This workflow briefly describes necessary procedures to explore and reproduce the statistical, graphical and imaging-based (examples only) analyses underpinning the article "Reticular adhesions are a distinct class of cell-matrix adhesions that mediate attachment during mitosis" by Lock et al, published in Nature Cell Biology, 2018.

This workflow requires the following free software tools:

1. R (https://www.r-project.org) e.g. v3.5.1
2. RStudio (https://www.rstudio.com/products/rstudio/download/) e.g. v1.1.453
3. Knime (https://www.knime.com/downloads) e.g. v3.6.0
4. Knime community nodes including Knime Image Processing & HCS Tools

Go to github repository following links defined in Lock et al article

Download respoitory to desired location

Unzip knime workflows:
Reticular_Adhesion_Arp23_Inhibitor_Combining_All_Exp_Image_Quant_Outputs.zip
&
Reticular_Adhesion_Arp23_Inhibitor_Image_Analysis_Exp1.zip

Move knime workflows to local knime workspace

LOAD knime 'Image Analysis' workflow

Update input image file path locations in 'Image Reader' node e.g.:
.../Source_Data/Knime_Image_Analysis/Arp2-3 Inhibition studies/Input Data/Arp23 Inhibition Images/Exp1 Combined/Exp1_666_Composite_004.tif
(Load all images in folder)

Update 96 well plate layout file path locations in 'Load Layout' node e.g.:
.../Source_Data/Knime_Image_Analysis/Arp2-3 Inhibition studies/Input Data/Arp23 Inhibition Images/Plate_Layouts/Arp2-3 Inhibitor Exp1.xlsx

Update 'Table Writer' node (inside Data Export metanode) output file path location: this will define the location of the quantitative data file derived from image analysis (e.g. of Arp2/3 inhibition experiment 1), e.g.
.../Source_Data/Knime_Image_Analysis/Arp2-3 Inhibition studies/Input Data/Table Outputs/Arp2-3_Exp1_Table_All_Combined.table
This will be the location of the file imported into Exp1 import node of the 'Combining Data' knime workflow.

RUN knime 'Image Analysis' workflow
Repeat for image data sets from Exp2 & Exp3 (changing input and output paths/names as appropriate)

LOAD knime 'Combining Data' workflow

Update input data table path locations in 'Table Reader' node (within 'Import' metanode), e.g.:
.../Source_Data/Knime_Image_Analysis/Arp2-3 Inhibition studies/Input Data/Table Outputs/Arp2-3_Exp1_Table_All_Combined.table
(Repeat for Exp2 and Exp3 'Import' metanodes)

Update output .csv file path location in 'CSV Writer' node, e.g.:
.../Source_Data/Knime_Image_Analysis/Arp2-3 Inhibition studies/Output Data/Arp2-3 Three Experiment Integrated Data for R.csv

RUN knime 'Combining Data' workflow
Copy resulting data into sheet *'SuppFig5C'* of excel file: "*Supplementary Table 1 Statistics Source Data.xlsx*"

LOAD R markdown file
"Statistical_Analysis_Code_Lock_et_al_NCB_2018.Rmd"

Update: *> data_input_path <- ".../Source_Data"*
to match location path of *"Supplementary Table 1 Statistics Source Data.xlsx"*

RUN R markdown file
(required packages will load automatically)

Graphical outputs will be saved to:
"data_input_path/Graphical_Outputs/"
An HTML summary file (preview) will be saved to:
"data_input_path/Statistical_Analysis_Code_Lock_et_al_NCB_2018.nb.html"