User Input I

```
########## User Input ###########

#User Input I: Steps 1-4 below must be changed to tailor the analysis to a specific data set on a local computer.

#Step 1: Set the working directory
setwd("C:/Users/pippi/Downloads")

#Step 2: Select your input file (should be a csv file).
plate_no <- 'NO7.csv'

#Step 3: Name the treatments and/or lines used.
#Per specific experiment, please change sample names accordingly from A to H, OR from 1 to 12 as on the plate.
#The number and order of labels matters!! This is because the code counts the number (needs 8 or 12) and uses the order.
#Same treatment labels will combine into one group in the analysis.
#Please avoid using a backslash in any treatment names!! Please avoid "NA" as a label when using ANOVA!
treatment <- c(
'Sample1',
'Sample2',
'Sample3',
'Sample4',
'Sample5',
'Sample6',
'Sample7',
'Sample8'
  )


#Step 4: Indicate the relative start time for the assay.
#For example, if subjective dawn was 7 am and the luciferase assay was started at 9 am, the user would input 2 as the relative start time.
#This number must be an integer and cannot be negative!
RelativeTime <- 0


###############
```

User Input II

```
#User Input II: Options 1-7 can be changed per user's specific needs.

#Option 1: Include graphs?
#If you want basic graphs of the luminescent curves and the graphs of average statistics, type TRUE. If not, type FALSE.
GRAPHS <- TRUE

################

#Option 2: Run a One-Way ANOVA test with Tukey HSD post-hoc?
#Code will run the test if TRUE is selected. If FALSE is selected, it will not.
ANOVA <- TRUE

#Option 2 addition 1: What is your control?
#You can specify the output control for the ANOVA test.
#Leave empty to use each treatment as a control in a pairwise comparison.
A_CONTROL <- ''

#Option 2 addition 2: Number ANOVA output files?
#If we are doing all treatments as controls for an ANOVA, do you want the file names numbered for convenience?
#Type TRUE or FALSE for yes or no, respectively.
A_NumberLabel <- TRUE

################

#Option 3: Run a t-test?
#If yes, type TRUE; if no, type FALSE.
#If an error message says data is too similar, write FALSE and use ANOVA or do t-test by hand.
t_test <- TRUE

#Option 3 addition 1: Should the t-test be pairwise?
#If yes, type TRUE; if no, type FALSE
pairwise<- TRUE

#Option 3 addition 2: If the test is pairwise, are the data paired?
#If yes, type TRUE; if no, type FALSE
paired<- FALSE

#Option 3 addition 3: What treatment is the control?
#Leave the list empty to use each treatment as control -OR- write the treatment name of the single control.
T_CONTROL <- ''

#Option 3 addition 4: Number t-test output files?
#If we are doing all treatments as controls for a t-test, do you want the file names numbered for convenience?
#Type TRUE or FALSE for yes or no, respectively.
T_NumberLabel <- TRUE

################

#Option 4: "Shift" the phase values?
#To get low values or negative values instead of high values, the code can subtract by XX if the value is greater than YY.
#If you want to shift the phase, type TRUE; if you do not want to, type FALSE.
shift <- TRUE

#Option 4 additions: What values do you want to use for XX and YY?
#If shift<-TRUE and phase value n > YY, then n-XX = new phase value.
XX <- 24
YY <- 22

################

#Option 5: Round your time points?
#If yes, type TRUE. If no, type FALSE.
#ARSER analysis can only be run if the time series is consistent. If it is not, try rounding to the nearest hour.
#Not advisable if times are off by more than a couple of minutes from the hour interval!
roundTP <- TRUE

################

#Option 6: Does your data list wells by A1,A2,A3... OR by A1,B1,C1...?
#If your data lists wells by A1,A2,A3.... then type TRUE. Otherwise, type FALSE.
orientation <- TRUE


################################


#END OF USER INPUT
##########################################################################################################
```

Supplemental Figure S1