Creation of active gene-lists

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Contents

1 Active/Inactive Gene lists

Our aim is to create a unified table that assigns to each gene in the P.falicparum gnome a expresion state. We will define 5 possible expresion states:

- Active
  - Regular
  - Variant Active
  - Variant Repressed
- Inactive
- Not-Settable

1.1 Microarray Data: Red Signal

We willl load the red signal and transform it into percentiles. For each gene we pick the "Aver.2Higher" column from the original microarrays data table. This column corresponds to the average between the two highest red signals among available timepoints.

Red Signal DataFrame

```
             Gene_id     Red_12B     Red_10G    Red_3D7B Percent_12B
1         mal_mito_3 22579.33333 36436.73333 30636.82500  96.0335622
2 MAL13P1.415_oldname   770.82083   702.22292   640.11667  21.3196034
3  MAL13P1.65_oldname   111.33333    87.05833    91.05833   6.2166285
4  MAL7P1.142_oldname  5924.44167  5194.40000  5114.63333  75.4767353
5  MAL8P1.310_oldname    37.21250    35.37917    33.24167   0.8581236
6   MAL8P1.90_oldname    80.55417    46.18333    54.64167   4.1952708
  Percent_10G Percent_3D7B MaxRedPercentDif
1   98.474447   97.8832952        2.4408848
2   20.861937   18.4591915        2.8604119
3    5.053394    4.5194508        1.6971777
4   72.444699   71.7200610        3.7566743
5    1.115561    0.5911518        0.5244088
6    2.002288    2.2501907        2.1929825
```

1.2 Microarray Data: Areas

We will load the areas data to calculate FC among strains. For each gene, we select the time interval (right, left, mid or sides) for which we find the maximum difference among strains (between highest and lowest). We will also add a column to check if this time interval corresponds to the interval of maxium expression for each strain.

Areas DataFrame

```
              Gene_id     l_12B     r_12B     m_12B    s_12B     l_10G    r_10G
1          mal_mito_3 30.592496 61.080128 49.676556 41.99607 25.372470 62.38873
2 MAL13P1.415_oldname  5.423269  8.488971  1.289779 12.62246  6.117132 10.59524
3  MAL13P1.65_oldname 18.322430        NA 17.593468       NA 14.071128       NA
4  MAL7P1.142_oldname  9.389247 12.807814 10.340803 11.85626 13.661078 14.52676
5  MAL8P1.310_oldname        NA        NA        NA       NA        NA       NA
6   MAL8P1.90_oldname        NA        NA        NA       NA        NA       NA
      m_10G    s_10G    l_3D7B   r_3D7B    m_3D7B    s_3D7B   MaxLeft   MinLeft
1 49.805504 37.95570 25.484634 62.83441 50.462696 37.856349 30.592496 25.372470
2  3.676218 13.03616  1.789873 10.51234  3.691753  8.610459  6.117132  1.789873
3        NA       NA 19.333324       NA        NA        NA 19.333324 14.071128
4 13.401610 14.78623  7.099032 13.34518 12.041177  8.403034 13.661078  7.099032
5        NA       NA        NA       NA        NA        NA        NA        NA
6        NA       NA        NA       NA        NA        NA        NA        NA
  MaxRight  MinRight    MaxMid    MinMid MaxSides  MinSides  DifLeft DifRight
1 62.83441 61.080128 50.462696 49.676556 41.99607 37.856349 5.220025 1.754283
2 10.59524  8.488971  3.691753  1.289779 13.03616  8.610459 4.327259 2.106274
3       NA        NA        NA        NA       NA        NA 5.262196       NA
4 14.52676 12.807814 13.401610 10.340803 14.78623  8.403034 6.562046 1.718950
5       NA        NA        NA        NA       NA        NA       NA       NA
6       NA        NA        NA        NA       NA        NA       NA       NA
     DifMid DifSides Interval   MaxDif    areaFC  area_12B area_10G area_3D7B
1 0.7861401 4.139719     Left 5.220025 0.3881060 30.592496 25.37247 25.484634
2 2.4019733 4.425700    Sides 4.425700 0.3290483 12.622460 13.03616  8.610459
3        NA       NA     Left 5.262196 0.3912413 18.322430 14.07113 19.333324
4 3.0608067 6.383199     Left 6.562046 0.4878845  9.389247 13.66108  7.099032
5        NA       NA  No Data       NA        NA        NA       NA        NA
6        NA       NA  No Data       NA        NA        NA       NA        NA
   MaxArea   MinArea
1 30.59250 25.372470
2 13.03616  8.610459
3 19.33332 14.071128
4 13.66108  7.099032
5       NA        NA
6       NA        NA
```

1.3 Load RNA-Seq Data

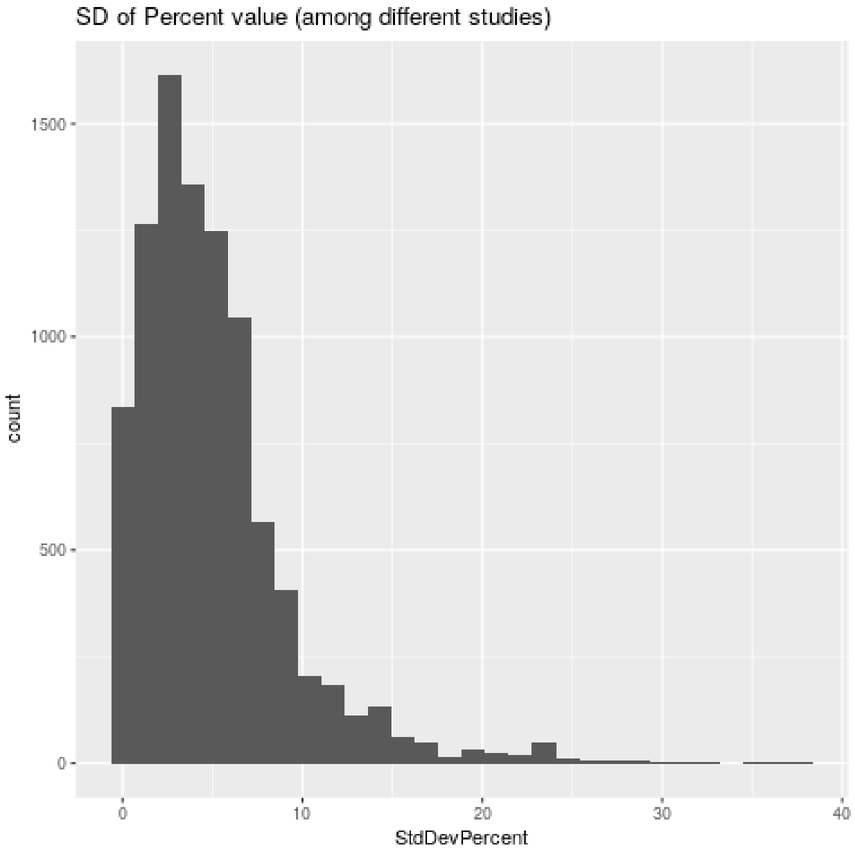
We will use publicly available data from PlasmoDB to create a reference expresion percentile for each gene. All data-sets are from RNA-Seq studies in the 3D7 strain. We are using 4 different data-sets:

- Otto et.al.
- Hoeijmakers et.al.
- Toenhake et.al.
- Bartfai et.al.

RNA-Seq DataFrame

```
        Gene_id MaxPercOtto MaxPercHoej MaxPercToen MaxPercBart MeanPercent
1 PF3D7_0100100        57.2        54.3        33.9        31.7      44.275
2 PF3D7_0100200        29.4        50.5        26.6        36.0      35.625
3 PF3D7_0100300        34.2         8.7         7.7         7.4      14.500
4 PF3D7_0100400        50.3        18.3        11.3        37.4      29.325
5 PF3D7_0100500        49.7        11.4        14.0        32.5      26.900
6 PF3D7_0100600        18.5         7.8         2.3        12.1      10.175
  StdDevPercent
1     11.546942
2      9.241313
3     11.383980
4     15.424068
5     15.474657
6      5.930167
```

We plot the standard deviation of the percentile values among different studies and we can see that for the vast majority of genes it doesn't go above 10.



1.4 Create table for classification

Joining and summarizing all the prevoius data we create a a table that will let us classify the genes according to their expression state.

To classify genes, we add a colum for each strain were we classify genes according to their expression relative to other strains. To create this column we have taken the maximum and minimum area value for each gene and divided this interval in 3 equal regions. Each strain then gets a value of man/mid/max according to which region it falls.

`gene-min---|--mid---|---gene-max`

Final DataFrame

```
              Gene_id Variant Percent_12B Percent_10G Percent_3D7B
1          mal_mito_3   FALSE  96.0335622   98.474447   97.8832952
```

```
2 MAL13P1.415_oldname   FALSE  21.3196034   20.861937   18.4591915
3  MAL13P1.65_oldname   FALSE   6.2166285    5.053394    4.5194508
4  MAL7P1.142_oldname   FALSE  75.4767353   72.444699   71.7200610
5  MAL8P1.310_oldname   FALSE   0.8581236    1.115561    0.5911518
6   MAL8P1.90_oldname   FALSE   4.1952708    2.002288    2.2501907
  MaxRedPercentDif Interval    areaFC  area_12B area_10G area_3D7B  MaxArea
1        2.4408848     Left 0.3881060 30.592496 25.37247 25.484634 30.59250
2        2.8604119    Sides 0.3290483 12.622460 13.03616  8.610459 13.03616
3        1.6971777     Left 0.3912413 18.322430 14.07113 19.333324 19.33332
4        3.7566743     Left 0.4878845  9.389247 13.66108  7.099032 13.66108
5        0.5244088  No Data        NA        NA       NA        NA       NA
6        2.1929825  No Data        NA        NA       NA        NA       NA
    MinArea MeanPercent rel_12B rel_10G rel_3D7B
1 25.372470      95.975     max     min      min
2  8.610459          NA     max     max      min
3 14.071128          NA     max     min      max
4  7.099032          NA     mid     max      min
5        NA          NA      NA      NA       NA
6        NA          NA      NA      NA       NA
```

1.5 Create Lists according to thresholds

Now that we have all the data loaded in, we can star to set labels for each gene.

We have set the following thresholds:

- (rna_pcnt) RNA-Seq mean percentile: 25%
- (red_pcnt) Red Signal Percentile (by sample): 25%
- (red_rescue) Red Signal Percentile (by sample) for "rescuing": 40%
- (red_dif) Red Signal percentile diference: 0 (we are currently not using it but it is set, just in case)
- (area_fc) Area log2 Fold-Change: 1

In addition to these thresholds we will use 2 more columns to set the categories:

- Variant: a column stating if gene is variant/non-variant

- Relative Expression (by strain): a colum were each gene is set to min/mid/max according to it's expression level relative to the other strains.

We will have the following categories with the following logic:

- Active :
    - Regular
        1. Non-Variant
        2. > rna_pcnt
    - Variant Active
        - Case 1 (no area_fc):
            1. Variant
            2. < area_fc
            3. > rna_pcnt
        - Case 2 (no area_fc, rescued):
            1. Variant
            2. < area_fc
            3. < rna_pcnt
            4. > red_rescue
        - Case 3 (area_fc, max):
            1. Variant
            2. > area_fc
            3. > red_dif
            4. > red_pcnt
            5. rel_exprs = max
        - Case 4 (area_fc, mid):
            1. Variant
            2. > area_fc
            3. > red_dif
            4. > red_pcnt
            5. rel_exprs = mid
    - Variant Repressed:
        - Case 1 (no area_fc, no rescue):
            1. Variant

        2. < area_fc
        3. < rna_pcnt
        4. < red_rescue
    - ∗ Case 2 (area_fc, rel_exprs = mid)
        1. Variant
        2. > area_fc
        3. > red_dif
        4. > red_pcnt
        5. rel_exprs = min
    - ∗ Case 3 (area_fc, low red_pcnt)
        1. Variant
        2. > area_fc
        3. > red_dif
        4. < red_pcnt

- Inactive:
    1. Non-Variant
    2. < rna_pcnt

- Not Settable:
    1. area_fc OR rna_pcnt are not set (NA).

Using these classification logic we get the following table:
Gene-State DataFrame

```
              Gene_id Variant Percent_12B Percent_10G Percent_3D7B
1          mal_mito_3   FALSE  96.0335622   98.474447   97.8832952
2 MAL13P1.415_oldname   FALSE  21.3196034   20.861937   18.4591915
3  MAL13P1.65_oldname   FALSE   6.2166285    5.053394    4.5194508
4  MAL7P1.142_oldname   FALSE  75.4767353   72.444699   71.7200610
5  MAL8P1.310_oldname   FALSE   0.8581236    1.115561    0.5911518
6   MAL8P1.90_oldname   FALSE   4.1952708    2.002288    2.2501907
  MaxRedPercentDif Interval    areaFC  area_12B area_10G area_3D7B  MaxArea
1        2.4408848     Left 0.3881060 30.592496 25.37247 25.484634 30.59250
2        2.8604119    Sides 0.3290483 12.622460 13.03616  8.610459 13.03616
3        1.6971777     Left 0.3912413 18.322430 14.07113 19.333324 19.33332
```

```
4        3.7566743     Left 0.4878845  9.389247 13.66108  7.099032 13.66108
5        0.5244088  No Data        NA        NA       NA        NA       NA
6        2.1929825  No Data        NA        NA       NA        NA       NA
    MinArea MeanPercent rel_12B rel_10G rel_3D7B    state_12B    state_10G
1 25.372470      95.975     max     min      min       Active       Active
2  8.610459          NA     max     max      min Not_settable Not_settable
3 14.071128          NA     max     min      max Not_settable Not_settable
4  7.099032          NA     mid     max      min Not_settable Not_settable
5        NA          NA      NA      NA       NA Not_settable Not_settable
6        NA          NA      NA      NA       NA Not_settable Not_settable
    state_3D7B
1       Active
2 Not_settable
3 Not_settable
4 Not_settable
5 Not_settable
6 Not_settable
```

1.6 Some results

This is a table with the number of genes in each state for each strain.

States Table

Strain	Active	Inactive	Not_settable	Var_Active	Var_Repressed	Var_Semiactive
12B	8302	306	246	167	265	1
10G	8302	306	246	164	269	0
3D7B	8302	306	246	249	184	0

And this are the Clag genes

States Table

```
        Gene_id Variant Percent_12B Percent_10G Percent_3D7B MaxRedPercentDif
1 PF3D7_0302200    TRUE    78.69947    99.58047     42.37223         57.20824
2 PF3D7_0302500    TRUE    98.81770    84.40122     98.98932         14.58810
  Interval   areaFC  area_12B area_10G area_3D7B   MaxArea  MinArea MeanPercent
1    Right 4.823089  37.32948 88.19577  23.32522  88.19577 23.32522       85.35
2    Right 3.452270 100.12065 53.68762  99.58767 100.12065 53.68762       94.90
  rel_12B rel_10G rel_3D7B     state_12B     state_10G    state_3D7B
1     min     max      min Var_Repressed    Var_Active Var_Repressed
2     max     min      max    Var_Active Var_Repressed    Var_Active
```

2 Code

2.1 Load Packages and functions

```
#### Imports ####

library(readxl)
library(tidyverse)

#### Max Dif function ####

max_dif <- function(vect){
  mx <- max(vect, na.rm = T)
  mn <- min(vect, na.rm = T)
  if (is.infinite(mx) | is.infinite(mn)) {
    md <- NA
  } else {
    md <- mx - mn
  }
  return(md)
}
```

2.2 Microarray Data: Red Signal

```
#### Red Signal DF ####

## Read translation table
map <- read.csv('./Data/oldnames_table.csv')
excl <- "./Data/3D7_Variantome_AllData_withGam.xls"

## Import Red Signal table
red <- read_excel(excl, sheet = 4)

colnames(red)[1] <- "Old_id"

red_df <- red %>%
  select(Old_id,
         Red_12B = `Aver.2Higher1.2B.`,
         Red_10G = `Aver.2Higher10G.`,
         Red_3D7B = `Aver.2Higher3D7-B.`) %>%
  left_join(map, by='Old_id') %>%
  select(-Old_id) %>%
  group_by(Gene_id) %>% summarize_all(list(mean))

## Transform into percentiles

red_df <- red_df %>%
  mutate(Percent_12B = (rank(Red_12B)/length(Red_12B))*100) %>%
  mutate(Percent_10G = (rank(Red_10G)/length(Red_10G))*100) %>%
  mutate(Percent_3D7B = (rank(Red_3D7B)/length(Red_3D7B))*100)

## Add max percentile dif

red_df <- red_df %>%
  mutate(MaxRedPercentDif= apply(select(., contains('Percent_')), 1, max_dif))

print(red_df, width = 200)
```

2.3 Microarray Data: Areas

```
#### Areas DF ####

# Import Areas table

area <- read_excel(excl, sheet = 2)

colnames(area)[1] <- "Old_id"

area_df <- area %>%
  select(Old_id,
         l_12B = `left.1.2b`,
         r_12B = `right.1.2b`,
         m_12B = `mid.1.2b`,
         s_12B = `sides.1.2b`,
         l_10G = `left.10g`,
         r_10G = `right.10g`,
         m_10G = `mid.10g`,
         s_10G = `sides.10g`,
         l_3D7B = `left.3d7b`,
         r_3D7B = `right.3d7b`,
         m_3D7B = `mid.3d7b`,
         s_3D7B = `sides.3d7b`) %>%

  mutate_at(vars(-Old_id), as.numeric) %>%


  left_join(map, by='Old_id') %>%
  select(-Old_id) %>%
  group_by(Gene_id) %>% summarize_all(list(mean))


print(area_df, width = 200)

area_df <- area_df %>%
  mutate(MaxLeft = apply(select(., contains('l_')), 1, max)) %>%
  mutate(MinLeft = apply(select(., contains('l_')), 1, min)) %>%

  mutate(MaxRight = apply(select(., contains('r_')), 1, max)) %>%
  mutate(MinRight = apply(select(., contains('r_')), 1, min)) %>%

  mutate(MaxMid = apply(select(., contains('m_')), 1, max)) %>%
  mutate(MinMid = apply(select(., contains('m_')), 1, min)) %>%

  mutate(MaxSides = apply(select(., contains('s_')), 1, max)) %>%
  mutate(MinSides = apply(select(., contains('s_')), 1, min)) %>%

  mutate(DifLeft = MaxLeft - MinLeft) %>%
  mutate(DifRight = MaxRight - MinRight) %>%
  mutate(DifMid = MaxMid - MinMid) %>%
  mutate(DifSides = MaxSides - MinSides)

print(area_df, width = 200)

## Add max interval and difference

maxinterval <- area_df %>%
  select(Gene_id, contains('Dif')) %>%
  pivot_longer(-Gene_id, names_to = 'Interval', values_to = 'MaxDif') %>%
  group_by(Gene_id) %>%
  filter(rank(-MaxDif, ties.method = "first") == 1) %>%
  mutate(Interval = ifelse(is.na(MaxDif), 'No Data', Interval)) %>%
  mutate(Interval = case_when(Interval == 'DifLeft' ~ 'Left',
                              Interval == 'DifRight' ~ 'Right',
                              Interval == 'DifMid' ~ 'Mid',
                              Interval == 'DifSides' ~ 'Sides',
                              Interval == 'No Data' ~ 'No Data')) %>%
  mutate(areaFC = MaxDif/13.45)

maxinterval

area_df <- area_df %>%
  left_join(maxinterval, by = 'Gene_id')

print(area_df, width = 400)

## Select appropiate area for each gene and add max and min areas

area_df <- area_df %>%
  mutate(area_12B = case_when(
           Interval == 'Left' ~ l_12B,
           Interval == 'Right' ~ r_12B,
           Interval == 'Mid' ~ m_12B,
           Interval == 'Sides' ~ s_12B,
           Interval == 'No Data' ~ NA_real_)) %>%
  mutate(area_10G = case_when(
           Interval == 'Left' ~ l_10G,
           Interval == 'Right' ~ r_10G,
           Interval == 'Mid' ~ m_10G,
           Interval == 'Sides' ~ s_10G,
           Interval == 'No Data' ~ NA_real_)) %>%
  mutate(area_3D7B = case_when(
           Interval == 'Left' ~ l_3D7B,
           Interval == 'Right' ~ r_3D7B,
           Interval == 'Mid' ~ m_3D7B,
           Interval == 'Sides' ~ s_3D7B,
           Interval == 'No Data' ~ NA_real_)) %>%
  mutate(MaxArea = apply(select(., contains('area_')), 1, max)) %>%
  mutate(MinArea = apply(select(., contains('area_')), 1, min))


print(area_df, width = 400)
```

2.4 Load RNA-Seq Data

```
#### Load Data-Sets ####

otto <- read_delim("./Data/RNA_Seq_Percentiles/PlasmoDB_Otto.csv", delim=";") %>%
  select(Gene_id = `Gene ID`, MaxPercOtto = `Max %ile (Within Chosen Samples)`)
hoej <- read_delim("./Data/RNA_Seq_Percentiles/PlasmoDB_Hoejimakers.csv", delim=";") %>
  select(Gene_id = `Gene ID`, MaxPercHoej = `Max %ile (Within Chosen Samples)`)
toen <- read_delim("./Data/RNA_Seq_Percentiles/PlasmoDB_Toenke.csv", delim=";") %>%
  select(Gene_id = `Gene ID`, MaxPercToen = `Max %ile (Within Chosen Samples)`)
bart <- read_delim("./Data/RNA_Seq_Percentiles/PlasmoDB_Bartfai.csv", delim=";") %>%
  select(Gene_id = `Gene ID`, MaxPercBart = `Max %ile (Within Chosen Samples)`)

## Join DF
rna_df <- full_join(otto, hoej) %>%
  full_join(hoej) %>%
  full_join(toen) %>%
  full_join(bart)

## Add mean and sd
rna_df <- rna_df %>%
  mutate(MeanPercent = apply(select(., -Gene_id), 1, mean)) %>%
  mutate(StdDevPercent = apply(select(., -Gene_id), 1, sd))


print(rna_df, width=200)
```

2.5 Create Join DF

```
red_df
print(area_df, width = 200)
rna_df

all_df <- select(red_df, Gene_id, contains('Percent')) %>%
  full_join(select(area_df, Gene_id, Interval, contains('area')), by = 'Gene_id') %>%
  full_join(select(rna_df, Gene_id, MeanPercent), by = 'Gene_id')

## Add Vartiant Genes information

cvg <- read_excel("./Data/CVG_list_jan2020_final.xlsx", sheet = "Final")
```

```
final_df <- cvg %>%
  select("Gene_id" = `Gene ID`, "Variant" = `Final Customized`) %>%
  right_join(all_df, by = 'Gene_id') %>%
  mutate(Variant = recode(Variant, YES = TRUE, NO = FALSE, .missing = FALSE))

print(final_df, width = 200)

## Here we create a dplyr function.
##To be able to use variables (for colnames) we needto use the special quote functions
## Colnames to use inside functions must be "enquoted" before usage and preceded by !!
## Colnames to assign must be "enquoted" first, preceded by !! and assigned by :=


## First create a col where we set categories for each gene according relative express
## For each gene: gene-min----|---mid----|----gene-max

relexprs <- function(vect){
  if (any(is.na(vect))){
    return(NA)
  } else {
    labs = c('min', 'mid', 'max')
    lab <- cut(vect, 3, labels = labs)[1]
    return(as.character(lab))
  }
}

set_relexprs <- function(df, outcol, areacol){
  outcol <- enquo(outcol)
  areacol <- enquo(areacol)
  df %>%
    mutate(!! outcol := apply(select(., !! areacol, MaxArea, MinArea), 1, relexprs))
}

final_df <- final_df %>%
  set_relexprs(rel_12B, area_12B) %>%
  set_relexprs(rel_10G, area_10G) %>%
  set_relexprs(rel_3D7B, area_3D7B)

print(final_df, width = 200)
```

2.6 Create Lists according to thresholds

```
print(final_df, width = 200)

th_rnapcnt <- 25
th_redpcnt <- 25
th_redrescue <- 40
th_red_difpcnt <- 0
th_areaFC <- 1

## Here we create a dplyr function.
##To be able to use variables (for colnames) we needto use the special quote functions
## Colnames to use inside functions must be "enquoted" before usage and preceded by !!
## Colnames to assign must be "enquoted" first, preceded by !! and assigned by :=

set_state <- function(df, statecol, redcol, relcol){

  statecol <- enquo(statecol)
  redcol <- enquo(redcol)
  relcol <- enquo(relcol)

  df <- df %>%
    mutate(!! statecol := case_when(
                ## Actiu
                !Variant & MeanPercent >= th_rnapcnt ~ 'Active',
                ## Inactiu
                !Variant & MeanPercent < th_rnapcnt ~ 'Inactive',

                ## Var actiu
                Variant &
                areaFC < th_areaFC &
                MeanPercent >= th_rnapcnt ~ 'Var_Active', # noFC

                Variant &
                areaFC < th_areaFC &
                MeanPercent < th_rnapcnt &
                !! redcol >= th_redrescue ~ 'Var_Active', # noFC, rescued

                Variant &
                areaFC >= th_areaFC &
```

```r
                MaxRedPercentDif >= th_red_difpcnt &
                !! redcol >= th_redpcnt &
                !! relcol == 'max' ~ 'Var_Active', # Variant, FC, redpcnt, max

                Variant &
                areaFC >= th_areaFC &
                MaxRedPercentDif >= th_red_difpcnt &
                !! redcol >= th_redpcnt &
                !! relcol == 'mid' ~ 'Var_Semiactive', # Variant, FC, redpcnt, mid

                ## Var repressed
                Variant &
                areaFC < th_areaFC &
                MeanPercent < th_rnapcnt &
                !! redcol < th_redrescue ~ 'Var_Repressed', # noFC, noRescued

                Variant &
                areaFC >= th_areaFC &
                MaxRedPercentDif >= th_red_difpcnt &
                !! redcol >= th_redpcnt &
                !! relcol == 'min' ~ 'Var_Repressed', # Variant, FC, redpcnt, min

                Variant &
                areaFC >= th_areaFC &
                MaxRedPercentDif >= th_red_difpcnt &
                !! redcol < th_redpcnt ~ 'Var_Repressed', # Variant, FC, NOredpcnt

                ## Not settable
                is.na(areaFC) | is.na(MeanPercent) ~ 'Not_settable',

                TRUE ~ 'Wrong!'))

  ## The 'TRUE ~ ...' handles rows that do not match any of previous patterns.
  ## Here we use it to make sure all rows are set (no "Wrong!" appearing)

  return(df)
}

## We now set each gene to it's state
```

```
state_df <- final_df %>%
  set_state(state_12B, Percent_12B, rel_12B) %>%
  set_state(state_10G, Percent_10G, rel_10G) %>%
  set_state(state_3D7B, Percent_3D7B, rel_3D7B)

## We check no rows are set to "Wrong!"
state_df %>%
  filter(state_12B == 'Wrong!' | state_10G == 'Wrong!' | state_3D7B == 'Wrong!') %>%
  print(width = 200)

## Save results
write.csv(state_df, './Results_Tables/state_df_rna25_red25_reddif0_area1.csv')

## Create a table with number of each state per strain
state_table <-  bind_rows(table(state_df$state_12B),
                          table(state_df$state_10G),
                          table(state_df$state_3D7B)) %>%
  replace_na(list(Var_Semiactive = 0)) %>%
  mutate(Strain = c('12B', '10G', '3D7B')) %>%
  select(Strain, everything())

## Create a table with differences between 12B and 10G
dif12B_10G <- state_df %>%
  filter(state_12B != state_10G) %>%
  select(contains('12B'), contains('10G'))

write.csv(dif12B_10G, './Results_Tables/gens_dif12B_10G.csv')

## Check Clags
clags <- state_df %>%
  filter(Gene_id == 'PF3D7_0302500' | Gene_id == 'PF3D7_0302200')

 write.csv(clags, './Results_Tables/clag_genes.csv')
```