

Gene Classification (adjusted from MG)

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Functions

```
classify_expressed <- function(row, names, cutoff){  
  #Checks if gene is expressed greater than [cutoff] in at least 1 of the tissues included in names.  
  #Returns boolean  
  
  row <- row[which(names(row) %in% names)]  
  for(i in seq(1, length(names))){  
    if (as.numeric(row[i]) > cutoff){  
      return(TRUE)  
    }  
  }  
  return(FALSE)  
}  
  
classify_trace <- function(row, names, cutoff){  
  #Checks if gene is expressed less than [cutoff] in ALL of the tissues included in names.  
  #Returns boolean  
  
  num_trace <- 0  
  
  row <- row[which(names(row) %in% names)]  
  for(i in seq(1, length(names))){  
    if (as.numeric(row[i]) < cutoff){  
      num_trace <- num_trace + 1  
    }  
  }  
  if (num_trace == length(names)){  
    return(TRUE)  
  }else{return(FALSE)}  
}  
  
#calculate tau measure of tissue specificity  
#https://github.com/severinEvo/gene_expression  
tau<-function(x){  
  if(any(is.na(x))) stop('NA\'s need to be 0.')  
  if(any(x<0)) stop('Negative input values not permitted.')  
  t<-sum(1-x/max(x))/(length(x)-1)  
}
```

Load data

melanogaster (ore)

```
mel <- read.table("~/Desktop/data/aim_3/dmel.transTPM.txt", header = T)

mel_FB <- read.table("~/Desktop/data/aim_3/GSE99574_HiSAT2_dmel.transcript_level_TPM.FB.txt", header = T)

mel_ore_f_full <- mel %>% select(1, 3, starts_with("oreR_f"))

mel_ore_f <- mel_ore_f_full %>%
  mutate(mean_head = rowMeans(select(mel_ore_f_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(mel_ore_f_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(mel_ore_f_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(mel_ore_f_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(mel_ore_f_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(mel_ore_f_full, contains("_re_"))),
         mean_genitalia = rowMeans(select(mel_ore_f_full, contains("_ge_")))) %>%
  select(1, 2, starts_with("mean"))

mel_ore_m_full <- mel %>% select(1, 3, starts_with("oreR_m"))

mel_ore_m <- mel_ore_m_full %>%
  mutate(mean_head = rowMeans(select(mel_ore_m_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(mel_ore_m_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(mel_ore_m_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(mel_ore_m_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(mel_ore_m_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(mel_ore_m_full, contains("_re_"))),
         mean_genitalia = rowMeans(select(mel_ore_m_full, contains("_ge_")))) %>%
  select(1, 2, starts_with("mean"))
```

melanogaster (w1118)

```
mel <- read.table("~/Desktop/data/aim_3/dmel.transTPM.txt", header = T)

mel_w1118_f_full <- mel %>% select(1, starts_with("w1118_f"))

mel_w1118_f <- mel_w1118_f_full %>%
  mutate(mean_head = rowMeans(select(mel_w1118_f_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(mel_w1118_f_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(mel_w1118_f_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(mel_w1118_f_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(mel_w1118_f_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(mel_w1118_f_full, contains("_re_"))),
         mean_genitalia = rowMeans(select(mel_w1118_f_full, contains("_ge_")))) %>%
  select(1, starts_with("mean"))

mel_w1118_m_full <- mel %>% select(1, starts_with("w1118_m"))
```

```

mel_w1118_m <- mel_w1118_m_full %>%
  mutate(mean_head = rowMeans(select(mel_w1118_m_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(mel_w1118_m_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(mel_w1118_m_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(mel_w1118_m_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(mel_w1118_m_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(mel_w1118_m_full, contains("_re_"))),
         mean_genitalia = rowMeans(select(mel_w1118_m_full, contains("_ge_")))) %>%
  select(1, starts_with("mean"))

```

ananassae

```

ana <- read.table("~/Desktop/data/aim_3/dana.transTPM.txt", header = T, fill = T)
ana <- na.omit(ana)

ana_f_full <- ana %>% select(1, starts_with("dana_f"))

ana_f <- ana_f_full %>%
  mutate(mean_head = rowMeans(select(ana_f_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(ana_f_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(ana_f_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(ana_f_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(ana_f_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(ana_f_full, contains("_re_")))) %>%
  select(1, starts_with("mean"))

ana_m_full <- ana %>% select(1, starts_with("dana_m"))

ana_m <- ana_m_full %>%
  mutate(mean_head = rowMeans(select(ana_m_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(ana_m_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(ana_m_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(ana_m_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(ana_m_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(ana_m_full, contains("_re_")))) %>%
  select(1, starts_with("mean"))

```

mojavensis

```

moj <- read.table("~/Desktop/data/aim_3/dmoj.transTPM.txt", header = T, fill = T)
moj <- na.omit(moj)

moj_f_full <- moj %>% select(1, starts_with("dmoj_f"))

moj_f <- moj_f_full %>%
  mutate(mean_head = rowMeans(select(moj_f_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(moj_f_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(moj_f_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(moj_f_full, contains("_dg_"))),

```

```

    mean_gonad = rowMeans(select(moj_f_full, contains("_go_"))),
    mean_reproductive = rowMeans(select(moj_f_full, contains("_re_")))) %>%
select(1, starts_with("mean"))

moj_m_full <- moj %>% select(1, starts_with("dmoj_m"))

moj_m <- moj_m_full %>%
  mutate(mean_head = rowMeans(select(moj_m_full, contains("_hd_"))),
    mean_thorax = rowMeans(select(moj_m_full, contains("_tx_"))),
    mean_abdomen = rowMeans(select(moj_m_full, contains("_ac_"))),
    mean_digestive = rowMeans(select(moj_m_full, contains("_dg_"))),
    mean_gonad = rowMeans(select(moj_m_full, contains("_go_"))),
    mean_reproductive = rowMeans(select(moj_m_full, contains("_re_")))) %>%
select(1, starts_with("mean"))

```

persimilis

```

per <- read.table("~/Desktop/data/aim_3/dper.transTPM.txt", header = T, fill = T)
per <- na.omit(per)

per_f_full <- per %>% select(1, starts_with("dper_f"))

per_f <- per_f_full %>%
  mutate(mean_head = rowMeans(select(per_f_full, contains("_hd_"))),
    mean_thorax = rowMeans(select(per_f_full, contains("_tx_"))),
    mean_abdomen = rowMeans(select(per_f_full, contains("_ac_"))),
    mean_digestive = rowMeans(select(per_f_full, contains("_dg_"))),
    mean_gonad = rowMeans(select(per_f_full, contains("_go_"))),
    mean_reproductive = rowMeans(select(per_f_full, contains("_re_")))) %>%
select(1, starts_with("mean"))

per_m_full <- per %>% select(1, starts_with("dper_m"))

per_m <- per_m_full %>%
  mutate(mean_head = rowMeans(select(per_m_full, contains("_hd_"))),
    mean_thorax = rowMeans(select(per_m_full, contains("_tx_"))),
    mean_abdomen = rowMeans(select(per_m_full, contains("_ac_"))),
    mean_digestive = rowMeans(select(per_m_full, contains("_dg_"))),
    mean_gonad = rowMeans(select(per_m_full, contains("_go_"))),
    mean_reproductive = rowMeans(select(per_m_full, contains("_re_")))) %>%
select(1, starts_with("mean"))

```

pseudoobscura

```

pse <- read.table("~/Desktop/data/aim_3/dpse.transTPM.txt", header = T, fill = T)
pse <- na.omit(pse)

pse_f_full <- pse %>% select(1, starts_with("dpse_f"))

```

```

pse_f <- pse_f_full %>%
  mutate(mean_head = rowMeans(select(pse_f_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(pse_f_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(pse_f_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(pse_f_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(pse_f_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(pse_f_full, contains("_re_")))) %>%
  select(1, starts_with("mean"))

pse_m_full <- pse %>% select(1, starts_with("dpse_m"))

pse_m <- pse_m_full %>%
  mutate(mean_head = rowMeans(select(pse_m_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(pse_m_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(pse_m_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(pse_m_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(pse_m_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(pse_m_full, contains("_re_")))) %>%
  select(1, starts_with("mean"))

```

virilis

```

vir <- read.table("~/Desktop/data/aim_3/dvir.transTPM.txt", header = T, fill = T)
vir <- na.omit(vir)

vir_f_full <- vir %>% select(1, starts_with("dvir_f"))

vir_f <- vir_f_full %>%
  mutate(mean_head = rowMeans(select(vir_f_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(vir_f_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(vir_f_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(vir_f_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(vir_f_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(vir_f_full, contains("_re_")))) %>%
  select(1, starts_with("mean"))

vir_m_full <- vir %>% select(1, starts_with("dvir_m"))

vir_m <- vir_m_full %>%
  mutate(mean_head = rowMeans(select(vir_m_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(vir_m_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(vir_m_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(vir_m_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(vir_m_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(vir_m_full, contains("_re_")))) %>%
  select(1, starts_with("mean"))

```

willistoni

```
wil <- read.table("~/Desktop/data/aim_3/dwil.transTPM.txt", header = T, fill = T)
wil <- na.omit(wil)

wil_f_full <- wil %>% select(1, starts_with("dwil_f"))

wil_f <- wil_f_full %>%
  mutate(mean_head = rowMeans(select(wil_f_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(wil_f_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(wil_f_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(wil_f_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(wil_f_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(wil_f_full, contains("_re_")))) %>%
  select(1, starts_with("mean"))

wil_m_full <- wil %>% select(1, starts_with("dwil_m"))

wil_m <- wil_m_full %>%
  mutate(mean_head = rowMeans(select(wil_m_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(wil_m_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(wil_m_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(wil_m_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(wil_m_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(wil_m_full, contains("_re_")))) %>%
  select(1, starts_with("mean"))
```

yakuba

```
yak <- read.table("~/Desktop/data/aim_3/dyak.transTPM.txt", header = T, fill = T)
yak <- na.omit(yak)

yak_f_full <- yak %>% select(1, starts_with("dyak_f"))

yak_f <- yak_f_full %>%
  mutate(mean_head = rowMeans(select(yak_f_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(yak_f_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(yak_f_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(yak_f_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(yak_f_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(yak_f_full, contains("_re_")))) %>%
  select(1, starts_with("mean"))

yak_m_full <- yak %>% select(1, starts_with("dyak_m"))

yak_m <- yak_m_full %>%
  mutate(mean_head = rowMeans(select(yak_m_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(yak_m_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(yak_m_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(yak_m_full, contains("_dg_"))),
```

```

mean_gonad = rowMeans(select(yak_m_full, contains("_go_"))),
mean_reproductive = rowMeans(select(yak_m_full, contains("_re_")))) %>%
select(1, starts_with("mean"))

```

grimshawi

```

haw <- read.table("~/Desktop/data/aim_3/haw.transTPM.txt", header = T, fill = T)
haw <- na.omit(haw)

gri_f_full <- haw %>% select(1, starts_with("dgriG1_f"))

gri_f <- gri_f_full %>%
  mutate(mean_head = rowMeans(select(gri_f_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(gri_f_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(gri_f_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(gri_f_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(gri_f_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(gri_f_full, contains("_re_"))),
         mean_genitalia = rowMeans(select(gri_f_full, contains("_ge_")))) %>%
  select(1, starts_with("mean"))

gri_m_full <- haw %>% select(1, starts_with("dgriG1_m"))

gri_m <- gri_m_full %>%
  mutate(mean_head = rowMeans(select(gri_m_full, contains("_hd_"))),
         mean_thorax = rowMeans(select(gri_m_full, contains("_tx_"))),
         mean_abdomen = rowMeans(select(gri_m_full, contains("_ac_"))),
         mean_digestive = rowMeans(select(gri_m_full, contains("_dg_"))),
         mean_gonad = rowMeans(select(gri_m_full, contains("_go_"))),
         mean_reproductive = rowMeans(select(gri_m_full, contains("_re_"))),
         mean_genitalia = rowMeans(select(gri_m_full, contains("_ge_")))) %>%
  select(1, starts_with("mean"))

```

Calculate Tau

mel (ore) female

```

mel_ore_f_NA <- replace(mel_ore_f, mel_ore_f < 1, NA)
mel_ore_f_NA_log <- log2(mel_ore_f_NA[,3:9])
mel_ore_f_log <- replace(mel_ore_f_NA_log, is.na(mel_ore_f_NA_log), 0)

mel_ore_f_log$tau <- apply(mel_ore_f_log, 1, tau)

mel_ore_f_tau <- cbind(mel_ore_f[,1:2], mel_ore_f_log)

#filter rows where reproductive tissues have highest gene expression
mel_ore_f_RP <- mel_ore_f_tau %>%
  filter(mean_gonad > mean_head & mean_gonad > mean_thorax & mean_gonad > mean_abdomen & mean_gonad > m

```

```
mean_reproductive > mean_head & mean_reproductive > mean_thorax & mean_reproductive > mean_abdomen &
mean_genitalia > mean_head & mean_genitalia > mean_thorax & mean_genitalia > mean_abdomen &

#filter tissue-specific, reproductive genes
mel_ore_f_RPspec <- mel_ore_f_RP %>% filter(tau > 0.8)
```

mel (ore) male

```
mel_ore_m_NA <- replace(mel_ore_m, mel_ore_m < 1, NA)
mel_ore_m_NA_log <- log2(mel_ore_m_NA[,3:9])
mel_ore_m_log <- replace(mel_ore_m_NA_log, is.na(mel_ore_m_NA_log), 0)

mel_ore_m_log$tau <- apply(mel_ore_m_log, 1, tau)

mel_ore_m_tau <- cbind(mel_ore_m[,1:2], mel_ore_m_log)

#filter rows where reproductive tissues have highest gene expression
mel_ore_m_RP <- mel_ore_m_tau %>%
  filter(mean_gonad > mean_head & mean_gonad > mean_thorax & mean_gonad > mean_abdomen & mean_gonad > mean_reproductive &
    mean_reproductive > mean_head & mean_reproductive > mean_thorax & mean_reproductive > mean_abdomen &
    mean_genitalia > mean_head & mean_genitalia > mean_thorax & mean_genitalia > mean_abdomen & mean_genitalia > mean_reproductive)

#filter tissue-specific, reproductive genes
mel_ore_m_RPspec <- mel_ore_m_RP %>% filter(tau > 0.8)
```

RP, SM, & GR

Classify

Overview of what I'm doing to classify genes:

For each species... 1. Identify SomExpressed genes (> 2 TPM in at least one somatic tissue; TRUE/FALSE) 2. Identify RepExpressed genes (> 2 TPM in at least one reproductive tissue; TRUE/FALSE) 3. Identify somatic trace expression genes (< 0.5 TPM in all som tissues; TRUE/FALSE) 4. Identify reproductive trace expression genes (< 0.5 TPM in all rep tissues; TRUE/FALSE)

5. Classify GR genes as those which are SomExpressed AND RepExpressed AND not expressed at trace levels in either (TRUE/FALSE)
6. Classify SM genes as those which are SomExpressed AND trace expressed in reproductive tissues AND not in the GR list (TRUE/FALSE)
7. Classify RP genes as those which are RepExpressed AND trace expressed in somatic tissues AND not in the GR list (TRUE/FALSE)

MELANOCASTER

```
upperCutoff <- 2
lowerCutoff <- 0.5
```


mel (ore) female

```
mel_ore_f <- mel_ore_f %>% mutate(SomExpressed = apply(mel_ore_f, 1, classify_expressed, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
  RepExpressed = apply(mel_ore_f, 1, classify_expressed, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
  SomTrace = apply(mel_ore_f, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive")),
  RepTrace = apply(mel_ore_f, 1, classify_trace, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
  mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
    SM = SomExpressed & RepTrace & !GR,
    RP = RepExpressed & SomTrace & !GR)

mel_ore_f_RP <- mel_ore_f %>% filter(RP == TRUE)
mel_ore_f_SM <- mel_ore_f %>% filter(SM == TRUE)
mel_ore_f_GR <- mel_ore_f %>% filter(GR == TRUE)
```

mel (ore) male

```
mel_ore_m <- mel_ore_m %>% mutate(SomExpressed = apply(mel_ore_m, 1, classify_expressed, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
  RepExpressed = apply(mel_ore_m, 1, classify_expressed, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
  SomTrace = apply(mel_ore_m, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive")),
  RepTrace = apply(mel_ore_m, 1, classify_trace, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
  mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
    SM = SomExpressed & RepTrace & !GR,
    RP = RepExpressed & SomTrace & !GR)

mel_ore_m_RP <- mel_ore_m %>% filter(RP == TRUE)
mel_ore_m_SM <- mel_ore_m %>% filter(SM == TRUE)
mel_ore_m_GR <- mel_ore_m %>% filter(GR == TRUE)
```

mel (w1118) female

```
mel_w1118_f <- mel_w1118_f %>% mutate(SomExpressed = apply(mel_w1118_f, 1, classify_expressed, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
  RepExpressed = apply(mel_w1118_f, 1, classify_expressed, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
  SomTrace = apply(mel_w1118_f, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive")),
  RepTrace = apply(mel_w1118_f, 1, classify_trace, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
  mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
    SM = SomExpressed & RepTrace & !GR,
    RP = RepExpressed & SomTrace & !GR)

mel_w1118_f_RP <- mel_w1118_f %>% filter(RP == TRUE)
mel_w1118_f_SM <- mel_w1118_f %>% filter(SM == TRUE)
mel_w1118_f_GR <- mel_w1118_f %>% filter(GR == TRUE)
```

mel (w1118) male

```
mel_w1118_m <- mel_w1118_m %>% mutate(SomExpressed = apply(mel_w1118_m, 1, classify_expressed, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
  RepExpressed = apply(mel_w1118_m, 1, classify_expressed, names = c("mean_gonad", "mean_head", "mean_thorax", "mean_reproductive")),
```

```

        SomTrace = apply(mel_w1118_m, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive"))
        RepTrace = apply(mel_w1118_m, 1, classify_trace, names = c("mean_gonad", "mean_reproductive"))
mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
       SM = SomExpressed & RepTrace & !GR,
       RP = RepExpressed & SomTrace & !GR)

mel_w1118_m_RP <- mel_w1118_m %>% filter(RP == TRUE)
mel_w1118_m_SM <- mel_w1118_m %>% filter(SM == TRUE)
mel_w1118_m_GR <- mel_w1118_m %>% filter(GR == TRUE)

```

ANANASSAE

ana female

```

ana_f <- ana_f %>% mutate(SomExpressed = apply(ana_f, 1, classify_expressed, names = c("mean_head", "mean_thorax", "mean_reproductive")),
                        RepExpressed = apply(ana_f, 1, classify_expressed, names = c("mean_gonad", "mean_reproductive")),
                        SomTrace = apply(ana_f, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive")),
                        RepTrace = apply(ana_f, 1, classify_trace, names = c("mean_gonad", "mean_reproductive")))
mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
       SM = SomExpressed & RepTrace & !GR,
       RP = RepExpressed & SomTrace & !GR)

ana_f_RP <- ana_f %>% filter(RP == TRUE)
ana_f_SM <- ana_f %>% filter(SM == TRUE)
ana_f_GR <- ana_f %>% filter(GR == TRUE)

```

ana male

```

ana_m <- ana_m %>% mutate(SomExpressed = apply(ana_m, 1, classify_expressed, names = c("mean_head", "mean_thorax", "mean_reproductive")),
                        RepExpressed = apply(ana_m, 1, classify_expressed, names = c("mean_gonad", "mean_reproductive")),
                        SomTrace = apply(ana_m, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive")),
                        RepTrace = apply(ana_m, 1, classify_trace, names = c("mean_gonad", "mean_reproductive")))
mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
       SM = SomExpressed & RepTrace & !GR,
       RP = RepExpressed & SomTrace & !GR)

ana_m_RP <- ana_m %>% filter(RP == TRUE)
ana_m_SM <- ana_m %>% filter(SM == TRUE)
ana_m_GR <- ana_m %>% filter(GR == TRUE)

```

MOJAVENSIS

moj female

```

moj_f <- moj_f %>% mutate(SomExpressed = apply(moj_f, 1, classify_expressed, names = c("mean_head", "mean_thorax", "mean_reproductive")),
                        RepExpressed = apply(moj_f, 1, classify_expressed, names = c("mean_gonad", "mean_reproductive")))

```

```

        SomTrace = apply(moj_f, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_gonad", "mean_reproductive"))
        RepTrace = apply(moj_f, 1, classify_trace, names = c("mean_gonad", "mean_reproductive"))
    mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
           SM = SomExpressed & RepTrace & !GR,
           RP = RepExpressed & SomTrace & !GR)

moj_f_RP <- moj_f %>% filter(RP == TRUE)
moj_f_SM <- moj_f %>% filter(SM == TRUE)
moj_f_GR <- moj_f %>% filter(GR == TRUE)

```

moj male

```

moj_m <- moj_m %>% mutate(SomExpressed = apply(moj_m, 1, classify_expressed, names = c("mean_head", "mean_thorax", "mean_gonad", "mean_reproductive")),
                        RepExpressed = apply(moj_m, 1, classify_expressed, names = c("mean_gonad", "mean_reproductive")),
                        SomTrace = apply(moj_m, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_gonad", "mean_reproductive")),
                        RepTrace = apply(moj_m, 1, classify_trace, names = c("mean_gonad", "mean_reproductive")))
    mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
           SM = SomExpressed & RepTrace & !GR,
           RP = RepExpressed & SomTrace & !GR)

moj_m_RP <- moj_m %>% filter(RP == TRUE)
moj_m_SM <- moj_m %>% filter(SM == TRUE)
moj_m_GR <- moj_m %>% filter(GR == TRUE)

```

PERSIMILIS

per female

```

per_f <- per_f %>% mutate(SomExpressed = apply(per_f, 1, classify_expressed, names = c("mean_head", "mean_thorax", "mean_gonad", "mean_reproductive")),
                        RepExpressed = apply(per_f, 1, classify_expressed, names = c("mean_gonad", "mean_reproductive")),
                        SomTrace = apply(per_f, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_gonad", "mean_reproductive")),
                        RepTrace = apply(per_f, 1, classify_trace, names = c("mean_gonad", "mean_reproductive")))
    mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
           SM = SomExpressed & RepTrace & !GR,
           RP = RepExpressed & SomTrace & !GR)

per_f_RP <- per_f %>% filter(RP == TRUE)
per_f_SM <- per_f %>% filter(SM == TRUE)
per_f_GR <- per_f %>% filter(GR == TRUE)

```

per male

```

per_m <- per_m %>% mutate(SomExpressed = apply(per_m, 1, classify_expressed, names = c("mean_head", "mean_thorax", "mean_gonad", "mean_reproductive")),
                        RepExpressed = apply(per_m, 1, classify_expressed, names = c("mean_gonad", "mean_reproductive")),
                        SomTrace = apply(per_m, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_gonad", "mean_reproductive")),
                        RepTrace = apply(per_m, 1, classify_trace, names = c("mean_gonad", "mean_reproductive")))

```

```

mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
       SM = SomExpressed & RepTrace & !GR,
       RP = RepExpressed & SomTrace & !GR)

per_m_RP <- per_m %>% filter(RP == TRUE)
per_m_SM <- per_m %>% filter(SM == TRUE)
per_m_GR <- per_m %>% filter(GR == TRUE)

```

PSEUDOOBSCURA

pse female

```

pse_f <- pse_f %>% mutate(SomExpressed = apply(pse_f, 1, classify_expressed, names = c("mean_head", "mean_gonad", "mean_thorax", "mean_reproductive"),
                                             RepExpressed = apply(pse_f, 1, classify_expressed, names = c("mean_gonad", "mean_thorax", "mean_reproductive"),
                                             SomTrace = apply(pse_f, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive"),
                                             RepTrace = apply(pse_f, 1, classify_trace, names = c("mean_gonad", "mean_thorax", "mean_reproductive")),
mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
       SM = SomExpressed & RepTrace & !GR,
       RP = RepExpressed & SomTrace & !GR)

pse_f_RP <- pse_f %>% filter(RP == TRUE)
pse_f_SM <- pse_f %>% filter(SM == TRUE)
pse_f_GR <- pse_f %>% filter(GR == TRUE)

```

pse male

```

pse_m <- pse_m %>% mutate(SomExpressed = apply(pse_m, 1, classify_expressed, names = c("mean_head", "mean_gonad", "mean_thorax", "mean_reproductive"),
                                             RepExpressed = apply(pse_m, 1, classify_expressed, names = c("mean_gonad", "mean_thorax", "mean_reproductive"),
                                             SomTrace = apply(pse_m, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive"),
                                             RepTrace = apply(pse_m, 1, classify_trace, names = c("mean_gonad", "mean_thorax", "mean_reproductive")),
mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
       SM = SomExpressed & RepTrace & !GR,
       RP = RepExpressed & SomTrace & !GR)

pse_m_RP <- pse_m %>% filter(RP == TRUE)
pse_m_SM <- pse_m %>% filter(SM == TRUE)
pse_m_GR <- pse_m %>% filter(GR == TRUE)

```

VIRILIS

vir female

```

vir_f <- vir_f %>% mutate(SomExpressed = apply(vir_f, 1, classify_expressed, names = c("mean_head", "mean_gonad", "mean_thorax", "mean_reproductive"),
                                             RepExpressed = apply(vir_f, 1, classify_expressed, names = c("mean_gonad", "mean_thorax", "mean_reproductive"),
                                             SomTrace = apply(vir_f, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive"),
                                             RepTrace = apply(vir_f, 1, classify_trace, names = c("mean_gonad", "mean_thorax", "mean_reproductive")),

```

```

mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
       SM = SomExpressed & RepTrace & !GR,
       RP = RepExpressed & SomTrace & !GR)

vir_f_RP <- vir_f %>% filter(RP == TRUE)
vir_f_SM <- vir_f %>% filter(SM == TRUE)
vir_f_GR <- vir_f %>% filter(GR == TRUE)

```

vir male

```

vir_m <- vir_m %>% mutate(SomExpressed = apply(vir_m, 1, classify_expressed, names = c("mean_head", "mean_gonad", "mean_thorax", "mean_reproductive")),
                        RepExpressed = apply(vir_m, 1, classify_expressed, names = c("mean_gonad", "mean_thorax", "mean_reproductive")),
                        SomTrace = apply(vir_m, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive")),
                        RepTrace = apply(vir_m, 1, classify_trace, names = c("mean_gonad", "mean_thorax", "mean_reproductive")),
                        mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
                               SM = SomExpressed & RepTrace & !GR,
                               RP = RepExpressed & SomTrace & !GR)

vir_m_RP <- vir_m %>% filter(RP == TRUE)
vir_m_SM <- vir_m %>% filter(SM == TRUE)
vir_m_GR <- vir_m %>% filter(GR == TRUE)

```

WILLISTONI

wil female

```

wil_f <- wil_f %>% mutate(SomExpressed = apply(wil_f, 1, classify_expressed, names = c("mean_head", "mean_gonad", "mean_thorax", "mean_reproductive")),
                        RepExpressed = apply(wil_f, 1, classify_expressed, names = c("mean_gonad", "mean_thorax", "mean_reproductive")),
                        SomTrace = apply(wil_f, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive")),
                        RepTrace = apply(wil_f, 1, classify_trace, names = c("mean_gonad", "mean_thorax", "mean_reproductive")),
                        mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
                               SM = SomExpressed & RepTrace & !GR,
                               RP = RepExpressed & SomTrace & !GR)

wil_f_RP <- wil_f %>% filter(RP == TRUE)
wil_f_SM <- wil_f %>% filter(SM == TRUE)
wil_f_GR <- wil_f %>% filter(GR == TRUE)

```

wil male

```

wil_m <- wil_m %>% mutate(SomExpressed = apply(wil_m, 1, classify_expressed, names = c("mean_head", "mean_gonad", "mean_thorax", "mean_reproductive")),
                        RepExpressed = apply(wil_m, 1, classify_expressed, names = c("mean_gonad", "mean_thorax", "mean_reproductive")),
                        SomTrace = apply(wil_m, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive")),
                        RepTrace = apply(wil_m, 1, classify_trace, names = c("mean_gonad", "mean_thorax", "mean_reproductive")),
                        mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
                               SM = SomExpressed & RepTrace & !GR,
                               RP = RepExpressed & SomTrace & !GR)

```

```

RP = RepExpressed & SomTrace & !GR)

wil_m_RP <- wil_m %>% filter(RP == TRUE)
wil_m_SM <- wil_m %>% filter(SM == TRUE)
wil_m_GR <- wil_m %>% filter(GR == TRUE)

```

YAKUBA

yak female

```

yak_f <- yak_f %>% mutate(SomExpressed = apply(yak_f, 1, classify_expressed, names = c("mean_head", "mean_gonad", "mean_thorax", "mean_reproductive"),
RepExpressed = apply(yak_f, 1, classify_expressed, names = c("mean_gonad", "mean_thorax", "mean_reproductive"),
SomTrace = apply(yak_f, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive"),
RepTrace = apply(yak_f, 1, classify_trace, names = c("mean_gonad", "mean_thorax", "mean_reproductive"),
mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
SM = SomExpressed & RepTrace & !GR,
RP = RepExpressed & SomTrace & !GR)

yak_f_RP <- yak_f %>% filter(RP == TRUE)
yak_f_SM <- yak_f %>% filter(SM == TRUE)
yak_f_GR <- yak_f %>% filter(GR == TRUE)

```

yak male

```

yak_m <- yak_m %>% mutate(SomExpressed = apply(yak_m, 1, classify_expressed, names = c("mean_head", "mean_gonad", "mean_thorax", "mean_reproductive"),
RepExpressed = apply(yak_m, 1, classify_expressed, names = c("mean_gonad", "mean_thorax", "mean_reproductive"),
SomTrace = apply(yak_m, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive"),
RepTrace = apply(yak_m, 1, classify_trace, names = c("mean_gonad", "mean_thorax", "mean_reproductive"),
mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
SM = SomExpressed & RepTrace & !GR,
RP = RepExpressed & SomTrace & !GR)

yak_m_RP <- yak_m %>% filter(RP == TRUE)
yak_m_SM <- yak_m %>% filter(SM == TRUE)
yak_m_GR <- yak_m %>% filter(GR == TRUE)

```

GRIMSHAWI

gri female

```

gri_f <- gri_f %>% mutate(SomExpressed = apply(gri_f, 1, classify_expressed, names = c("mean_head", "mean_gonad", "mean_thorax", "mean_reproductive"),
RepExpressed = apply(gri_f, 1, classify_expressed, names = c("mean_gonad", "mean_thorax", "mean_reproductive"),
SomTrace = apply(gri_f, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_reproductive"),
RepTrace = apply(gri_f, 1, classify_trace, names = c("mean_gonad", "mean_thorax", "mean_reproductive"),
mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
SM = SomExpressed & RepTrace & !GR,
RP = RepExpressed & SomTrace & !GR)

```

```
RP = RepExpressed & SomTrace & !GR)
```

```
gri_f_RP <- gri_f %>% filter(RP == TRUE)
gri_f_SM <- gri_f %>% filter(SM == TRUE)
gri_f_GR <- gri_f %>% filter(GR == TRUE)
```

gri male

```
gri_m <- gri_m %>% mutate(SomExpressed = apply(gri_m, 1, classify_expressed, names = c("mean_head", "mean_thorax", "mean_gonad", "mean_reproductive")),
  RepExpressed = apply(gri_m, 1, classify_expressed, names = c("mean_gonad", "mean_reproductive")),
  SomTrace = apply(gri_m, 1, classify_trace, names = c("mean_head", "mean_thorax", "mean_gonad", "mean_reproductive")),
  RepTrace = apply(gri_m, 1, classify_trace, names = c("mean_gonad", "mean_reproductive")),
  mutate(GR = SomExpressed & RepExpressed & !SomTrace & !RepTrace,
    SM = SomExpressed & RepTrace & !GR,
    RP = RepExpressed & SomTrace & !GR)

gri_m_RP <- gri_m %>% filter(RP == TRUE)
gri_m_SM <- gri_m %>% filter(SM == TRUE)
gri_m_GR <- gri_m %>% filter(GR == TRUE)
```