ARP2/3 complex associates with peroxisomes to participate in pexophagy in plants

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Statistical analysis

Full R source code written by Stanislav Vosolsobě

Required libraries

```
library(betareg) # for beta regression
library(lmtest)  # for LR test after BetaReg
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
library(pscl)    # for zero-inflated Poisson model
```

```
## Classes and Methods for R developed in the
## Political Science Computational Laboratory
## Department of Political Science
## Stanford University
## Simon Jackman
## hurdle and zeroinfl functions by Achim Zeileis
```

```
library(emmeans) # for multiple comparison
```

Figure 2b

```
fig2b <- read.table("Fig2b",header = T)

m0 <- lm(data=fig2b,speed~variant)
anova(m0)
```

```
## Analysis of Variance Table
##
## Response: speed
##           Df  Sum Sq  Mean Sq F value Pr(>F)
## variant    2 0.03623 0.018113  0.3099 0.7351
## Residuals 45 2.63031 0.058451
```

```
em1 <- emmeans(m0,pairwise~variant,type="response")
summary(em1)
```

```
## $emmeans
```

```
##  variant emmean     SE df lower.CL upper.CL
##  arpc2    0.580 0.0646 45    0.450    0.710
##  arpc5    0.511 0.0604 45    0.390    0.633
##  WT       0.533 0.0570 45    0.418    0.648
##
## Confidence level used: 0.95
##
## $contrasts
##  contrast      estimate     SE df t.ratio p.value
##  arpc2 - arpc5   0.0685 0.0885 45   0.774  0.7206
##  arpc2 - WT      0.0468 0.0862 45   0.544  0.8502
##  arpc5 - WT     -0.0217 0.0831 45  -0.261  0.9632
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
plot(em1,type="response",comparisons = T)
```

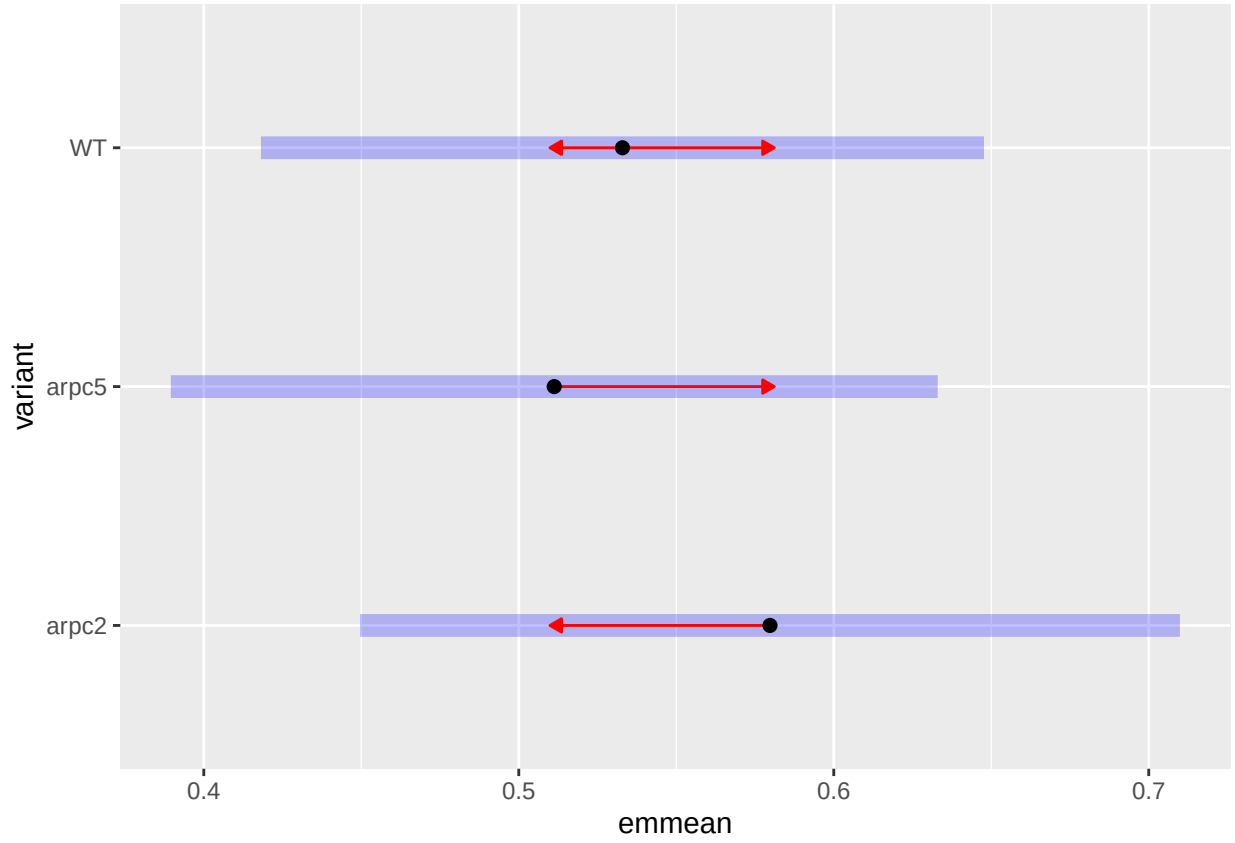

Figure 3e

```
fig3e <- read.table("Fig3e",header = T)

m0 <- glm(data=fig3e,diffused~variant,family = quasibinomial)
anova(m0,test="LRT")
```

```
## Analysis of Deviance Table
##
```

```
## Model: quasibinomial, link: logit
##
## Response: diffused
##
## Terms added sequentially (first to last)
##
##
##         Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                       59     53.630
## variant  2   22.217        57     31.413 7.703e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
em1 <- emmeans(m0,pairwise~variant,type="response")
summary(em1)
```

```
## $emmeans
##  variant  prob     SE  df asymp.LCL asymp.UCL
##  c2      0.850 0.0567 Inf    0.7029     0.931
##  c5      0.136 0.0605 Inf    0.0543     0.302
##  nap1    0.398 0.0759 Inf    0.2622     0.552
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
##
## $contrasts
##  contrast  odds.ratio     SE  df null z.ratio p.value
##  c2 / c5       35.879 24.392 Inf    1   5.266  <.0001
##  c2 / nap1      8.543  4.662 Inf    1   3.931  0.0002
##  c5 / nap1      0.238  0.144 Inf    1  -2.374  0.0463
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log odds ratio scale
```

```
summary(em1)$contrasts$p.value
```

```
## [1] 4.174639e-07 2.491940e-04 4.625254e-02
```

```
plot(em1,type="response",comparisons = T)
```

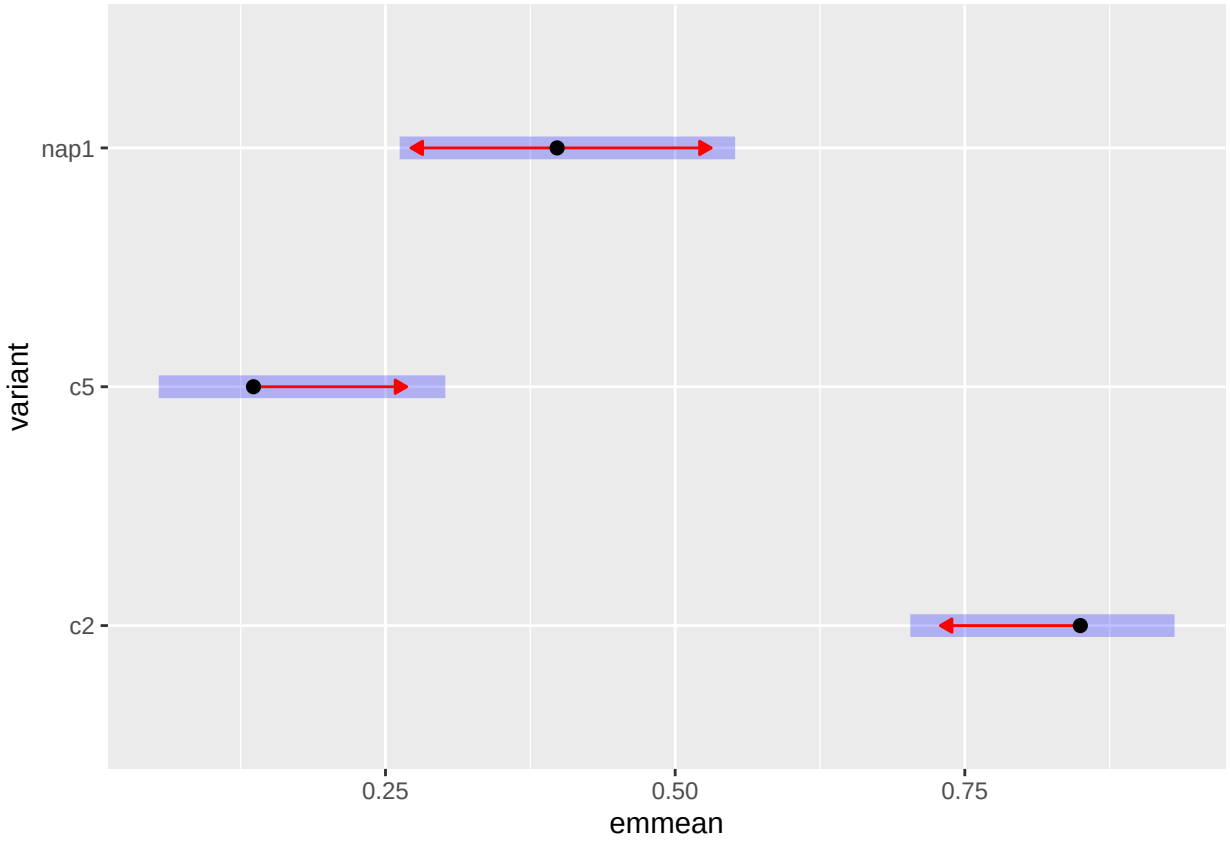

Figure 4a

```
fig4a <- read.table("Fig4a",header = T)

m0 <- glm(data=fig4a,peroxisomes~variant,family = poisson)
anova(m0,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: peroxisomes
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                       225     1494.9
## variant  2    463.9       223     1031.0 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
em1 <- emmeans(m0,pairwise~variant,type="response")
summary(em1)
```

```
## $emmeans
```

```
##  variant rate    SE  df asymp.LCL asymp.UCL
##  arpc2   48.0 1.206 Inf      45.7      50.5
##  arpc5   40.8 0.799 Inf      39.3      42.4
##  WT      26.8 0.456 Inf      25.9      27.7
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
##
## $contrasts
##  contrast      ratio     SE  df null z.ratio p.value
##  arpc2 / arpc5  1.18 0.0375 Inf    1   5.114  <.0001
##  arpc2 / WT     1.79 0.0544 Inf    1  19.244  <.0001
##  arpc5 / WT     1.52 0.0395 Inf    1  16.235  <.0001
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log scale
```

```
summary(em1)$contrasts$p.value
```

```
## [1] 9.415278e-07 0.000000e+00 0.000000e+00
```

```
plot(em1,comparisons = T)
```

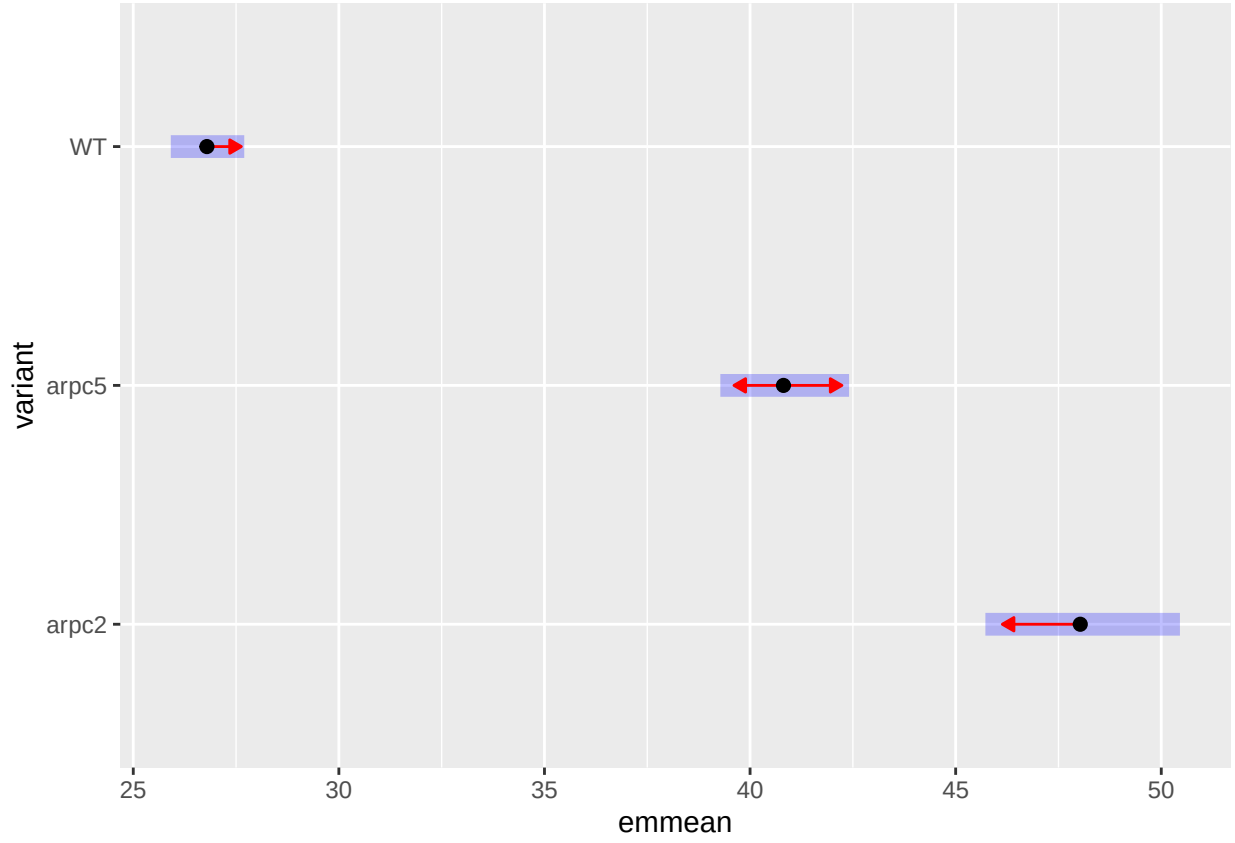

Figure 4b

```
fig4b <- read.table("Fig4b",header = T)

m0 <- glm(data=fig4b, area~varianta,family = Gamma)
anova(m0,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: Gamma, link: inverse
##
## Response: area
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                       667     251.32
## varianta  1   51.052       666     200.26 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- lm(data=fig4b, log(area)~varianta)
anova(m1)
```

```
## Analysis of Variance Table
##
## Response: log(area)
##            Df  Sum Sq Mean Sq F value    Pr(>F)
## varianta    1  46.161  46.161  154.21 < 2.2e-16 ***
## Residuals 666 199.355   0.299
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 4c

```
fig4c <- read.table("Fig4c",header = T)

m0 <- glm(data=fig4c, area~variant,family = Gamma)
anova(m0,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: Gamma, link: inverse
##
## Response: area
##
## Terms added sequentially (first to last)
##
##
##         Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                      967     268.36
## variant  1   41.335       966     227.02 < 2.2e-16 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- lm(data=fig4c, log(area)~variant)
anova(m1)
```

```
## Analysis of Variance Table
##
## Response: log(area)
##            Df  Sum Sq Mean Sq F value    Pr(>F)
## variant     1  37.382  37.382  155.89 < 2.2e-16 ***
## Residuals 966 231.646   0.240
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 4d

```
fig4d <- read.table("Fig4d",header = T)

m1 <- lm(data=fig4d, log(length) ~ variant * treatment  )
anova(m1)
```

```
## Analysis of Variance Table
##
## Response: log(length)
##                   Df  Sum Sq Mean Sq  F value    Pr(>F)
## variant            3  4.3999  1.4666  40.5654 3.066e-16 ***
## treatment          1 17.1267 17.1267 473.6989 < 2.2e-16 ***
## variant:treatment  3  0.3684  0.1228   3.3963   0.02161 *
## Residuals         83  3.0009  0.0362
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
em1 <- emmeans(m1, pairwise ~ treatment | variant, type="response")
summary(em1)
```

```
## $emmeans
## variant = arp2:
##  treatment response    SE df lower.CL upper.CL
##  IBA           12.8 0.772 83    11.40     14.5
##  mock          30.4 1.828 83    26.98     34.3
##
## variant = arpc4:
##  treatment response    SE df lower.CL upper.CL
##  IBA           13.8 0.877 83    12.20     15.7
##  mock          26.7 1.603 83    23.66     30.0
##
## variant = arpc5:
##  treatment response    SE df lower.CL upper.CL
##  IBA           11.2 0.756 83     9.83     12.8
##  mock          26.1 1.655 83    23.02     29.6
##
## variant = WT:
##  treatment response    SE df lower.CL upper.CL
##  IBA            7.5 0.336 83     6.86      8.2
##  mock          20.4 0.940 83    18.59     22.3
```

```
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
##
## $contrasts
## variant = arp2:
##  contrast   ratio     SE df null t.ratio p.value
##  IBA / mock 0.422 0.0359 83    1 -10.133  <.0001
##
## variant = arpc4:
##  contrast   ratio     SE df null t.ratio p.value
##  IBA / mock 0.519 0.0454 83    1  -7.503  <.0001
##
## variant = arpc5:
##  contrast   ratio     SE df null t.ratio p.value
##  IBA / mock 0.430 0.0398 83    1  -9.125  <.0001
##
## variant = WT:
##  contrast   ratio     SE df null t.ratio p.value
##  IBA / mock 0.368 0.0237 83    1 -15.545  <.0001
##
## Tests are performed on the log scale
```

```
summary(em1)$contrasts$p.value
```

```
## [1] 3.575741e-16 6.307242e-11 3.677664e-14 2.636529e-26
```

Figure 4h

```
fig4h <- read.table("Fig4h",header = T)

m0 <- glm(data=fig4h,coloc~variant,family = quasibinomial)
anova(m0,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: quasibinomial, link: logit
##
## Response: coloc
##
## Terms added sequentially (first to last)
##
##
##         Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                      247     75.953
## variant  1   13.444       246     62.509 3.401e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
em1 <- emmeans(m0,pairwise~variant,type="response")
summary(em1)
```

```
## $emmeans
##  variant   prob      SE  df asymp.LCL asymp.UCL
##  LSCM    0.0393 0.00906 Inf     0.025    0.0615
```

```
##  VAEM_M  0.1811 0.02357 Inf     0.139    0.2320
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
##
## $contrasts
##  contrast      odds.ratio     SE  df null z.ratio p.value
##  LSCM / VAEM_M      0.185 0.0532 Inf    1  -5.864  <.0001
##
## Tests are performed on the log odds ratio scale
```

```
summary(em1)$contrasts$p.value
```

```
## [1] 4.51307e-09
```

```
plot(em1,type="response",comparisons = T)
```

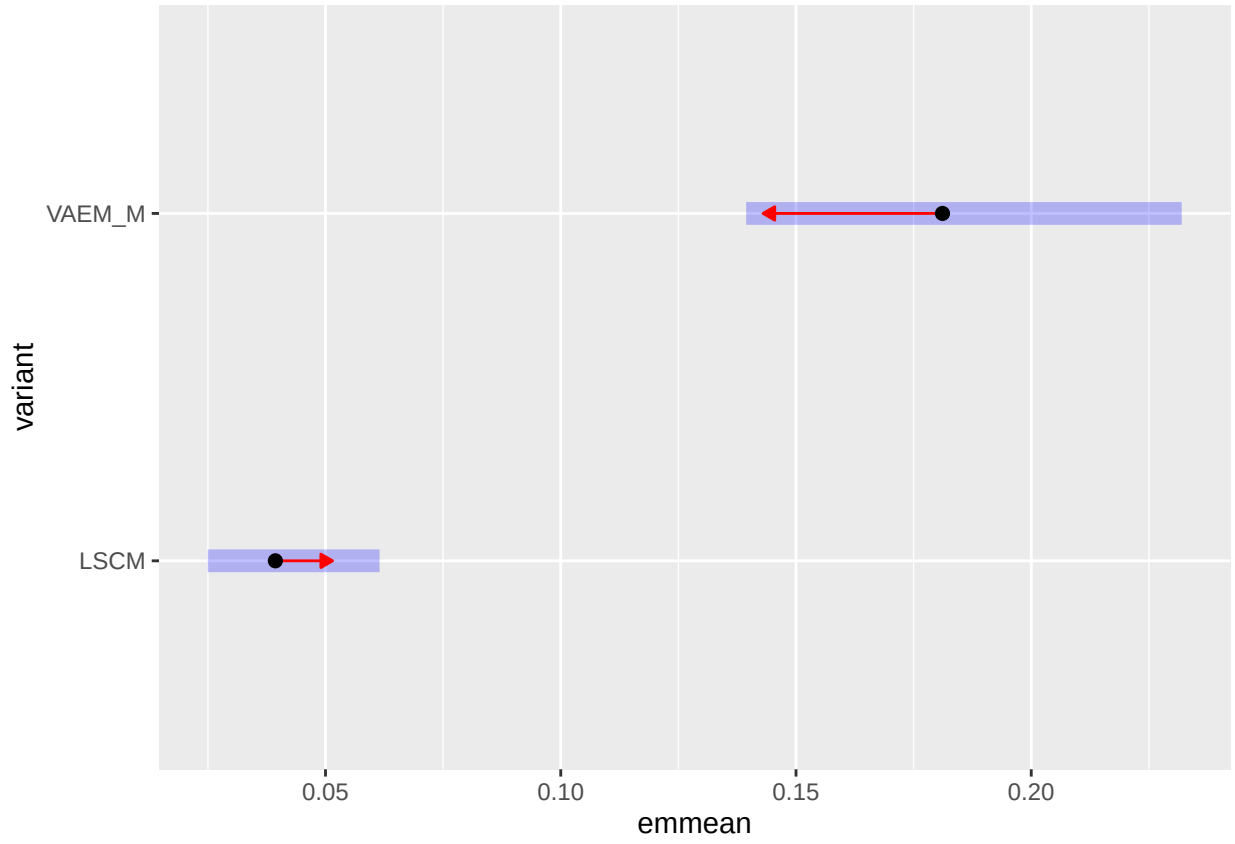

Figure 4o

```
fig4o <- read.table("Fig4o",header = T)

anova(lm(data=fig4o,tm~autophagosome))
```

```
## Analysis of Variance Table
##
## Response: tm
```

```
##               Df  Sum Sq Mean Sq F value   Pr(>F)
## autophagosome  1  727685  727685  15.847 0.000299 ***
## Residuals     38 1744983   45921
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure S4a

```
figS4a <- read.table("FigS4a",header = T)

m1 <- aov(data=figS4a,density~variant)
summary(m1)
```

```
##             Df   Sum Sq  Mean Sq F value   Pr(>F)
## variant      2 42287384 21143692   44.71 0.000249 ***
## Residuals    6  2837368   472895
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
em1 <- emmeans(m1,pairwise~variant,type="response")
summary(em1)
```

```
## $emmeans
##  variant emmean  SE df lower.CL upper.CL
##  C2-K     13017 397  6    12046    13989
##  C5-K     12619 397  6    11648    13591
##  WT-K      8233 397  6     7261     9204
##
## Confidence level used: 0.95
##
## $contrasts
##  contrast        estimate  SE df t.ratio p.value
##  (C2-K) - (C5-K)      398 561  6   0.708  0.7678
##  (C2-K) - (WT-K)     4784 561  6   8.521  0.0004
##  (C5-K) - (WT-K)     4387 561  6   7.812  0.0006
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
summary(em1)$contrasts$p.value
```

```
## [1] 0.7678493786 0.0003515171 0.0005682736
```

```
plot(em1,type="response",comparisons = T)
```

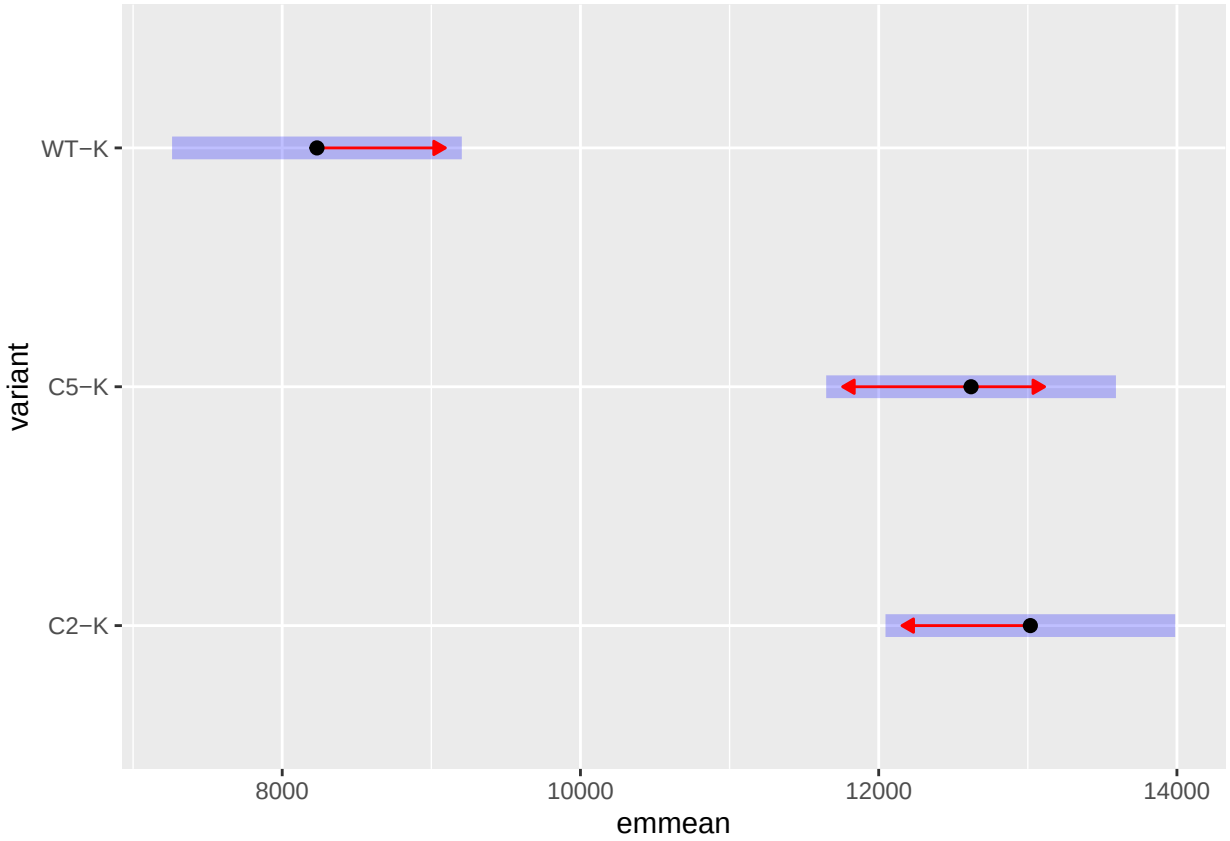

Figure S4c

```
figS4c <- read.table("FigS4c",header = T)

m0 <- aov(data=figS4c,fluorescence~variant)
summary(m0)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## variant       5 0.2387 0.04775    9.56 1.67e-07 ***
## Residuals   102 0.5095 0.00499
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
em1 <- emmeans(m0,pairwise~variant,type="response")
summary(em1)
```

```
## $emmeans
##  variant emmean     SE  df lower.CL upper.CL
##  arp2     0.455 0.0167 102    0.422    0.488
##  arpc2    0.485 0.0167 102    0.452    0.518
##  arpc4    0.437 0.0167 102    0.404    0.470
##  arpc5    0.436 0.0167 102    0.403    0.469
##  atg5     0.447 0.0167 102    0.414    0.480
##  WT       0.334 0.0167 102    0.301    0.367
##
## Confidence level used: 0.95
```

```
##
## $contrasts
##  contrast       estimate     SE  df t.ratio p.value
##  arp2 - arpc2  -0.030120 0.0236 102  -1.279  0.7960
##  arp2 - arpc4   0.018739 0.0236 102   0.795  0.9677
##  arp2 - arpc5   0.019057 0.0236 102   0.809  0.9653
##  arp2 - atg5    0.008612 0.0236 102   0.366  0.9991
##  arp2 - WT      0.121348 0.0236 102   5.151  <.0001
##  arpc2 - arpc4  0.048859 0.0236 102   2.074  0.3091
##  arpc2 - arpc5  0.049176 0.0236 102   2.087  0.3021
##  arpc2 - atg5   0.038732 0.0236 102   1.644  0.5716
##  arpc2 - WT     0.151468 0.0236 102   6.430  <.0001
##  arpc4 - arpc5  0.000318 0.0236 102   0.013  1.0000
##  arpc4 - atg5  -0.010127 0.0236 102  -0.430  0.9981
##  arpc4 - WT     0.102609 0.0236 102   4.356  0.0004
##  arpc5 - atg5  -0.010445 0.0236 102  -0.443  0.9978
##  arpc5 - WT     0.102292 0.0236 102   4.342  0.0005
##  atg5 - WT      0.112736 0.0236 102   4.786  0.0001
##
## P value adjustment: tukey method for comparing a family of 6 estimates
```

```
summary(em1)$contrasts$p.value
```

```
##  [1] 7.960011e-01 9.677057e-01 9.652896e-01 9.991227e-01 1.850841e-05
##  [6] 3.091474e-01 3.020741e-01 5.715834e-01 6.219121e-08 1.000000e+00
## [11] 9.980844e-01 4.449431e-04 9.977795e-01 4.681686e-04 8.319533e-05
```

```
plot(em1,type="response",comparisons = T)
```

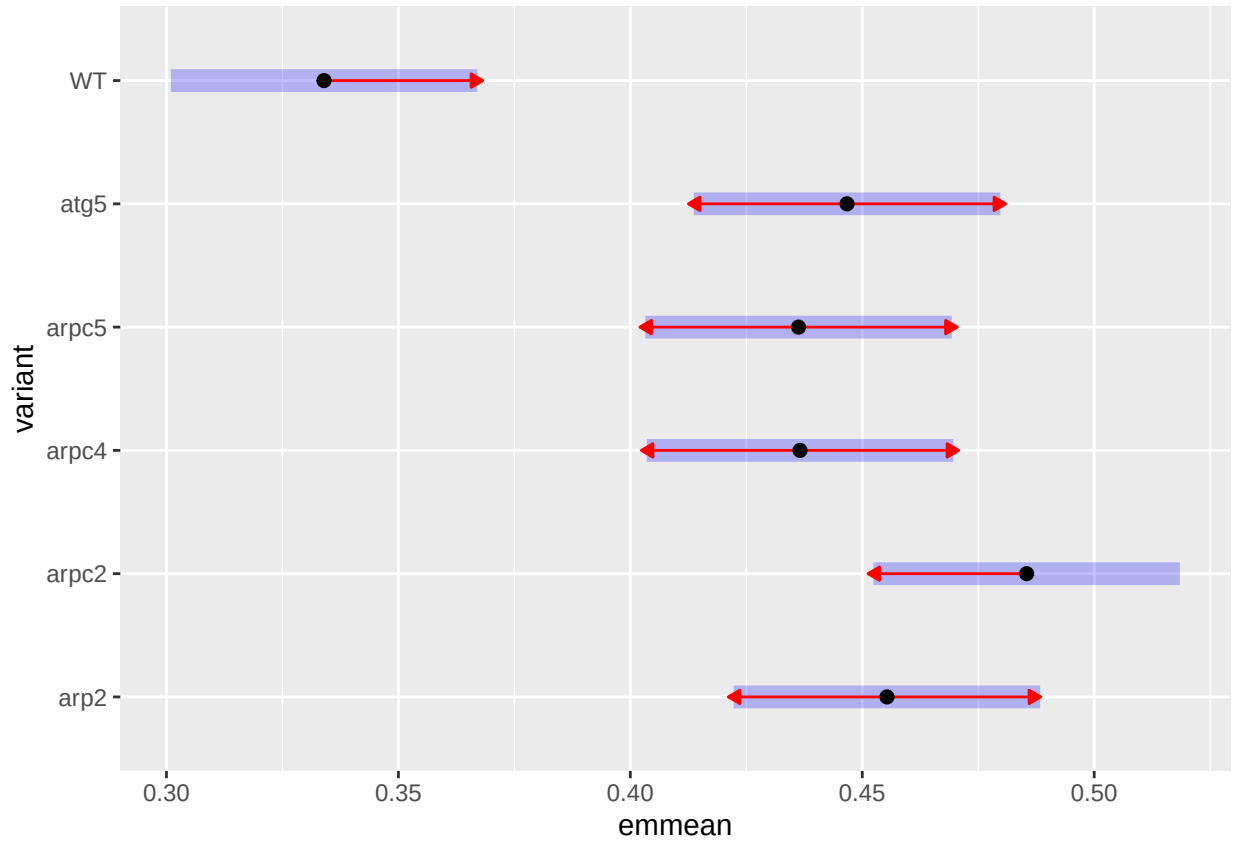

Figure S4d

```
figS4d <- read.table("FigS4d",header = T)


m1 <- lm(data=figS4d, log(primcm)~variant*treatment)
anova(m1)
```

```
## Analysis of Variance Table
##
## Response: log(primcm)
##                   Df Sum Sq Mean Sq  F value    Pr(>F)
## variant            2 0.5365  0.2682   7.3526  0.006564 **
## treatment          1 5.5441  5.5441 151.9640 6.616e-09 ***
## variant:treatment  2 0.0708  0.0354   0.9699  0.403183
## Residuals         14 0.5108  0.0365
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m2 <- lm(data=figS4d, log(primcm)~variant+treatment)
anova(m2)
```

```
## Analysis of Variance Table
##
## Response: log(primcm)
##           Df Sum Sq Mean Sq  F value    Pr(>F)
```

```
## variant    2 0.5365  0.2682   7.3803  0.005358 **
## treatment  1 5.5441  5.5441 152.5372 1.354e-09 ***
## Residuals 16 0.5815  0.0363
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
em1 <- emmeans(m1, pairwise ~ treatment | variant, type="response")
summary(em1)
```

```
## $emmeans
## variant = C4:
##  treatment response    SE df lower.CL upper.CL
##  IBA          13.58 1.297 14    11.06    16.67
##  mock          5.18 0.571 14     4.09     6.56
##
## variant = C5:
##  treatment response    SE df lower.CL upper.CL
##  IBA          13.48 1.287 14    10.98    16.54
##  mock          3.96 0.437 14     3.13     5.02
##
## variant = WT:
##  treatment response    SE df lower.CL upper.CL
##  IBA          19.46 2.146 14    15.36    24.65
##  mock          7.27 0.802 14     5.74     9.22
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
##
## $contrasts
## variant = C4:
##  contrast   ratio    SE df null t.ratio p.value
##  IBA / mock  2.62 0.382 14    1   6.607  <.0001
##
## variant = C5:
##  contrast   ratio    SE df null t.ratio p.value
##  IBA / mock  3.40 0.496 14    1   8.392  <.0001
##
## variant = WT:
##  contrast   ratio    SE df null t.ratio p.value
##  IBA / mock  2.68 0.417 14    1   6.310  <.0001
##
## Tests are performed on the log scale
```

```
summary(em1)$contrasts$p.value
```

```
## [1] 1.175403e-05 7.807748e-07 1.923172e-05
```

```
plot(em1, comparison=T)
```

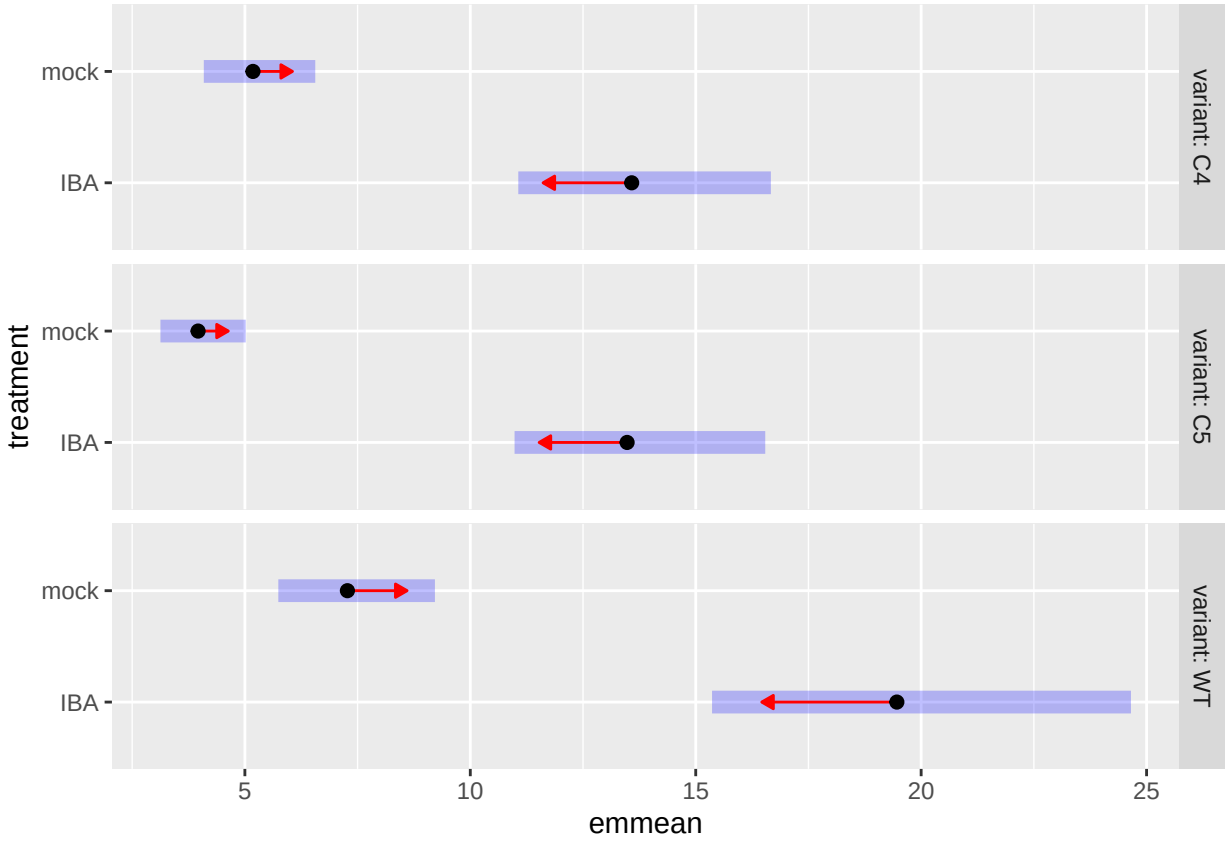

Figure S4e

```
figS4e <- read.table("FigS4e",header = T)

m1 <- betareg(data=figS4e,I(percarea/100)~variant)
lrtest(m1)
```

```
## Likelihood ratio test
##
## Model 1: I(percarea/100) ~ variant
## Model 2: I(percarea/100) ~ 1
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1   5 83.760
## 2   2 82.934 -3 1.6514     0.6478
```

```
em1 <- emmeans(m1,pairwise~variant,type="response")
summary(em1)
```

```
## $emmeans
##  variant       response     SE  df asymp.LCL asymp.UCL
##  arpc5            0.118 0.0221 Inf    0.0746     0.161
##  C2_induced       0.155 0.0254 Inf    0.1052     0.205
##  C2_noninduced    0.125 0.0224 Inf    0.0811     0.169
##  WT               0.121 0.0219 Inf    0.0777     0.164
##
## Confidence level used: 0.95
```

```
##
## $contrasts
##  contrast                   estimate     SE  df z.ratio p.value
##  arpc5 - C2_induced         -0.03707 0.0322 Inf  -1.149  0.6588
##  arpc5 - C2_noninduced      -0.00710 0.0299 Inf  -0.237  0.9953
##  arpc5 - WT                 -0.00278 0.0296 Inf  -0.094  0.9997
##  C2_induced - C2_noninduced  0.02997 0.0324 Inf   0.923  0.7923
##  C2_induced - WT             0.03429 0.0321 Inf   1.068  0.7093
##  C2_noninduced - WT          0.00432 0.0298 Inf   0.145  0.9989
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
plot(em1,type="response",comparisons = T)
```

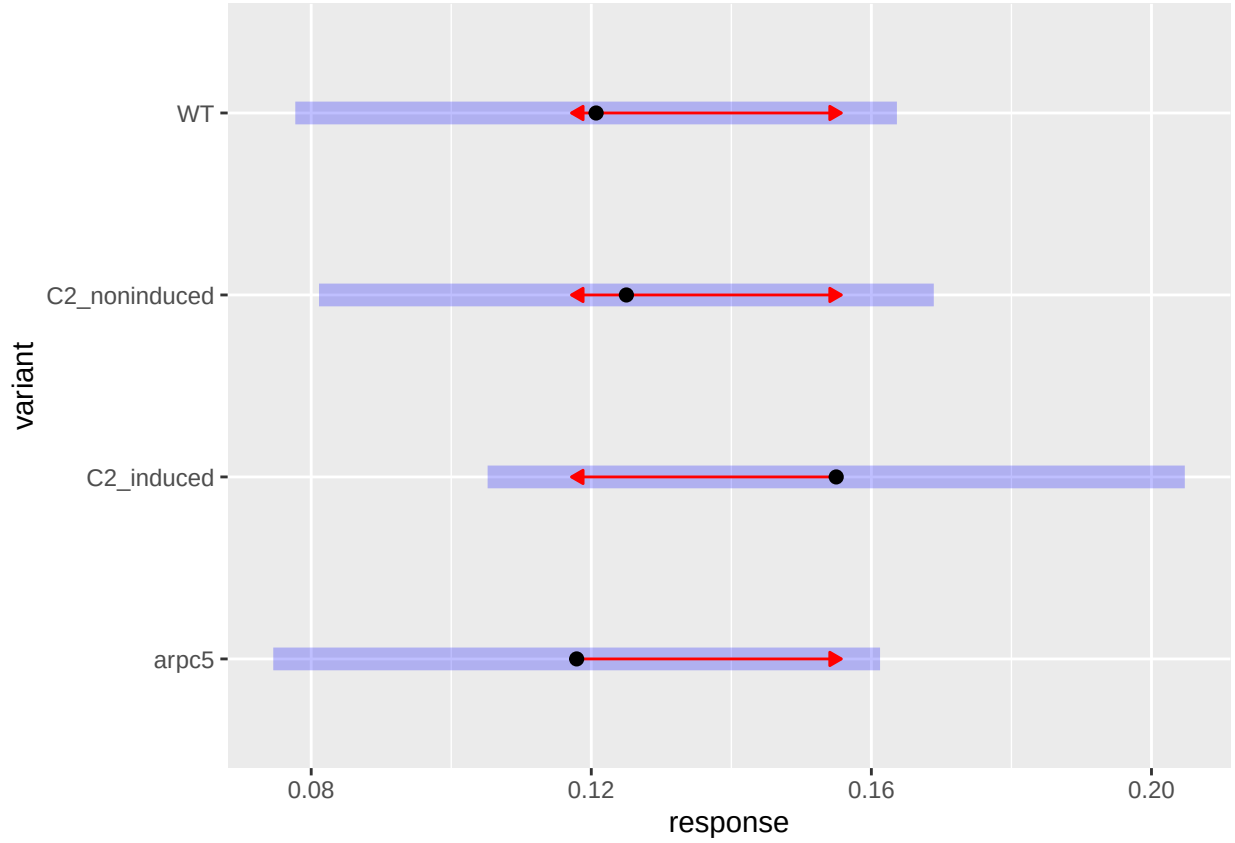

Figure 5a-d

```
fig5ad <- read.table("Fig5ad",header = T)

# Counts were normalized by scanning areas (~ divided approx. by 2), thus the
# multiplication by 2 was necessary to prevent the loss of complexity in data
# after rounding (to get discrete values for Poisson model).
m1 <- glm(data=fig5ad,round(2*autophagosomes)~variant,family = poisson)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
##
```

```
## Model: poisson, link: log
##
## Response: round(2 * autophagosomes)
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                       242     797.00
## variant   1   61.964       241     735.04 3.499e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- glm(data=fig5ad,round(2*arposomes)~variant,family = poisson)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: round(2 * arposomes)
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                       242     1252.3
## variant   1   192.24       241     1060.0 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- glm(data=fig5ad,round(2*colocalization)~variant,family = poisson)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: round(2 * colocalization)
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                       242     254.04
## variant   1   9.1169       241     244.92 0.002533 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- glm(data=fig5ad,col_aut~variant,family = quasibinomial)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: quasibinomial, link: logit
##
```

```
## Response: col_aut
##
## Terms added sequentially (first to last)
##
##
##         Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                      242     88.322
## variant  1 0.033692       241     88.288   0.8026
```

Figure 5e-h

```
fig5eh <- read.table("Fig5efh",header = T)

m1 <- glm(data=fig5eh,round(autophagosomes)~variant,family = poisson)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: round(autophagosomes)
##
## Terms added sequentially (first to last)
##
##
##         Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                      60     250.71
## variant  1   31.797        59     218.91 1.711e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- glm(data=fig5eh,round(arposomes)~variant,family = poisson)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: round(arposomes)
##
## Terms added sequentially (first to last)
##
##
##         Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                      60    1054.90
## variant  1   377.33        59     677.58 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- glm(data=fig5eh,round(colocalization)~variant,family = poisson)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
```

```
##
## Response: round(colocalization)
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                        60     96.910
## variant  1   20.535        59     76.375 5.855e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- glm(data=fig5eh,col_aut~variant,family = quasibinomial)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: quasibinomial, link: logit
##
## Response: col_aut
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                        60     8.5090
## variant  1  0.81906        59     7.6899  0.01129 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
em1 <- emmeans(m1,pairwise~variant,type="response")
summary(em1)
```

```
## $emmeans
##  variant   prob     SE  df asymp.LCL asymp.UCL
##  3-MA    0.1137 0.0200 Inf    0.0799    0.1592
##  ctrl    0.0505 0.0145 Inf    0.0286    0.0879
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
##
## $contrasts
##  contrast      odds.ratio    SE  df null z.ratio p.value
##  (3-MA) / ctrl       2.41 0.873 Inf    1   2.427  0.0152
##
## Tests are performed on the log odds ratio scale
```

```
summary(em1)$contrasts$p.value
```

```
## [1] 0.01521345
```

```
plot(em1,comparisons = T)
```

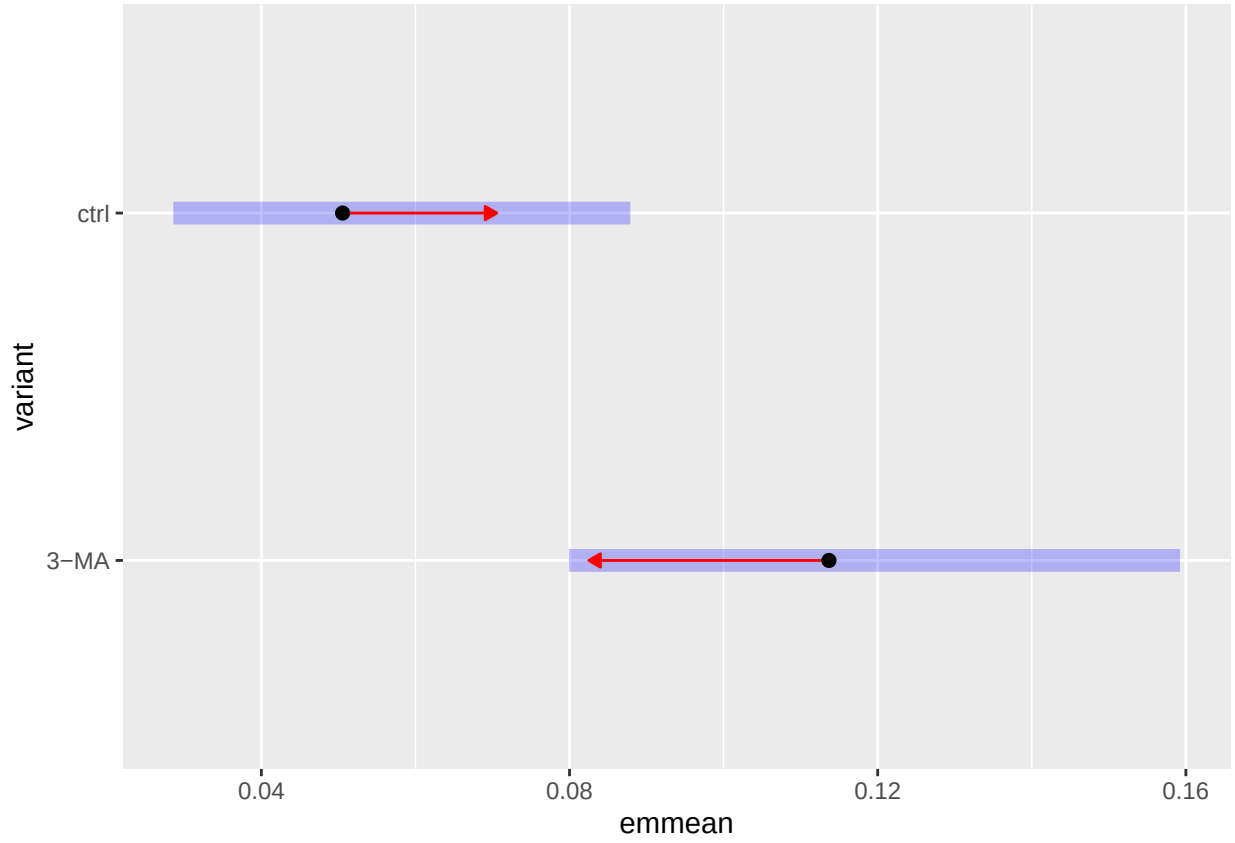

Figure 5i-k

```
fig5ijk <- read.table("Fig5ijk",header = T)

m1 <- glm(data=fig5ijk,arposomes~variant,family = poisson)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: arposomes
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                        24    2543.39
## variant  1   1995.2         23     548.14 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- glm(data=fig5ijk,peroxisomes~variant,family = poisson)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
```

```
##
## Model: poisson, link: log
##
## Response: peroxisomes
##
## Terms added sequentially (first to last)
##
##
##         Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                       24     3651.3
## variant  1   2882.5        23      768.8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- betareg(data=fig5ijk,I(ap_ratio/100)~variant)
lrtest(m1)
```

```
## Likelihood ratio test
##
## Model 1: I(ap_ratio/100) ~ variant
## Model 2: I(ap_ratio/100) ~ 1
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1   3 27.515
## 2   2 14.816 -1 25.398  4.665e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure S5

```
figS5 <- read.table("FigS5",header = T)

m1 <- glm(data=figS5,coloc~variant,family = quasibinomial)
anova(m1,test="LRT")
```

```
## Analysis of Deviance Table
##
## Model: quasibinomial, link: logit
##
## Response: coloc
##
## Terms added sequentially (first to last)
##
##
##         Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                      304     106.58
## variant  2   16.415       302      90.17 2.698e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
em1 <- emmeans(m1,pairwise~variant,type="response")
summary(em1)
```

```
## $emmeans
##  variant   prob      SE  df asymp.LCL asymp.UCL
##  LSCM    0.0393 0.00947 Inf    0.0244    0.0627
```

```
##  VAEM_A  0.1741 0.03066 Inf    0.1219    0.2425
##  VAEM_M  0.1811 0.02464 Inf    0.1377    0.2345
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
##
## $contrasts
##  contrast        odds.ratio     SE  df null z.ratio p.value
##  LSCM / VAEM_A        0.194 0.0639 Inf    1  -4.981  <.0001
##  LSCM / VAEM_M        0.185 0.0557 Inf    1  -5.610  <.0001
##  VAEM_A / VAEM_M      0.953 0.2576 Inf    1  -0.178  0.9827
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log odds ratio scale
```

```
summary(em1)$contrasts$p.value
```

```
## [1] 1.894299e-06 6.050313e-08 9.827059e-01
```

```
plot(em1,comparisons = T)
```