Transporter Colocalization Analysis (ImageJ Coloc2)

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2022-12-01

M1 = occludin overlapping P-gp/Bcrp/Mrp2 M2 = P-gp/Bcrp/Mrp2 overlapping occludin

Reading in the data

P-gp

```
#starting with the raw data
#pgp_filelist <- list.files(path="../data/IHC/coloc2_results_pgp/",
#                           pattern="*.txt", full.names = TRUE)
#pgp_cols <- c("sample", "m1", "m2", "r_pearson", "Pval", "r_rand", "sd_rand")
#pgp_coloc2 <- as.data.frame(matrix(,1,length(pgp_cols)))
#names(pgp_coloc2) <- pgp_cols

#for (i in pgp_filelist) {
#  test <- read_lines(i)
#  sample <- str_subset(test, "Working on") %>%
#    str_extract(., "(?<=:[:space:]).*")
#  r_pearson <- str_subset(test, "no threshold") %>%
#    str_extract(., "(?<=,[:space:]).*")
#  m1 <- str_subset(test, "tM1") %>% str_extract(., "(?<=,[:space:]).*")
#  m2 <- str_subset(test, "tM2") %>% str_extract(., "(?<=,[:space:]).*")
#  Pval <- str_subset(test, "P-Value") %>% str_extract(., "(?<=,[:space:]).*")
#  r_rand <- str_subset(test, "Costes Shuffled Mean") %>%
#    str_extract(., "(?<=,[:space:]).*")
#  sd_rand <- str_subset(test, "Costes Shuffled Std") %>%
#    str_extract(., "(?<=,[:space:]).*")
#  res <- c(all_of(sample), all_of(m1), all_of(m2), all_of(r_pearson),
#           all_of(Pval), all_of(r_rand), all_of(sd_rand))
#  pgp_coloc2 <- rbind(pgp_coloc2, res)
#}

#pgp_coloc2 <- pgp_coloc2 %>% na.omit(pgp_coloc2) %>%
#  mutate(sex = as.factor(str_sub(sample, start=1L, end=1L)),
#         mouseID = as.factor(str_extract(sample, "(?<=-)[:digit:]+")),
#        #prep = as.factor(str_extract(sample, "[:lower:]{2,}")),
#         prep = as.factor(str_extract(sample, "wm|section")),
#         image = str_extract(sample, "[:alpha:]{2,}.*"), .before=m1)

#pgp_coloc2 <- pgp_coloc2 %>% select(-sample) %>%
```

```
#   mutate(m1 = as.double(m1),
#          m2 = as.double(m2),
#          r_pearson = as.double(r_pearson),
#          Pval = as.double(Pval),
#          r_rand = as.double(r_rand),
#          sd_rand = as.double(sd_rand),
#          coloc = Pval>0.95)

#write.xlsx(pgp_coloc2, "../data/IHC/coloc2-pgp-totals.xlsx")

#starting from the processed excel sheet
pgp_coloc2 <- readxl::read_excel("../data/IHC/coloc2-pgp-totals.xlsx") %>%
  mutate(coloc = as.logical(coloc),
         sex = as.factor(sex),
         mouseID = as.factor(mouseID),
         prep = as.factor(prep))

head(pgp_coloc2)
```

```
## # A tibble: 6 x 11
##   sex   mouseID prep    image         m1    m2 r_pea~1  Pval r_rand sd_rand coloc
##   <fct> <fct>   <fct>   <chr>      <dbl> <dbl>   <dbl> <dbl>  <dbl>   <dbl> <lgl>
## 1 F     20      section slide1-s~  0.816 0.76     0.64     1      0       0 TRUE
## 2 F     20      section slide1-s~  0.789 0.77     0.58     1      0       0 TRUE
## 3 F     20      section slide1-s~  0.845 0.64     0.5      1      0       0 TRUE
## 4 F     20      section slide1-s~  0.063 0.057    0.61     1      0       0 TRUE
## 5 F     20      section slide2-s~  0.613 0.361    0.62     1      0       0 TRUE
## 6 F     20      section slide2-s~  0.778 0.772    0.62     1      0       0 TRUE
## # ... with abbreviated variable name 1: r_pearson
```

Bcrp

```
#starting with the raw data
#bcrp_filelist <- list.files(path="../data/IHC/coloc2_results_bcrp/",
#                            pattern=".*.txt", full.names = TRUE)
#bcrp_cols <- c("sample", "m1", "m2", "r_pearson", "Pval", "r_rand", "sd_rand")
#bcrp_coloc2 <- as.data.frame(matrix(,1,length(bcrp_cols)))
#names(bcrp_coloc2) <- bcrp_cols

#for (i in bcrp_filelist) {
#  test <- read_lines(i)
#  sample <- str_subset(test, "Working on") %>%
#    str_extract(., "(?<=:[:space:]).*")
#  r_pearson <- str_subset(test, "no threshold") %>%
#    str_extract(., "(?<=,[:space:]).*")
#  m1 <- str_subset(test, "tM1") %>% str_extract(., "(?<=,[:space:]).*")
#  m2 <- str_subset(test, "tM2") %>% str_extract(., "(?<=,[:space:]).*")
#  Pval <- str_subset(test, "P-Value") %>% str_extract(., "(?<=,[:space:]).*")
#  r_rand <- str_subset(test, "Costes Shuffled Mean") %>%
#    str_extract(., "(?<=,[:space:]).*")
#  sd_rand <- str_subset(test, "Costes Shuffled Std") %>%
```

```r
#     str_extract(., "(?<=,[:space:]).*")
#   print(sample)
#   res <- c(all_of(sample), all_of(m1), all_of(m2), all_of(r_pearson),
#            all_of(Pval), all_of(r_rand), all_of(sd_rand))
#   bcrp_coloc2 <- rbind(bcrp_coloc2, res)
#}

#bcrp_coloc2 <- bcrp_coloc2 %>% na.omit(bcrp_coloc2) %>%
#  mutate(sex = as.factor(str_sub(sample, start=1L, end=1L)),
#         mouseID = as.factor(str_extract(sample, "(?<=-)[:digit:]+")),
#         prep = as.factor(str_extract(sample, "[:lower:]{2,}")),
#         image = str_extract(sample, "[:alpha:]{2,}.*"), .before=m1)

#bcrp_coloc2 <- bcrp_coloc2 %>% select(-sample) %>%
#  mutate(m1 = as.double(m1),
#         m2 = as.double(m2),
#         r_pearson = as.double(r_pearson),
#         Pval = as.double(Pval),
#         r_rand = as.double(r_rand),
#         sd_rand = as.double(sd_rand),
#         coloc = Pval>0.95)

#write.xlsx(bcrp_coloc2, "../data/IHC/coloc2-bcrp-totals.xlsx")

#starting from processed excel file
bcrp_coloc2 <- readxl::read_excel("../data/IHC/coloc2-bcrp-totals.xlsx") %>%
  mutate(coloc = as.logical(coloc),
         sex = as.factor(sex),
         mouseID = as.factor(mouseID),
         prep = as.factor(prep))

head(bcrp_coloc2)
```

```
## # A tibble: 6 x 11
##   sex   mouseID prep    image        m1    m2 r_pea~1  Pval r_rand sd_rand coloc
##   <fct> <fct>   <fct>   <chr>     <dbl> <dbl>   <dbl> <dbl>  <dbl>   <dbl> <lgl>
## 1 F     22      section section1~ 0.618 0.229    0.32     1      0       0 TRUE
## 2 F     22      section section1~ 0.787 0.359    0.63     1      0       0 TRUE
## 3 F     22      section section1~ 0.782 0.29     0.51     1      0       0 TRUE
## 4 F     22      section section3~ 0.517 0.461    0.49     1      0       0 TRUE
## 5 F     22      section section3~ 0.687 0.541    0.58     1      0       0 TRUE
## 6 F     22      section section3~ 0.555 0.431    0.58     1      0       0 TRUE
## # ... with abbreviated variable name 1: r_pearson
```

Mrp2

```r
#starting with raw data
#mrp2_filelist <- list.files(path="../data/IHC/coloc2_results_mrp2/",
#                            pattern="*.txt", full.names = TRUE)
#mrp2_cols <- c("sample", "m1", "m2", "r_pearson", "Pval", "r_rand", "sd_rand")
#mrp2_coloc2 <- as.data.frame(matrix(,1,length(mrp2_cols)))
```

```r
#names(mrp2_coloc2) <- mrp2_cols

#for (i in mrp2_filelist) {
#  test <- read_lines(i)
#  sample <- str_subset(test, "Working on") %>%
#    str_extract(., "(?<=:[:space:]).*")
#  r_pearson <- str_subset(test, "no threshold") %>%
#    str_extract(., "(?<=,[:space:]).*")
#  m1 <- str_subset(test, "tM1") %>% str_extract(., "(?<=,[:space:]).*")
#  m2 <- str_subset(test, "tM2") %>% str_extract(., "(?<=,[:space:]).*")
#  Pval <- str_subset(test, "P-Value") %>% str_extract(., "(?<=,[:space:]).*")
#  r_rand <- str_subset(test, "Costes Shuffled Mean") %>%
#    str_extract(., "(?<=,[:space:]).*")
#  sd_rand <- str_subset(test, "Costes Shuffled Std") %>%
#    str_extract(., "(?<=,[:space:]).*")
#  res <- c(all_of(sample), all_of(m1), all_of(m2), all_of(r_pearson),
#           all_of(Pval), all_of(r_rand), all_of(sd_rand))
#  mrp2_coloc2 <- rbind(mrp2_coloc2, res)
#}

#mrp2_coloc2 <- mrp2_coloc2 %>% na.omit(mrp2_coloc2) %>%
#  mutate(sex = as.factor(str_sub(sample, start=1L, end=1L)),
#         mouseID = as.factor(str_extract(sample, "(?<=-)[:digit:]+")),
#         image = str_extract(sample, "s.*(?=_)"),
#         roi = str_extract(sample, "(?<=_).*"), .before=m1)

#mrp2_coloc2 <- mrp2_coloc2 %>% select(-sample) %>%
#  mutate(m1 = as.double(m1),
#         m2 = as.double(m2),
#         r_pearson = as.double(r_pearson),
#         Pval = as.double(Pval),
#         r_rand = as.double(r_rand),
#         sd_rand = as.double(sd_rand),
#         coloc = Pval>0.95)

#write.xlsx(mrp2_coloc2, "../data/IHC/coloc2-mrp2-totals.xlsx")

#starting with processed excel file
mrp2_coloc2 <- readxl::read_excel("../data/IHC/coloc2-mrp2-totals.xlsx") %>%
  mutate(coloc = as.logical(coloc),
         sex = as.factor(sex),
         mouseID = as.factor(mouseID))


head(mrp2_coloc2)
```

```
## # A tibble: 6 x 11
##   sex   mouseID image       roi      m1    m2 r_pea~1  Pval r_rand sd_rand coloc
##   <fct> <fct>   <chr>       <chr> <dbl> <dbl>   <dbl> <dbl>  <dbl>   <dbl> <lgl>
## 1 F     22      section2-4~ gcl1  0.063 0.36     0.12 1      -0.01    0.04 TRUE
## 2 F     22      section2-4~ inl1  0     0.087   -0.01 0.34    0       0.02 FALSE
## 3 F     22      section2-4~ inl2  0     0.097   -0.03 0.12    0       0.02 FALSE
## 4 F     22      section2-4~ gcl1  0.111 0.001    0.01 0.77    0       0.01 FALSE
```

```
## 5 F       22      section2-4~ inl1  0      0.183   -0.02  0.18   0        0.03 FALSE
## 6 F       22      section2-4~ gcl1  0      0.181   -0.02  0.14   0        0.02 FALSE
## # ... with abbreviated variable name 1: r_pearson
```

Generating summary statistics

P-gp

```
pgp_sumstats <- pgp_coloc2 %>% summarise(m1_mean = mean(m1),
                    m1_sd = sd(m1),
                    m2_mean = mean(m2),
                    m2_sd = sd(m2),
                    r_mean = mean(r_pearson),
                    r_sd = sd(r_pearson),
                    n_total = n(),
                    n_coloc = sum(coloc)
                    )
pgp_sumstats
```

```
## # A tibble: 1 x 8
##   m1_mean m1_sd m2_mean m2_sd r_mean   r_sd n_total n_coloc
##     <dbl> <dbl>   <dbl> <dbl>  <dbl>  <dbl>   <int>   <int>
## 1   0.298 0.315   0.229 0.264  0.325 0.164      51      51
```

```
bcrp_sumstats <- bcrp_coloc2 %>% summarise(m1_mean = mean(m1),
                    m1_sd = sd(m1),
                    m2_mean = mean(m2),
                    m2_sd = sd(m2),
                    r_mean = mean(r_pearson),
                    r_sd = sd(r_pearson),
                    n_total = n(),
                    n_coloc = sum(coloc),
                    mean_P = mean(Pval)
                    )
bcrp_sumstats
```

```
## # A tibble: 1 x 9
##   m1_mean m1_sd m2_mean  m2_sd r_mean   r_sd n_total n_coloc mean_P
##     <dbl> <dbl>   <dbl>  <dbl>  <dbl>  <dbl>   <int>   <int>  <dbl>
## 1   0.737 0.132   0.266 0.0870  0.460 0.104      42      42      1
```

```
mrp2_sumstats <- mrp2_coloc2 %>% summarise(m1_mean = mean(m1),
                    m1_sd = sd(m1),
                    m2_mean = mean(m2),
                    m2_sd = sd(m2),
                    r_mean = mean(r_pearson),
                    r_sd = sd(r_pearson),
                    n_total = n(),
                    n_coloc = sum(coloc)
                    )
mrp2_sumstats
```

```
## # A tibble: 1 x 8
##   m1_mean m1_sd m2_mean m2_sd  r_mean   r_sd n_total n_coloc
##     <dbl> <dbl>   <dbl> <dbl>   <dbl>  <dbl>   <int>   <int>
## 1   0.110 0.144   0.208 0.157  0.0350 0.0713     145      55
```

```r
mrp2_sumstats_image <- mrp2_coloc2 %>% group_by(image,mouseID,sex,coloc) %>%
  summarise(m1_mean = mean(m1),
            m1_sd = sd(m1),
            m2_mean = mean(m2),
            m2_sd = sd(m2),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            n_coloc = sum(coloc)
            )
```

```
## 'summarise()' has grouped output by 'image', 'mouseID', 'sex'. You can override
## using the '.groups' argument.
```

```r
pgp_sumstats_animals <- pgp_coloc2 %>% group_by(mouseID,sex,prep) %>%
  summarise(m1_mean = mean(m1),
            m1_sd = sd(m1),
            m2_mean = mean(m2),
            m2_sd = sd(m2),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            n_coloc = sum(coloc)
            )
```

```
## 'summarise()' has grouped output by 'mouseID', 'sex'. You can override using
## the '.groups' argument.
```

```r
pgp_sumstats_animals
```

```
## # A tibble: 10 x 11
## # Groups:   mouseID, sex [10]
##    mouseID sex   prep    m1_mean   m1_sd m2_mean  m2_sd r_mean   r_sd n_total
##    <fct>   <fct> <fct>     <dbl>   <dbl>   <dbl>  <dbl>  <dbl>  <dbl>   <int>
## 1 10       M     wm       0.01    0.00784 0.043  0.0168 0.128  0.0295       5
## 2 11       M     wm       0.0258  0.0409  0.0503 0.0192 0.145  0.0191       4
## 3 20       F     section  0.651   0.299   0.56   0.293  0.595  0.0505       6
## 4 39       F     wm       0.227   0.258   0.0782 0.135  0.375  0.0947       4
## 5 80       M     section  0.320   0.282   0.246  0.290  0.37   0.140        6
## 6 81       M     section  0.283   0.251   0.204  0.286  0.377  0.0838       6
## 7 82       M     section  0.381   0.325   0.208  0.270  0.352  0.183        6
## 8 83       M     wm       0.430   0.373   0.368  0.274  0.328  0.0804       5
## 9 87       F     wm       0.416   0.366   0.297  0.247  0.3    0.0628       5
## 10 9       M     wm       0.0265  0.0155  0.0812 0.0538 0.138  0.0419       4
## # ... with 1 more variable: n_coloc <int>
```

```r
bcrp_sumstats_animals <- bcrp_coloc2 %>% group_by(mouseID,sex,prep) %>%
  summarise(m1_mean = mean(m1),
            m1_sd = sd(m1),
            m2_mean = mean(m2),
            m2_sd = sd(m2),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            n_coloc = sum(coloc),
           mean_P = mean(Pval)
            )
```

```
## 'summarise()' has grouped output by 'mouseID', 'sex'. You can override using
## the '.groups' argument.
```

```r
bcrp_sumstats_animals
```

```
## # A tibble: 7 x 12
## # Groups:   mouseID, sex [7]
##    mouseID sex    prep     m1_mean  m1_sd m2_mean  m2_sd r_mean    r_sd n_total
##    <fct>   <fct>  <fct>      <dbl>  <dbl>   <dbl>  <dbl>  <dbl>   <dbl>   <int>
## 1 22       F      section   0.658 0.114    0.385 0.115   0.518 0.110         6
## 2 40       F      section   0.774 0.0717   0.274 0.0454  0.502 0.117         6
## 3 80       M      section   0.775 0.0587   0.162 0.0183  0.443 0.0638        6
## 4 81       M      section   0.663 0.127    0.276 0.0642  0.42  0.103         6
## 5 82       M      section   0.754 0.0375   0.275 0.0144  0.408 0.0337        6
## 6 92       M      section   0.806 0.0483   0.264 0.0486  0.503 0.0403        6
## 7 98       F      section   0.732 0.280    0.226 0.0874  0.428 0.177         6
## # ... with 2 more variables: n_coloc <int>, mean_P <dbl>
```

```r
mrp2_sumstats_animals <- mrp2_coloc2 %>% group_by(mouseID,sex,coloc) %>%
  summarise(m1_mean = mean(m1),
            m1_sd = sd(m1),
            m2_mean = mean(m2),
            m2_sd = sd(m2),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            n_coloc = sum(coloc)
            )
```

```
## 'summarise()' has grouped output by 'mouseID', 'sex'. You can override using
## the '.groups' argument.
```

```r
dropped <- mrp2_sumstats_animals %>% group_by(mouseID) %>%
  summarise(n = n(), coloc = coloc, sex=sex) %>%
  filter(n==1) %>% select(-n) %>%
  mutate(coloc = toString(as.integer(coloc))) %>%
  mutate(coloc = str_replace(toString(coloc), pattern = "0", replacement = "1")) %>%
  mutate(coloc = as.logical(as.integer(coloc)))
```

```
## 'summarise()' has grouped output by 'mouseID'. You can override using the
## '.groups' argument.

mrp2_sumstats_animals <- rbind(mrp2_sumstats_animals, dropped) %>% arrange(., mouseID)
mrp2_sumstats_animals <- mrp2_sumstats_animals %>% ungroup() %>% group_by(mouseID)

pgp_sumstats_sex <- pgp_coloc2 %>% group_by(sex) %>%
  summarise(m1_mean = mean(m1),
            m1_sd = sd(m1),
            m2_mean = mean(m2),
            m2_sd = sd(m2),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            n_coloc = sum(coloc)
            )
pgp_sumstats_sex
```

```
## # A tibble: 2 x 9
##   sex   m1_mean m1_sd m2_mean m2_sd r_mean  r_sd n_total n_coloc
##   <fct>   <dbl> <dbl>   <dbl> <dbl>  <dbl> <dbl>   <int>   <int>
## 1 F       0.459 0.341   0.344 0.305  0.438 0.150      15      15
## 2 M       0.231 0.282   0.181 0.234  0.278 0.147      36      36
```

```
bcrp_sumstats_sex <- bcrp_coloc2 %>% group_by(sex) %>%
  summarise(m1_mean = mean(m1),
            m1_sd = sd(m1),
            m2_mean = mean(m2),
            m2_sd = sd(m2),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            n_coloc = sum(coloc)
            )
bcrp_sumstats_sex
```

```
## # A tibble: 2 x 9
##   sex   m1_mean  m1_sd m2_mean  m2_sd r_mean   r_sd n_total n_coloc
##   <fct>   <dbl>  <dbl>   <dbl>  <dbl>  <dbl>  <dbl>   <int>   <int>
## 1 F       0.721 0.176    0.295 0.107   0.483 0.136      18      18
## 2 M       0.750 0.0896   0.244 0.0623  0.444 0.0719     24      24
```

```
mrp2_sumstats_sex <- mrp2_coloc2 %>% group_by(sex) %>%
  summarise(m1_mean = mean(m1),
            m1_sd = sd(m1),
            m2_mean = mean(m2),
            m2_sd = sd(m2),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            n_coloc = sum(coloc)
            )
mrp2_sumstats_sex
```

```
## # A tibble: 2 x 9
##   sex   m1_mean m1_sd m2_mean m2_sd r_mean   r_sd n_total n_coloc
##   <fct>   <dbl> <dbl>   <dbl> <dbl>  <dbl>  <dbl>   <int>   <int>
## 1 F       0.104 0.124   0.201 0.113 0.0411 0.0794      53      24
## 2 M       0.113 0.154   0.212 0.178 0.0314 0.0664      92      31
```

```
pgp_sumstats_prep <- pgp_coloc2 %>% group_by(prep) %>%
  summarise(m1_mean = mean(m1),
            m1_sd = sd(m1),
            m2_mean = mean(m2),
            m2_sd = sd(m2),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            mean_P = mean(Pval)
            )
pgp_sumstats_prep
```

```
## # A tibble: 2 x 9
##   prep    m1_mean m1_sd m2_mean m2_sd r_mean  r_sd n_total mean_P
##   <fct>     <dbl> <dbl>   <dbl> <dbl>  <dbl> <dbl>   <int>  <dbl>
## 1 section   0.408 0.308   0.304 0.306  0.423 0.155      24      1
## 2 wm        0.200 0.292   0.162 0.205  0.237 0.116      27      1
```

```
mrp2_sumstats_coloc <- mrp2_coloc2 %>% group_by(coloc) %>%
  summarise(m1_mean = mean(m1),
            m1_sd = sd(m1),
            m2_mean = mean(m2),
            m2_sd = sd(m2),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            mean_P = mean(Pval)
            )
mrp2_sumstats_coloc
```

```
## # A tibble: 2 x 9
##   coloc m1_mean  m1_sd m2_mean m2_sd   r_mean   r_sd n_total mean_P
##   <lgl>   <dbl>  <dbl>   <dbl> <dbl>    <dbl>  <dbl>   <int>  <dbl>
## 1 FALSE  0.0393 0.0672   0.187 0.166 -0.00622 0.0329      90  0.431
## 2 TRUE   0.225  0.160    0.243 0.136  0.102   0.0656      55  0.996
```

Plotting the data

```
pgp_coloc2$coloc <- as.logical(pgp_coloc2$coloc)
pgp_coloc2$mouseID <- as.factor(pgp_coloc2$mouseID)

pgp_coloc2_long <- pgp_coloc2 %>% pivot_longer(cols = m1:m2, names_to = "m_stat_type", values_to = "m_s

pgp_coloc2_long <- pgp_coloc2_long %>% group_by(mouseID, m_stat_type, prep, sex) %>%
```

```
    summarise(m_mean = mean(m_stat_val),
              m_sd = sd(m_stat_val),
              r_mean = mean(r_pearson),
              r_sd = sd(r_pearson),
              n_total = n(),
              n_coloc = sum(coloc))
```

'summarise()' has grouped output by 'mouseID', 'm_stat_type', 'prep'. You can
override using the '.groups' argument.

```
#per animal
pgp_animal_r_plot <- pgp_sumstats_animals %>%
  ggplot(aes(x=prep, y=r_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.2) +
  geom_jitter(color="black", width=0.1, aes(shape=sex)) +
  theme_bw(12) +
  guides(shape=guide_legend("Sex")) +
  ylim(-0.05,0.65) +
  ggtitle("P-gp")

pgp_animal_r_plot
```
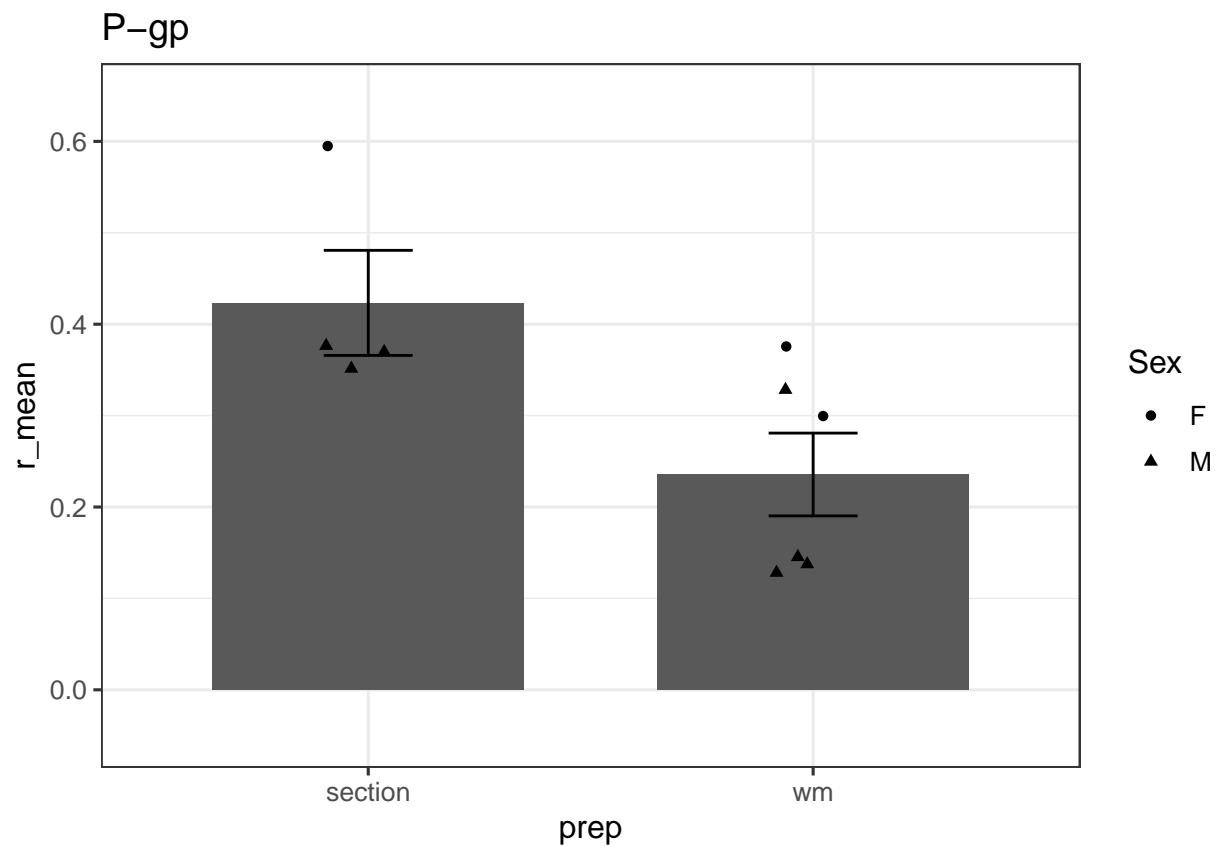
```
ggsave("../figures/pgp_r_plot.png", plot=pgp_animal_r_plot, width=3, height=3)
ggsave("../figures/pgp_r_plot.svg", plot=pgp_animal_r_plot, width=3, height=3)

pgp_animal_m_plot <- ggplot(pgp_coloc2_long, aes(x=prep, y=m_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.2) +
  geom_jitter(color="black", width=0.1, aes(shape=sex)) +
  facet_wrap(~m_stat_type) +
  theme_bw(12) +
  guides(shape=guide_legend("Sex")) +
  ylim(-0.05,0.9) +
  ggtitle("P-gp")

pgp_animal_m_plot
```
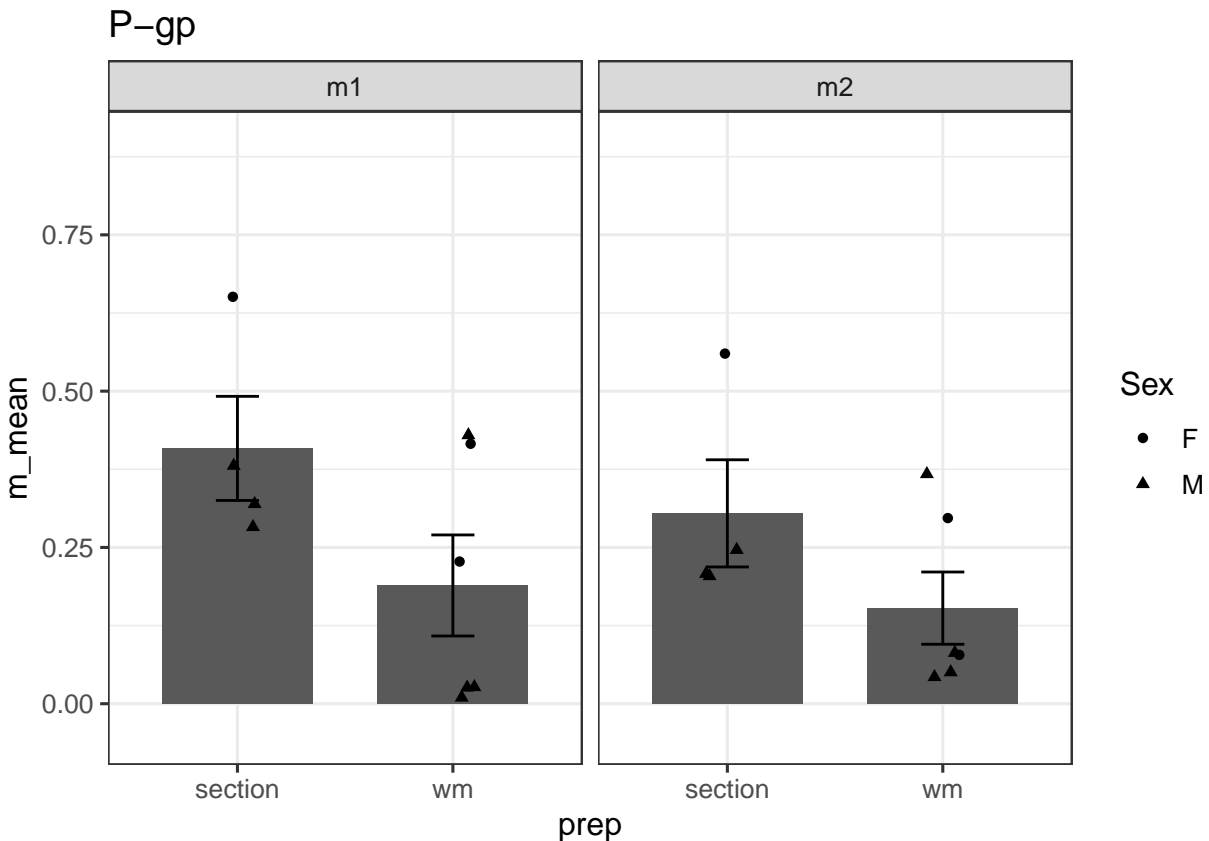


```
ggsave("../figures/pgp_m_plot.png", plot=pgp_animal_m_plot, width=5, height=3)
ggsave("../figures/pgp_m_plot.svg", plot=pgp_animal_m_plot, width=5, height=3)

#males v females
pgp_r_plot_sex <- pgp_sumstats_animals %>%
  ggplot(aes(x=sex, y=r_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.2) +
```

```
geom_jitter(color="black", width=0.1, aes(shape=sex)) +
theme_bw(12) +
guides(shape=guide_legend("Sex")) +
ylim(-0.05,0.65) +
ggtitle("P-gp")

pgp_r_plot_sex
```
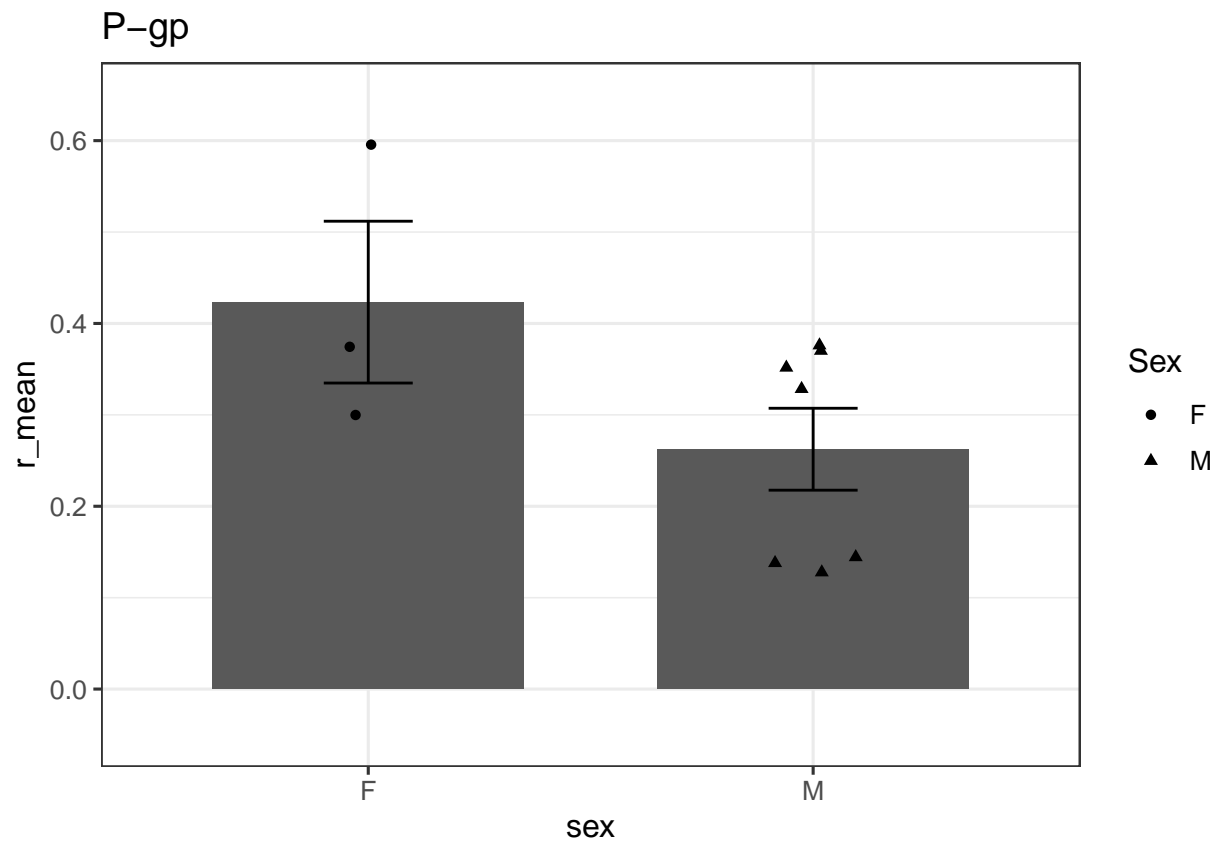


```
ggsave("../figures/pgp_r_plot_sex.png", plot=pgp_r_plot_sex, width=3, height=3)
ggsave("../figures/pgp_r_plot_sex.svg", plot=pgp_r_plot_sex, width=3, height=3)

pgp_m_plot_sex <- ggplot(pgp_coloc2_long, aes(x=sex, y=m_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.2) +
  geom_jitter(color="black", width=0.1, aes(shape=sex)) +
  facet_wrap(~m_stat_type) +
  theme_bw(12) +
  guides(shape=guide_legend("Sex")) +
  ylim(-0.05,0.9) +
  ggtitle("P-gp")

pgp_m_plot_sex
```

P–gp
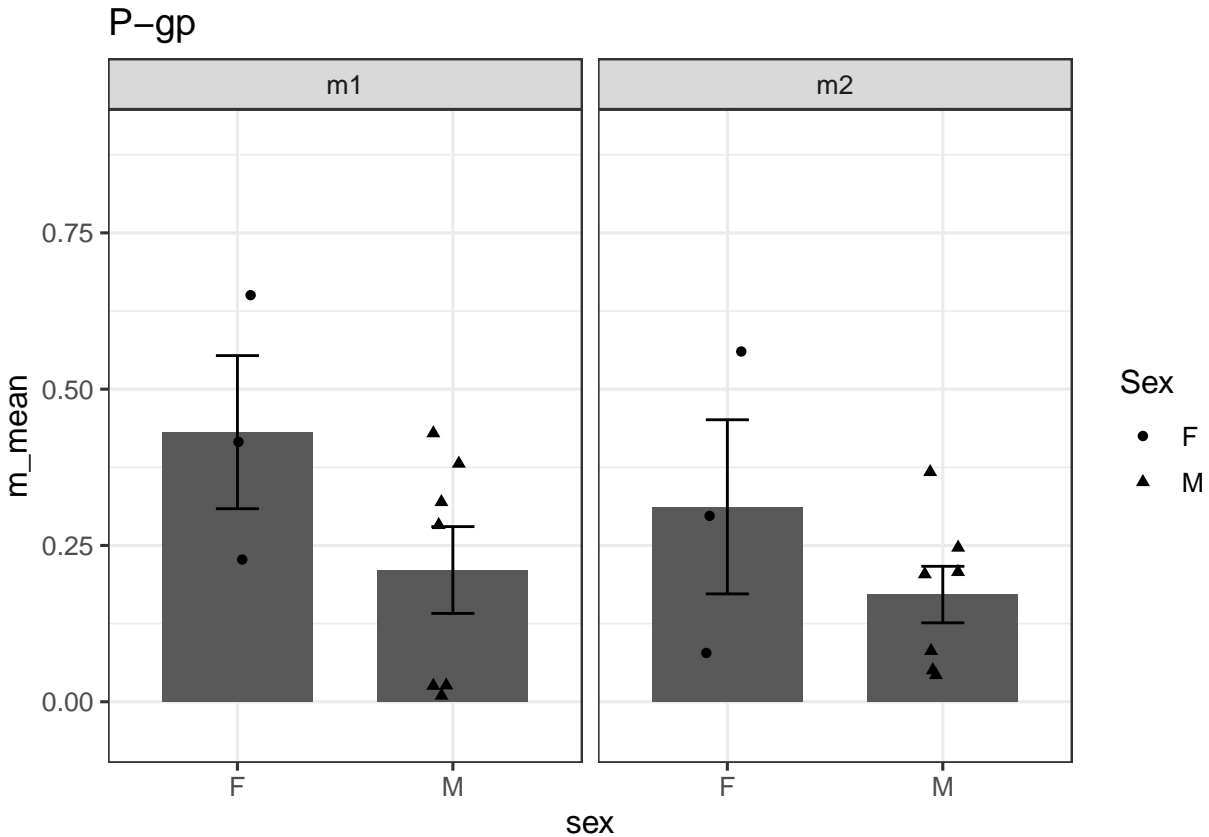

```
ggsave("../figures/pgp_m_plot_sex.png", plot=pgp_m_plot_sex, width=5, height=3)
ggsave("../figures/pgp_m_plot_sex.svg", plot=pgp_m_plot_sex, width=5, height=3)
```

```
bcrp_coloc2_long <- bcrp_coloc2 %>% pivot_longer(cols = m1:m2, names_to = "m_stat_type", values_to = "m_

bcrp_coloc2_long <- bcrp_coloc2_long %>% group_by(mouseID, m_stat_type, sex) %>%
  summarise(m_mean = mean(m_stat_val),
            m_sd = sd(m_stat_val),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            n_coloc = sum(coloc))
```

```
## 'summarise()' has grouped output by 'mouseID', 'm_stat_type'. You can override
## using the '.groups' argument.
```

```
#per animal
bcrp_animal_r_plot <- bcrp_sumstats_animals %>%
  ggplot(aes(x=sex, y=r_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.2) +
  geom_jitter(color="black", width=0.1, aes(shape=sex)) +
  theme_bw(12)  +
  guides(shape=guide_legend("Sex")) +
```

```
  ylim(-0.05,0.65) +
  ggtitle("Bcrp")

bcrp_animal_r_plot
```
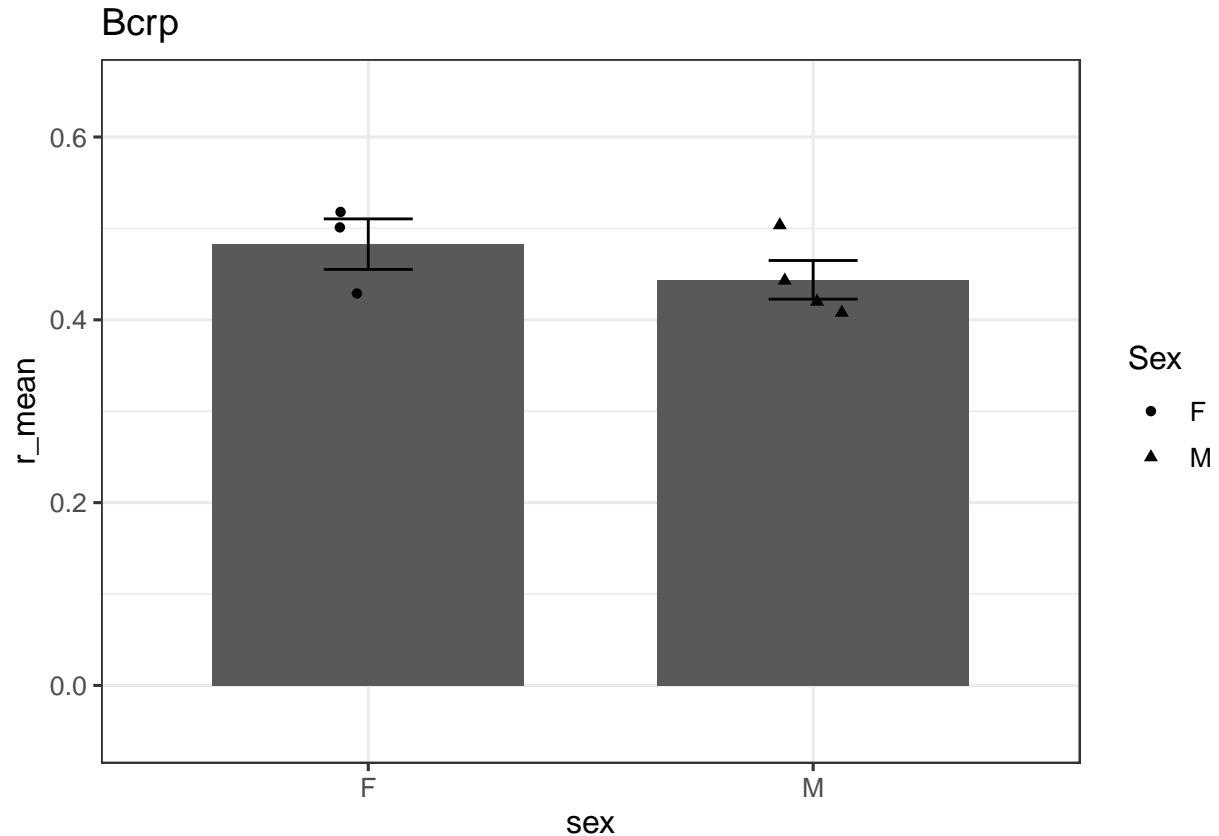
Bcrp


```
ggsave("../figures/bcrp_r_plot.png", plot=bcrp_animal_r_plot, width=3, height=3)
ggsave("../figures/bcrp_r_plot.svg", plot=bcrp_animal_r_plot, width=3, height=3)

bcrp_animal_m_plot <- ggplot(bcrp_coloc2_long, aes(x=sex, y=m_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.2) +
  geom_jitter(color="black", width=0.1, aes(shape=sex)) +
  facet_wrap(~m_stat_type) +
  theme_bw(12)  +
  guides(shape=guide_legend("Sex")) +
  ylim(-0.05,0.9) +
  ggtitle("Bcrp")

bcrp_animal_m_plot
```
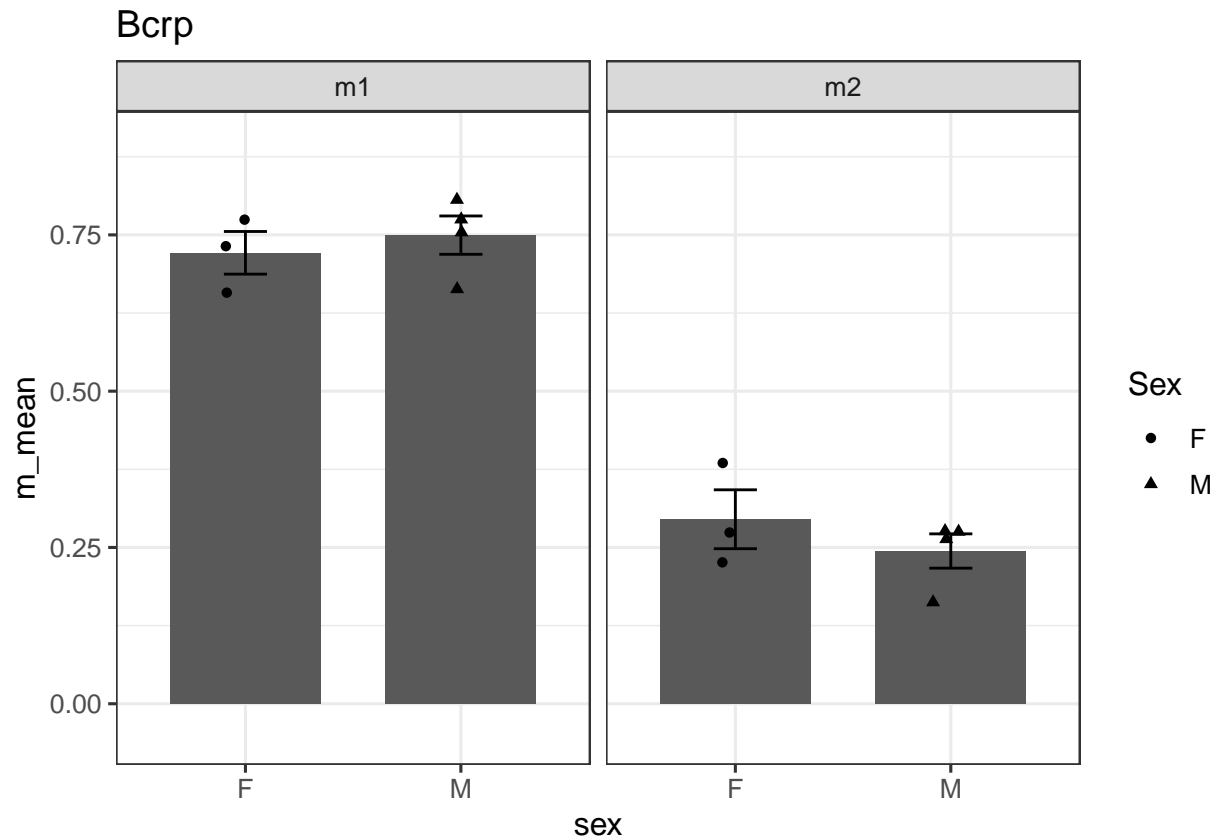
Bcrp


```
ggsave("../figures/bcrp_m_plot.png", plot=bcrp_animal_m_plot, width=5, height=3)
ggsave("../figures/bcrp_m_plot.svg", plot=bcrp_animal_m_plot, width=5, height=3)
```

```
mrp2_coloc2$coloc <- as.logical(mrp2_coloc2$coloc)

mrp2_coloc2_long <- mrp2_coloc2 %>% pivot_longer(cols = m1:m2, names_to = "m_stat_type", values_to = "m_

mrp2_coloc2_long <- mrp2_coloc2_long %>% group_by(mouseID, coloc, m_stat_type, sex) %>%
  summarise(m_stat_type = as.factor(m_stat_type),
            m_mean = mean(m_stat_val),
            m_sd = sd(m_stat_val),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            n_coloc = sum(coloc))
```

```
## `summarise()` has grouped output by 'mouseID', 'coloc', 'm_stat_type', 'sex'.
## You can override using the `.groups` argument.
```

```
mrp2_sumstats_animals_long <- mrp2_sumstats_animals %>% pivot_longer(cols = c(m1_mean,m2_mean), names_to

#per animal
mrp2_animal_r_plot <- mrp2_sumstats_animals %>%
  ggplot(aes(x=coloc, y=r_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
```

```
    stat_summary(fun.data = mean_se,
                 geom = "errorbar", width=0.2) +
    geom_jitter(color="black", width=0.1, aes(shape=sex)) +
    geom_line(aes(group=mouseID, color=mouseID)) +
    scale_color_viridis(discrete="TRUE") +
    theme_bw(12) +
    guides(shape=guide_legend("Sex"), color = "none") +
    ylim(-0.1,0.65) +
    ggtitle("Mrp2")

mrp2_animal_r_plot
```
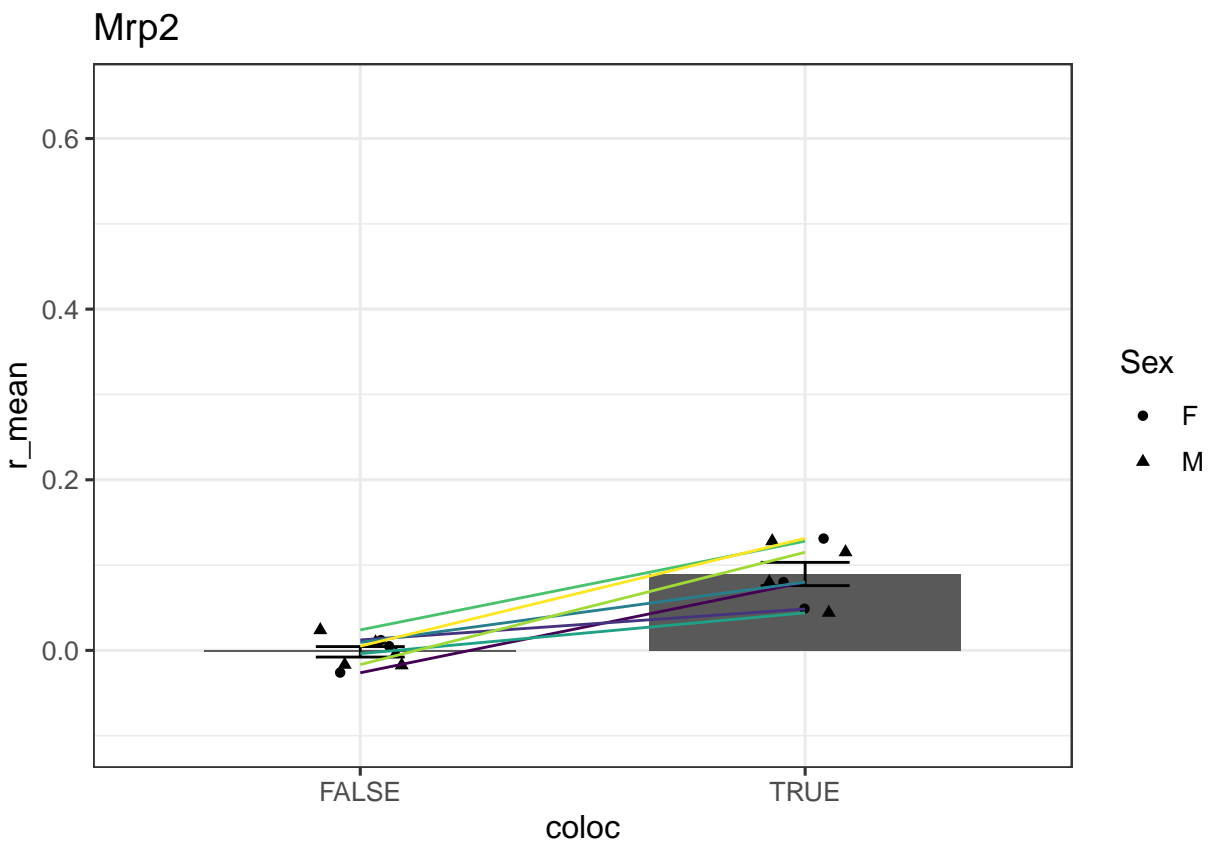
```
## Warning: Removed 1 rows containing non-finite values ('stat_summary()').
## Removed 1 rows containing non-finite values ('stat_summary()').

## Warning: Removed 1 rows containing missing values ('geom_point()').

## Warning: Removed 1 row containing missing values ('geom_line()').
```



```
ggsave("../figures/mrp2_r_plot.png", plot=mrp2_animal_r_plot, width=3, height=3)
```

```
## Warning: Removed 1 rows containing non-finite values ('stat_summary()').

## Warning: Removed 1 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 1 rows containing missing values ('geom_point()').
```

```
## Warning: Removed 1 row containing missing values ('geom_line()').
```

```
ggsave("../figures/mrp2_r_plot.svg", plot=mrp2_animal_r_plot, width=3, height=3)
```

```
## Warning: Removed 1 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 1 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 1 rows containing missing values ('geom_point()').
```

```
## Warning: Removed 1 row containing missing values ('geom_line()').
```

```r
mrp2_animal_m_plot <- ggplot(mrp2_sumstats_animals_long, aes(x=coloc, y=m_stat_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.2) +
  geom_jitter(color="black", width=0.1, aes(shape=sex)) +
  geom_line(aes(group=mouseID, color=mouseID)) +
  facet_wrap(~m_stat_type) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw(12) +
  guides(shape=guide_legend("Sex"), color = "none") +
  ylim(-0.05,0.9) +
  ggtitle("Mrp2")

mrp2_animal_m_plot
```
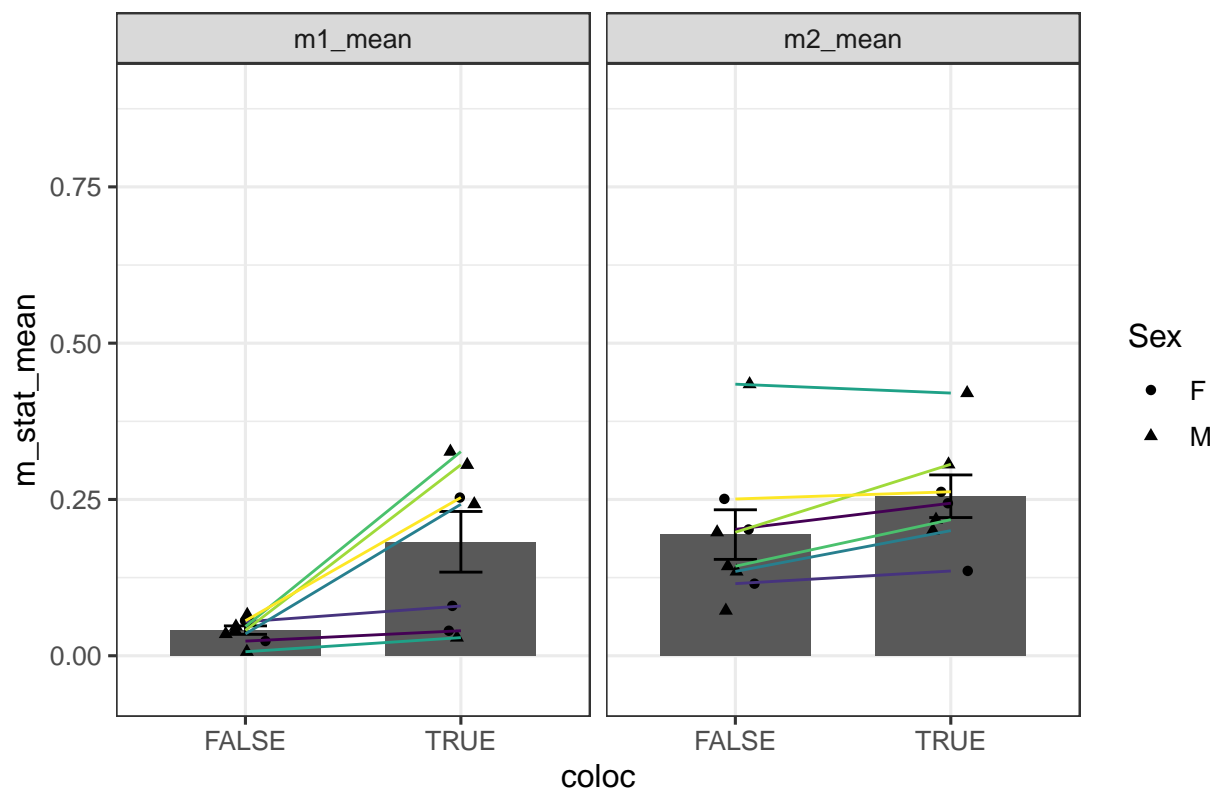
```
## Warning: Removed 2 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 2 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 2 rows containing missing values ('geom_point()').
```

```
## Warning: Removed 1 row containing missing values ('geom_line()').
```

Mrp2

```
ggsave("../figures/mrp2_m_plot.png", plot=mrp2_animal_m_plot, width=5, height=3)
```

```
## Warning: Removed 2 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 2 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 2 rows containing missing values ('geom_point()').
```

```
## Warning: Removed 1 row containing missing values ('geom_line()').
```

```
ggsave("../figures/mrp2_m_plot.svg", plot=mrp2_animal_m_plot, width=5, height=3)
```

```
## Warning: Removed 2 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 2 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 2 rows containing missing values ('geom_point()').
```

```
## Warning: Removed 1 row containing missing values ('geom_line()').
```

Statistical Tests

did sex affect pgp bcrp or mrp2_coloc2 did prep affect pgp parameters were true and false coloc in mrp2 statistically different

```
#normality
#pgp
car::qqPlot(pgp_sumstats_animals$r_mean)
```
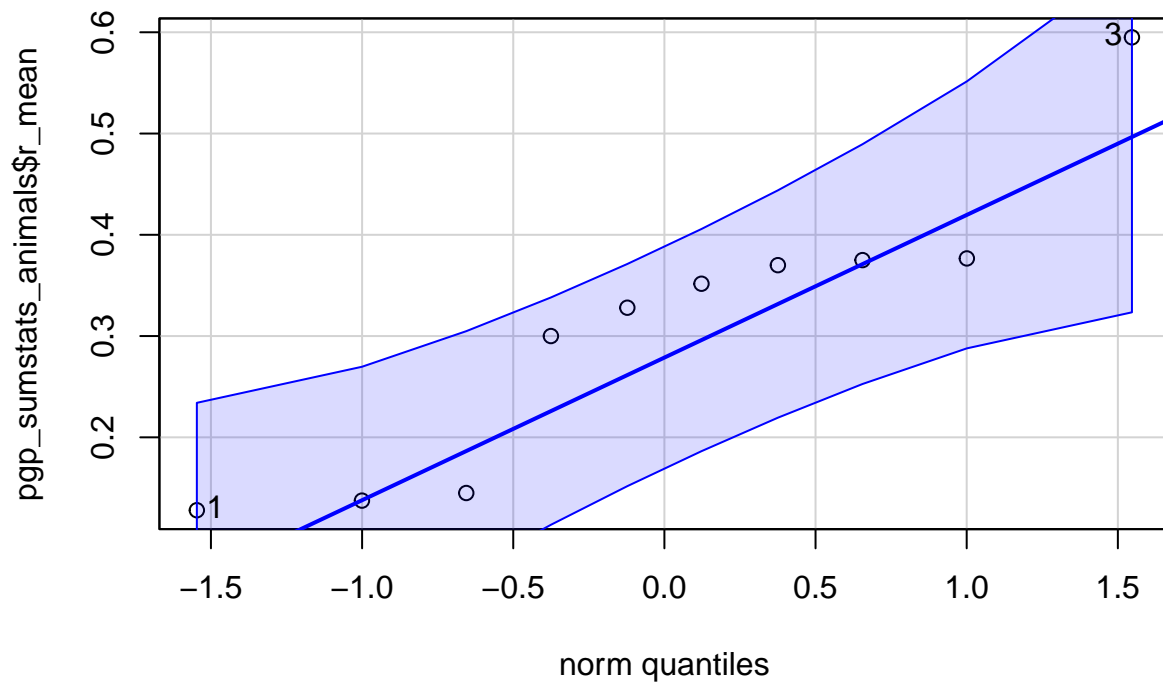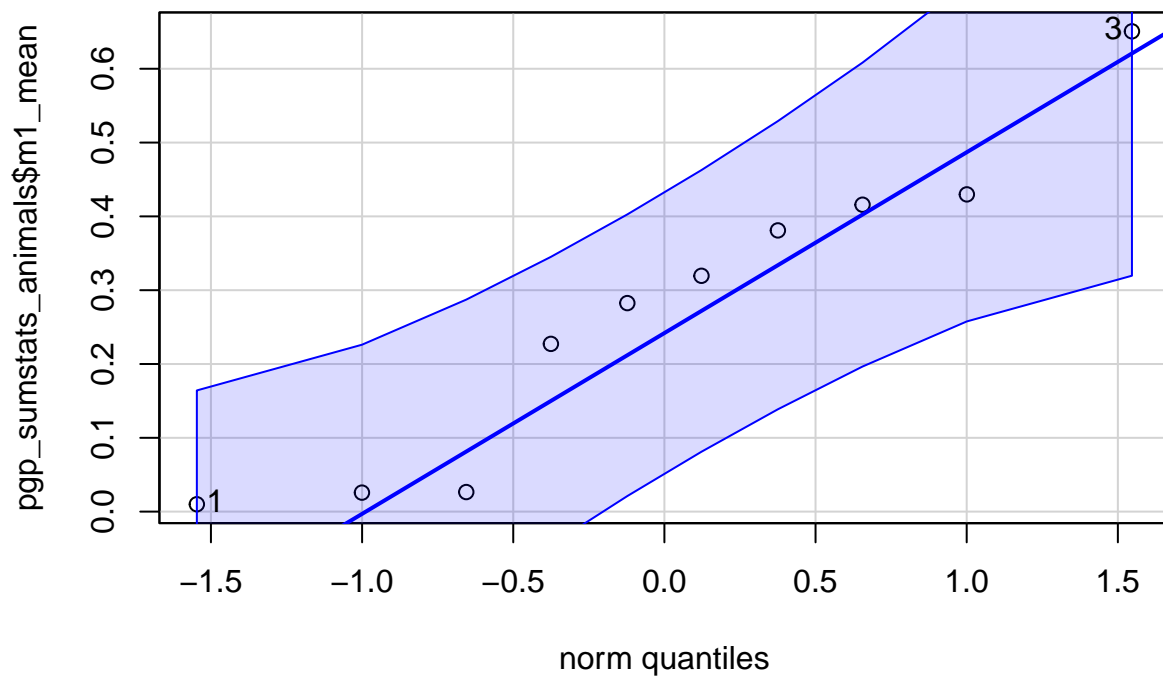


```
## [1] 3 1
```

```
shapiro.test(pgp_sumstats_animals$r_mean)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  pgp_sumstats_animals$r_mean
## W = 0.88497, p-value = 0.1487
```
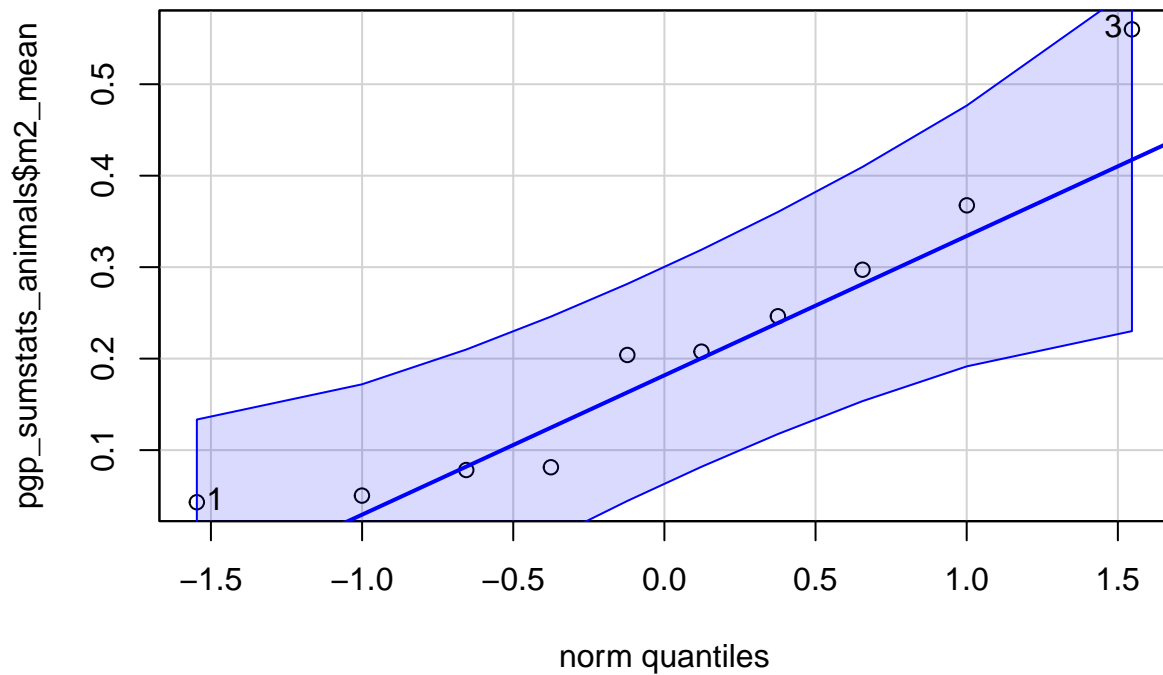
```
car::qqPlot(pgp_sumstats_animals$m1_mean)
```

```
## [1] 3 1
```

```
shapiro.test(pgp_sumstats_animals$m1_mean)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  pgp_sumstats_animals$m1_mean
## W = 0.92556, p-value = 0.4057
```

```
car::qqPlot(pgp_sumstats_animals$m2_mean)
```

```
## [1] 3 1
```

```
shapiro.test(pgp_sumstats_animals$m2_mean)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  pgp_sumstats_animals$m2_mean
## W = 0.90079, p-value = 0.2235
```

```
#hom variance
#pgp
leveneTest(pgp_sumstats_animals$r_mean ~ pgp_sumstats_animals$prep)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.6631  0.439
##        8
```

```
leveneTest(pgp_sumstats_animals$m1_mean ~ pgp_sumstats_animals$prep)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.7174 0.4216
##        8
```

21

```
leveneTest(pgp_sumstats_animals$m2_mean ~ pgp_sumstats_animals$prep)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.0011 0.9746
##        8
```

```
leveneTest(pgp_sumstats_animals$r_mean ~ pgp_sumstats_animals$sex)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1       0 0.9992
##        8
```

```
leveneTest(pgp_sumstats_animals$m1_mean ~ pgp_sumstats_animals$sex)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.0206 0.8893
##        8
```

```
leveneTest(pgp_sumstats_animals$m2_mean ~ pgp_sumstats_animals$sex)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  1.0683 0.3316
##        8
```

```
t.test(pgp_sumstats_animals$r_mean ~ pgp_sumstats_animals$prep)
```

```
##
##  Welch Two Sample t-test
##
## data:  pgp_sumstats_animals$r_mean by pgp_sumstats_animals$prep
## t = 2.5661, df = 6.4019, p-value = 0.04019
## alternative hypothesis: true difference in means between group section and group wm is not equal to 0
## 95 percent confidence interval:
##   0.01140926 0.36409074
## sample estimates:
## mean in group section      mean in group wm
##            0.4233333             0.2355833
```

```
t.test(pgp_sumstats_animals$m1_mean ~ pgp_sumstats_animals$prep)
```

```
##
##  Welch Two Sample t-test
##
## data:  pgp_sumstats_animals$m1_mean by pgp_sumstats_animals$prep
## t = 1.8892, df = 7.3837, p-value = 0.09861
```

```
## alternative hypothesis: true difference in means between group section and group wm is not equal to 0
## 95 percent confidence interval:
##  -0.05230006  0.49076672
## sample estimates:
## mean in group section     mean in group wm
##             0.4084167            0.1891833
```

```
t.test(pgp_sumstats_animals$m2_mean ~ pgp_sumstats_animals$prep)
```

```
##
##  Welch Two Sample t-test
##
## data:  pgp_sumstats_animals$m2_mean by pgp_sumstats_animals$prep
## t = 1.4663, df = 5.6489, p-value = 0.1959
## alternative hypothesis: true difference in means between group section and group wm is not equal to 0
## 95 percent confidence interval:
##  -0.1052348  0.4083848
## sample estimates:
## mean in group section     mean in group wm
##             0.304500             0.152925
```

```
t.test(pgp_sumstats_animals$r_mean ~ pgp_sumstats_animals$sex)
```

```
##
##  Welch Two Sample t-test
##
## data:  pgp_sumstats_animals$r_mean by pgp_sumstats_animals$sex
## t = 1.6219, df = 3.0889, p-value = 0.2007
## alternative hypothesis: true difference in means between group F and group M is not equal to 0
## 95 percent confidence interval:
##  -0.1497504  0.4716075
## sample estimates:
## mean in group F mean in group M
##       0.4233333       0.2624048
```

```
t.test(pgp_sumstats_animals$m1_mean ~ pgp_sumstats_animals$sex)
```

```
##
##  Welch Two Sample t-test
##
## data:  pgp_sumstats_animals$m1_mean by pgp_sumstats_animals$sex
## t = 1.5664, df = 3.3755, p-value = 0.2052
## alternative hypothesis: true difference in means between group F and group M is not equal to 0
## 95 percent confidence interval:
##  -0.2005908  0.6416257
## sample estimates:
## mean in group F mean in group M
##       0.4312389       0.2107214
```

```
t.test(pgp_sumstats_animals$m2_mean ~ pgp_sumstats_animals$sex)
```

```
##
##  Welch Two Sample t-test
##
## data:  pgp_sumstats_animals$m2_mean by pgp_sumstats_animals$sex
## t = 0.95877, df = 2.4344, p-value = 0.4229
## alternative hypothesis: true difference in means between group F and group M is not equal to 0
## 95 percent confidence interval:
##  -0.3932192  0.6739668
## sample estimates:
## mean in group F mean in group M
##       0.3118167       0.1714429
```

```
#normality
car::qqPlot(bcrp_sumstats_animals$r_mean)
```
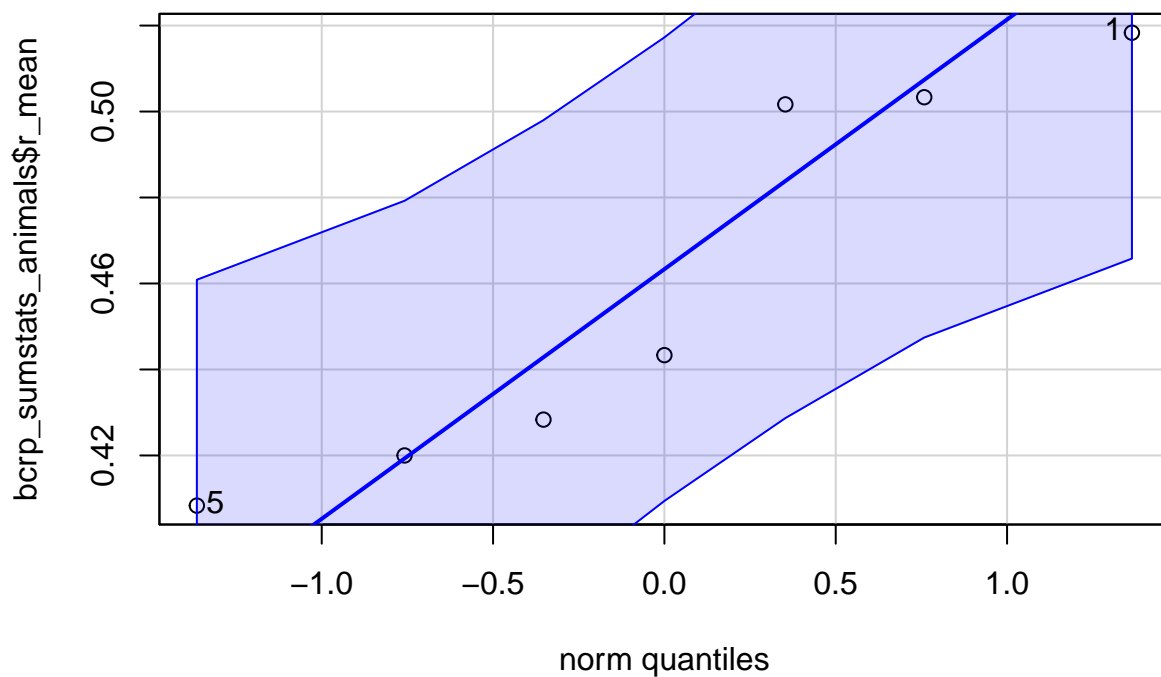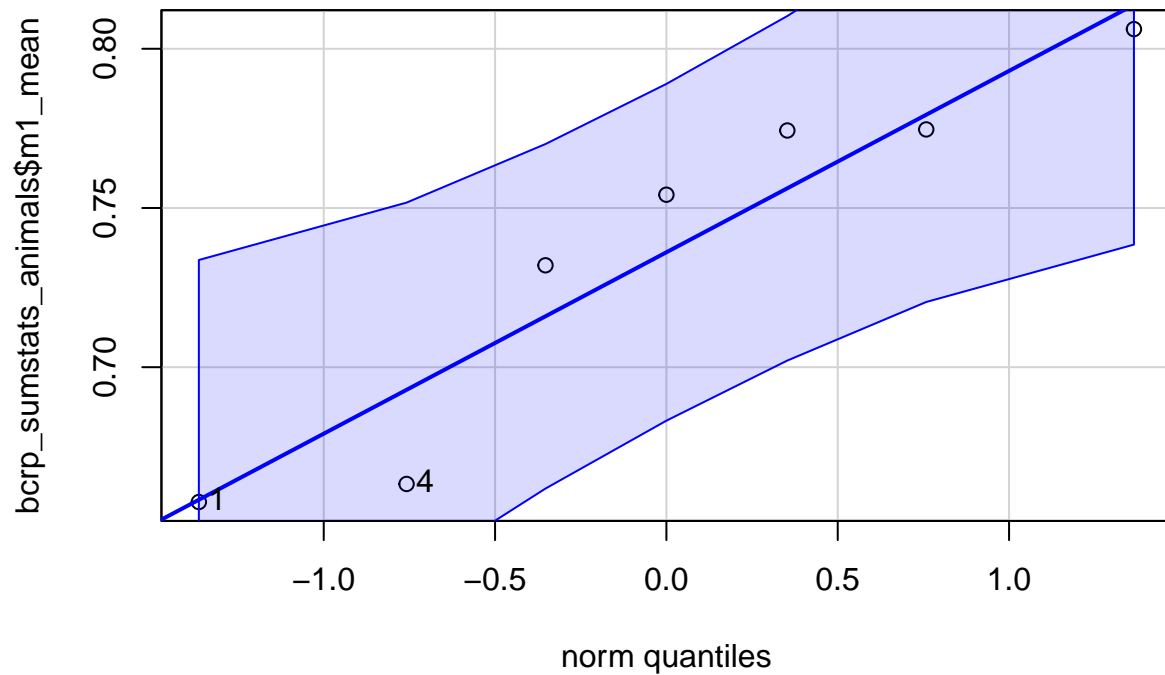


```
## [1] 1 5
```

```
shapiro.test(bcrp_sumstats_animals$r_mean)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  bcrp_sumstats_animals$r_mean
## W = 0.86316, p-value = 0.1616
```

```
car::qqPlot(bcrp_sumstats_animals$m1_mean)
```
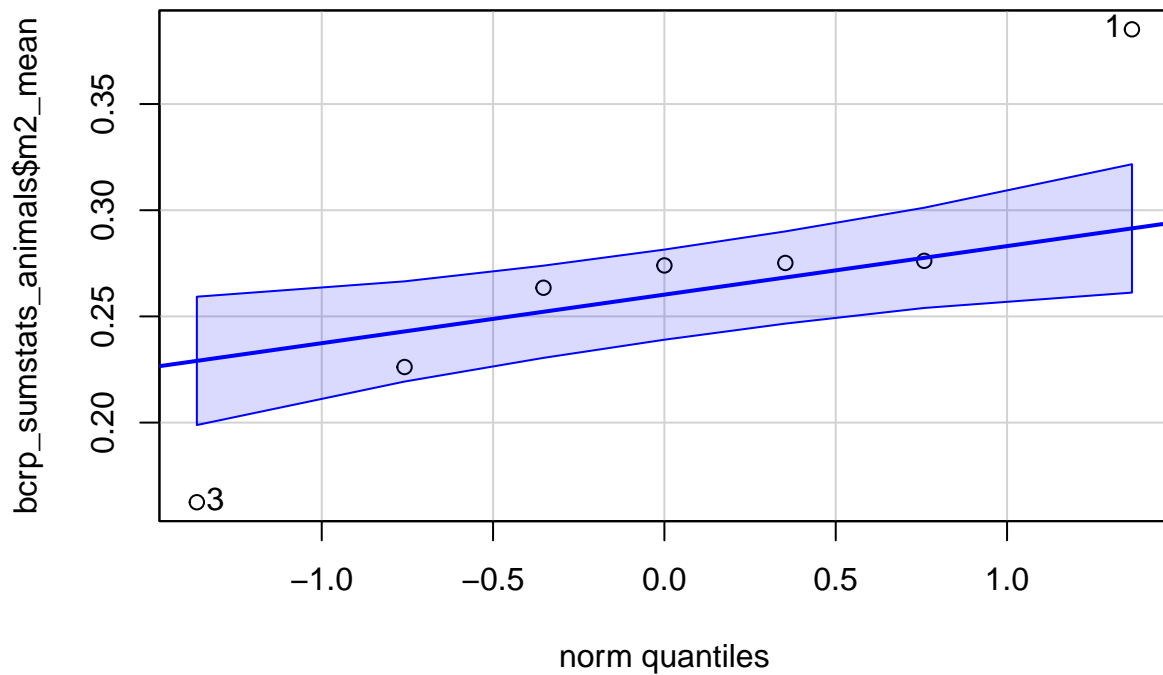


```
## [1] 1 4
```

```
shapiro.test(bcrp_sumstats_animals$m1_mean)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  bcrp_sumstats_animals$m1_mean
## W = 0.89064, p-value = 0.278
```

```
car::qqPlot(bcrp_sumstats_animals$m2_mean)
```

```
## [1] 1 3
```

```
shapiro.test(bcrp_sumstats_animals$m2_mean)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  bcrp_sumstats_animals$m2_mean
## W = 0.90418, p-value = 0.3571
```

```
#hom variance
leveneTest(bcrp_sumstats_animals$r_mean ~ bcrp_sumstats_animals$sex)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1   3e-04 0.9874
##        5
```

```
leveneTest(bcrp_sumstats_animals$m1_mean ~ bcrp_sumstats_animals$sex)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.0039 0.9525
##        5
```

```
leveneTest(bcrp_sumstats_animals$m2_mean ~ bcrp_sumstats_animals$sex)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.2912 0.6126
##        5
```

```
t.test(bcrp_sumstats_animals$r_mean ~ bcrp_sumstats_animals$sex)
```

```
##
##  Welch Two Sample t-test
##
## data:  bcrp_sumstats_animals$r_mean by bcrp_sumstats_animals$sex
## t = 1.1212, df = 4.0922, p-value = 0.3236
## alternative hypothesis: true difference in means between group F and group M is not equal to 0
## 95 percent confidence interval:
##  -0.05676176  0.13481732
## sample estimates:
## mean in group F mean in group M
##       0.4827778       0.4437500
```

```
t.test(bcrp_sumstats_animals$m1_mean ~ bcrp_sumstats_animals$sex)
```

```
##
##  Welch Two Sample t-test
##
## data:  bcrp_sumstats_animals$m1_mean by bcrp_sumstats_animals$sex
## t = -0.61594, df = 4.5571, p-value = 0.5674
## alternative hypothesis: true difference in means between group F and group M is not equal to 0
## 95 percent confidence interval:
##  -0.14968102  0.09318102
## sample estimates:
## mean in group F mean in group M
##       0.7213333       0.7495833
```

```
t.test(bcrp_sumstats_animals$m2_mean ~ bcrp_sumstats_animals$sex)
```

```
##
##  Welch Two Sample t-test
##
## data:  bcrp_sumstats_animals$m2_mean by bcrp_sumstats_animals$sex
## t = 0.93166, df = 3.3313, p-value = 0.414
## alternative hypothesis: true difference in means between group F and group M is not equal to 0
## 95 percent confidence interval:
##  -0.1133118  0.2148674
## sample estimates:
## mean in group F mean in group M
##       0.2951111       0.2443333
```

```
mrp2_sumstats_animals_wide <- mrp2_sumstats_animals %>%
  pivot_wider(id_cols=!c(n_coloc, n_total), names_from = coloc,
              values_from = c(r_mean, r_sd, m1_mean, m1_sd, m2_mean, m2_sd))

colnames(mrp2_sumstats_animals_wide)
```
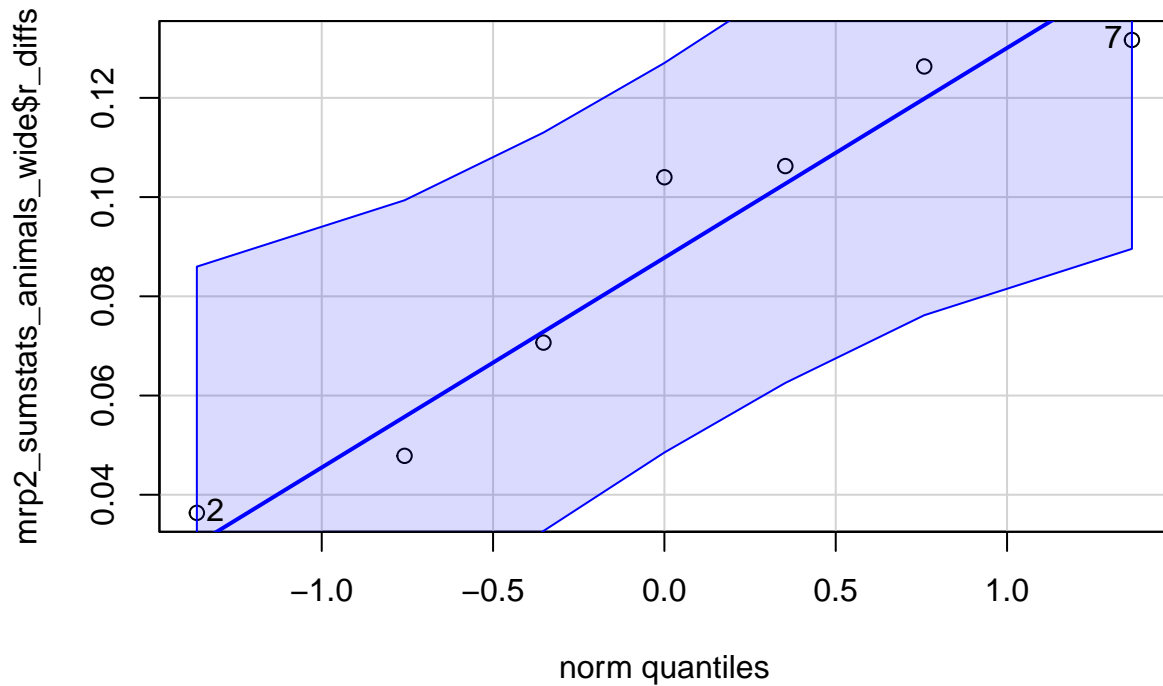
```
## [1] "mouseID"        "sex"           "r_mean_FALSE"  "r_mean_TRUE"
## [5] "r_sd_FALSE"     "r_sd_TRUE"     "m1_mean_FALSE" "m1_mean_TRUE"
## [9] "m1_sd_FALSE"    "m1_sd_TRUE"    "m2_mean_FALSE" "m2_mean_TRUE"
## [13] "m2_sd_FALSE"   "m2_sd_TRUE"
```

```
#checking normality of differences for paired t test
```

```
mrp2_sumstats_animals_wide <- mrp2_sumstats_animals_wide %>%
  mutate(r_diffs = r_mean_TRUE - r_mean_FALSE,
         m1_diffs = m1_mean_TRUE - m1_mean_FALSE,
         m2_diffs = m2_mean_TRUE - m2_mean_FALSE)
```

```
car::qqPlot(mrp2_sumstats_animals_wide$r_diffs)
```
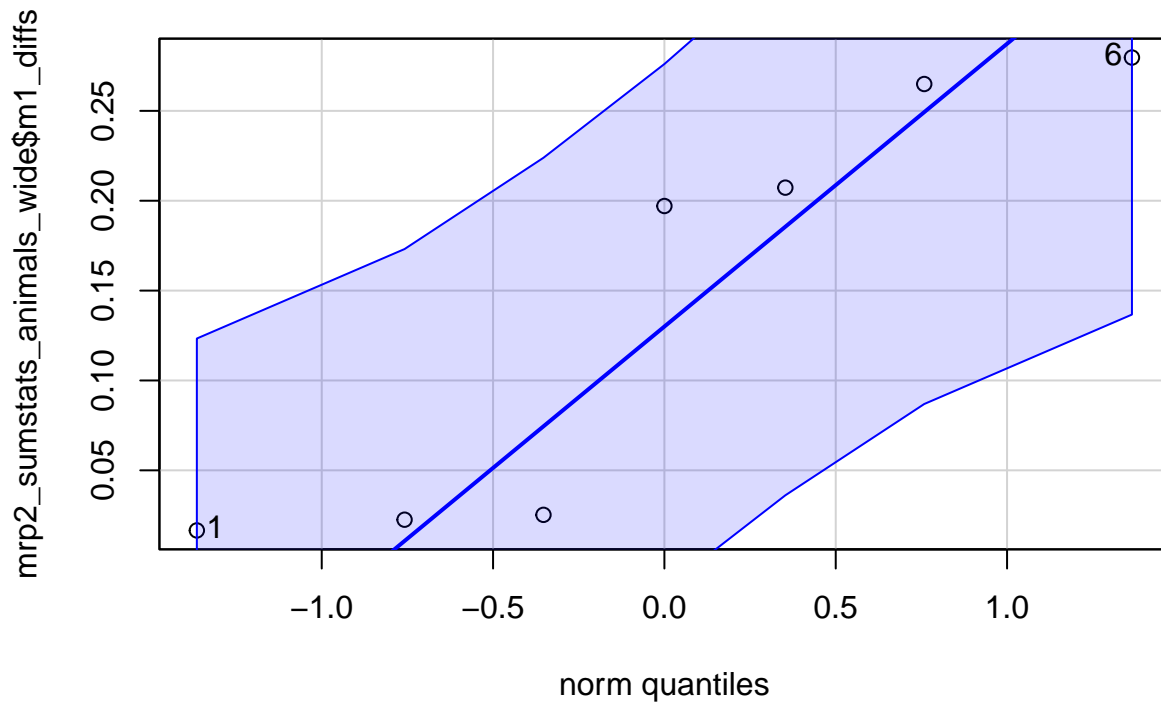


```
## [1] 2 7
```

```
shapiro.test(mrp2_sumstats_animals_wide$r_diffs)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  mrp2_sumstats_animals_wide$r_diffs
## W = 0.91102, p-value = 0.403
```

```
mrp2_sumstats_animals_wide %>% rstatix::identify_outliers(r_diffs)
```

```
##  [1] mouseID        sex            r_mean_FALSE   r_mean_TRUE    r_sd_FALSE
##  [6] r_sd_TRUE      m1_mean_FALSE  m1_mean_TRUE   m1_sd_FALSE    m1_sd_TRUE
## [11] m2_mean_FALSE  m2_mean_TRUE   m2_sd_FALSE    m2_sd_TRUE     r_diffs
## [16] m1_diffs       m2_diffs       is.outlier     is.extreme
## <0 rows> (or 0-length row.names)
```

```
car::qqPlot(mrp2_sumstats_animals_wide$m1_diffs)
```
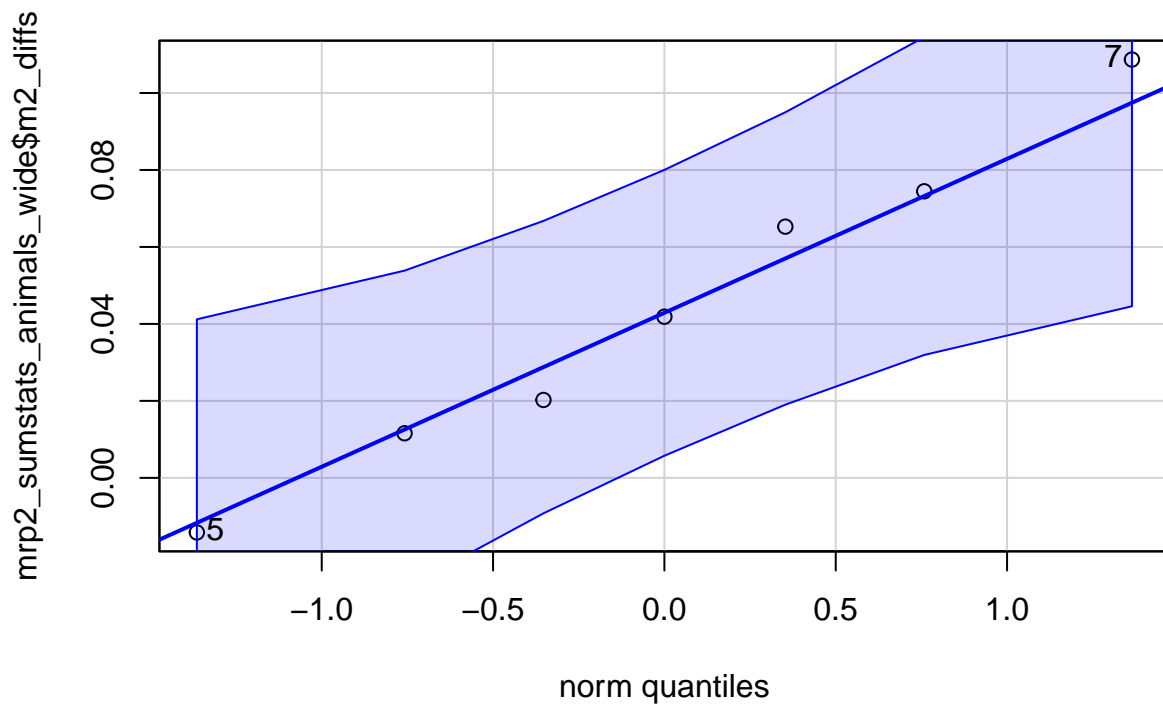


```
## [1] 6 1
```

```
shapiro.test(mrp2_sumstats_animals_wide$m1_diffs)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  mrp2_sumstats_animals_wide$m1_diffs
## W = 0.8148, p-value = 0.0572
```

```
mrp2_sumstats_animals_wide %>% rstatix::identify_outliers(m1_diffs)
```

```
##  [1] mouseID       sex           r_mean_FALSE  r_mean_TRUE   r_sd_FALSE
##  [6] r_sd_TRUE     m1_mean_FALSE m1_mean_TRUE  m1_sd_FALSE   m1_sd_TRUE
## [11] m2_mean_FALSE m2_mean_TRUE  m2_sd_FALSE   m2_sd_TRUE    r_diffs
## [16] m1_diffs      m2_diffs      is.outlier    is.extreme
## <0 rows> (or 0-length row.names)
```

```
car::qqPlot(mrp2_sumstats_animals_wide$m2_diffs)
```



```
## [1] 7 5
```

```
shapiro.test(mrp2_sumstats_animals_wide$m2_diffs)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  mrp2_sumstats_animals_wide$m2_diffs
## W = 0.98371, p-value = 0.9756
```

```
mrp2_sumstats_animals_wide %>% rstatix::identify_outliers(m2_diffs)
```

```
## [1] mouseID        sex            r_mean_FALSE  r_mean_TRUE    r_sd_FALSE
## [6] r_sd_TRUE      m1_mean_FALSE  m1_mean_TRUE  m1_sd_FALSE    m1_sd_TRUE
## [11] m2_mean_FALSE m2_mean_TRUE   m2_sd_FALSE   m2_sd_TRUE     r_diffs
## [16] m1_diffs      m2_diffs       is.outlier    is.extreme
## <0 rows> (or 0-length row.names)
```

```
mrp2_sumstats_animals$r_mean <- replace_na(mrp2_sumstats_animals$r_mean, 0)
mrp2_sumstats_animals$m1_mean <- replace_na(mrp2_sumstats_animals$m1_mean, 0)
mrp2_sumstats_animals$m2_mean <- replace_na(mrp2_sumstats_animals$m2_mean, 0)

t.test(mrp2_sumstats_animals$r_mean ~ mrp2_sumstats_animals$coloc, paired = TRUE)
```

```
##
##  Paired t-test
##
## data:  mrp2_sumstats_animals$r_mean by mrp2_sumstats_animals$coloc
## t = -5.2485, df = 7, p-value = 0.001188
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.11613005 -0.04399006
## sample estimates:
## mean difference
##     -0.08006006
```

```
t.test(mrp2_sumstats_animals$m1_mean ~ mrp2_sumstats_animals$coloc, paired = TRUE)
```

```
##
##  Paired t-test
##
## data:  mrp2_sumstats_animals$m1_mean by mrp2_sumstats_animals$coloc
## t = -2.5217, df = 7, p-value = 0.03971
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.229578325 -0.007378891
## sample estimates:
## mean difference
##      -0.1184786
```

```
t.test(mrp2_sumstats_animals$m2_mean ~ mrp2_sumstats_animals$coloc, paired = TRUE)
```

```
##
##  Paired t-test
##
## data:  mrp2_sumstats_animals$m2_mean by mrp2_sumstats_animals$coloc
## t = -1.4724, df = 7, p-value = 0.1844
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.07675553  0.01784720
## sample estimates:
## mean difference
##     -0.02945417
```

```
# sex effect within positive regions
t.test(mrp2_sumstats_animals_wide$r_mean_TRUE ~ mrp2_sumstats_animals_wide$sex)
```

```
##
##  Welch Two Sample t-test
##
## data:  mrp2_sumstats_animals_wide$r_mean_TRUE by mrp2_sumstats_animals_wide$sex
## t = -0.16703, df = 4.1587, p-value = 0.8752
## alternative hypothesis: true difference in means between group F and group M is not equal to 0
## 95 percent confidence interval:
##  -0.08887805  0.07864789
## sample estimates:
## mean in group F mean in group M
##      0.08663492      0.09175000
```

```
t.test(mrp2_sumstats_animals_wide$m1_mean_TRUE ~ mrp2_sumstats_animals_wide$sex)
```

```
##
##  Welch Two Sample t-test
##
## data:  mrp2_sumstats_animals_wide$m1_mean_TRUE by mrp2_sumstats_animals_wide$sex
## t = -1.0766, df = 4.8677, p-value = 0.3321
## alternative hypothesis: true difference in means between group F and group M is not equal to 0
## 95 percent confidence interval:
##  -0.3461774  0.1429766
## sample estimates:
## mean in group F mean in group M
##       0.1242127       0.2258131
```

```
t.test(mrp2_sumstats_animals_wide$m2_mean_TRUE ~ mrp2_sumstats_animals_wide$sex)
```

```
##
##  Welch Two Sample t-test
##
## data:  mrp2_sumstats_animals_wide$m2_mean_TRUE by mrp2_sumstats_animals_wide$sex
## t = -1.1256, df = 4.9927, p-value = 0.3115
## alternative hypothesis: true difference in means between group F and group M is not equal to 0
## 95 percent confidence interval:
##  -0.23682453  0.09263127
## sample estimates:
## mean in group F mean in group M
##       0.2139683       0.2860649
```

```
mrp2_r_plot_sex <- mrp2_sumstats_animals_wide %>%
  ggplot(aes(x=sex, y=r_mean_TRUE)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.2) +
  geom_jitter(color="black", width=0.1, aes(shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw(12) +
```

```
  guides(shape=guide_legend("Sex"), color = "none") +
  ylim(-0.1,0.65) +
  ggtitle("Mrp2")
```
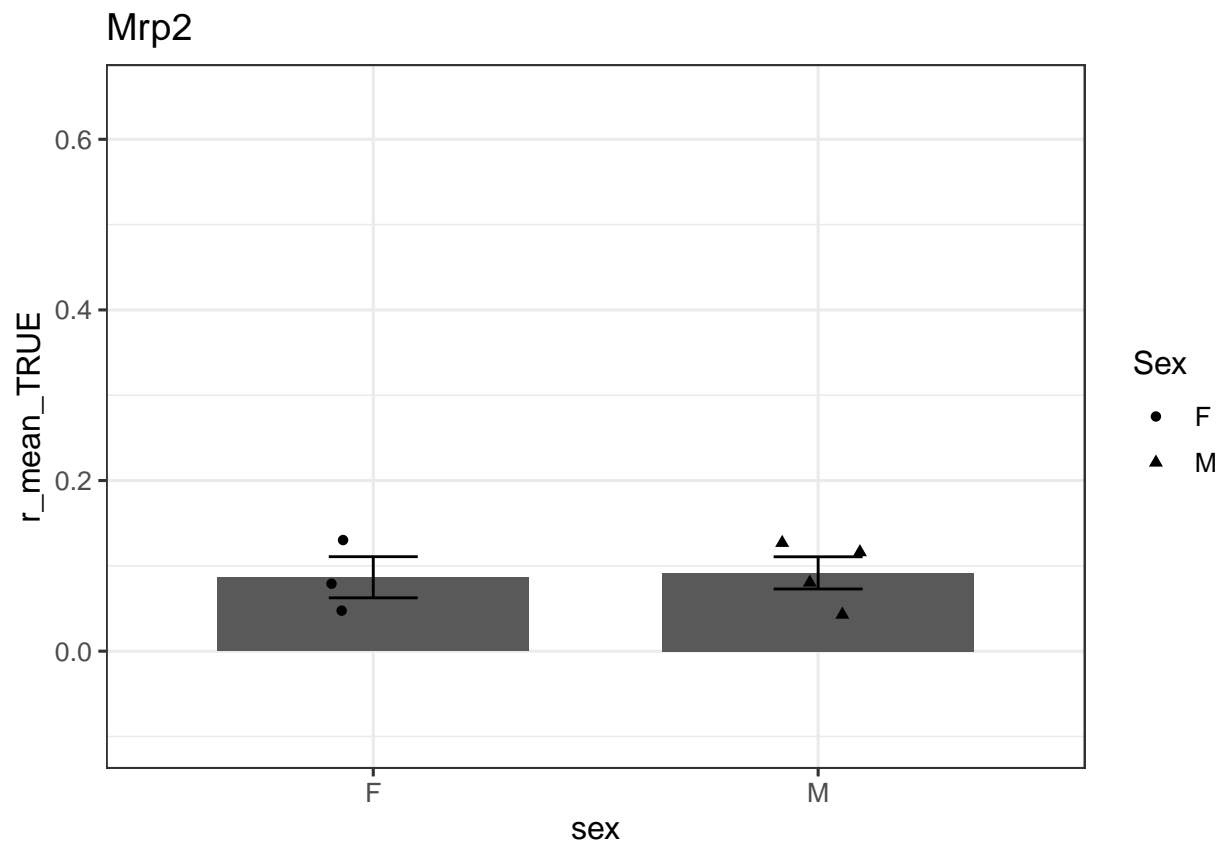
```
mrp2_r_plot_sex
```

Warning: Removed 1 rows containing non-finite values ('stat_summary()').
Removed 1 rows containing non-finite values ('stat_summary()').

Warning: Removed 1 rows containing missing values ('geom_point()').


```
ggsave("../figures/mrp2_r_plot_sex.png", plot=mrp2_r_plot_sex, width=3, height=3)
```

Warning: Removed 1 rows containing non-finite values ('stat_summary()').

Warning: Removed 1 rows containing non-finite values ('stat_summary()').

Warning: Removed 1 rows containing missing values ('geom_point()').

```
ggsave("../figures/mrp2_r_plot_sex.svg", plot=mrp2_r_plot_sex, width=3, height=3)
```

Warning: Removed 1 rows containing non-finite values ('stat_summary()').

Warning: Removed 1 rows containing non-finite values (‘stat_summary()‘).

Warning: Removed 1 rows containing missing values (‘geom_point()‘).

```
mrp2_m1_plot_sex <- ggplot(mrp2_sumstats_animals_wide, aes(x=sex, y=m1_mean_TRUE)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.2) +
  geom_jitter(color="black", width=0.1, aes(shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw(12) +
  guides(shape=guide_legend("Sex"), color = "none") +
  ylim(-0.05,0.9) +
  ggtitle("Mrp2")

mrp2_m1_plot_sex
```

Warning: Removed 1 rows containing non-finite values (‘stat_summary()‘).

Warning: Removed 1 rows containing non-finite values (‘stat_summary()‘).

Warning: Removed 1 rows containing missing values (‘geom_point()‘).
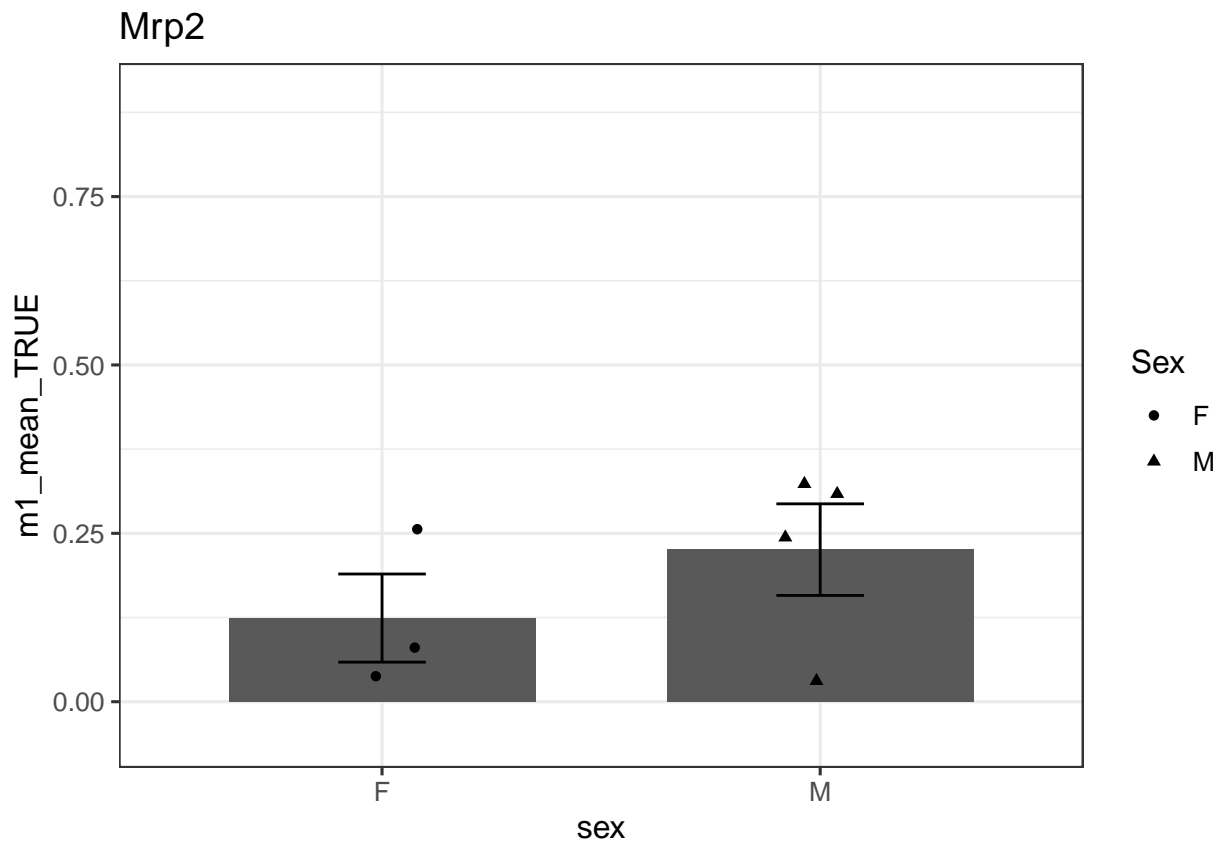
```
ggsave("../figures/mrp2_m1_plot_sex.png", plot=mrp2_m1_plot_sex, width=3, height=3)
```

Warning: Removed 1 rows containing non-finite values ('stat_summary()').

Warning: Removed 1 rows containing non-finite values ('stat_summary()').

Warning: Removed 1 rows containing missing values ('geom_point()').

```
ggsave("../figures/mrp2_m1_plot_sex.svg", plot=mrp2_m1_plot_sex, width=3, height=3)
```

Warning: Removed 1 rows containing non-finite values ('stat_summary()').

Warning: Removed 1 rows containing non-finite values ('stat_summary()').

Warning: Removed 1 rows containing missing values ('geom_point()').

```
mrp2_m2_plot_sex <- ggplot(mrp2_sumstats_animals_wide, aes(x=sex, y=m2_mean_TRUE)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.2) +
  geom_jitter(color="black", width=0.1, aes(shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw(12) +
  guides(shape=guide_legend("Sex"), color = "none") +
  ylim(-0.05,0.9) +
  ggtitle("Mrp2")

mrp2_m2_plot_sex
```

Warning: Removed 1 rows containing non-finite values ('stat_summary()').

Warning: Removed 1 rows containing non-finite values ('stat_summary()').

Warning: Removed 1 rows containing missing values ('geom_point()').

```
ggsave("../figures/mrp2_m2_plot_sex.png", plot=mrp2_m2_plot_sex, width=3, height=3)
```

```
## Warning: Removed 1 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 1 rows containing non-finite values ('stat_summary()').
```
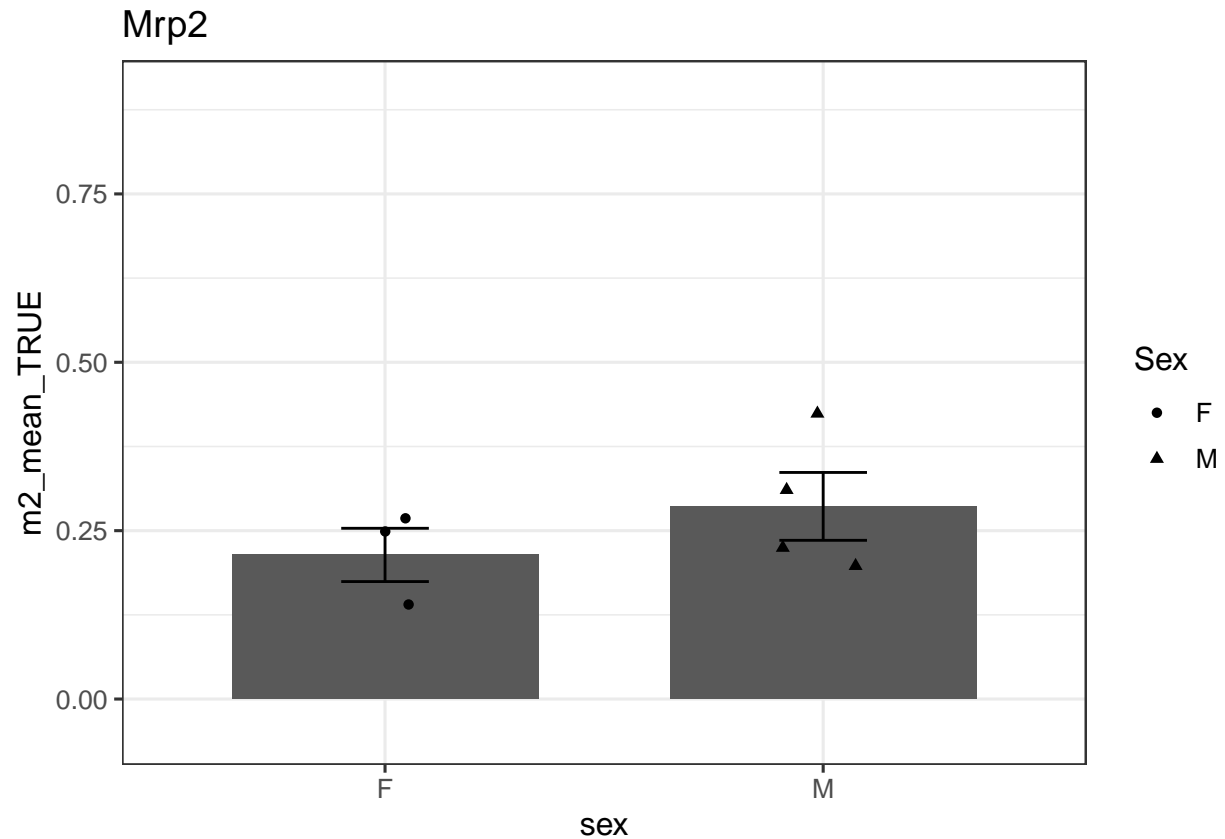
```
## Warning: Removed 1 rows containing missing values ('geom_point()').
```

```
ggsave("../figures/mrp2_m2_plot_sex.svg", plot=mrp2_m2_plot_sex, width=3, height=3)
```

```
## Warning: Removed 1 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 1 rows containing non-finite values ('stat_summary()').
```

```
## Warning: Removed 1 rows containing missing values ('geom_point()').
```

```
intersect(pgp_sumstats_animals$mouseID,bcrp_sumstats_animals$mouseID)
```

```
## [1] "80" "81" "82"
```

```
intersect(pgp_sumstats_animals$mouseID,mrp2_sumstats_animals$mouseID)
```

```
## [1] "81" "82"
```

```
intersect(bcrp_sumstats_animals$mouseID,mrp2_sumstats_animals$mouseID)
```

```
## [1] "22" "40" "81" "82" "92" "98"
```

```
intersect(intersect(pgp_sumstats_animals$mouseID,bcrp_sumstats_animals$mouseID),mrp2_sumstats_animals$mo
```

```
## [1] "81" "82"
```