QC inForm Phenotype Outputs

Since we run multiple cell segmentations and rounds of phenotyping, we had to develop a code capable of analyzing the inForm phenotypes for each individual marker, assign the correct phenotype based on a hierarchy method, and align the different cell segmentations to ensure we aren’t counting too many or too few cells.

1. Go to the Clinical\_Specimen\_Y folder (Y is number associated with your cohort)
2. Open the ‘Upkeep and Progress’ folder
3. Open the ‘inform\_QC’ spreadsheet
   1. Running down the first column is a list of all specimens in the cohort
   2. The first row lists all the phenotypes that were run for the cohort
4. Go to the QC images for a case
   1. \\bkiZZ\Clinical\_Specimen\_Y\XX1\inform\_data\Phenotyped\Results\QA\_QC\Phenotype
      1. ZZ: Which BKI server your data is stored on
      2. Y: Clinical Specimen number associated with your cohort
      3. XX: Reassigned Specimen ID
   2. Each phenotype is broken up into an individual folder, with up to 20 im3s represented
   3. There are seven versions of each image:
      1. cell\_stamp\_mosiacs\_pos\_neg: shows 20 positive and 20 negative cells from one image with the stain in white, DAPI in blue, and the cell segmentation shown in red
         1. White + indicates a cell being phenotyped as positive by the algorithm
      2. cell\_stamp\_mosiacs\_pos\_neg\_no\_dapi: same as previous image without DAPI
      3. cell\_stamp\_mosiacs\_pos\_neg\_no\_dapi\_no\_seg: same as previous without cell segmentation
      4. cell\_stamp\_mosiacs\_pos\_neg\_no\_seg: same as first image without cell segmentation
      5. full\_color\_expression\_image\_no\_seg: shows whole image with each all markers shown in original pseudocolor
         1. useful in determining if background/nonspecific staining is present
      6. single\_color\_expression\_image: shows whole image with only the marker of interest shown in white
      7. single\_color\_expression\_image\_no\_seg: same as previous without cell segmentation
5. Flip through the images for the first phenotype
6. Recording QC:
   1. If the phenotype and cell segmentation are correct, place an X in the corresponding cell for that case and phenotype
   2. If there are issues, record notes in the corresponding cell
   3. Up to researcher to determine what level of error they deem acceptable
7. Once finished with QC for a case, place the date in the corresponding cell
8. Save this file
   1. Keep the file as a .csv and ignore the pop-up warning the formatting data will be lost
9. See examples of good/bad phenotyping in PPT