Transporter (P-gp) Colocalization Analysis (ImageJ Coloc2)

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

Reading in the data

P-gp

```
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_
  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,}")),
         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)
```

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

head(pgp_coloc2)
```

```
##   sex mouseID prep         image    m1    m2 r_pearson Pval r_rand sd_rand coloc
## 2   F      87   wm       wm-20x-1 0.010 0.047      0.21    1   0.01       0  TRUE
## 3   F      87   wm       wm-20x-2 0.021 0.044      0.28    1  -0.01       0  TRUE
## 4   F      87   wm       wm-20x-3 0.655 0.585      0.33    1   0.00       0  TRUE
## 5   F      87   wm       wm-20x-4 0.719 0.479      0.38    1  -0.01       0  TRUE
## 6   F      87   wm       wm-20x-5 0.674 0.331      0.30    1   0.00       0  TRUE
## 7   M      10   wm GFP-wm-20x-1 0.012 0.040      0.13    1  -0.01       0  TRUE
```

Bcrp

```r
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") %>% 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_
  bcrp_coloc2 <- rbind(bcrp_coloc2, res)
}
```

```
## [1] "F-22-section1-40x-1-avg4"
## [1] "F-22-section1-40x-2-avg4"
## [1] "F-22-section1-40x-3-avg4"
## [1] "F-22-section3-40x-1-avg4"
## [1] "F-22-section3-40x-2-avg4"
## [1] "F-22-section3-40x-3-avg4"
## [1] "F-GTL-section1-40x-1-avg4"
## [1] "F-GTL-section1-40x-2-avg4"
## [1] "F-GTL-section1-40x-3-avg4"
## [1] "F-GTL-section3-40x-1-avg4"
## [1] "F-GTL-section3-40x-2-avg4"
## [1] "F-GTL-section3-40x-3-avg4"
## [1] "F-McKO-98-section1-40x-1-avg4"
## [1] "F-McKO-98-section1-40x-2-avg4"
## [1] "F-McKO-98-section1-40x-3-avg4"
## [1] "F-McKO-98-section3-40x-1-avg4"
## [1] "F-McKO-98-section3-40x-2-avg4"
## [1] "F-McKO-98-section3-40x-3-avg4"
```

```
## [1] "M-80-section1-40x-1-avg4"
## [1] "M-80-section1-40x-2-avg4"
## [1] "M-80-section1-40x-3-avg4"
## [1] "M-80-section3-40x-1-avg4"
## [1] "M-80-section3-40x-2-avg4"
## [1] "M-80-section3-40x-3-avg4"
## [1] "M-81-section1-40x-1-avg4"
## [1] "M-81-section1-40x-2-avg4"
## [1] "M-81-section1-40x-3-avg4"
## [1] "M-81-section3-40x-1-avg4"
## [1] "M-81-section3-40x-2-avg4"
## [1] "M-81-section3-40x-3-avg4"
## [1] "M-82-section1-40x-1-avg4"
## [1] "M-82-section1-40x-2-avg4"
## [1] "M-82-section1-40x-3-avg4"
## [1] "M-82-section3-40x-1-avg4"
## [1] "M-82-section3-40x-2-avg4"
## [1] "M-82-section3-40x-3-avg4"
## [1] "M-McKO-92-section1-40x-1-avg4"
## [1] "M-McKO-92-section1-40x-2-avg4"
## [1] "M-McKO-92-section1-40x-3-avg4"
## [1] "M-McKO-92-section3-40x-1-avg4"
## [1] "M-McKO-92-section3-40x-2-avg4"
## [1] "M-McKO-92-section3-40x-3-avg4"
```

```r
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")

head(bcrp_coloc2)
```

```
##   sex mouseID    prep              image    m1    m2 r_pearson Pval r_rand
## 2   F      22 section section1-40x-1-avg4 0.618 0.229      0.32    1      0
## 3   F      22 section section1-40x-2-avg4 0.787 0.359      0.63    1      0
## 4   F      22 section section1-40x-3-avg4 0.782 0.290      0.51    1      0
## 5   F      22 section section3-40x-1-avg4 0.517 0.461      0.49    1      0
## 6   F      22 section section3-40x-2-avg4 0.687 0.541      0.58    1      0
## 7   F      22 section section3-40x-3-avg4 0.555 0.431      0.58    1      0
##   sd_rand coloc
## 2       0  TRUE
## 3       0  TRUE
```

```
## 4          0  TRUE
## 5          0  TRUE
## 6          0  TRUE
## 7          0  TRUE
```

Mrp2

```r
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)))
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")

head(mrp2_coloc2)
```

```
##   sex mouseID          image  roi    m1    m2 r_pearson Pval r_rand sd_rand
## 2   F      22 section2-40x-1 gcl1 0.063 0.360      0.12 1.00  -0.01    0.04
## 3   F      22 section2-40x-1 inl1 0.000 0.087     -0.01 0.34   0.00    0.02
## 4   F      22 section2-40x-1 inl2 0.000 0.097     -0.03 0.12   0.00    0.02
## 5   F      22 section2-40x-2 gcl1 0.111 0.001      0.01 0.77   0.00    0.01
## 6   F      22 section2-40x-2 inl1 0.000 0.183     -0.02 0.18   0.00    0.03
## 7   F      22 section2-40x-3 gcl1 0.000 0.181     -0.02 0.14   0.00    0.02
##   coloc
```

```
## 2  TRUE
## 3 FALSE
## 4 FALSE
## 5 FALSE
## 6 FALSE
## 7 FALSE
```

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
```

```
##     m1_mean    m1_sd m2_mean     m2_sd    r_mean      r_sd n_total n_coloc
## 1 0.2532927 0.294287 0.195439 0.2355011 0.2804878 0.1387795      41      41
```

```
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)
                    )
bcrp_sumstats
```

```
##     m1_mean    m1_sd  m2_mean     m2_sd    r_mean     r_sd n_total n_coloc
## 1 0.7374762 0.1322315 0.2660952 0.08701775 0.4604762 0.104437      42      42
```

```
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
```

```
##      m1_mean      m1_sd   m2_mean     m2_sd     r_mean        r_sd n_total n_coloc
## 1 0.1098828 0.1436731 0.2081172 0.1569569 0.03496552 0.07127923     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
mrp2_sumstats_image
```

```
## # A tibble: 59 x 12
## # Groups:   image, mouseID, sex [40]
##      image   mouseID sex   coloc m1_mean  m1_sd m2_mean  m2_sd r_mean      r_sd
##      <chr>   <fct>   <fct> <lgl>   <dbl>  <dbl>   <dbl>  <dbl>  <dbl>     <dbl>
##  1 section~ 40      F     FALSE  0.0527 0.0352  0.0933  0.107  0.0167  0.00577
##  2 section~ 92      M     FALSE  0       0       0.204  0.0566 -0.055  0.0778
##  3 section~ 40      F     FALSE  0.155  NA      0.023  NA      0.02    NA
##  4 section~ 40      F     TRUE   0.127  0.0396  0.129  0.0465  0.0533  0.00577
##  5 section~ 92      M     FALSE  0.019  0.0329  0.213  0.0721  0       0.0346
##  6 section~ 40      F     FALSE  0      NA      0.079  NA      0       NA
##  7 section~ 40      F     TRUE   0.0465 0.0573  0.102  0.0983  0.025   0.00707
##  8 section~ 92      M     FALSE  0      NA      0.352  NA      -0.02   NA
##  9 section~ 92      M     TRUE   0.308  0.0629  0.258  0.0643  0.11    0.0283
## 10 section~ 40      F     FALSE  0.013  NA      0.362  NA      0.02    NA
## # ... with 49 more rows, and 2 more variables: n_total <int>, n_coloc <int>
```

```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: 8 x 11
## # Groups:   mouseID, sex [8]
##   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 80      M     section   0.320  0.282    0.246 0.290   0.37  0.140        6
## 4 81      M     section   0.283  0.251    0.204 0.286   0.377 0.0838       6
## 5 82      M     section   0.381  0.325    0.208 0.270   0.352 0.183        6
## 6 83      M     wm        0.430  0.373    0.368 0.274   0.328 0.0804       5
## 7 87      F     wm        0.416  0.366    0.297 0.247   0.3   0.0628       5
## 8 9       M     wm        0.0265 0.0155  0.0812 0.0538  0.138 0.0419       4
## # ... with 1 more variable: n_coloc <int>
```

```
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)
            )
```

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

```
bcrp_sumstats_animals
```

```
## # A tibble: 7 x 11
## # 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 1 more variable: n_coloc <int>
```

```
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.
```

```
mrp2_sumstats_animals
```

```
## # A tibble: 15 x 11
## # Groups:   mouseID, sex [8]
##    mouseID sex   coloc m1_mean   m1_sd m2_mean  m2_sd   r_mean    r_sd n_total
##    <fct>   <fct> <lgl>   <dbl>   <dbl>   <dbl>  <dbl>    <dbl>   <dbl>   <int>
## 1  22      F     FALSE 0.0234  0.0497    0.202  0.118 -0.0262  0.0421      16
## 2  22      F     TRUE  0.04    0.0325    0.244  0.164  0.08    0.0566       2
## 3  40      F     FALSE 0.0543  0.0658    0.115  0.117  0.0122  0.0109       9
## 4  40      F     TRUE  0.0796  0.0552    0.136  0.0669 0.0486  0.0177       7
## 5  62      M     FALSE 0.0655  0.0959    0.0723 0.0747 -0.0174 0.0254      19
## 6  77      M     FALSE 0.035   0.0492    0.135  0.0385 0.00933 0.0249      15
## 7  77      M     TRUE  0.242   0.142     0.200  0.0504 0.08    0.0486       7
## 8  81      M     FALSE 0.00646 0.00785   0.434  0.239 -0.00385 0.0112      13
## 9  81      M     TRUE  0.029   0.0428    0.420  0.291  0.044   0.0313       5
## 10 82      M     FALSE 0.0468  0.0604    0.143  0.0994 0.024   0.0397       5
## 11 82      M     TRUE  0.326   0.170     0.218  0.116  0.128   0.0669      15
## 12 92      M     FALSE 0.0406  0.0896    0.198  0.103 -0.0167  0.0424       9
## 13 92      M     TRUE  0.306   0.0802    0.306  0.0831 0.115   0.03         4
## 14 98      F     FALSE 0.056   0.0752    0.251  0.0982 0.005   0.0404       4
## 15 98      F     TRUE  0.253   0.124     0.262  0.0856 0.131   0.0752      15
## # ... with 1 more variable: n_coloc <int>
```

```
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       0.416 0.366   0.297 0.247  0.3   0.0628       5       5
## 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    0.328 0.273   0.219 0.266  0.366 0.133      18      1
## 2 wm         0.195 0.303   0.177 0.213  0.213 0.103      23      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
```

Statistical Tests

```
coin::wilcox_test(pgp_sumstats_animals$r_mean ~ pgp_sumstats_animals$prep, conf.int=TRUE, distribution=
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  pgp_sumstats_animals$r_mean by pgp_sumstats_animals$prep (section, wm)
## Z = 2.2361, p-value = 0.03571
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  0.02366667 0.24866667
## sample estimates:
## difference in location
##              0.2141667
```

```
coin::wilcox_test(pgp_sumstats_animals$m1_mean ~ pgp_sumstats_animals$prep, conf.int=TRUE, distribution=
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  pgp_sumstats_animals$m1_mean by pgp_sumstats_animals$prep (section, wm)
## Z = 0.44721, p-value = 0.7857
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  -0.1473  0.3710
## sample estimates:
## difference in location
##                0.25675
```

```
coin::wilcox_test(pgp_sumstats_animals$m2_mean ~ pgp_sumstats_animals$prep, conf.int=TRUE, distribution=
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  pgp_sumstats_animals$m2_mean by pgp_sumstats_animals$prep (section, wm)
```

```
## Z = 0.44721, p-value = 0.7857
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  -0.1636000  0.2033333
## sample estimates:
## difference in location
##               0.1264167
```

```
pgp_wm_sumstats <- pgp_sumstats_animals %>% filter(prep == "wm")
```

```
coin::wilcox_test(pgp_wm_sumstats$r_mean ~ pgp_wm_sumstats$sex, conf.int=TRUE, distribution="exact")
```

```
## Warning in cci(alpha): cannot compute confidence interval
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  pgp_wm_sumstats$r_mean by pgp_wm_sumstats$sex (F, M)
## Z = 0.70711, p-value = 0.8
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  NA NA
## sample estimates:
## difference in location
##               0.15875
```

```
coin::wilcox_test(pgp_wm_sumstats$m1_mean ~ pgp_wm_sumstats$sex, conf.int=TRUE, distribution="exact")
```

```
## Warning in cci(alpha): cannot compute confidence interval
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  pgp_wm_sumstats$m1_mean by pgp_wm_sumstats$sex (F, M)
## Z = 0.70711, p-value = 0.8
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  NA NA
## sample estimates:
## difference in location
##               0.389675
```

```
coin::wilcox_test(pgp_wm_sumstats$m2_mean ~ pgp_wm_sumstats$sex, conf.int=TRUE, distribution="exact")
```

```
## Warning in cci(alpha): cannot compute confidence interval
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  pgp_wm_sumstats$m2_mean by pgp_wm_sumstats$sex (F, M)
## Z = 0.70711, p-value = 0.8
```

```
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  NA NA
## sample estimates:
## difference in location
##                0.23145
```

```
coin::wilcox_test(bcrp_sumstats_animals$r_mean ~ bcrp_sumstats_animals$sex, conf.int=TRUE, distribution=
```

```
## Warning in cci(alpha): cannot compute confidence interval
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  bcrp_sumstats_animals$r_mean by bcrp_sumstats_animals$sex (F, M)
## Z = 1.0607, p-value = 0.4
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  NA NA
## sample estimates:
## difference in location
##             0.03916667
```

```
coin::wilcox_test(bcrp_sumstats_animals$m1_mean ~ bcrp_sumstats_animals$sex, conf.int=TRUE, distribution
```

```
## Warning in cci(alpha): cannot compute confidence interval
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  bcrp_sumstats_animals$m1_mean by bcrp_sumstats_animals$sex (F, M)
## Z = -1.0607, p-value = 0.4
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  NA NA
## sample estimates:
## difference in location
##                 -0.027
```

```
coin::wilcox_test(bcrp_sumstats_animals$m2_mean ~ bcrp_sumstats_animals$sex, conf.int=TRUE, distribution
```

```
## Warning in cci(alpha): cannot compute confidence interval
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  bcrp_sumstats_animals$m2_mean by bcrp_sumstats_animals$sex (F, M)
## Z = 0.35355, p-value = 0.8571
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  NA NA
```

```
## sample estimates:
## difference in location
##                0.03708333
```

```
mrp2_sumstats_animals$coloc <- as.factor(mrp2_sumstats_animals$coloc)
```

```
coin::wilcox_test(mrp2_sumstats_animals$r_mean ~ mrp2_sumstats_animals$coloc, conf.int=TRUE, distributi
```

```
##
##   Exact Wilcoxon-Mann-Whitney Test
##
## data:  mrp2_sumstats_animals$r_mean by
##   mrp2_sumstats_animals$coloc (FALSE, TRUE)
## Z = -3.2433, p-value = 0.0003108
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  -0.1316667 -0.0560000
## sample estimates:
## difference in location
##               -0.09666667
```

```
coin::wilcox_test(mrp2_sumstats_animals$m1_mean ~ mrp2_sumstats_animals$coloc, conf.int=TRUE, distributi
```

```
##
##   Exact Wilcoxon-Mann-Whitney Test
##
## data:  mrp2_sumstats_animals$m1_mean by
##   mrp2_sumstats_animals$coloc (FALSE, TRUE)
## Z = -1.9674, p-value = 0.05408
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  -0.2649444444  0.0005555556
## sample estimates:
## difference in location
##                -0.191719
```

```
#coin::wilcox_test(mrp2_sumstats_animals$m1_mean ~ mrp2_sumstats_animals$coloc, conf.int=TRUE)
coin::wilcox_test(mrp2_sumstats_animals$m2_mean ~ mrp2_sumstats_animals$coloc, conf.int=TRUE, distributi
```

```
##
##   Exact Wilcoxon-Mann-Whitney Test
##
## data:  mrp2_sumstats_animals$m2_mean by
##   mrp2_sumstats_animals$coloc (FALSE, TRUE)
## Z = -1.5045, p-value = 0.152
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  -0.17138333  0.03308333
## sample estimates:
## difference in location
##                -0.06502698
```

```
coin::wilcox_test(mrp2_sumstats_animals$r_mean ~ mrp2_sumstats_animals$sex, conf.int=TRUE, distribution=
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  mrp2_sumstats_animals$r_mean by mrp2_sumstats_animals$sex (F, M)
## Z = 0.17693, p-value = 0.8881
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  -0.06777778  0.06593985
## sample estimates:
## difference in location
##            0.003111111
```

```
coin::wilcox_test(mrp2_sumstats_animals$m1_mean ~ mrp2_sumstats_animals$sex, conf.int=TRUE, distribution
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  mrp2_sumstats_animals$m1_mean by mrp2_sumstats_animals$sex (F, M)
## Z = 0, p-value = 1
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  -0.21884821  0.04457143
## sample estimates:
## difference in location
##            0.002222222
```

```
coin::wilcox_test(mrp2_sumstats_animals$m2_mean ~ mrp2_sumstats_animals$sex, conf.int=TRUE, distribution
```

```
##
##  Exact Wilcoxon-Mann-Whitney Test
##
## data:  mrp2_sumstats_animals$m2_mean by mrp2_sumstats_animals$sex (F, M)
## Z = -0.11785, p-value = 0.9546
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  -0.17205128  0.06725833
## sample estimates:
## difference in location
##            -0.01158512
```

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_st
```

```
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 image
pgp_coloc2 %>% ggplot(aes(x=prep, y=r_pearson)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw()
```
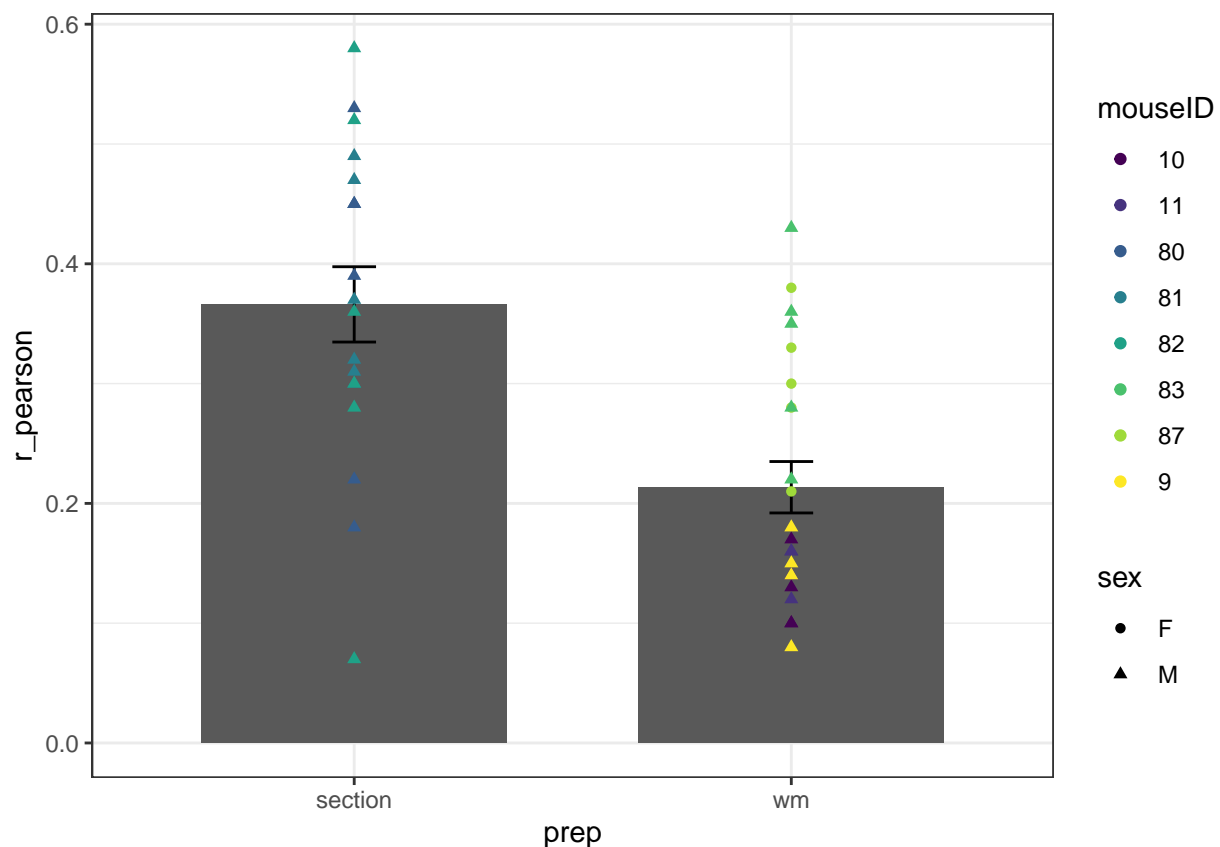


```
pgp_m1_plot <- ggplot(pgp_coloc2, aes(x=prep, y=m1)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
```

```
    geom_point(aes(color=mouseID, shape=sex)) +
    scale_color_viridis(discrete="TRUE") +
    theme_bw()

pgp_m2_plot <- ggplot(pgp_coloc2, aes(x=prep, y=m2)) +
    stat_summary(fun = 'mean', geom="bar", width=0.7) +
    stat_summary(fun.data = mean_se,
                 geom = "errorbar", width=0.1) +
    geom_point(aes(color=mouseID, shape=sex)) +
    scale_color_viridis(discrete="TRUE") +
    theme_bw()

ggarrange(pgp_m1_plot, pgp_m2_plot, common.legend=TRUE, legend="right")
```
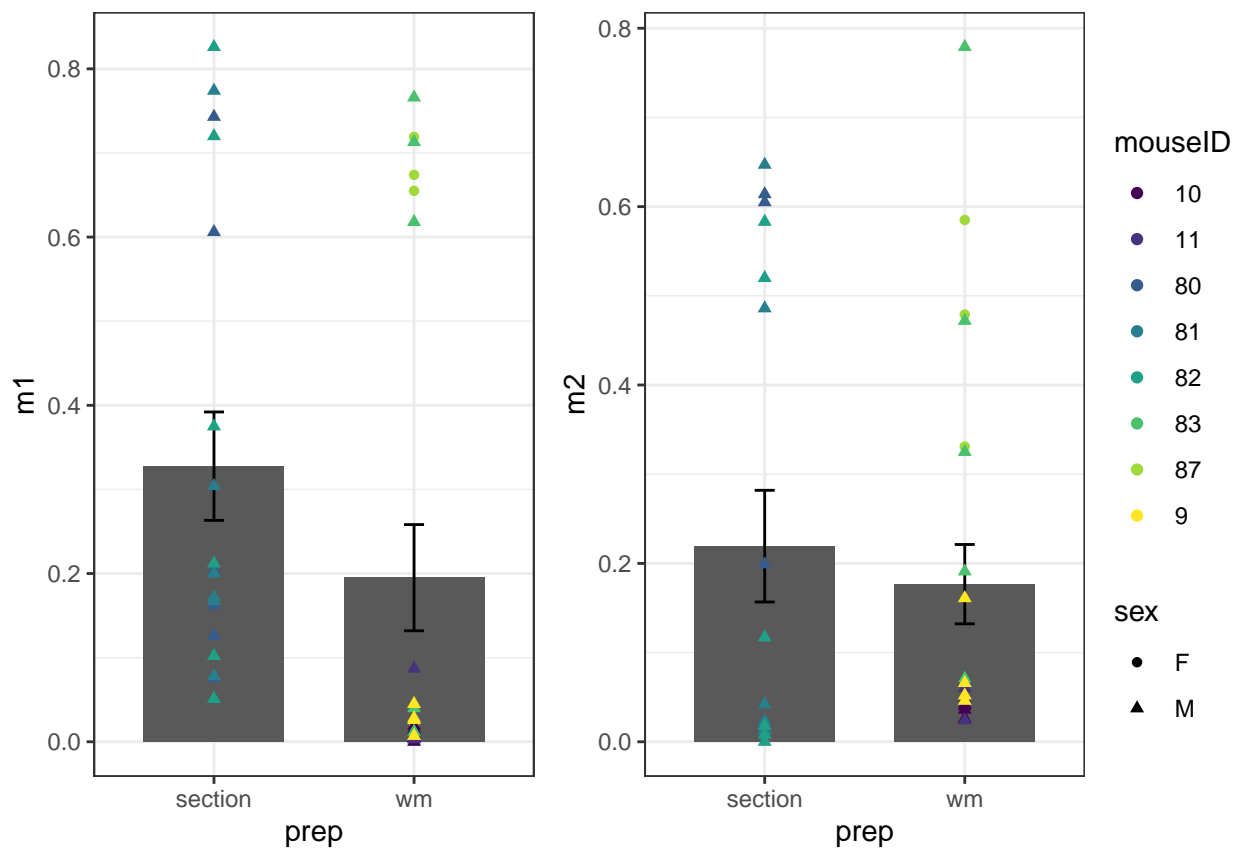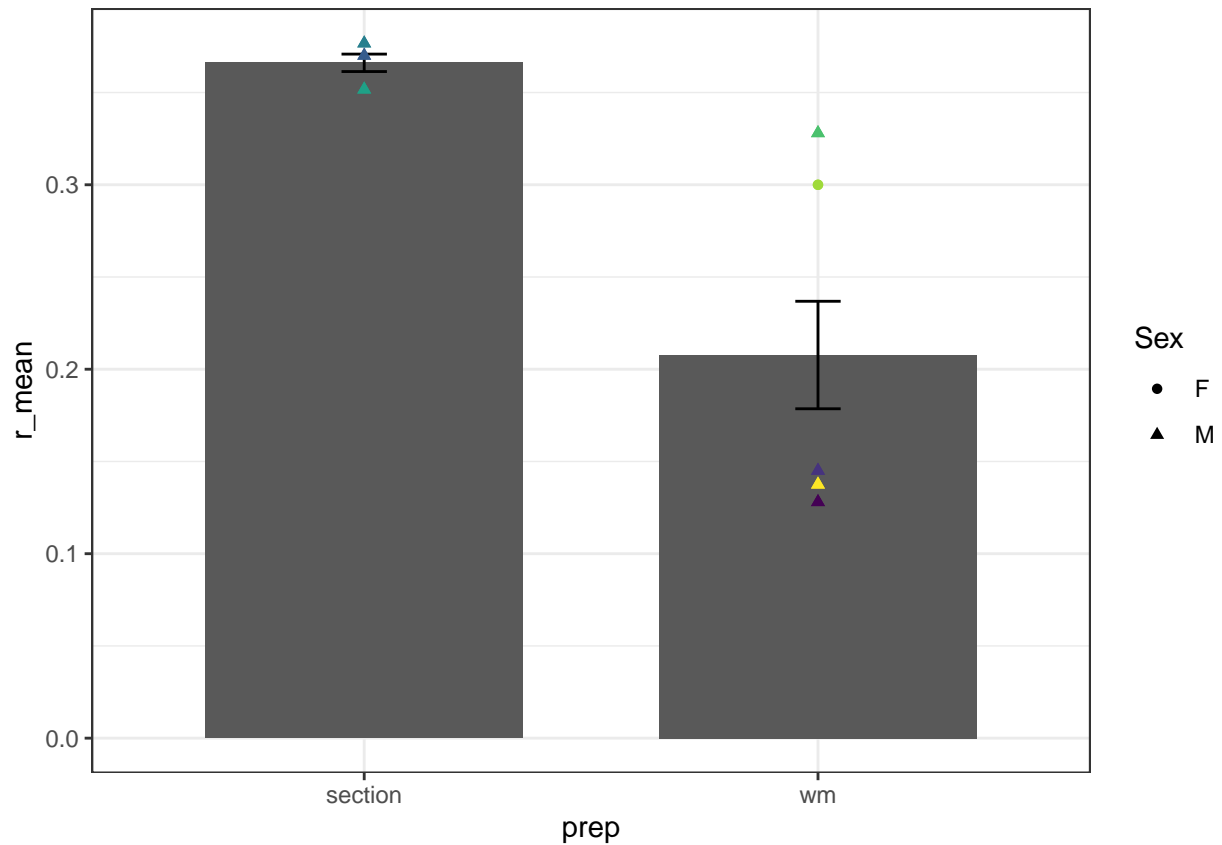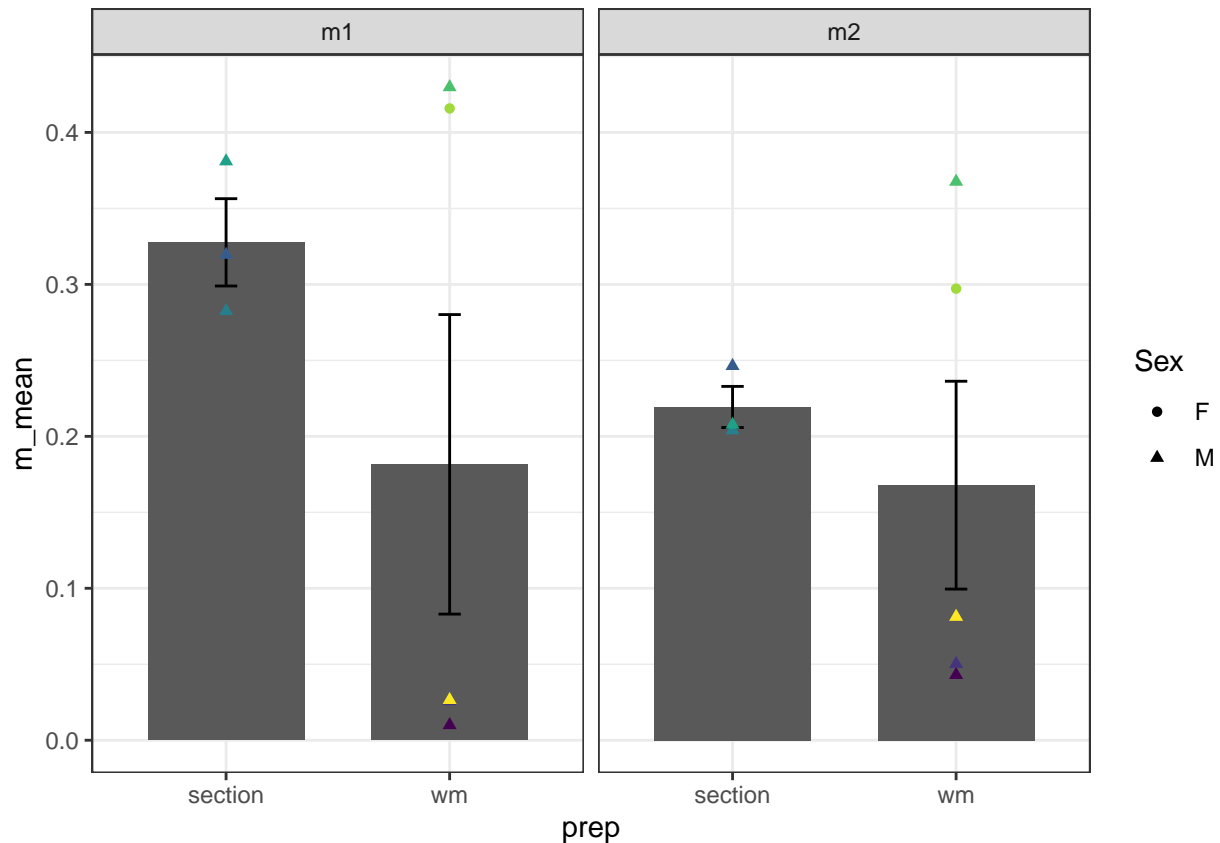


```
#per animal
pgp_animal_r_plot <- pgp_coloc2_long %>% ggplot(aes(x=prep, y=r_mean)) +
    stat_summary(fun = 'mean', geom="bar", width=0.7) +
    stat_summary(fun.data = mean_se,
                 geom = "errorbar", width=0.1) +
    geom_point(aes(color=mouseID, shape=sex)) +
    scale_color_viridis(discrete="TRUE") +
    theme_bw() +
    guides(shape=guide_legend("Sex"), color = "none")

pgp_animal_r_plot
```

```
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=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  facet_wrap(~m_stat_type) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw() +
  guides(shape=guide_legend("Sex"), color = "none")

pgp_animal_m_plot
```

```
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 image
bcrp_coloc2 %>% ggplot(aes(x=sex, y=r_pearson)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw()
```
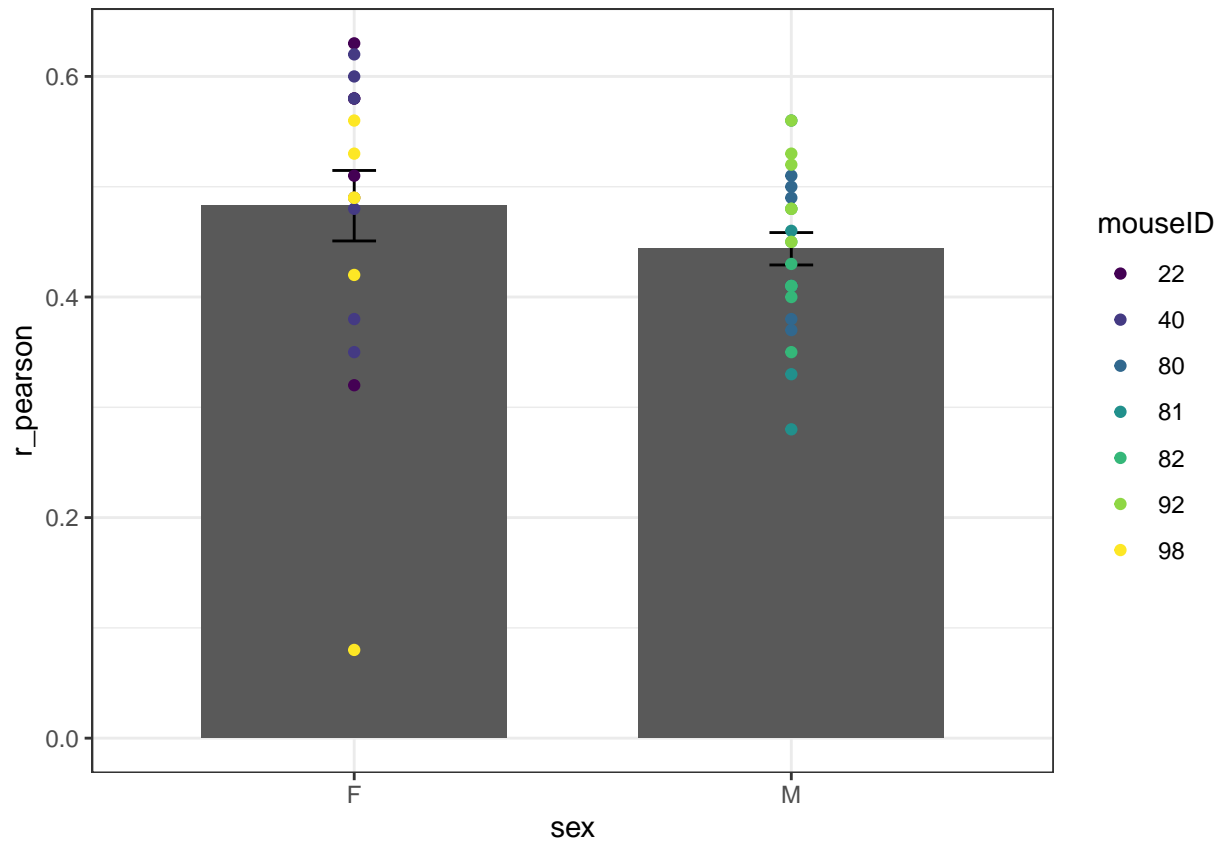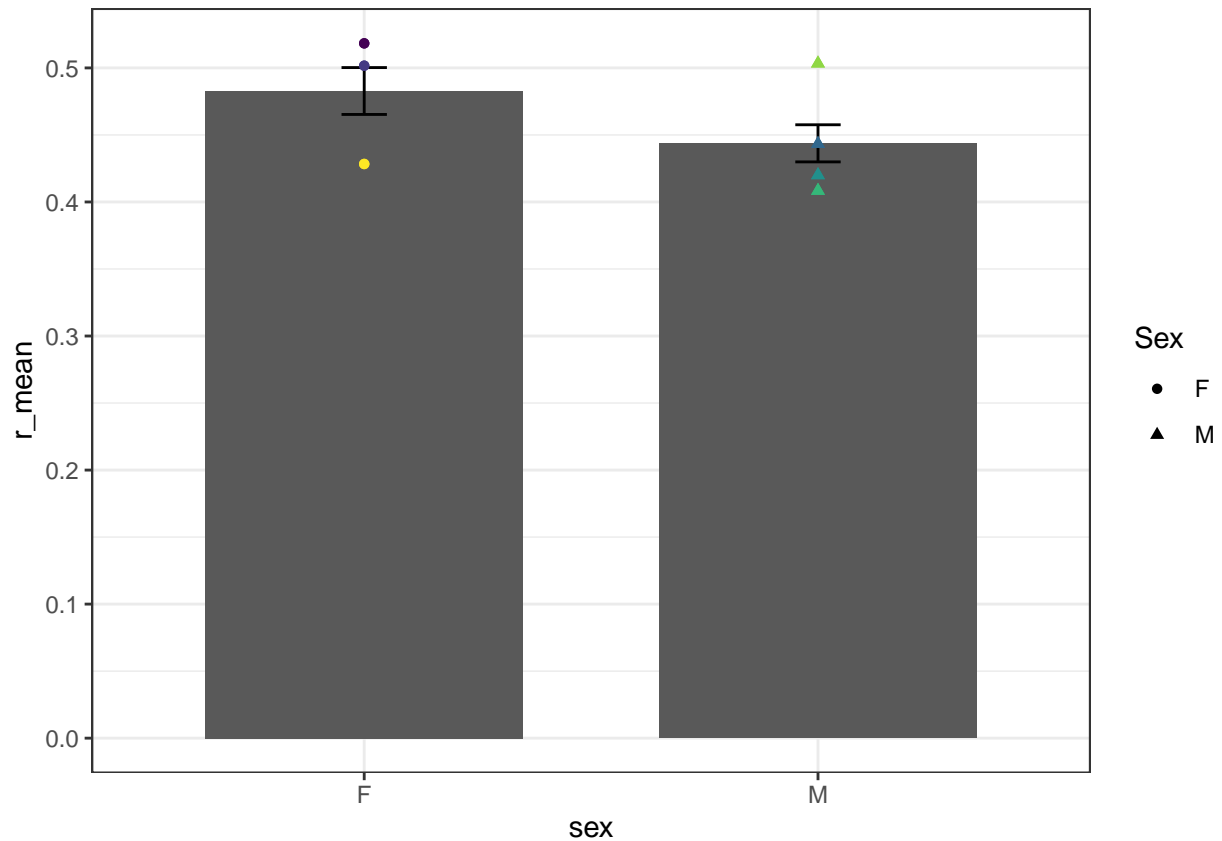
```
bcrp_m1_plot <- ggplot(bcrp_coloc2, aes(x=sex, y=m1)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw()

bcrp_m2_plot <- ggplot(bcrp_coloc2, aes(x=sex, y=m2)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw()

ggarrange(bcrp_m1_plot, bcrp_m2_plot, common.legend=TRUE, legend="right")
```
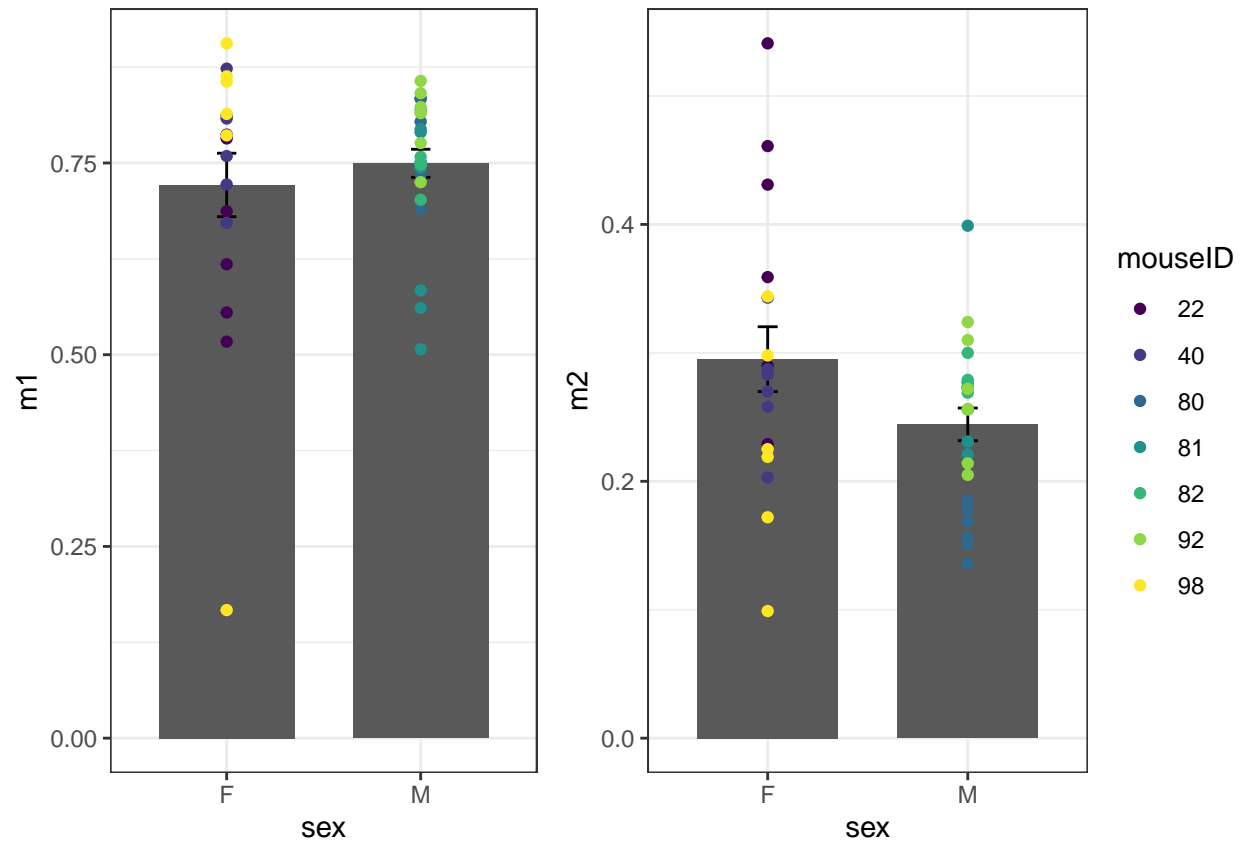
```
#per animal
bcrp_animal_r_plot <- bcrp_coloc2_long %>% ggplot(aes(x=sex, y=r_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw() +
  guides(shape=guide_legend("Sex"), color = "none")

bcrp_animal_r_plot
```

```
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=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  facet_wrap(~m_stat_type) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw() +
  guides(shape=guide_legend("Sex"), color = "none")

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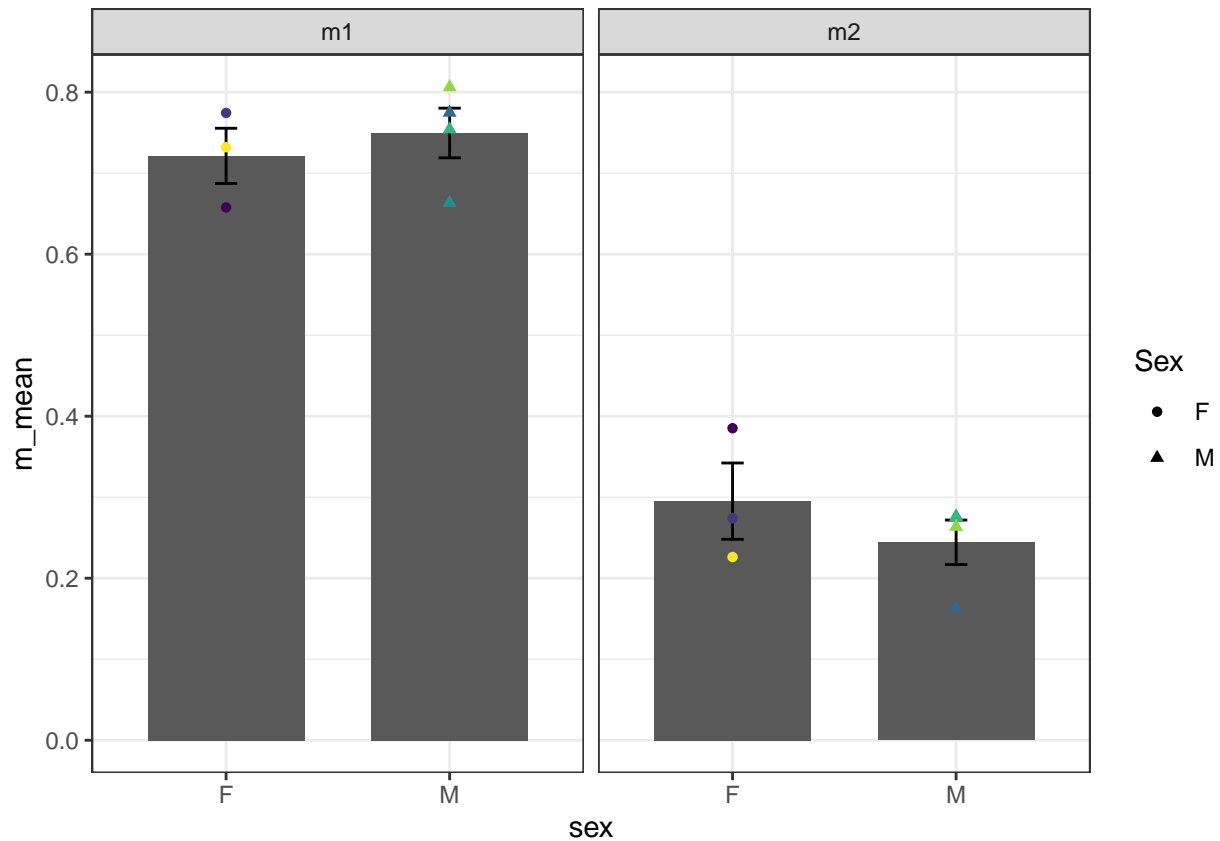
```
mrp2_coloc2$coloc <- as.logical(mrp2_coloc2$coloc)

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)) %>% ungroup()
```

```
## 'summarise()' has grouped output by 'mouseID', 'coloc', 'm_stat_type', 'sex'.
## You can override using the '.groups' argument.
```
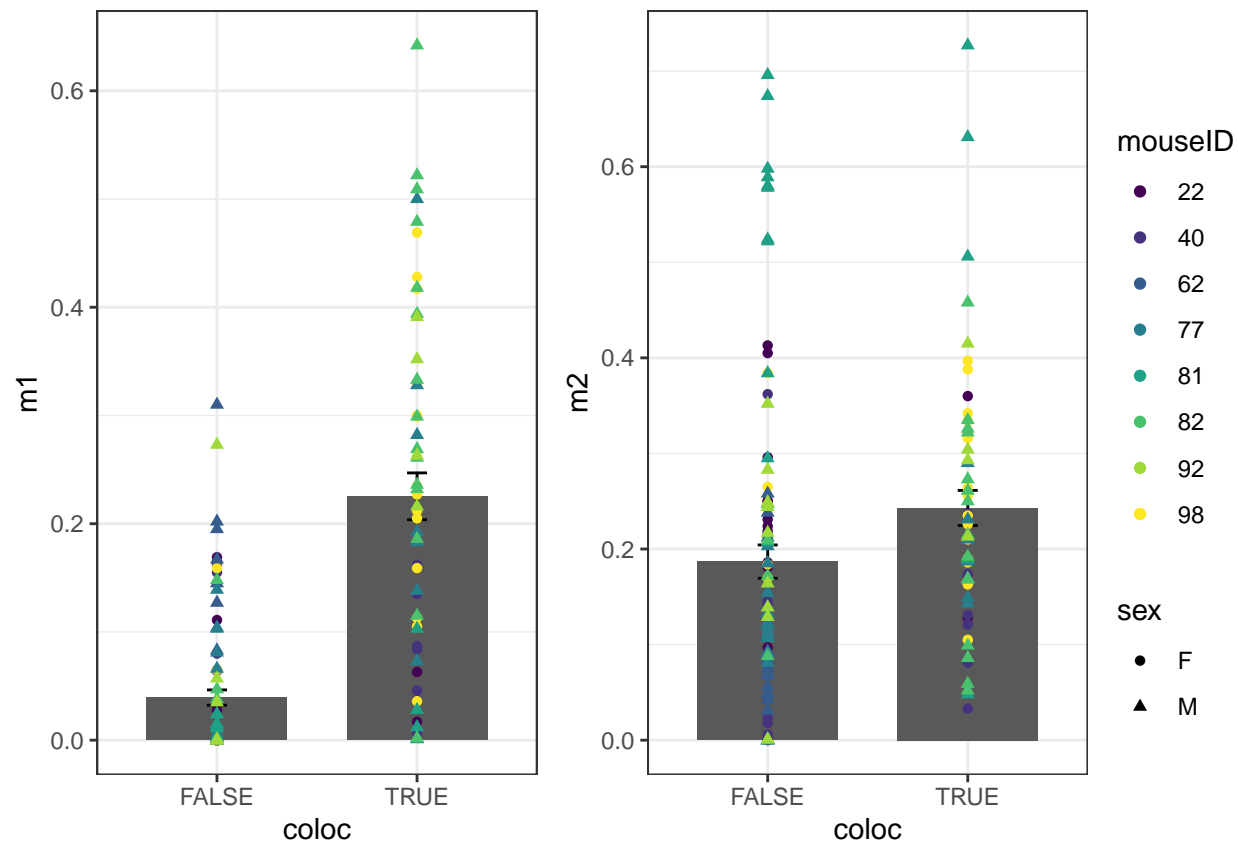
```
#per roi
mrp2_coloc2 %>% ggplot(aes(x=coloc, y=r_pearson)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw()
```
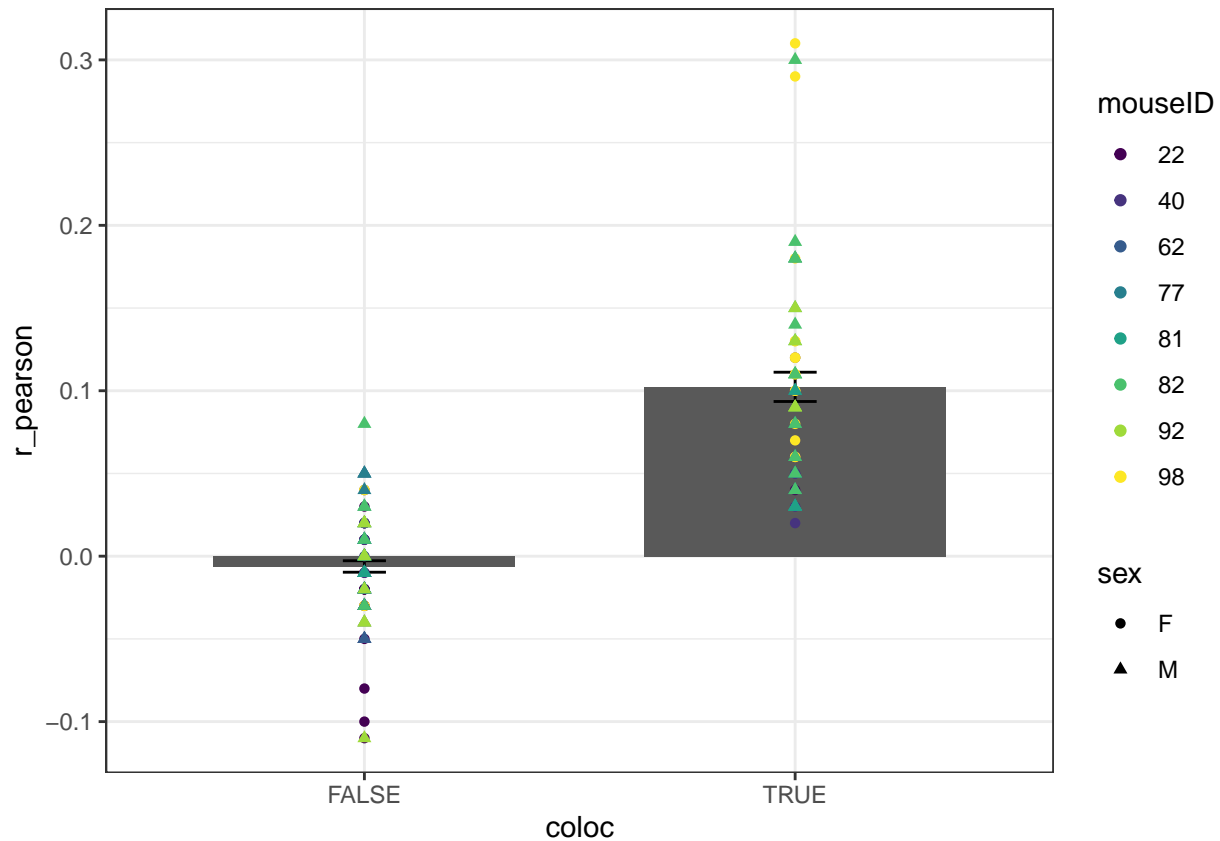
```
mrp2_m1_plot <- ggplot(mrp2_coloc2, aes(x=coloc, y=m1)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw()

mrp2_m2_plot <- ggplot(mrp2_coloc2, aes(x=coloc, y=m2)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw()

ggarrange(mrp2_m1_plot, mrp2_m2_plot, common.legend=TRUE, legend="right")
```
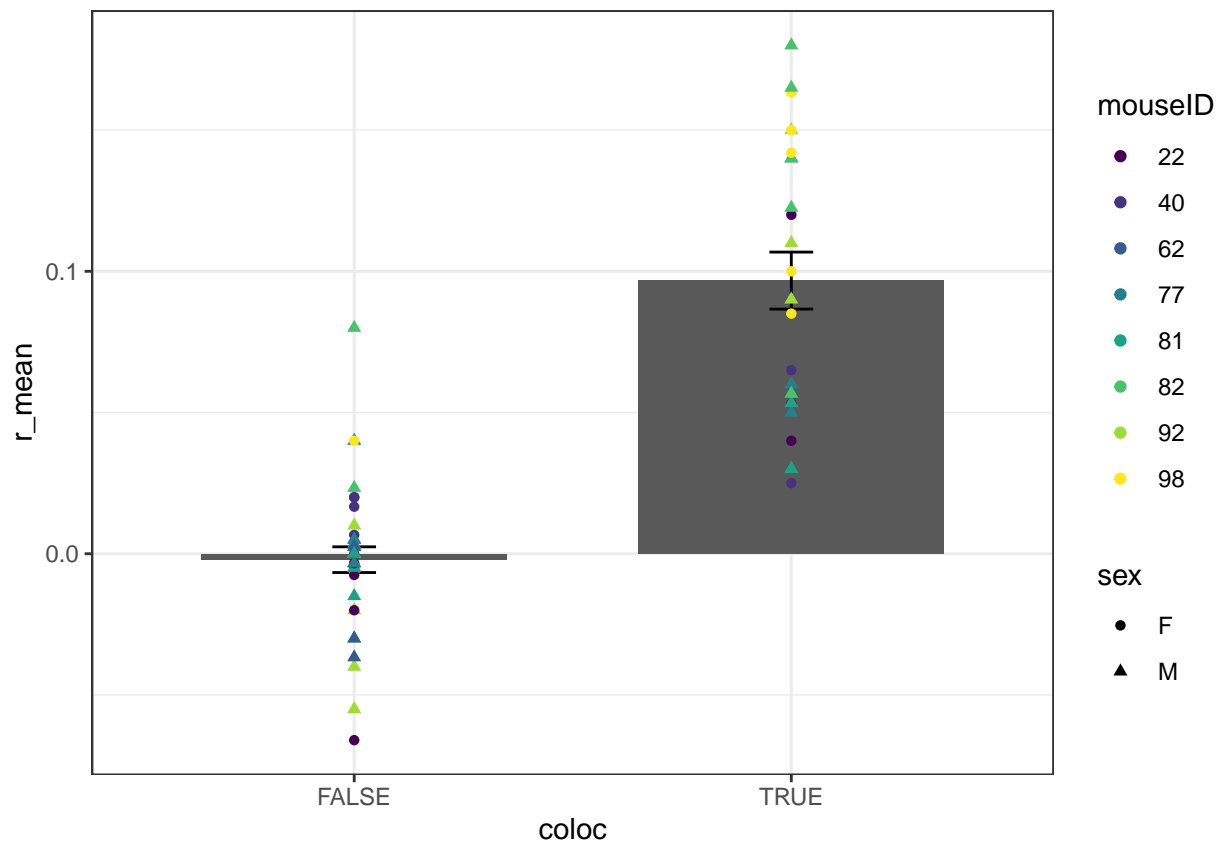
```
#per image
mrp2_sumstats_image %>% ggplot(aes(x=coloc, y=r_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw()
```
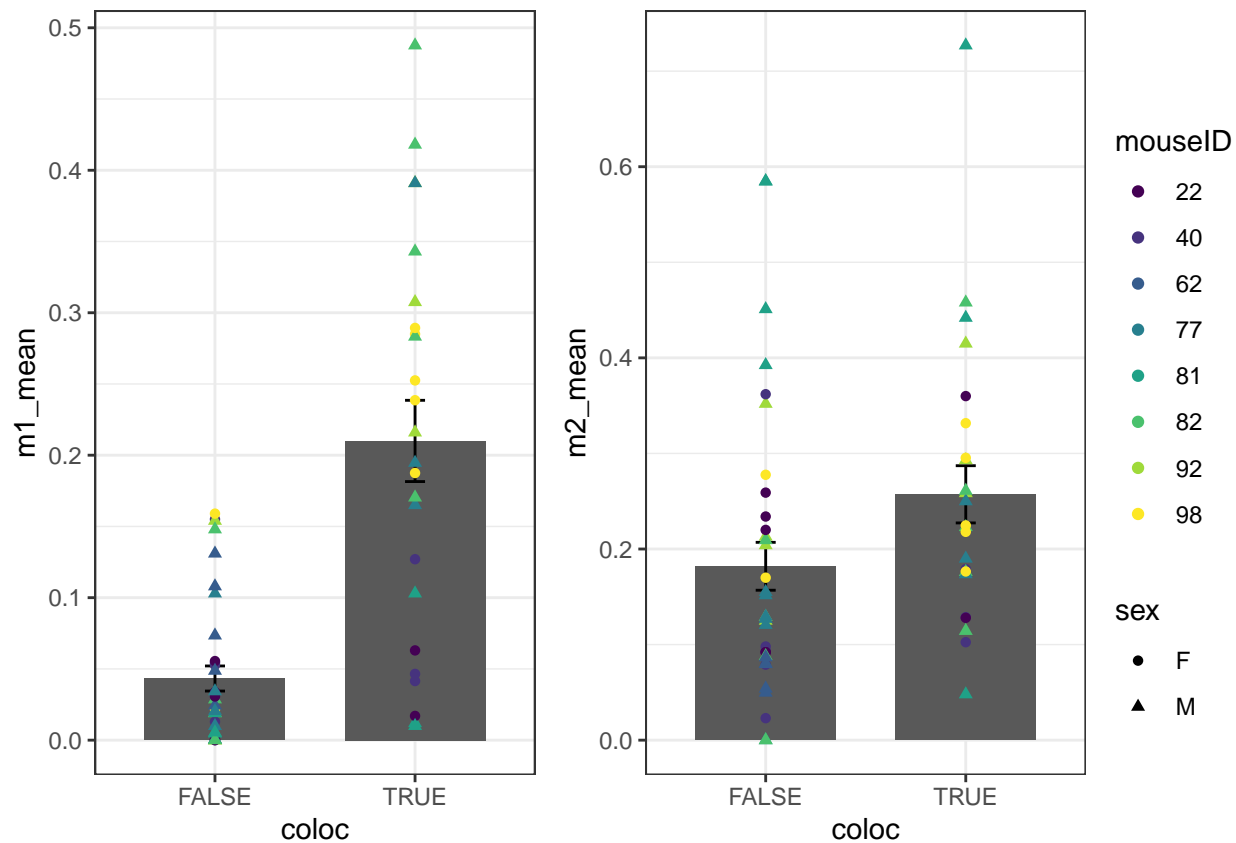
```
mrp2_m1_plot_image <- mrp2_sumstats_image %>% ggplot(aes(x=coloc, y=m1_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw()

mrp2_m2_plot_image <- mrp2_sumstats_image %>% ggplot(aes(x=coloc, y=m2_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw()

ggarrange(mrp2_m1_plot_image, mrp2_m2_plot_image, common.legend=TRUE, legend="right")
```
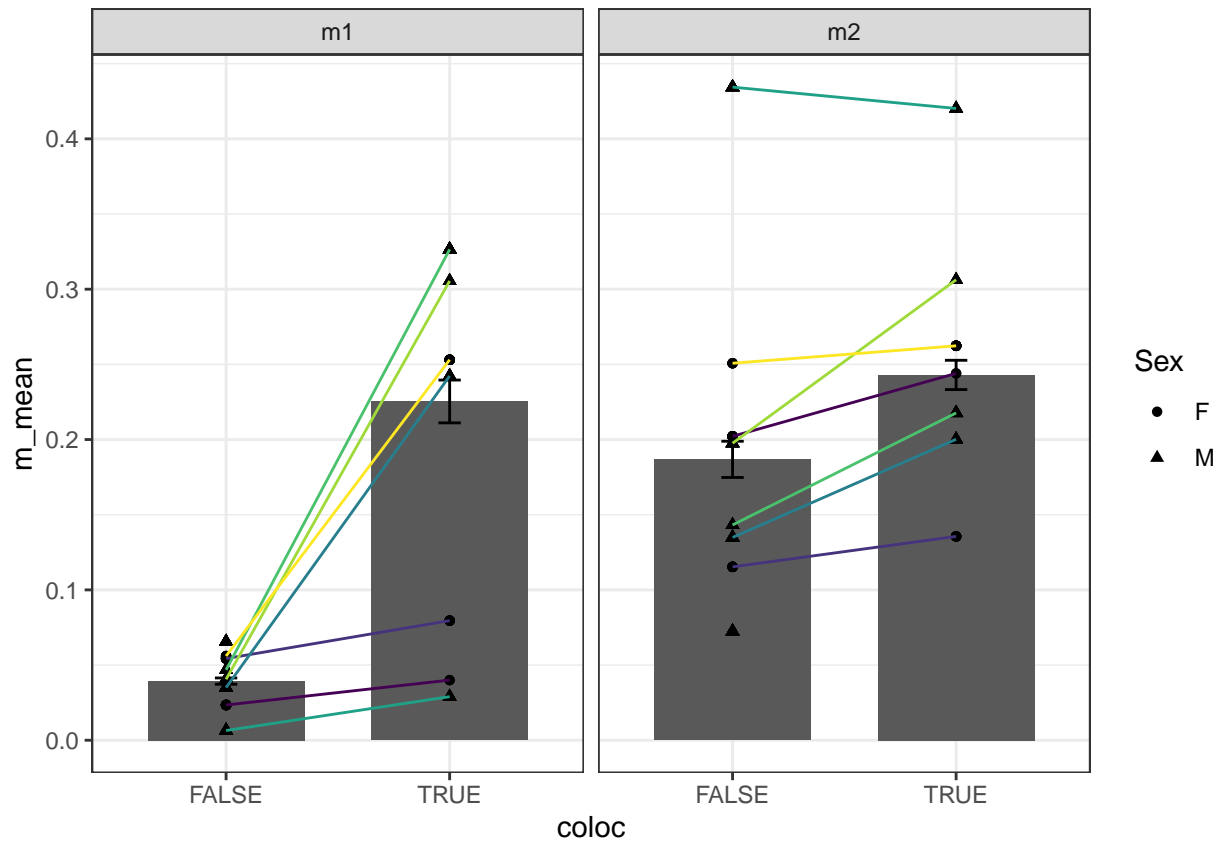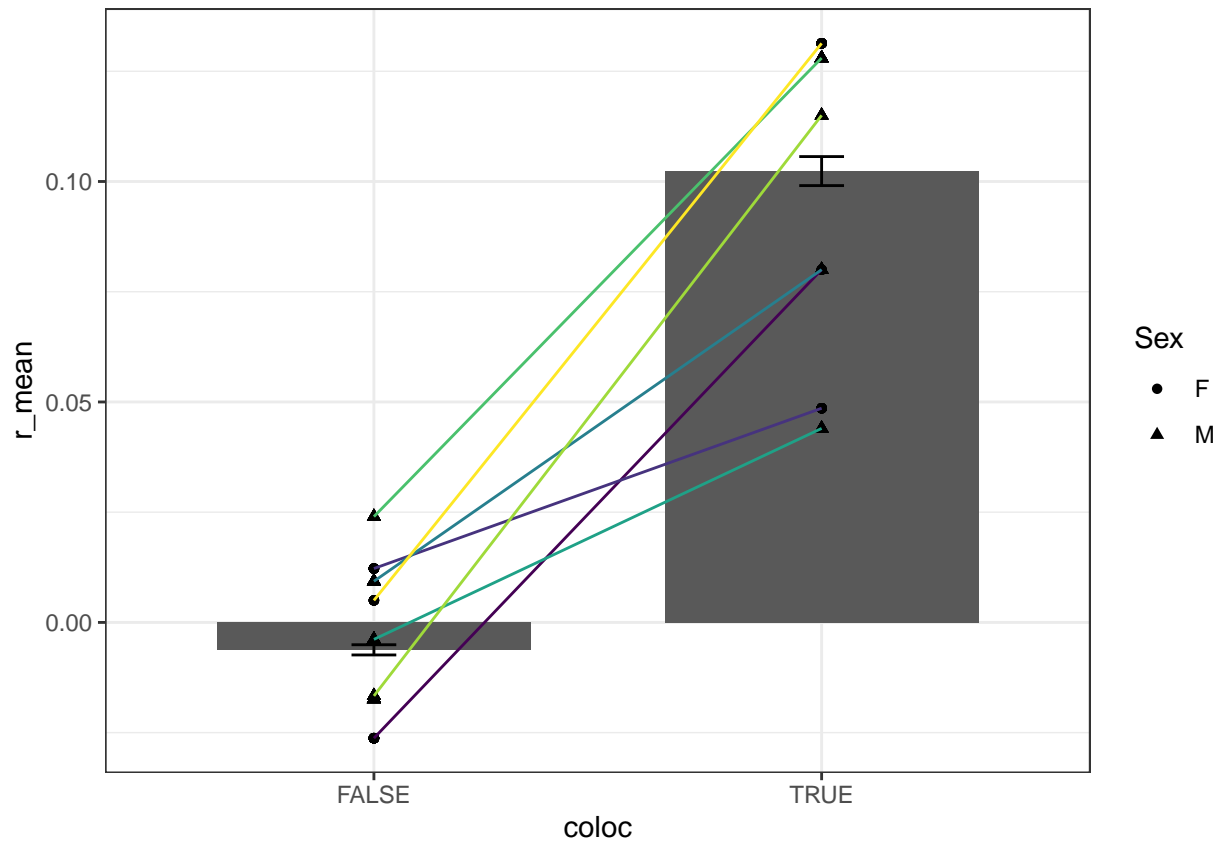
```
#per animal
mrp2_animal_m_plot <- ggplot(mrp2_coloc2_long, aes(x=coloc, y=m_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(shape=sex)) +
  geom_line(aes(group=mouseID, color=mouseID)) +
  facet_wrap(~m_stat_type) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw() +
  guides(shape=guide_legend("Sex"), color = "none")

mrp2_animal_m_plot
```

```
mrp2_animal_r_plot <- ggplot(mrp2_coloc2_long, aes(x=coloc, y=r_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(shape=sex)) +
  geom_line(aes(group=mouseID, color=mouseID)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw() +
  guides(shape=guide_legend("Sex"), color = "none")

mrp2_animal_r_plot
```

```
pgp_animal_r_plot1 <- pgp_animal_r_plot + ylim(-0.05,0.6) + ggtitle("P-gp")
bcrp_animal_r_plot1 <- bcrp_animal_r_plot + ylim(-0.05,0.6) + ggtitle("Bcrp")
mrp2_animal_r_plot1 <- mrp2_animal_r_plot + ylim(-0.05,0.6) + ggtitle("Mrp2")

all_r_plot <- ggarrange(pgp_animal_r_plot1, bcrp_animal_r_plot1, mrp2_animal_r_plot1, ncol=3, common.leg
ggsave("../figures/all_r_plot.png", plot=all_r_plot, width=7, height=4)
ggsave("../figures/all_r_plot.svg", plot=all_r_plot, width=7, height=4)

pgp_animal_m1_plot <- ggplot(pgp_sumstats_animals, aes(x=prep, y=m1_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw(12) +
  ylim(0,0.9) +
  ggtitle("P-gp") +
  guides(shape=guide_legend("Sex"), color = "none")

bcrp_animal_m1_plot <- ggplot(bcrp_sumstats_animals, aes(x=sex, y=m1_mean)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  stat_summary(fun.data = mean_se,
               geom = "errorbar", width=0.1) +
  geom_point(aes(color=mouseID, shape=sex)) +
  scale_color_viridis(discrete="TRUE") +
  theme_bw(12) +
```

```
    ylim(0,0.9) +
    ggtitle("Bcrp") +
    guides(shape=guide_legend("Sex"), color = "none")

mrp2_animal_m1_plot <- ggplot(mrp2_sumstats_animals, aes(x=coloc, y=m1_mean)) +
    stat_summary(fun = 'mean', geom="bar", width=0.7) +
    stat_summary(fun.data = mean_se,
                 geom = "errorbar", width=0.1) +
    geom_point(aes(shape=sex)) +
    geom_line(aes(group=mouseID, color=mouseID)) +
    scale_color_viridis(discrete="TRUE") +
    theme_bw(12) +
    ylim(0,0.9) +
    ggtitle("Mrp2") +
    guides(shape=guide_legend("Sex"), color = "none")


all_m1_plot <- ggarrange(pgp_animal_m1_plot, bcrp_animal_m1_plot, mrp2_animal_m1_plot, ncol=3, common.l
ggsave("../figures/all_m1_plot.png", plot=all_m1_plot, width=7, height=4)
ggsave("../figures/all_m1_plot.svg", plot=all_m1_plot, width=7, height=4)



pgp_animal_m2_plot <- ggplot(pgp_sumstats_animals, aes(x=prep, y=m2_mean)) +
    stat_summary(fun = 'mean', geom="bar", width=0.7) +
    stat_summary(fun.data = mean_se,
                 geom = "errorbar", width=0.1) +
    geom_point(aes(color=mouseID, shape=sex)) +
    scale_color_viridis(discrete="TRUE") +
    theme_bw() +
    ylim(0,0.5) +
    ggtitle("P-gp") +
    guides(shape=guide_legend("Sex"), color = "none")

bcrp_animal_m2_plot <- ggplot(bcrp_sumstats_animals, aes(x=sex, y=m2_mean)) +
    stat_summary(fun = 'mean', geom="bar", width=0.7) +
    stat_summary(fun.data = mean_se,
                 geom = "errorbar", width=0.1) +
    geom_point(aes(color=mouseID, shape=sex)) +
    scale_color_viridis(discrete="TRUE") +
    theme_bw() +
    ylim(0,0.5) +
    ggtitle("Bcrp") +
    guides(shape=guide_legend("Sex"), color = "none")

mrp2_animal_m2_plot <- ggplot(mrp2_sumstats_animals, aes(x=coloc, y=m2_mean)) +
    stat_summary(fun = 'mean', geom="bar", width=0.7) +
    stat_summary(fun.data = mean_se,
                 geom = "errorbar", width=0.1) +
    geom_point(aes(shape=sex)) +
    geom_line(aes(group=mouseID, color=mouseID)) +
    scale_color_viridis(discrete="TRUE") +
```

```
  theme_bw() +
  ylim(0,0.5) +
  ggtitle("Mrp2") +
  guides(shape=guide_legend("Sex"), color = "none")


all_m2_plot <- ggarrange(pgp_animal_m2_plot, bcrp_animal_m2_plot, mrp2_animal_m2_plot, ncol=3, common.l
ggsave("../figures/all_m2_plot.png", plot=all_m1_plot, width=7, height=4)
ggsave("../figures/all_m2_plot.svg", plot=all_m1_plot, width=7, height=4)
```