

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)

anova(lm(data=fig2b,speed~variant))

## 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
```

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)

```

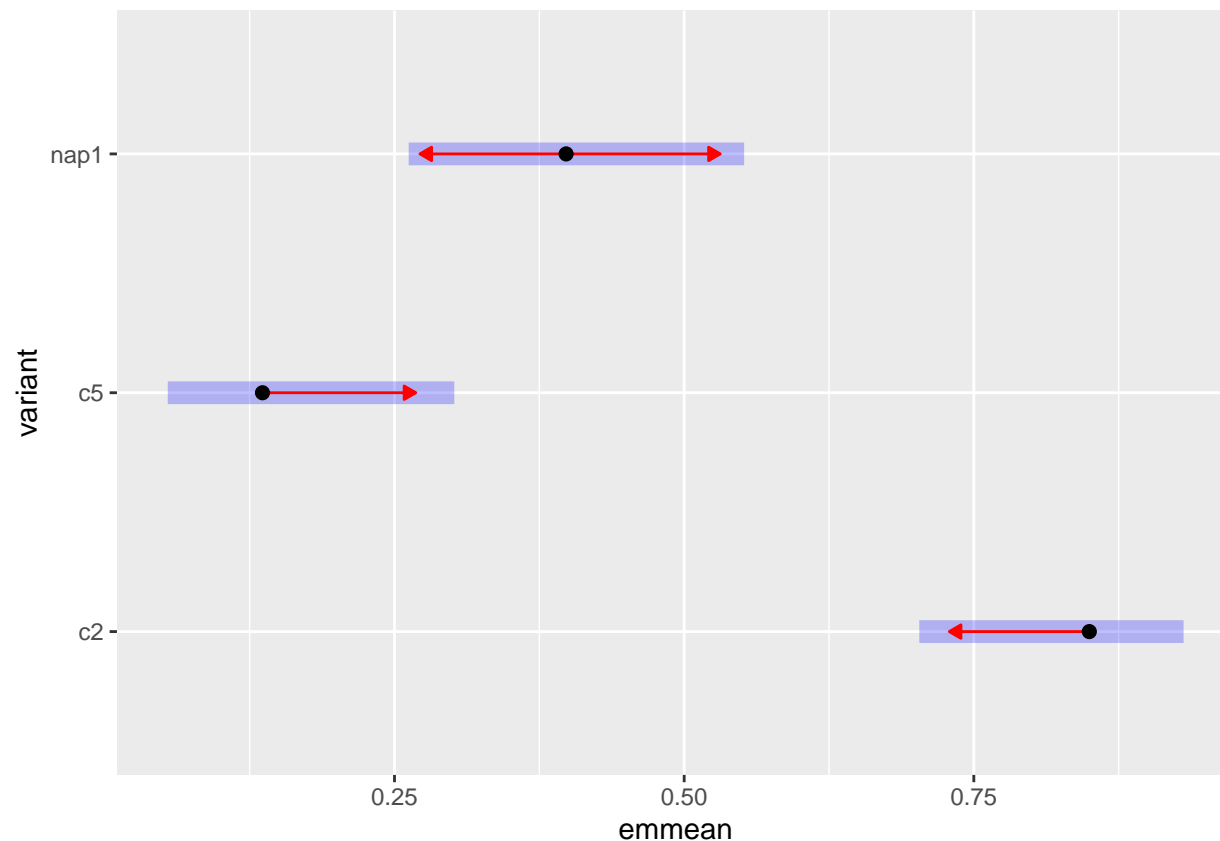


Figure 4a

```
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)
```

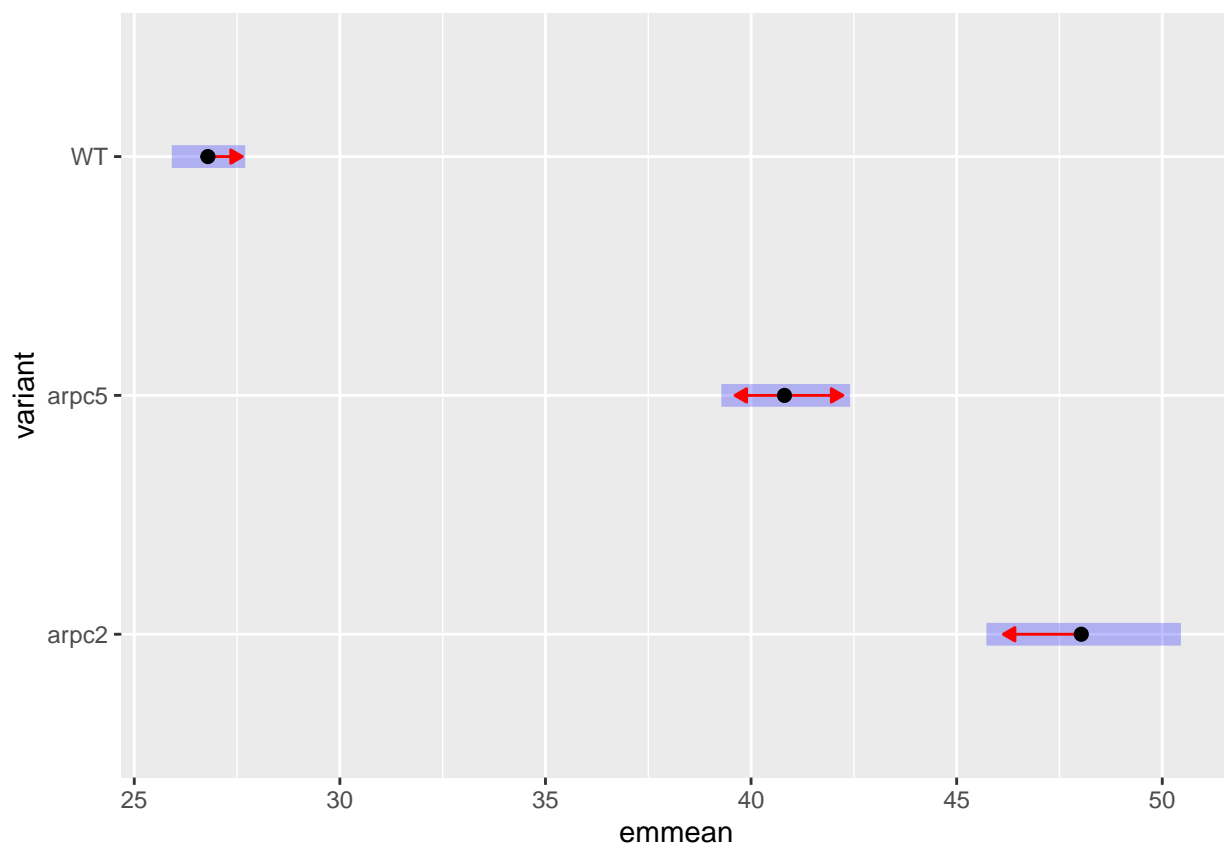


Figure 4b

```
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)
```

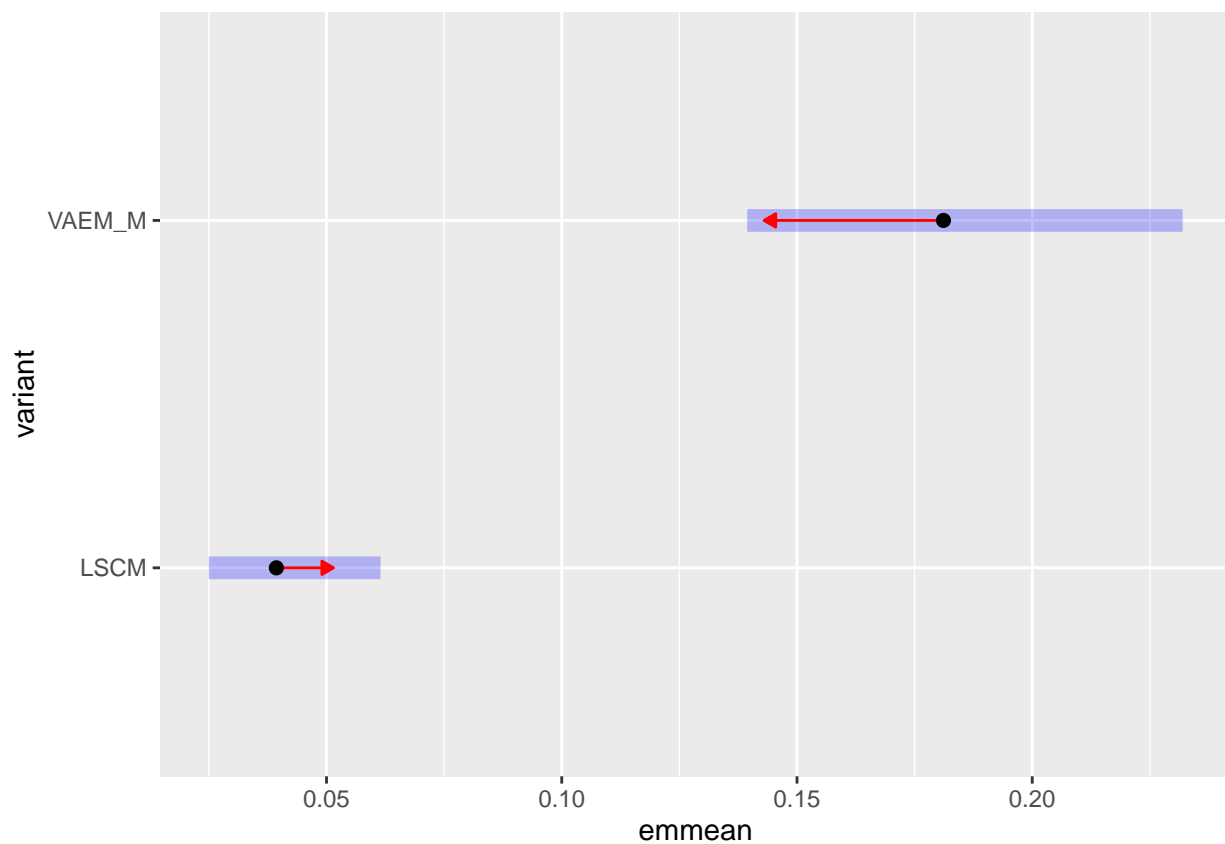


Figure 4o

```
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)
```

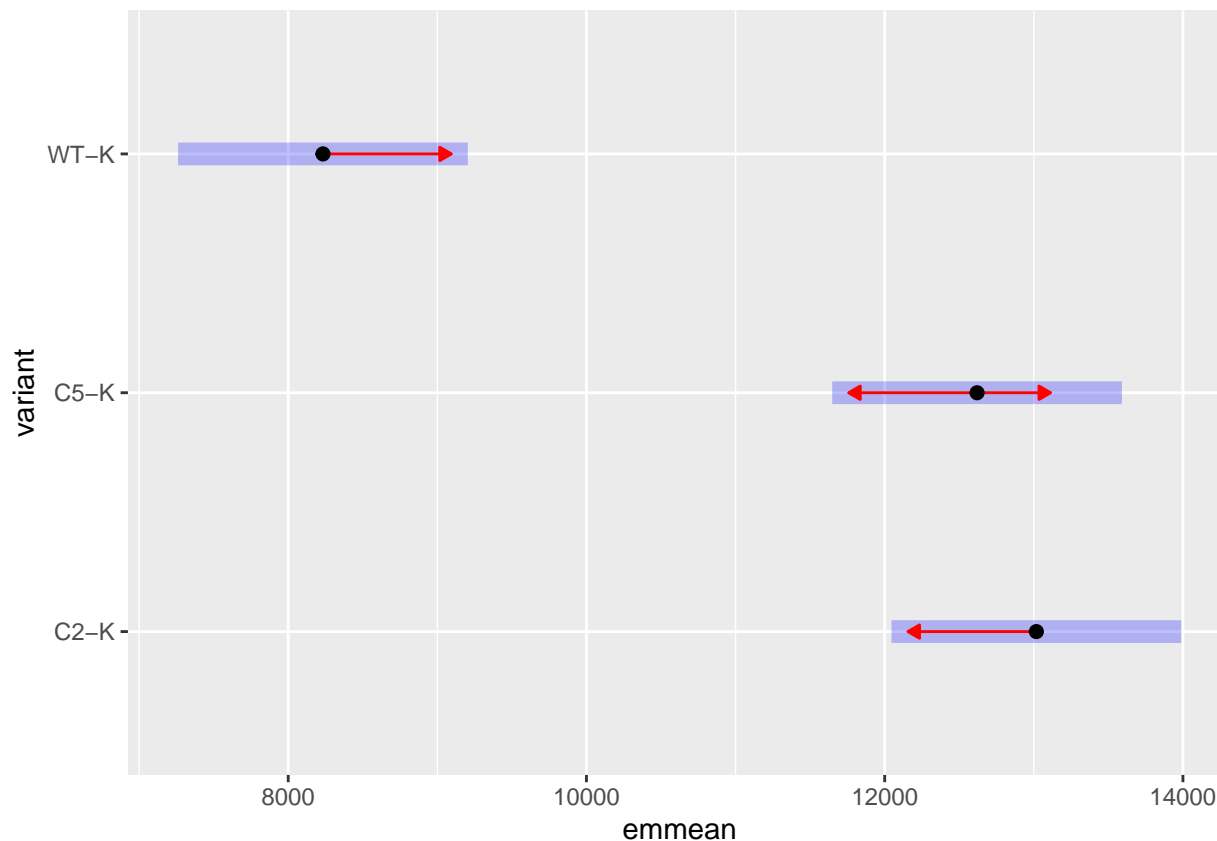


Figure S4c

```
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)
```

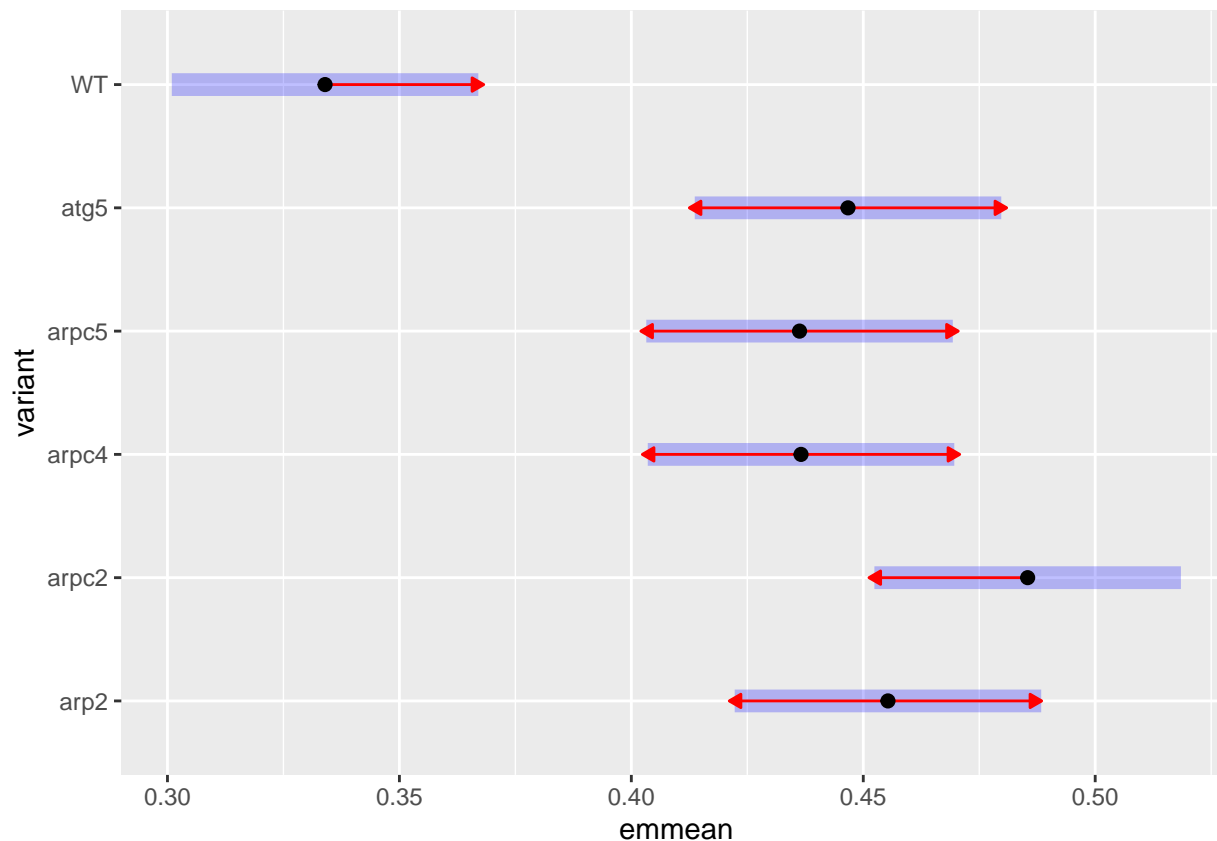


Figure S4d

```
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)
```

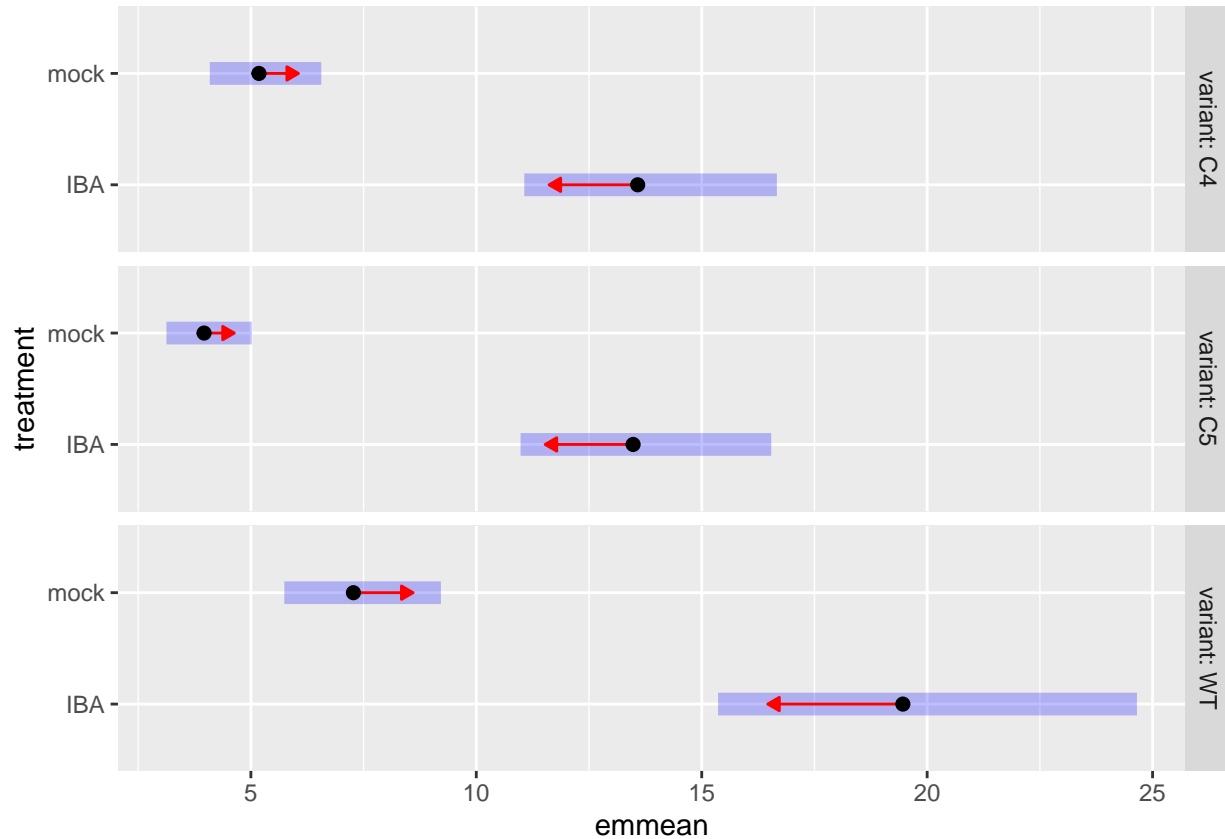


Figure S4e

```
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
```

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)
```

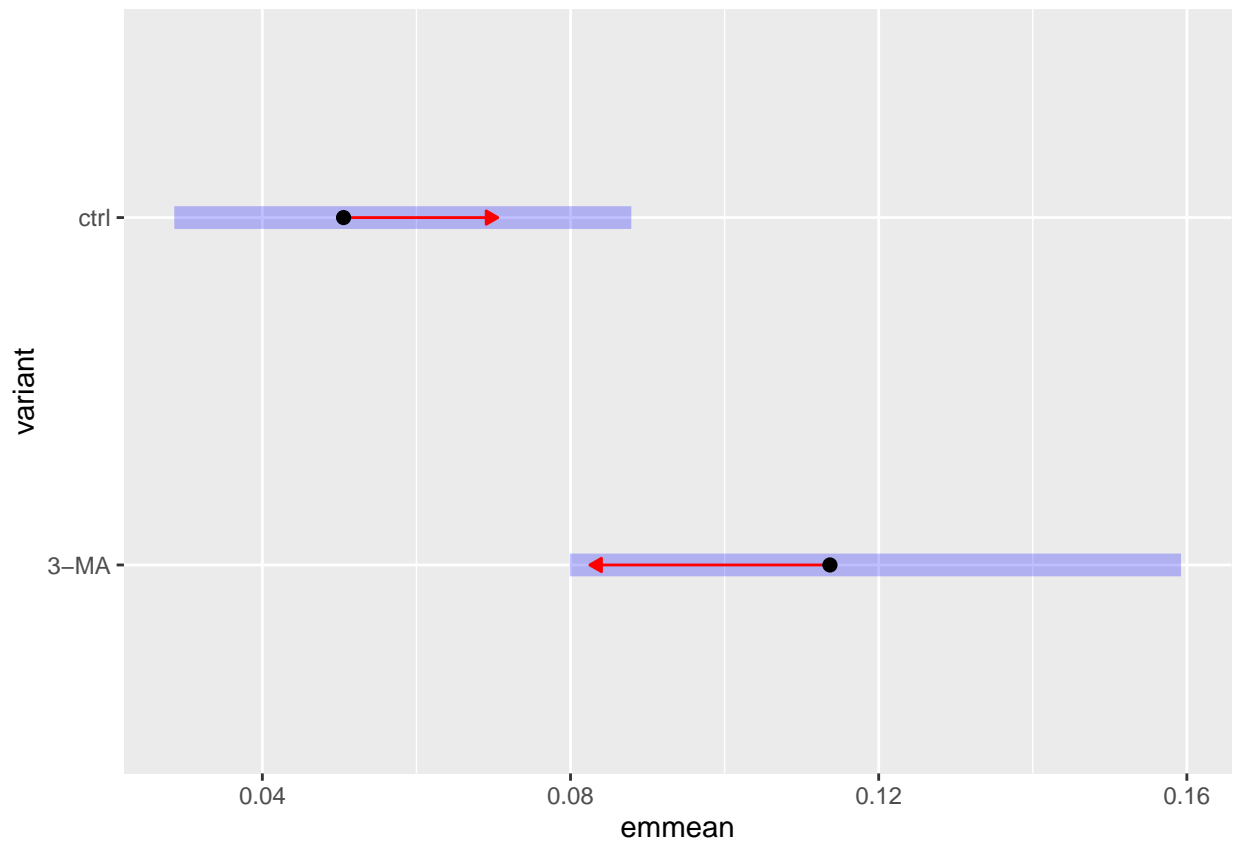


Figure 5i-k

```
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)
```

