To run the QC on-the-fly workflow:

* Prerequisites:
  + Download and install CellProfiler version 4.1.3 desktop client
  + Download Knime ([current version](https://www.knime.com/downloads))
    - Within Knime client, Install HCS Tools
  + Download the CellProfiler pipeline ([link](https://github.com/broadinstitute/imaging-platform-pipelines/tree/master/JUMP_production)) *[to be put there]*
  + Download the Knime workflow ([link](https://github.com/broadinstitute/imaging-platform-pipelines/tree/master/JUMP_production)) *[to be put there]*
* Run CellProfiler QC on-the-fly pipeline
  + Notes for most modules are documented within the pipeline Notes, but in brief:
    - Drag your exported images folder(s) onto the Images module
    - Set Output Folder
    - Check segmentation settings
      * Enter Test Mode
      * Run pipeline through the Identify\* modules
      * Adjust threshold settings as necessary
    - Run full set of images
      * Ensure to turn off window display for faster processing (Window -> Turn off…)
* Run Knime and load Knime workflow
  + Open the CSV Reader “Top Line Per-Image”  
    A picture containing chart

    Description automatically generated
    - Set the File path
  + Open the CSV Reader “Top Line Per-Object”  
    A picture containing graphical user interface

    Description automatically generated
    - Set the File path
  + Run the workflow  
    
  + Inspect the plots
    - Right-click the final nodes and select “View …”