CellProfiler\_Version 4.2.1

Images:

ChannelType\_Acti Grayscale
ChannelType\_DAPI Grayscale
ChannelType\_Tubu Grayscale

#### Metadata:

Metadata extraction method: Extract from file/folder names

Metadata source: File name

Regular expression to extract from file name:^(?P<Date>.\*)\_(?P<CellLine>.\*)\_(?P<DiffState>.\*)\_(?P<Substrate>.\*)\_(?P<Site>[0-9]{1,2}) c(?P<Chanel>[0-9])

#### **Modules:**

RescaleIntensity:

Select the input image:DAPI

Name the output image:RescaledDAPI

Rescaling method: Choose specific values to be reset to a custom range Method to calculate the minimum intensity: Minimum for each image Method to calculate the maximum intensity: Maximum for each image

Lower intensity limit for the input image:0 Upper intensity limit for the input image:1

Intensity range for the input image:0.000000,1.000000 Intensity range for the output image:0.000000,1.000000

### Smooth:

Select the input image:RescaledDAPI

Name the output image:rescaledDAPIsmooth Select smoothing method:Gaussian Filter Calculate artifact diameter automatically?:No

Typical artifact diameter:3.0 Edge intensity difference:0.1 Clip intensities to 0 and 1?:Yes

## RescaleIntensity:

Select the input image:Acti

Name the output image:RescaledActi

Rescaling method:Choose specific values to be reset to a custom range Method to calculate the minimum intensity:Minimum for each image Method to calculate the maximum intensity:Maximum for each image

Lower intensity limit for the input image:0 Upper intensity limit for the input image:1

Intensity range for the input image:0.000000,1.000000

Intensity range for the output image: 0.000000, 1.000000

## RescaleIntensity:

Select the input image:Tubu

Name the output image:RescaledTubu

Rescaling method:Choose specific values to be reset to a custom range Method to calculate the minimum intensity:Minimum for each image Method to calculate the maximum intensity:Maximum for each image

Lower intensity limit for the input image:0
Upper intensity limit for the input image:1
Intensity range for the input image:0.000000,1.000000
Intensity range for the output image:0.000000,1.000000
Select image to match in maximum intensity:None

### GrayToColor:

Select a color scheme:RGB

Rescale intensity:No

Select the image to be colored red:RescaledActi

Select the image to be colored green:RescaledTubu

Select the image to be colored blue:rescaledDAPIsmooth

Name the output image:RGBImage Relative weight for the red image:1.0 Relative weight for the green image:1.0 Relative weight for the blue image:1.0

#### Savelmages:

Select the type of image to save:Image Select the image to save:RGBImage Saved file format:tiff

## IdentifyPrimaryObjects:

Select the input image:rescaledDAPIsmooth

Name the primary objects to be identified: Nuclei

Typical diameter of objects, in pixel units (Min,Max):30,70

Discard objects outside the diameter range?:Yes

Discard objects touching the border of the image?:Yes

Method to distinguish clumped objects:Shape

Method to draw dividing lines between clumped objects:Shape

Size of smoothing filter:10

Suppress local maxima that are closer than this minimum allowed distance:8

Speed up by using lower-resolution image to find local maxima?:Yes

Fill holes in identified objects?: After both thresholding and declumping

Automatically calculate size of smoothing filter for declumping?:No

Automatically calculate minimum allowed distance between local maxima?:No

Handling of objects if excessive number of objects identified:Continue

Maximum number of objects:500

Use advanced settings?:Yes

Threshold setting version:12

Threshold strategy:Global

Thresholding method: Minimum Cross-Entropy

Threshold smoothing scale: 1.3488

Threshold correction factor:2

Lower and upper bounds on threshold:0.000000,1.000000

#### IdentifySecondaryObjects:

Select the input objects:Nuclei

Name the objects to be identified:Cells

Select the method to identify the secondary objects:Propagation

Select the input image:RescaledActi

Regularization factor:0.05

Discard secondary objects touching the border of the image?:Yes

Discard the associated primary objects?:Yes

Name the new primary objects: NucleiOK

Fill holes in identified objects?:Yes

Threshold setting version:12

Threshold strategy:Global

Thresholding method:Otsu

Threshold smoothing scale:0

Threshold correction factor:0.4

Lower and upper bounds on threshold:0.000000,1.000000

Manual threshold:0.0

Select the measurement to threshold with: None

Two-class or three-class thresholding?:Two classes

Log transform before thresholding?:No

## MeasureObjectSizeShape:

Select object sets to measure:Cells Calculate the Zernike features?:No

Calculate the advanced features?:No

# MeasureObjectIntensity:

Select images to measure: Acti, Rescaled Acti, Rescaled Tubu, Tubu

Select objects to measure: Cells

#### OverlayOutlines:

Display outlines on a blank image?:No

Select image on which to display outlines:RGBImage

Name the output image: Overlay

Outline display mode:Color

Select method to determine brightness of outlines: Max of image

How to outline:Inner

Select outline color:yellow

Select objects to display:Cells

Select outline color:red

Select objects to display:Nuclei

### Savelmages:

Select the type of image to save:Image

Select the image to save: Overlay

Select method for constructing file names: From image filename

Select image name for file prefix:DAPI

Enter single file name:OrigBlue

Saved file format:tiff

Image bit depth:8-bit integer

When to save: Every cycle

Record the file and path information to the saved image?:No

Create subfolders in the output folder?:No

Base image folder:Default Input Folder

Save with lossless compression?:No

### IdentifySecondaryObjects:

Select the input objects: Nuclei

Name the objects to be identified: Nuclei Big

Select the method to identify the secondary objects: Distance - N

Select the input image:RescaledActi

Number of pixels by which to expand the primary objects:55

Regularization factor:0.05

Discard secondary objects touching the border of the image?:Yes

Discard the associated primary objects?:Yes

Name the new primary objects: Nuclei Big OK

Fill holes in identified objects?:Yes

# ConvertObjectsToImage

Select the input objects:Cells

Name the output image:CellBinary

Select the color format:Binary (black & white)

Select the colormap:Default

# Morph:

Select the input image:CellBinary

Name the output image:SkelCell

Select the operation to perform:skelpe

Number of times to repeat operation:Custom

Repetition number:10

Rescale values from 0 to 1?:Yes

#### MeasureObjectSkeleton:

Select the seed objects: Nuclei Big

Select the skeletonized image:SkelCell

Retain the branchpoint image?:Yes

Name the branchpoint image:BranchpointImage

Fill small holes?:Yes

Maximum hole size:10

Export the skeleton graph relationships?:No

### Savelmages:

Select the type of image to save:Image

Select the image to save:BranchpointImage

Saved file format:tiff

Save with lossless compression?:No

### MeasureObjectIntensityDistribution:

Select images to measure: Acti, Rescaled Acti, Rescaled Tubu, Tubu

Calculate intensity Zernikes?: Magnitudes and phase

Maximum zernike moment:6

Select objects to measure: Cells

Object to use as center?: Centers of other objects

Select objects to use as centers: Nuclei

Scale the bins?:Yes

Number of bins:4

Maximum radius:100

# MeasureTexture:

Select images to measure: Acti, Rescaled Acti, Rescaled Tubu, Tubu

Select objects to measure:Cells
Enter how many gray levels to measure the texture at:256
Texture scale to measure:3

#### ExportToSpreadsheet

### ExportToDatabase:

Database type:SQLite

Calculate the per-image mean values of object measurements?:Yes

Calculate the per-image median values of object measurements?:Yes

Calculate the per-image standard deviation values of object measurements?:Yes

Calculate the per-well mean values of object measurements?:No

Calculate the per-well median values of object measurements?:No

Calculate the per-well standard deviation values of object measurements?:No

Export measurements for all objects to the database?:Select...

Select the objects:Cells,NucleiOK

Maximum # of characters in a column name:64

Create one table per object, a single object table or a single object view?:Single object table

Enter an image url prepend if you plan to access your files via http:

Write image thumbnails directly to the database?:Yes

Select the images for which you want to save thumbnails:RGBImage

Which objects should be used for locations?: NucleiOK

Enter a phenotype class table name if using the Classifier tool in CellProfiler Analyst:

Select the classification type:Object

Select an image to include: None

Use the image name for the display?:Yes

Do you want to add group fields?:Yes

Enter the name of the group:Date

Enter the per-image columns which define the group, separated by commas:ImageNumber, Image Metadata Date

Enter the name of the group:CellLine

Enter the per-image columns which define the group, separated by commas:ImageNumber, Image Metadata CellLine

Enter the name of the group:DiffState

Enter the per-image columns which define the group, separated by commas:ImageNumber, Image\_Metadata\_DiffState

Enter the name of the group:Substrate

Enter the per-image columns which define the group, separated by commas:ImageNumber, Image\_Metadata\_Substrate

Do you want to add filter fields?:No