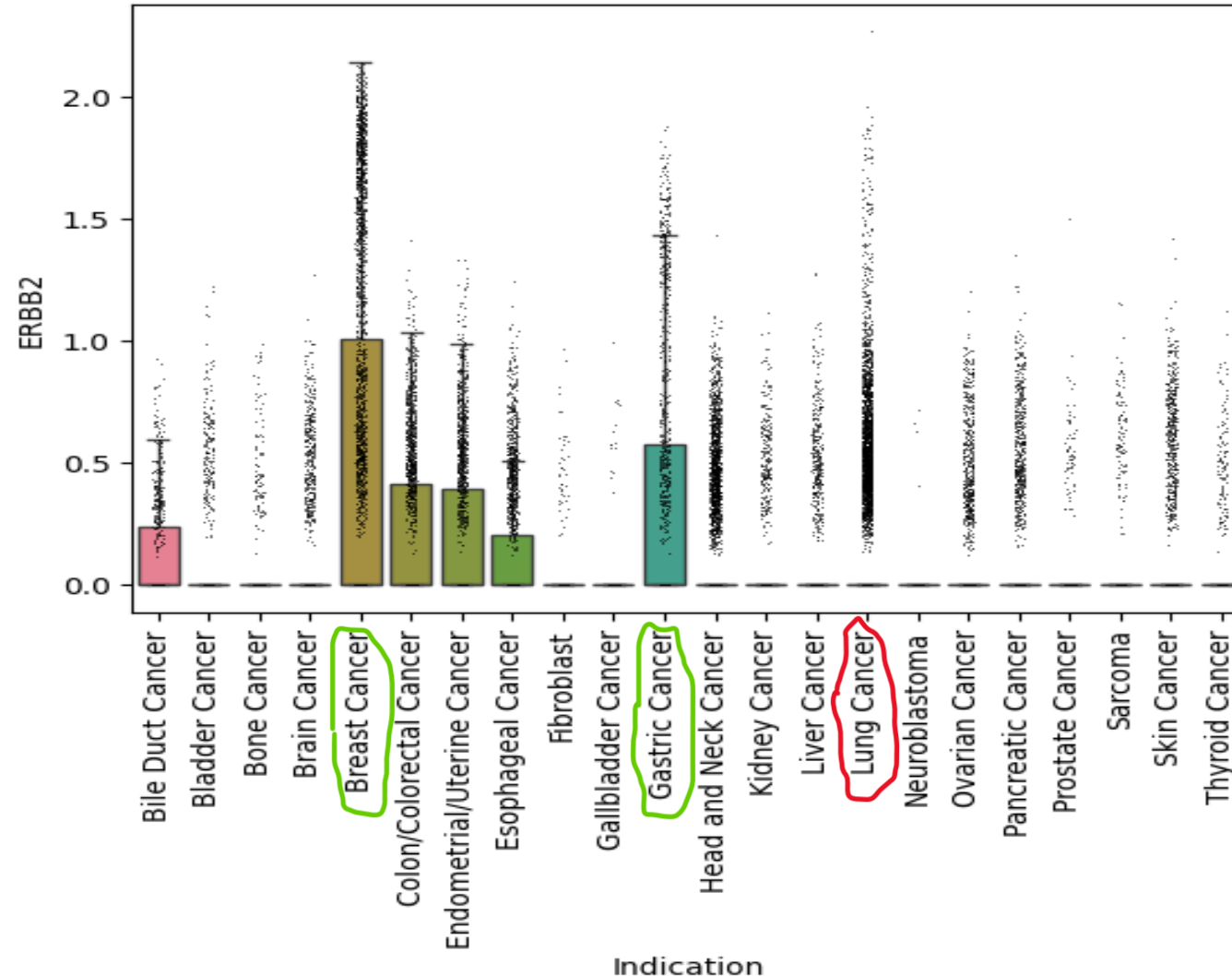


tSNE plot

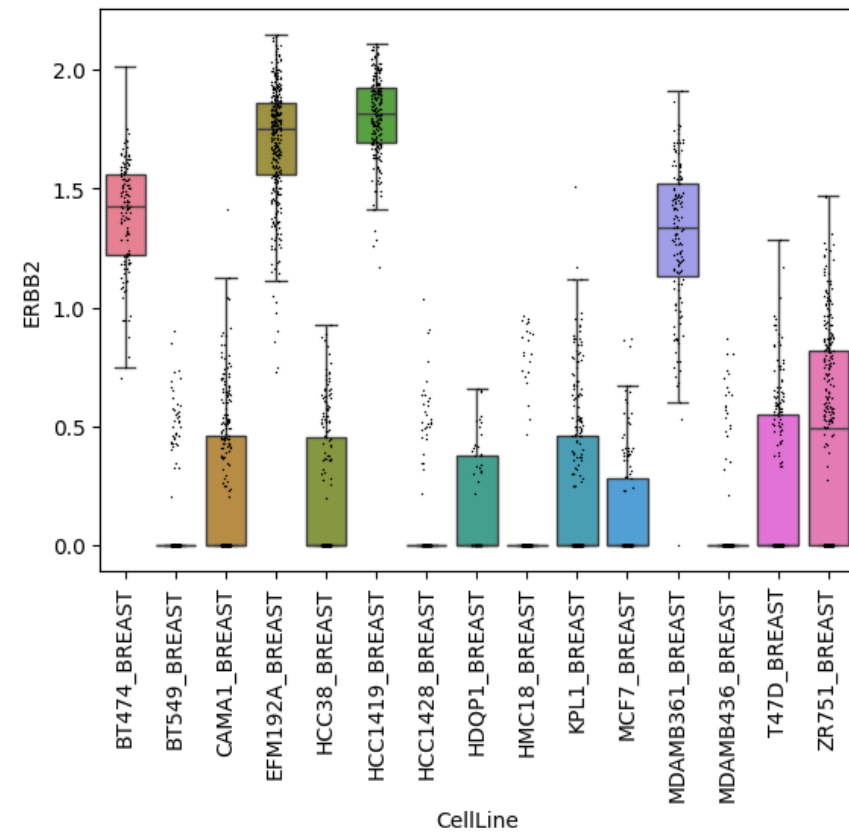


Trastuzumab Target Exploration

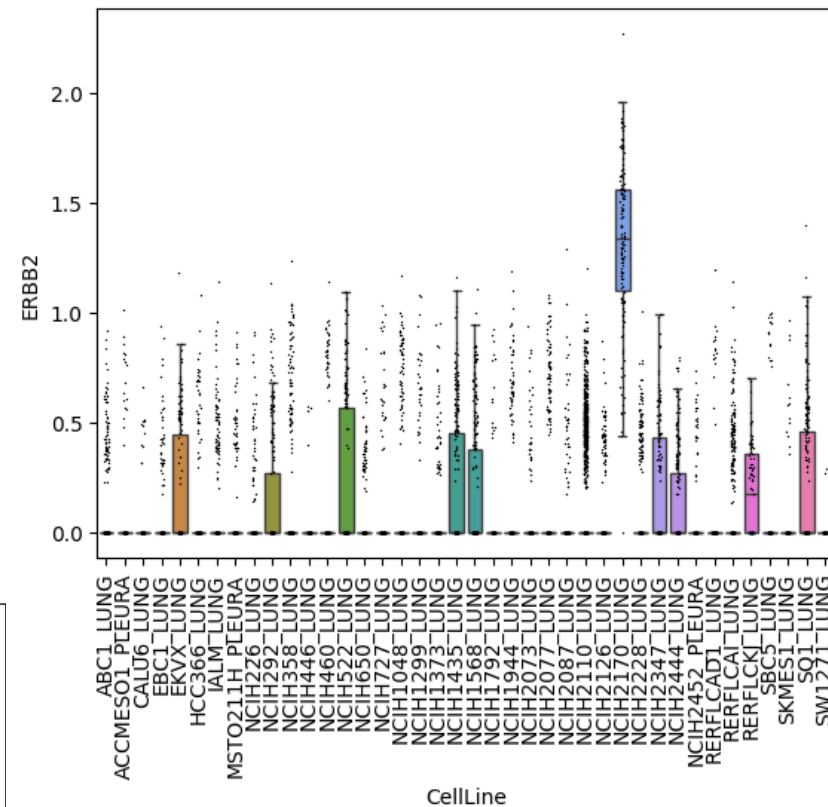
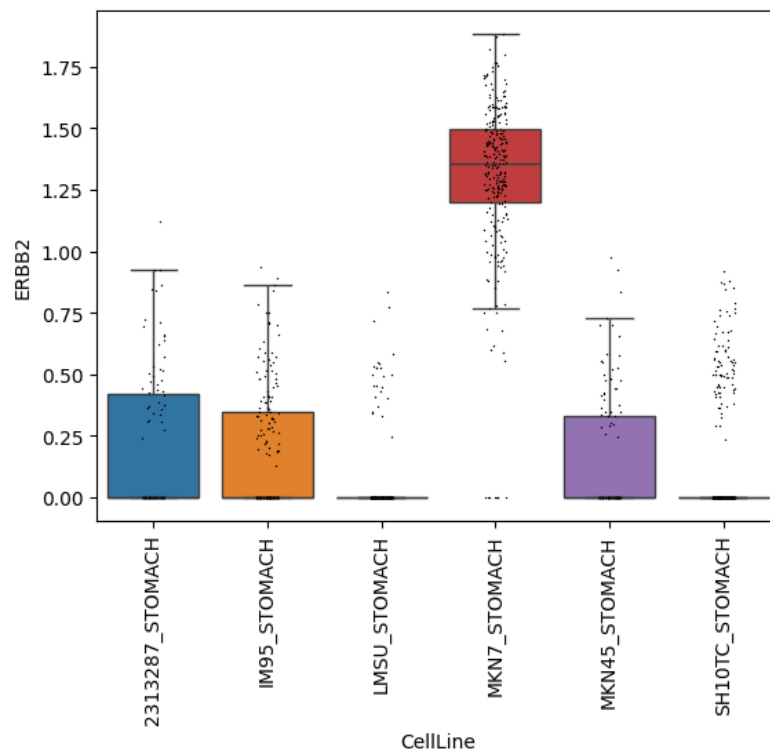
Expression of ERBB2 gene by Indication



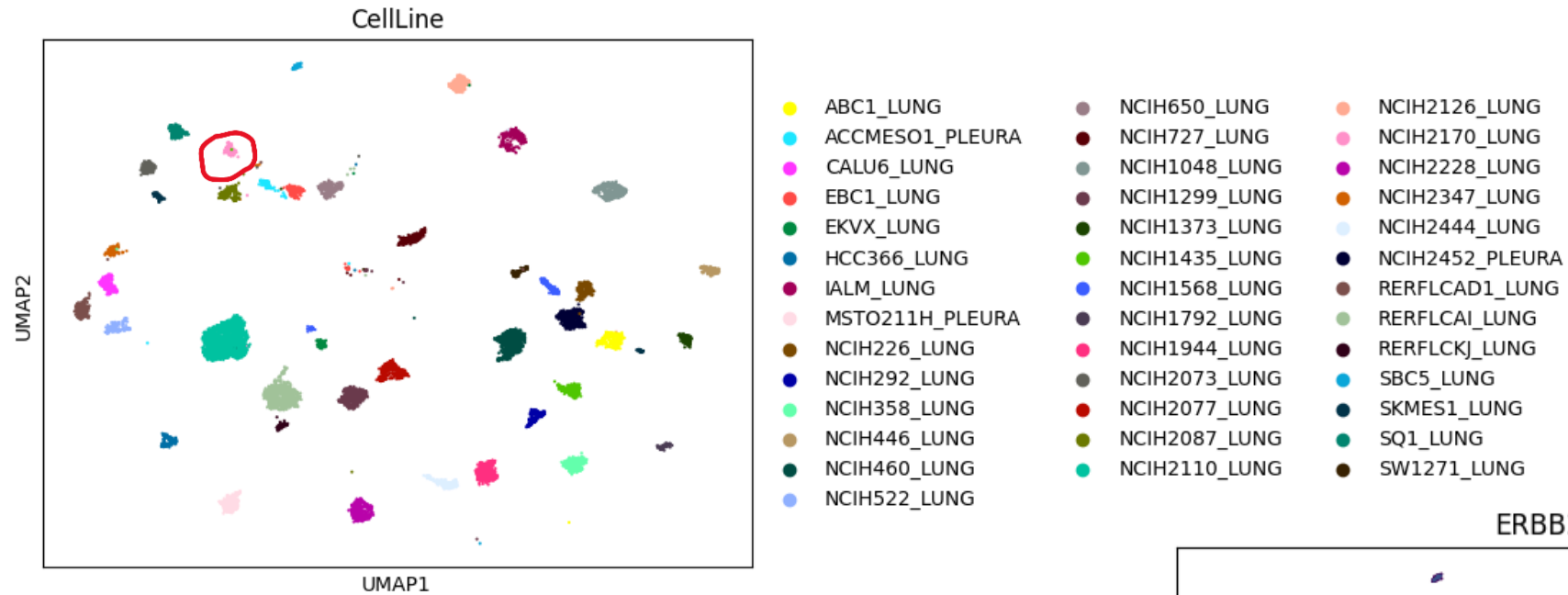
Cancers for which the drug is currently approved have been outlined in green. Additional cancers – lung cancer, in this case – in which the ERBB2 gene appears to be strongly expressed have been outlined in red. This may indicate a potential application of the drug in the treatment of this type of cancer.



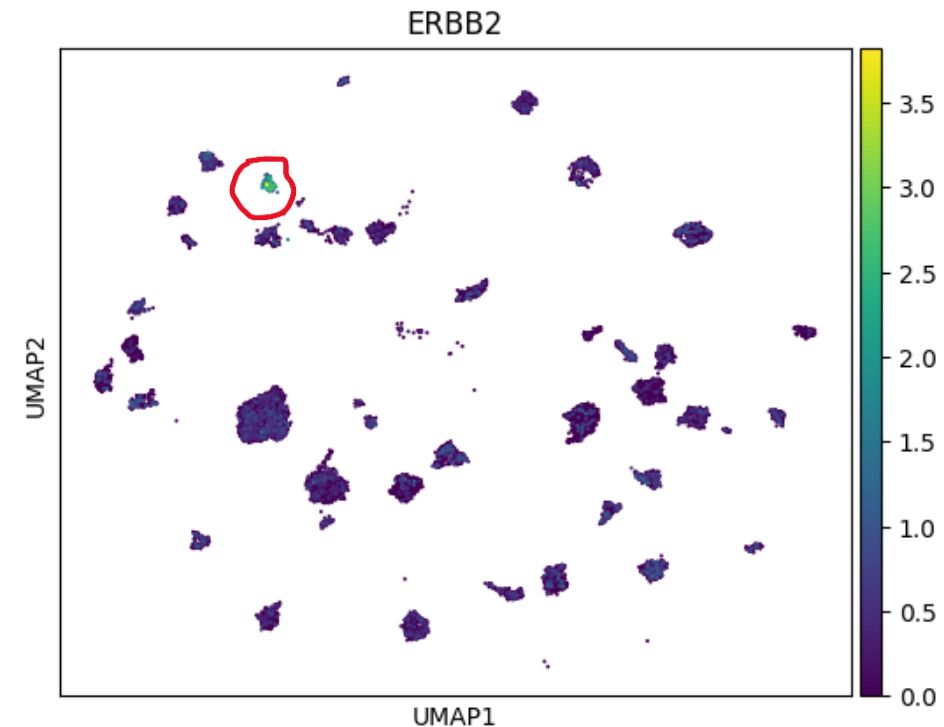
Expression of ERBB2 by Cell Line for Breast, Gastric and Lung Cancers



Mapping of Lung Cancer Cell Lines to Varying Levels of ERBB2 Expression



Clusters of cells that express a significantly higher level of the ERBB2 gene compared to other clusters have been outlined in red in both plots. A comparison of the two UMAPs will indicate that the NCIH2170_LUNG cell line appears to have a significantly higher expression level for this gene.



Differential Gene Expression Analysis

Differential gene expression analysis revealed that the NCIH2170_LUNG cell line had a significantly higher level of ERBB2 expression.

p-value = $2.532832e-59$

adjusted p-value = $9.444313e-58$

Statistical Tests

Three statistical tests – the t-test, the one-way ANOVA and the pairwise Tukey's HSD test – were conducted in order to determine if the expression of ERBB2 differed among the lung cancer cell lines that were analysed. The statistic and p-values of the first two tests are provided below:

- t-test

T statistic: 38.66725312879398

P value: 2.551458288533391e-77

- ANOVA

F statistic: 4005.561594678734

P value: 0.0

Conclusions for Trastuzumab

From multiple lines of evidence, it may be inferred that the ERBB2 gene, which is targeted by the drug Trastuzumab is differentially expressed in certain cell lines of lung cancer.

These results appear to indicate that the potential use and regulatory approval of this drug in the treatment of lung cancer should be explored through further analysis.