%% README:
Accompanying files for :

Gould, P.D., Domijan, M. , Greenwood, M., Tokuda I.T., Rees, H., Kozma-Bognar, L., Hall A.J., and Locke, J.C.W. (2017) “Coordination of robust single cell rhythms in the Arabidopsis circadian clock via spatial waves of gene expression”.

This folder comes with several files and subfolders.

**Data_singlecell** folder contains the data for WT, WT repeat and CCA1-long experiments.

In the folder WT_final_coordinates:

Positions from root tip to cotyledon are labelled pos1 to pos6, respectively. WT_pos1-6_RFP_YFP_BF_median_tracked_background_Plot.xlsx is the file stating the background subtracted for SI Figure 5. YFP levels of all the cells for each section imaged are start with the label ‘mean’. Their positions are in the files starting with label ‘pos’. Timestamp_WT.xlsx contains all the imaging times. Subfolder interpolated you will find the interpolated YFP traces for all positions. File individual_results.xlss contains the period analysis output of the Biodare for all these interpolated data files.

In WTrepeat_final_coordinates:

Positions from root tip to cotyledon are labelled pos13 to pos20, respectively. YFP levels of all the cells for each section imaged are start with the label ‘mean’ or ‘new_mean’. Their positions are in the files starting with label ‘pos’ or ‘new_pos’. Timestamp_WTrepeat.xlsx contains all the imaging times for different sections. Subfolder interpolated you will find the interpolated YFP traces for all positions. File individual_results.xls contains the period analysis output of the Biodare for all these interpolated data files.

In CCA1-long_final_coordinates:

Positions from root tip to cotyledon are labelled pos12 to pos18, respectively. YFP levels of all the cells for each section imaged are start with the label ‘mean’ or ‘new_mean’. Their positions are in the files starting with label ‘pos’ or ‘new_pos’. Timestamp_CCA1-long.xlsx contains all the imaging times for different sections. Subfolder interpolated you will find the interpolated YFP traces for all positions. File individual_results.xls contains the period analysis output of the Biodare for all these interpolated data files.

**Pictures** folder contains the stitched images of the experiment’s measurement positions.

**Analysis** Matlab files for each experiment producing some of the figures from the paper.

To make the sequential montages (Figure 3G, Figure 2 supplement 1 G and Figure 2 supplement 2 G) you need to download the following toolbox (Controllable tight subplot) from FileExchange:
https://uk.mathworks.com/matlabcentral/fileexchange/30884-controllable-tight-subplot
in this folder.