

Adiposity and TG

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```
load(file="Effect_Size_All_Traits.RData")
load(file="Effect_Size_All_Traits_lnCVR.RData")

Adiposity_lnRR <- subset(Effect_Size_All_Traits, Effect_Size_All_Traits$Trait == "Adiposity")

Adiposity_lnRR_MG <- subset(Adiposity_lnRR, Adiposity_lnRR$Exposure_Type == "Multigenerational")
Adiposity_lnRR_OF <- subset(Adiposity_lnRR, Adiposity_lnRR$Exposure_Type == "One off")
```

Adiposity

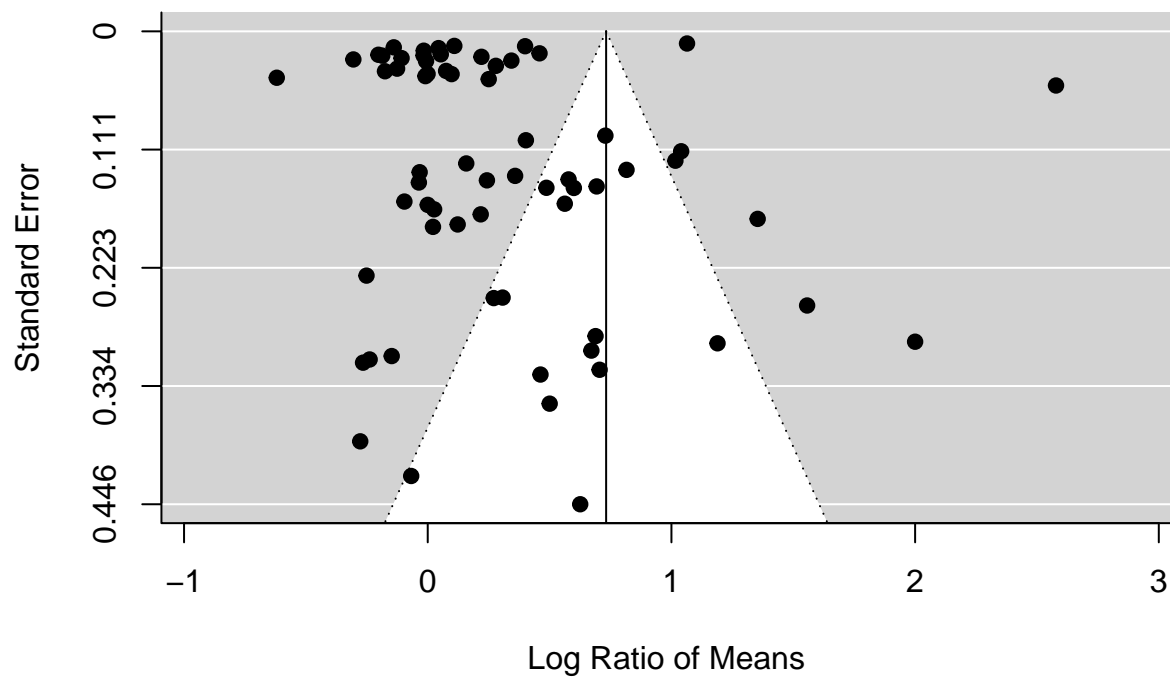
```
#Overall analysis, not split
```

```
Adiposity_overall_lnRR_Omods <- rma.mv(yi, vi, random = list(~1|Paper_ID, ~1|Cohort_ID, ~1|ES_ID), data=Adiposity_overall_lnRR_Omods)

summary(Adiposity_overall_lnRR_Omods)
```

```
##
## Multivariate Meta-Analysis Model (k = 65; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -20.0481    40.0962    48.0962    56.7318    48.7742
##
## Variance Components:
##
##              estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.6537  0.8085     10     no    Paper_ID
## sigma^2.2  0.0645  0.2541     25     no    Cohort_ID
## sigma^2.3  0.0253  0.1591     65     no      ES_ID
##
## Test for Heterogeneity:
## Q(df = 64) = 11279.9263, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    0.7321    0.2675    2.7368    0.0062    0.2078    1.2563    **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

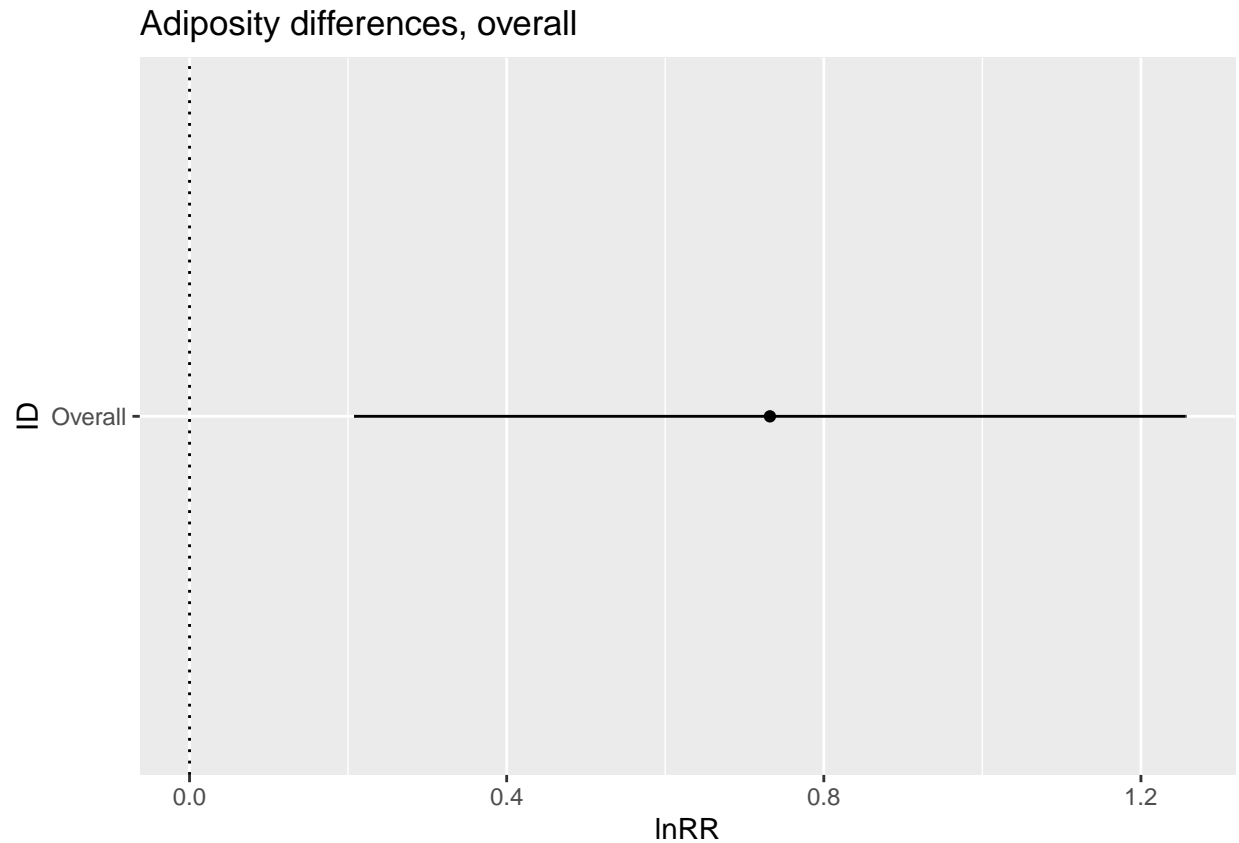
```
funnel(Adiposity_overall_lnRR_Omods)
```



#Tibble of overall results

```
Adiposity_overall_lnRR <- tibble(
  ID = "Overall",
  lnRR = Adiposity_overall_lnRR_Omods$b[1],
  ci.lb = Adiposity_overall_lnRR_Omods$ci.lb[1],
  ci.ub = Adiposity_overall_lnRR_Omods$ci.ub[1]
)

plot_adiposity_overall <- ggplot(Adiposity_overall_lnRR, aes(x=ID, y=lnRR)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +
  geom_point(aes(x = ID, y = lnRR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(title = "Adiposity differences, overall", x = "ID", y = "lnRR") +
  coord_flip()
plot_adiposity_overall
```



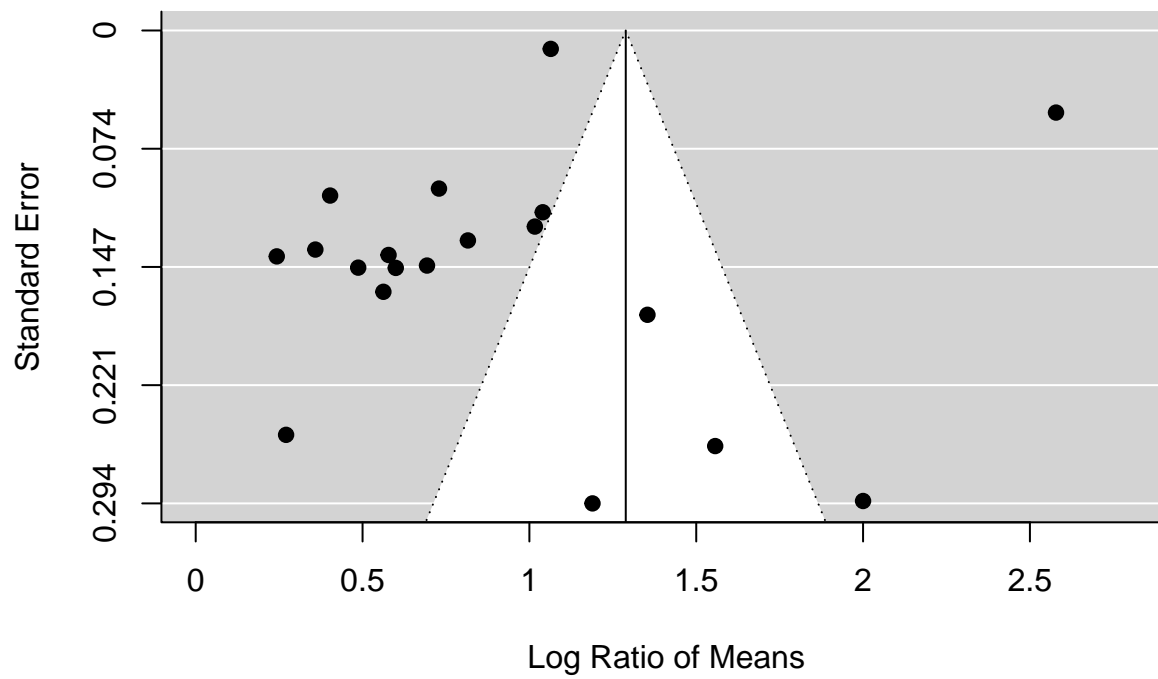
Splitting by exposure type

```
Adiposity_overall_lnRR_MG <- rma.mv(yi, vi, random = list(~1|Paper_ID, ~1|Cohort_ID, ~1|ES_ID), data=Adiposity_overall)
summary(Adiposity_overall_lnRR_MG)
```

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -10.4863   20.9725   28.9725   32.5340   32.0494
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.5856  0.7652     6    no   Paper_ID
## sigma^2.2  0.0000  0.0000     9    no   Cohort_ID
## sigma^2.3  0.0652  0.2553    19    no     ES_ID
##
## Test for Heterogeneity:
## Q(df = 18) = 1067.4729, p-val < .0001
##
## Model Results:
```

```
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 1.2888 0.3264 3.9478 <.0001 0.6489 1.9286 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel (Adiposity_overall_lnRR_MG)
```

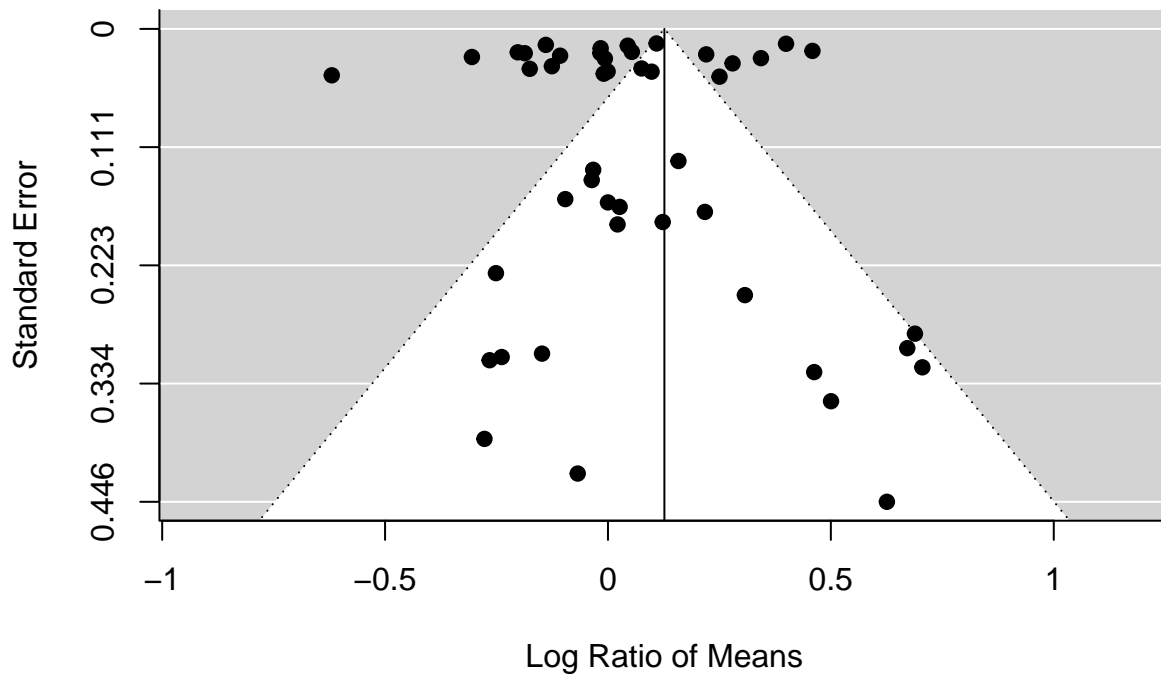


```
Adiposity_overall_lnRR_OF <- rma.mv(yi, vi, random = list(~1|Paper_ID, ~1|Cohort_ID, ~1|ES_ID), data=Adipos)
summary(Adiposity_overall_lnRR_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
## logLik Deviance      AIC      BIC      AICc
## 3.9950 -7.9900 0.0100 7.2367 1.0100
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed  factor
## sigma^2.1 0.0133 0.1152    6    no  Paper_ID
## sigma^2.2 0.0419 0.2048   16    no Cohort_ID
## sigma^2.3 0.0162 0.1271   46    no    ES_ID
```

```
##
## Test for Heterogeneity:
## Q(df = 45) = 2227.1441, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    0.1266    0.0841    1.5058    0.1321   -0.0382    0.2914
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel (Adiposity_overall_lnRR_OF)
```



```
Adiposity_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnRR = c(Adiposity_overall_lnRR_MG$b[1], Adiposity_overall_lnRR_OF$b[1]),
  ci.lb = c(Adiposity_overall_lnRR_MG$ci.lb[1], Adiposity_overall_lnRR_OF$ci.lb[1]),
  ci.ub = c(Adiposity_overall_lnRR_MG$ci.ub[1], Adiposity_overall_lnRR_OF$ci.ub[1])
)
```

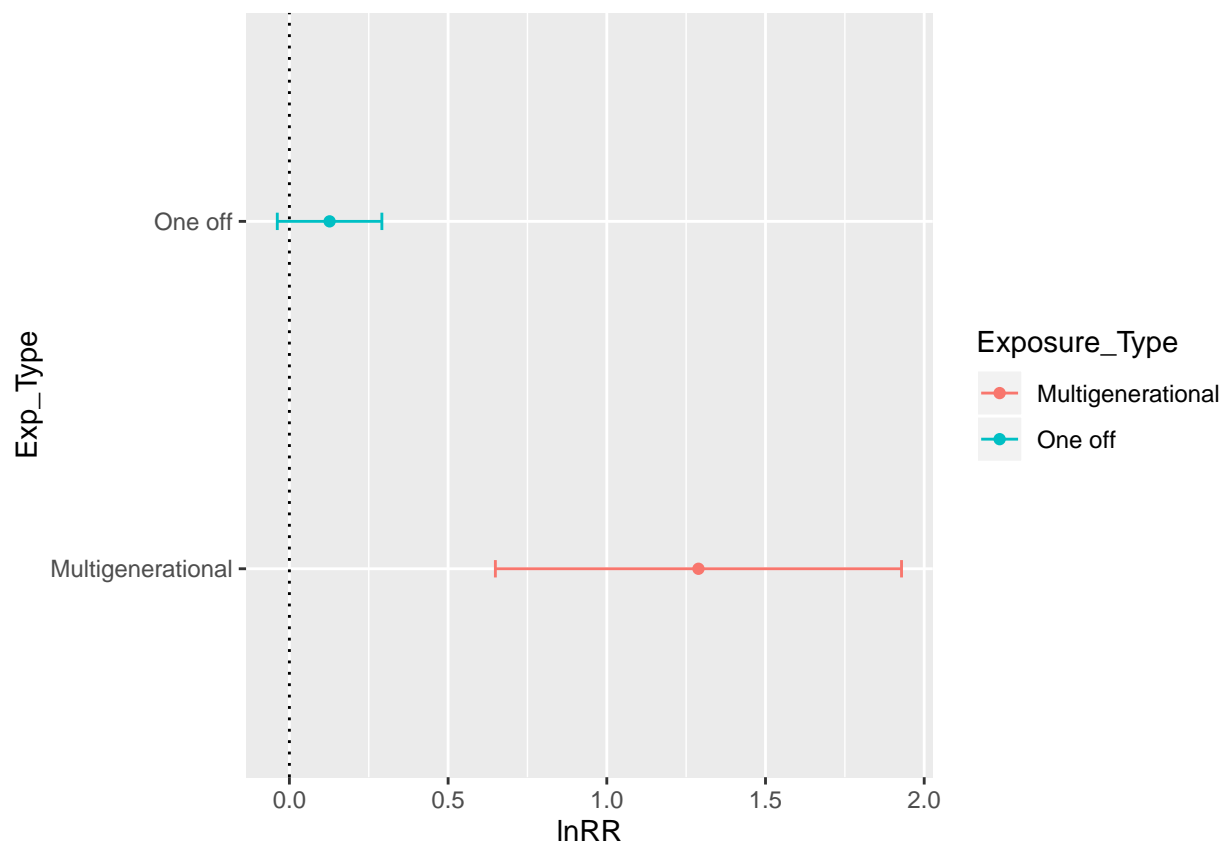
```
Adiposity_Exp_lnRR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnRR    ci.lb ci.ub
```

```
##      <chr>          <dbl>   <dbl> <dbl>
## 1 Multigenerational 1.29    0.649 1.93
## 2 One off          0.127 -0.0382 0.291
```

#Plotting when split by exp type

```
plot_Adiposity_exp_type <- ggplot(Adiposity_Exp_lnRR, aes(x=Exposure_Type, y=lnRR, colour = Exposure_Type)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0.05, position = position_dodge(0.3)) +
  geom_point(aes(x = Exposure_Type, y = lnRR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(x = "Exp_Type", y = "lnRR") +
  coord_flip()
plot_Adiposity_exp_type
```



#Adiposity analysis with moderators (split by exposure type)

```
Adiposity_MG_F0 <- rma.mv(yi, vi, mods = ~F0_Parent_Exposed-1, random = list(~1|Paper_ID,~1|Cohort_ID,~1|Study))
```

```
## Warning in rma.mv(yi, vi, mods = ~F0_Parent_Exposed - 1, random = list(~1
## | : Redundant predictors dropped from the model.
```

Adiposity_MG_F0

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
```

```

##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.6260  0.7912     6     no   Paper_ID
## sigma^2.2  0.0000  0.0000     9     no   Cohort_ID
## sigma^2.3  0.0652  0.2553    19     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 17) = 999.6668, p-val < .0001
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 15.4776, p-val = 0.0004
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## F0_Parent_ExposedFemale    1.4288  0.3713  3.8481  0.0001    0.7011  2.1566
## F0_Parent_ExposedMale      0.6531  0.7980  0.8184  0.4131   -0.9110  2.2173
##
## F0_Parent_ExposedFemale ***
## F0_Parent_ExposedMale
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Adiposity_OF_F0 <- rma.mv(yi, vi, mods = ~F0_Parent_Exposed-1, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID))

## Warning in rma.mv(yi, vi, mods = ~F0_Parent_Exposed - 1, random = list(~1
## | : Redundant predictors dropped from the model.

Adiposity_OF_F0

##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0176  0.1326     6     no   Paper_ID
## sigma^2.2  0.0437  0.2089    16     no   Cohort_ID
## sigma^2.3  0.0161  0.1270    46     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 44) = 2225.9395, p-val < .0001
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 2.4066, p-val = 0.3002
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb
## F0_Parent_ExposedFemale    0.1489  0.0960  1.5509  0.1209   -0.0393

```

```
## F0_Parent_ExposedMale      -0.0098  0.2577  -0.0379  0.9698  -0.5149
##                               ci.ub
## F0_Parent_ExposedFemale  0.3370
## F0_Parent_ExposedMale      0.4953
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Adiposity_MG_Sex <- rma.mv(yi, vi, mods = ~Sex-1, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), data=dat)
Adiposity_MG_Sex
```

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.6013  0.7754      6      no  Paper_ID
## sigma^2.2  0.0000  0.0000      9      no  Cohort_ID
## sigma^2.3  0.0699  0.2643     19      no    ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 17) = 1023.3387, p-val < .0001
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 15.4592, p-val = 0.0004
##
## Model Results:
##
##      estimate      se    zval    pval    ci.lb    ci.ub
## SexFemale      1.2410  0.3418  3.6310  0.0003  0.5711  1.9108 ***
## SexMale        1.3367  0.3420  3.9081 <.0001  0.6663  2.0071 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Adiposity_OF_Sex <- rma.mv(yi, vi, mods = ~Sex-1, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), data=dat)
Adiposity_OF_Sex
```

```
##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0219  0.1479      6      no  Paper_ID
## sigma^2.2  0.0301  0.1734     16      no  Cohort_ID
## sigma^2.3  0.0141  0.1189     46      no    ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 44) = 2169.3337, p-val < .0001
```

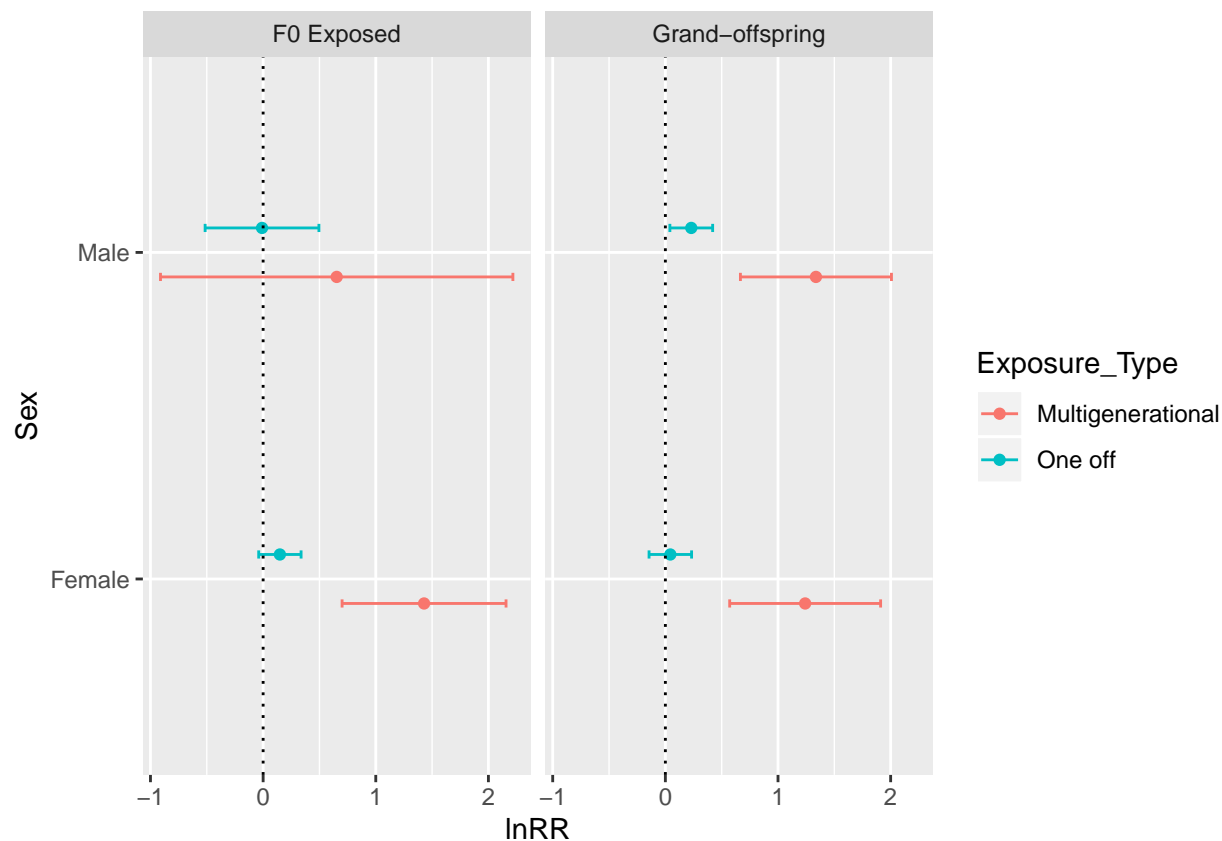


```
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 8.2387, p-val = 0.0163
##
## Model Results:
##
##          estimate      se    zval    pval    ci.lb    ci.ub
## SexFemale    0.0440  0.0963  0.4572  0.6475  -0.1447  0.2328
## SexMale      0.2299  0.0969  2.3731  0.0176   0.0400  0.4199  *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Adiposity_Exp_mods_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "Multigenerational", "One off", "One off", "Multigenerational",
  Sex = c("Female", "Male", "Female", "Male", "Female", "Male", "Female", "Male"),
  Mod = c("F0 Exposed", "F0 Exposed", "F0 Exposed", "F0 Exposed", "Grand-offspring", "Grand-offspring", "Grand-offspring", "Grand-offspring"),
  lnRR = c(Adiposity_MG_F0$b[1], Adiposity_MG_F0$b[2], Adiposity_OF_F0$b[1], Adiposity_OF_F0$b[2], Adiposity_OF_F0$b[3], Adiposity_OF_F0$b[4], Adiposity_OF_F0$b[5], Adiposity_OF_F0$b[6]),
  ci.lb = c(Adiposity_MG_F0$ci.lb[1], Adiposity_MG_F0$ci.lb[2], Adiposity_OF_F0$ci.lb[1], Adiposity_OF_F0$ci.lb[2], Adiposity_OF_F0$ci.lb[3], Adiposity_OF_F0$ci.lb[4], Adiposity_OF_F0$ci.lb[5], Adiposity_OF_F0$ci.lb[6]),
  ci.ub = c(Adiposity_MG_F0$ci.ub[1], Adiposity_MG_F0$ci.ub[2], Adiposity_OF_F0$ci.ub[1], Adiposity_OF_F0$ci.ub[2], Adiposity_OF_F0$ci.ub[3], Adiposity_OF_F0$ci.ub[4], Adiposity_OF_F0$ci.ub[5], Adiposity_OF_F0$ci.ub[6])
)

plot_Adiposity_lnRR_mods_exp <- ggplot(Adiposity_Exp_mods_lnRR, aes(x=Sex, y=lnRR, colour=Exposure_Type)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0.05, position = position_dodge(0.3)) +
  geom_point(aes(x = Sex, y = lnRR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(x = "Sex", y = "lnRR") +
  coord_flip() +
  facet_grid(~Mod)

plot_Adiposity_lnRR_mods_exp
```



Adiposity lnCVR

```
#Subset Adiposity lnCVR Data
Adiposity_lnCVR <- subset(Effect_Size_All_Traits_lnCVR, Effect_Size_All_Traits_lnCVR$Trait == "Adiposity")

Adiposity_lnCVR_MG <- subset(Adiposity_lnCVR, Adiposity_lnCVR$Exposure_Type == "Multigenerational")
Adiposity_lnCVR_OF <- subset(Adiposity_lnCVR, Adiposity_lnCVR$Exposure_Type == "One off")

Adiposity_overall_lnCVR_0mods <- rma.mv(yi, vi, random = list(~1|Paper_ID, ~1|Cohort_ID, ~1|ES_ID), data=Adiposity_lnCVR)
summary(Adiposity_overall_lnCVR_0mods)

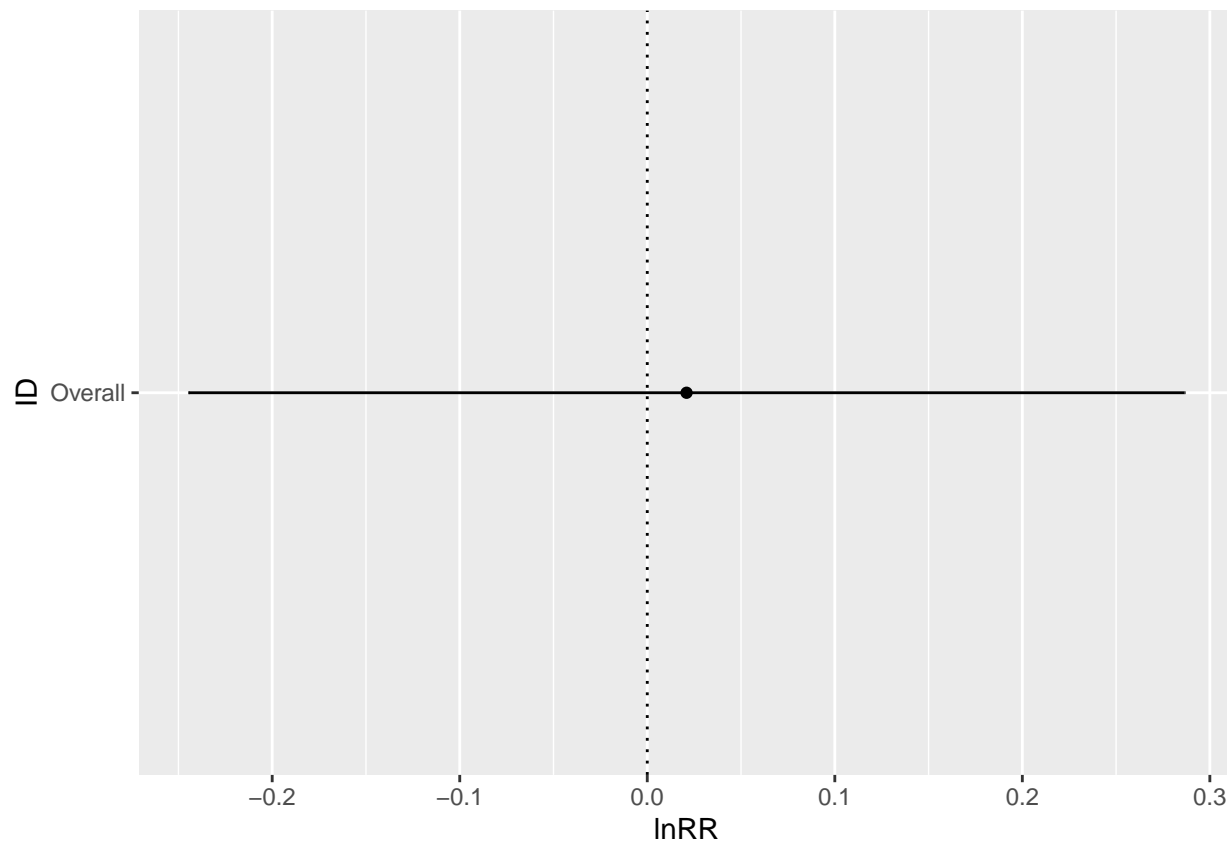
##
## Multivariate Meta-Analysis Model (k = 65; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -49.6278   99.2556  107.2556  115.8911  107.9335
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
```

```
## sigma^2.1 0.0663 0.2575 10 no Paper_ID
## sigma^2.2 0.1403 0.3745 25 no Cohort_ID
## sigma^2.3 0.0027 0.0515 65 no ES_ID
##
## Test for Heterogeneity:
## Q(df = 64) = 121.4021, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.0210 0.1355 0.1547 0.8771 -0.2446 0.2865
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#Tibble of overall results

```
Adiposity_overall_lnCVR <- tibble(
  ID = "Overall",
  lnCVR = Adiposity_overall_lnCVR_Omods$b[1],
  ci.lb = Adiposity_overall_lnCVR_Omods$ci.lb[1],
  ci.ub = Adiposity_overall_lnCVR_Omods$ci.ub[1]
)

plot_adiposity_overall_lnCVR <- ggplot(Adiposity_overall_lnCVR, aes(x=ID, y=lnCVR)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +
  geom_point(aes(x = ID, y = lnCVR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(x = "ID", y = "lnRR") +
  coord_flip()
plot_adiposity_overall_lnCVR
```



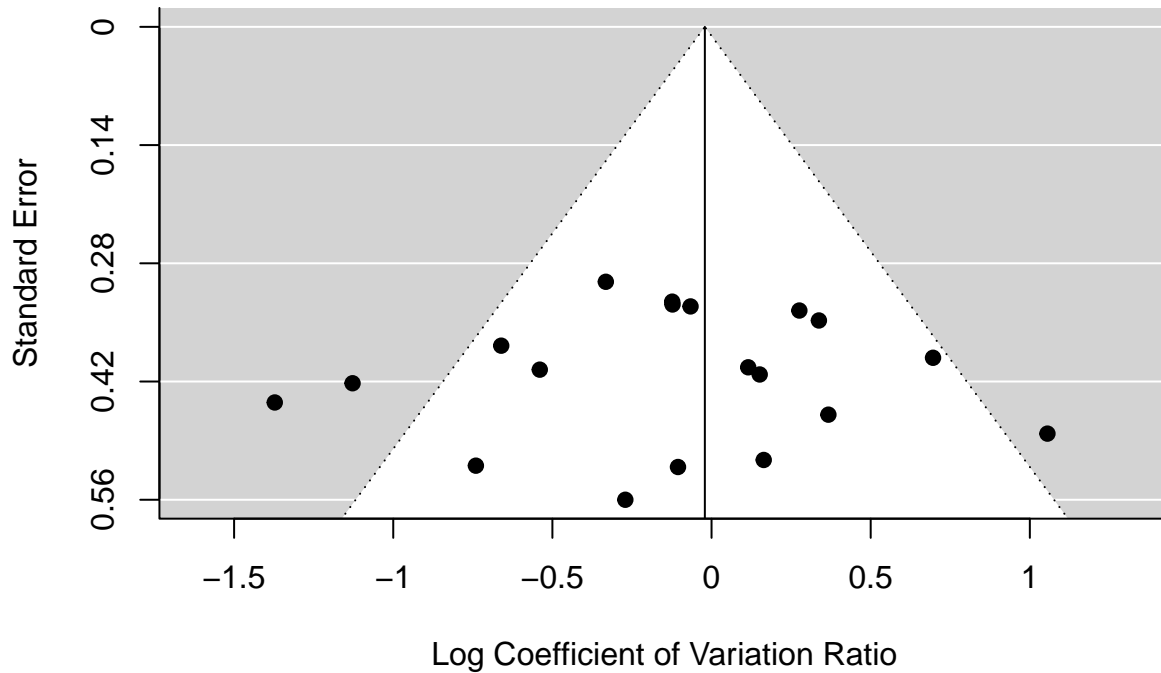
#Adiposity lnCVR (split by exposure type)

```
Adiposity_overall_lnCVR_MG <- rma.mv(yi, vi, random = list(~1|Paper_ID, ~1|Cohort_ID, ~1|ES_ID), data=Adiposity_overall_lnCVR_MG)
summary(Adiposity_overall_lnCVR_MG)
```

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -15.1516   30.3033   38.3033   41.8648   41.3802
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed    factor
## sigma^2.1  0.0000  0.0000     6    no   Paper_ID
## sigma^2.2  0.1150  0.3392     9    no   Cohort_ID
## sigma^2.3  0.0682  0.2612    19    no     ES_ID
##
## Test for Heterogeneity:
## Q(df = 18) = 34.4038, p-val = 0.0112
##
## Model Results:
##
## estimate      se      zval    pval    ci.lb    ci.ub
## -0.0210  0.1742  -0.1207  0.9039  -0.3625  0.3204
```

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

```
funnel (Adiposity_overall_lnCVR_MG)
```

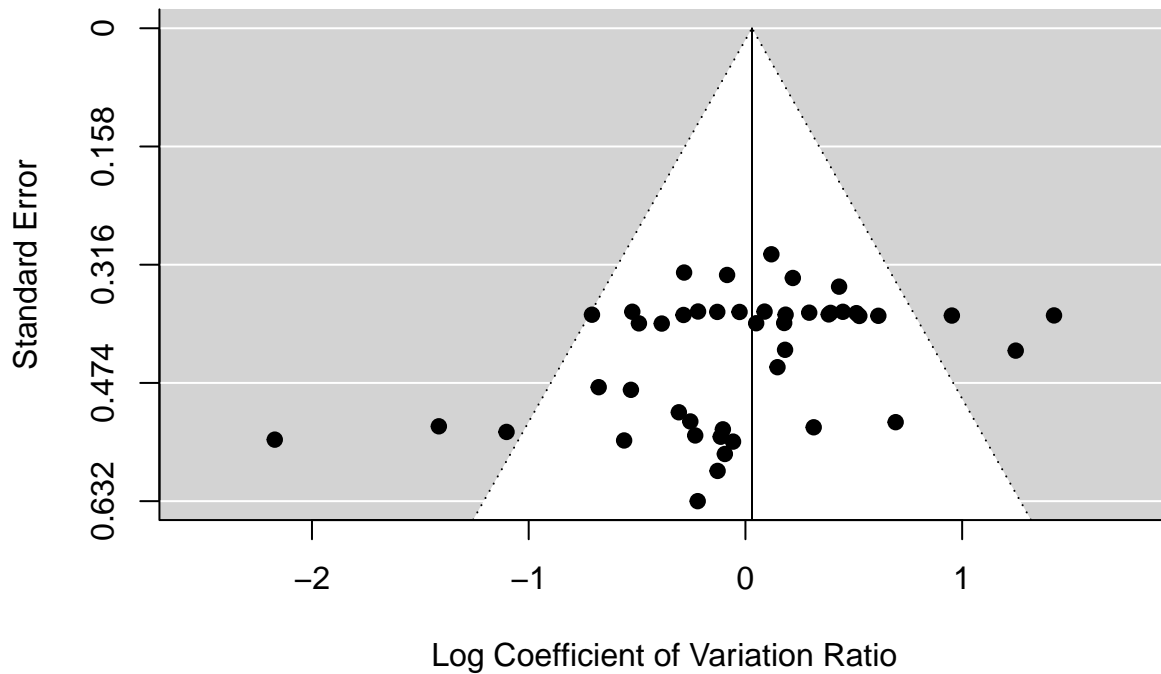


```
Adiposity_overall_lnCVR_OF <- rma.mv(yi, vi, random = list(~1|Paper_ID, ~1|Cohort_ID, ~1|ES_ID), data=Adiposity_overall_lnCVR_MG)
summary(Adiposity_overall_lnCVR_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -32.9893   65.9786   73.9786   81.2053   74.9786
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed  factor
## sigma^2.1 0.0984 0.3137    6    no  Paper_ID
## sigma^2.2 0.1595 0.3994   16    no  Cohort_ID
## sigma^2.3 0.0000 0.0000   46    no    ES_ID
##
## Test for Heterogeneity:
## Q(df = 45) = 85.1607, p-val = 0.0003
```

```
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.0304 0.1917 0.1584 0.8742 -0.3453 0.4061
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel (Adiposity_overall_lnCVR_OF)
```



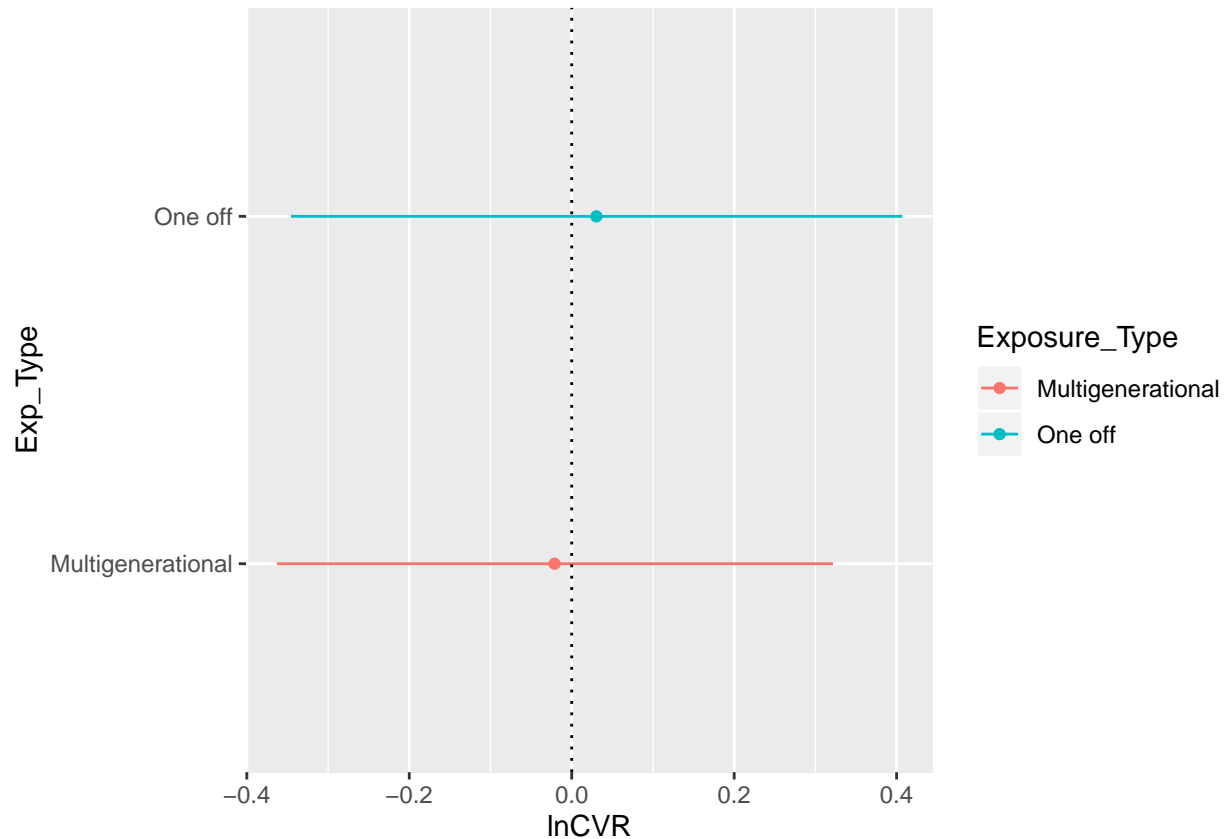
```
Adiposity_Exp_lnCVR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnCVR = c(Adiposity_overall_lnCVR_MG$b[1], Adiposity_overall_lnCVR_OF$b[1]),
  ci.lb = c(Adiposity_overall_lnCVR_MG$ci.lb[1], Adiposity_overall_lnCVR_OF$ci.lb[1]),
  ci.ub = c(Adiposity_overall_lnCVR_MG$ci.ub[1], Adiposity_overall_lnCVR_OF$ci.ub[1])
)
```

```
Adiposity_Exp_lnCVR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnCVR ci.lb ci.ub
##   <chr>          <dbl> <dbl> <dbl>
## 1 Multigenerational -0.0210 -0.363 0.320
## 2 One off           0.0304 -0.345 0.406
```

```
#Plotting when split by exp type
```

```
plot_Adiposity_exp_type_lnCVR <- ggplot(Adiposity_Exp_lnCVR, aes(x=Exposure_Type, y=lnCVR, colour = Exp
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +
  geom_point(aes(x = Exposure_Type, y = lnCVR), position = position_dodge(0.3))+
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(x = "Exp_Type", y = "lnCVR") +
  coord_flip()
plot_Adiposity_exp_type_lnCVR
```



Adiposity analysis with moderators (split by exposure type)

```
Adiposity_MG_F0_lnCVR <- rma.mv(yi, vi, mods = ~F0_Parent_Exposed-1, random = list(~1|Paper_ID,~1|Cohor
```

```
## Warning in rma.mv(yi, vi, mods = ~F0_Parent_Exposed - 1, random = list(~1
## | : Redundant predictors dropped from the model.
```

```
Adiposity_MG_F0_lnCVR
```

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
```

```

##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0001     6     no   Paper_ID
## sigma^2.2  0.1840  0.4289     9     no   Cohort_ID
## sigma^2.3  0.0635  0.2519    19     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 17) = 34.2930, p-val = 0.0077
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 0.0468, p-val = 0.9769
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb
## F0_Parent_ExposedFemale    0.0236  0.2173   0.1084  0.9137  -0.4024
## F0_Parent_ExposedMale    -0.0863  0.4611  -0.1873  0.8514  -0.9901
##              ci.ub
## F0_Parent_ExposedFemale    0.4495
## F0_Parent_ExposedMale     0.8174
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Adiposity_OF_F0_lnCVR <- rma.mv(yi, vi, mods = ~F0_Parent_Exposed-1, random = list(~1|Paper_ID,~1|Cohort_ID))

## Warning in rma.mv(yi, vi, mods = ~F0_Parent_Exposed - 1, random = list(~1
## | : Redundant predictors dropped from the model.

Adiposity_OF_F0_lnCVR

##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.1312  0.3622     6     no   Paper_ID
## sigma^2.2  0.1718  0.4144    16     no   Cohort_ID
## sigma^2.3  0.0000  0.0000    46     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 44) = 85.1309, p-val = 0.0002
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 0.0320, p-val = 0.9841
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## F0_Parent_ExposedFemale    0.0325  0.2250   0.1446  0.8850  -0.4085   0.4736

```



```
## F0_Parent_ExposedMale      0.0600  0.5683  0.1055  0.9160  -1.0539  1.1738
##
## F0_Parent_ExposedFemale
## F0_Parent_ExposedMale
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Adiposity_MG_Sex_lnCVR <- rma.mv(yi, vi, mods = ~Sex-1, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID))
Adiposity_MG_Sex_lnCVR
```

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000     6     no  Paper_ID
## sigma^2.2  0.1213  0.3484     9     no  Cohort_ID
## sigma^2.3  0.0824  0.2870    19     no    ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 17) = 33.9703, p-val = 0.0085
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 0.0181, p-val = 0.9910
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## SexFemale   -0.0111  0.2369   -0.0468   0.9627   -0.4754   0.4532
## SexMale     -0.0288  0.2148   -0.1341   0.8933   -0.4498   0.3922
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Adiposity_OF_Sex_lnCVR <- rma.mv(yi, vi, mods = ~Sex-1, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID))
Adiposity_OF_Sex_lnCVR
```

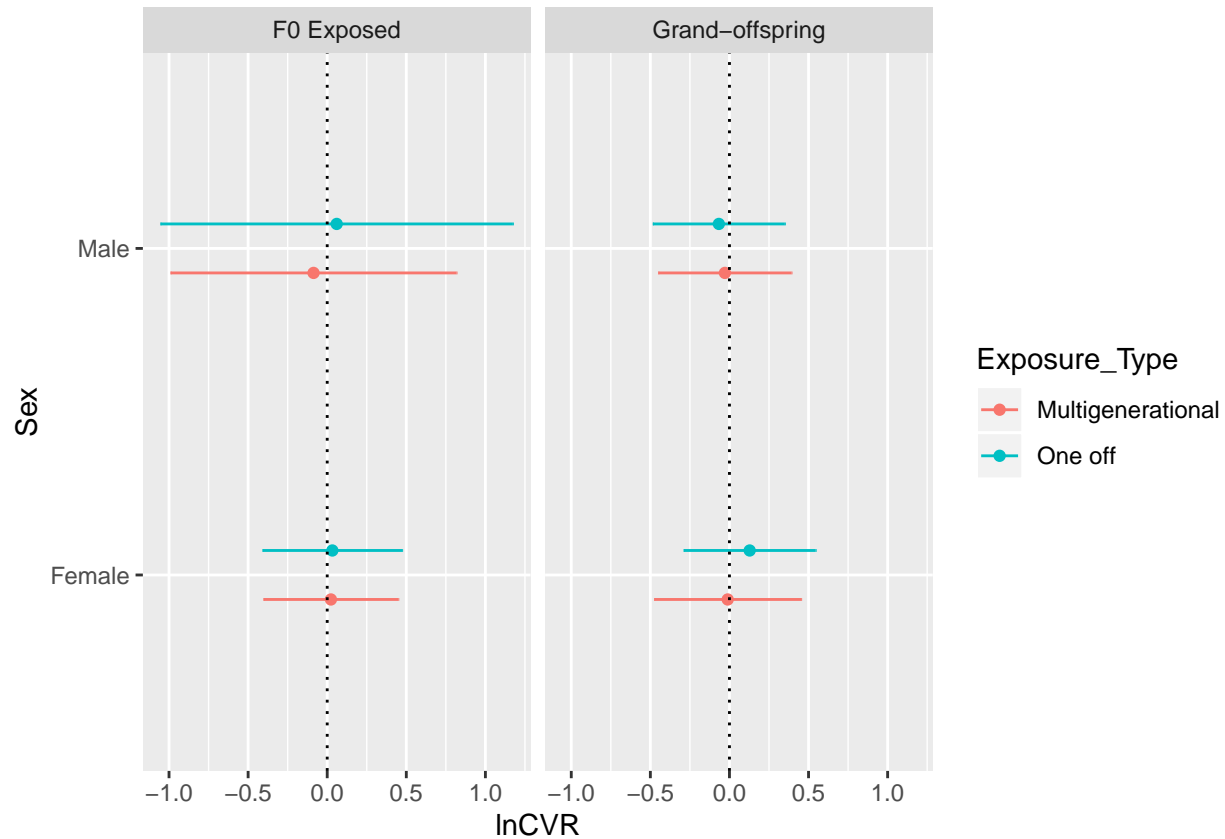
```
##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0993  0.3152     6     no  Paper_ID
## sigma^2.2  0.1567  0.3958    16     no  Cohort_ID
## sigma^2.3  0.0000  0.0000    46     no    ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 44) = 84.3253, p-val = 0.0002
```

```
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 1.1317, p-val = 0.5679
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## SexFemale      0.1280  0.2128   0.6014  0.5476  -0.2891  0.5450
## SexMale       -0.0670  0.2129  -0.3145  0.7531  -0.4843  0.3503
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Adiposity_Exp_mods_lnCVR <- tibble(
  Exposure_Type = c("Multigenerational", "Multigenerational", "One off", "One off", "Multigenerational",
  Sex = c("Female", "Male", "Female", "Male", "Female", "Male", "Female", "Male"),
  Mod = c("F0 Exposed", "F0 Exposed", "F0 Exposed", "F0 Exposed", "Grand-offspring", "Grand-offspring", "Grand-offspring", "Grand-offspring"),
  lnCVR = c(Adiposity_MG_F0_lnCVR$b[1], Adiposity_MG_F0_lnCVR$b[2], Adiposity_OF_F0_lnCVR$b[1], Adiposity_OF_F0_lnCVR$b[2],
  ci.lb = c(Adiposity_MG_F0_lnCVR$ci.lb[1], Adiposity_MG_F0_lnCVR$ci.lb[2], Adiposity_OF_F0_lnCVR$ci.lb[1], Adiposity_OF_F0_lnCVR$ci.lb[2],
  ci.ub = c(Adiposity_MG_F0_lnCVR$ci.ub[1], Adiposity_MG_F0_lnCVR$ci.ub[2], Adiposity_OF_F0_lnCVR$ci.ub[1], Adiposity_OF_F0_lnCVR$ci.ub[2])
)

plot_Adiposity_lnCVR_mods_exp <- ggplot(Adiposity_Exp_mods_lnCVR, aes(x=Sex, y=lnCVR, colour=Exposure_Type)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +
  geom_point(aes(x = Sex, y = lnCVR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(x = "Sex", y = "lnCVR") +
  coord_flip() +
  facet_grid(~Mod)

plot_Adiposity_lnCVR_mods_exp
```



#Triglycerides lnRR

#Subsetting Data for lnRR

```
Triglycerides_lnRR <- subset(Effect_Size_All_Traits, Effect_Size_All_Traits$Trait == "Triglycerides")
```

```
Triglycerides_lnRR_MG <- subset(Triglycerides_lnRR, Triglycerides_lnRR$Exposure_Type == "Multigenerational")
```

```
Triglycerides_lnRR_OF <- subset(Triglycerides_lnRR, Triglycerides_lnRR$Exposure_Type == "One off")
```

#Subsetting Data for lnCVR

```
Triglycerides_lnCVR <- subset(Effect_Size_All_Traits_lnCVR, Effect_Size_All_Traits_lnCVR$Trait == "Triglycerides")
```

```
Triglycerides_lnCVR_MG <- subset(Triglycerides_lnCVR, Triglycerides_lnCVR$Exposure_Type == "Multigenerational")
```

```
Triglycerides_lnCVR_OF <- subset(Triglycerides_lnCVR, Triglycerides_lnCVR$Exposure_Type == "One off")
```

Overall Triglycerides analysis

```
TG_overall_lnRR_0mods <- rma.mv(yi, vi, random = list(~1|Cohort_ID, ~1|ES_ID), data=Triglycerides_lnRR, method="REML")
summary(TG_overall_lnRR_0mods)
```

##

Multivariate Meta-Analysis Model (k = 33; method: REML)

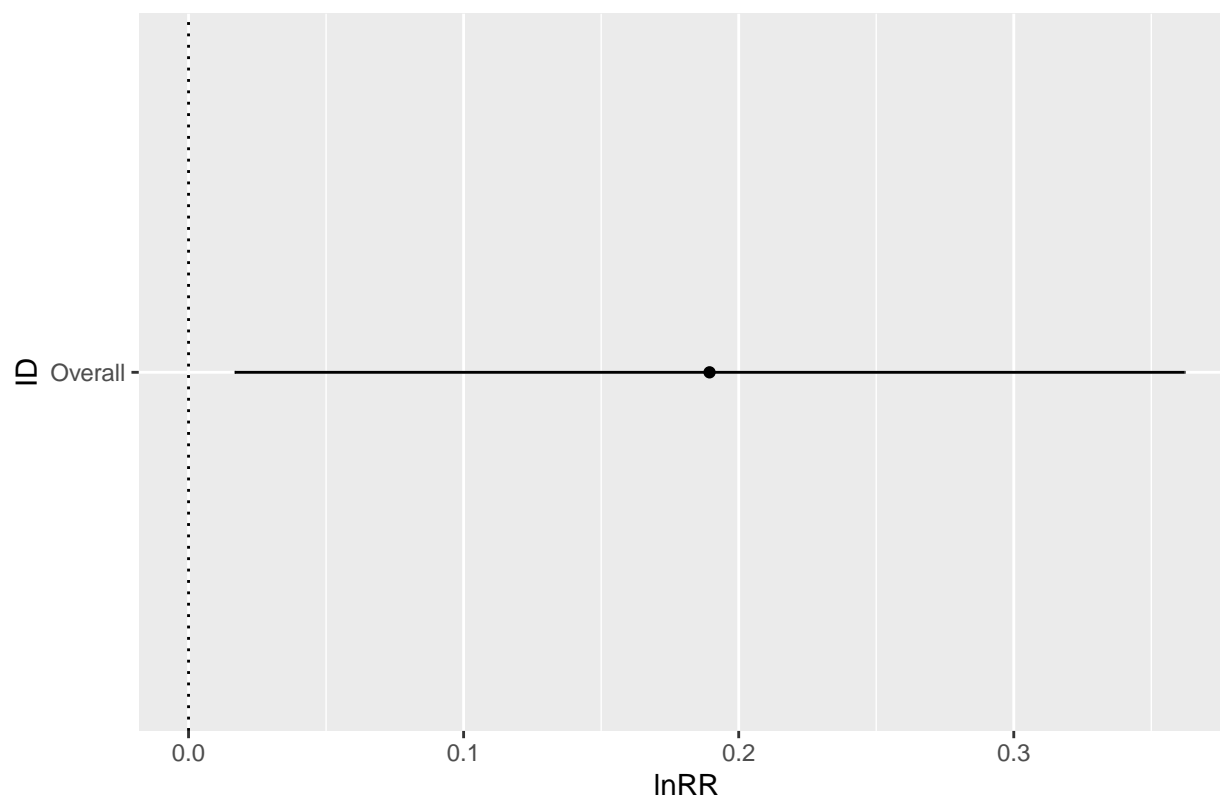
##

```
##   logLik  Deviance      AIC      BIC      AICc
## -13.9786   27.9572   33.9572   38.3544   34.8143
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.1439  0.3793     22     no  Cohort_ID
## sigma^2.2  0.0092  0.0961     33     no     ES_ID
##
## Test for Heterogeneity:
## Q(df = 32) = 262.1206, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##   0.1894  0.0881  2.1502  0.0315  0.0168  0.3621  *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TG_overall_lnRR <- tibble(
  ID = "Overall",
  lnRR = 0.1894,
  ci.lb = 0.0168,
  ci.ub = 0.3621
)
```

```
plot_tg_overall <- ggplot(TG_overall_lnRR, aes(x=ID, y=lnRR)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +
  geom_point(aes(x = ID, y = lnRR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(title = "TG differences, overall", x = "ID", y = "lnRR") +
  coord_flip()
plot_tg_overall
```

TG differences, overall



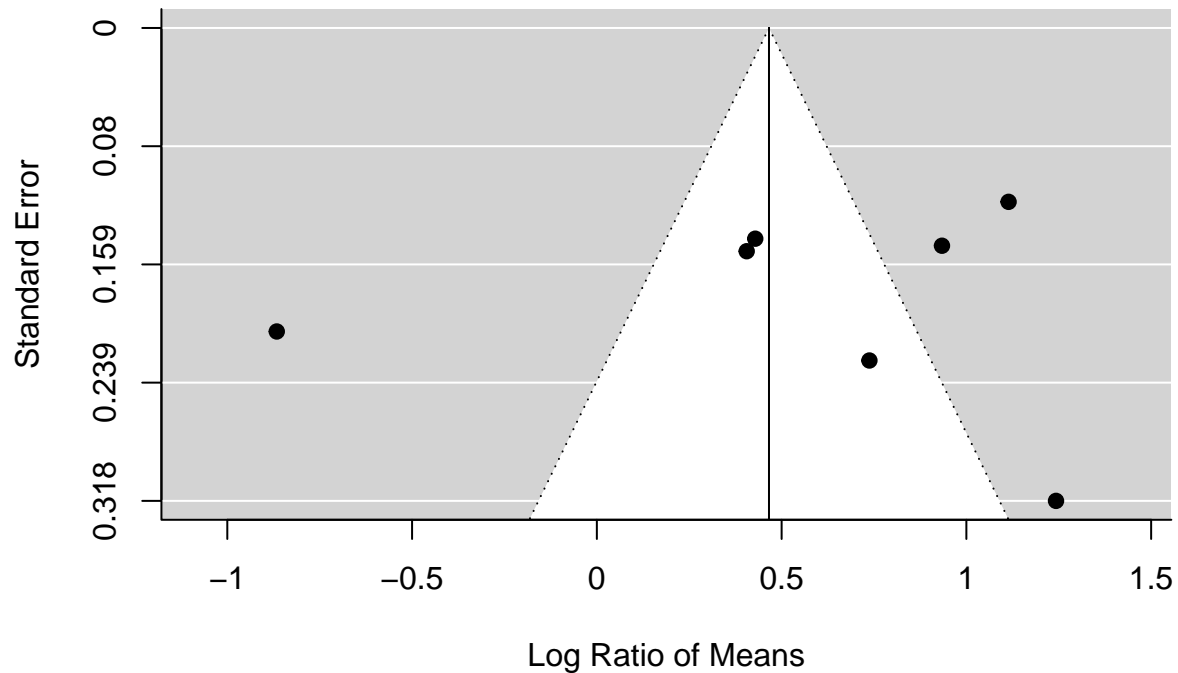
#Triglycerides analysis (split by exposure type)

```
Triglycerides_overall_lnRR_MG <- rma.mv(yi, vi, random = list(~1|Cohort_ID, ~1|ES_ID), data=Triglycerides.
summary(Triglycerides_overall_lnRR_MG)
```

```
##
## Multivariate Meta-Analysis Model (k = 7; method: REML)
##
##   logLik  Deviance      AIC      BIC     AICc
## -4.7574    9.5149   15.5149   14.8902   27.5149
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.6116  0.7821     5    no  Cohort_ID
## sigma^2.2  0.0038  0.0618     7    no    ES_ID
##
## Test for Heterogeneity:
## Q(df = 6) = 83.2645, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb    ci.ub
##   0.4658    0.3607  1.2915  0.1965   -0.2411   1.1727
##
```

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

```
funnel (Triglycerides_overall_lnRR_MG)
```

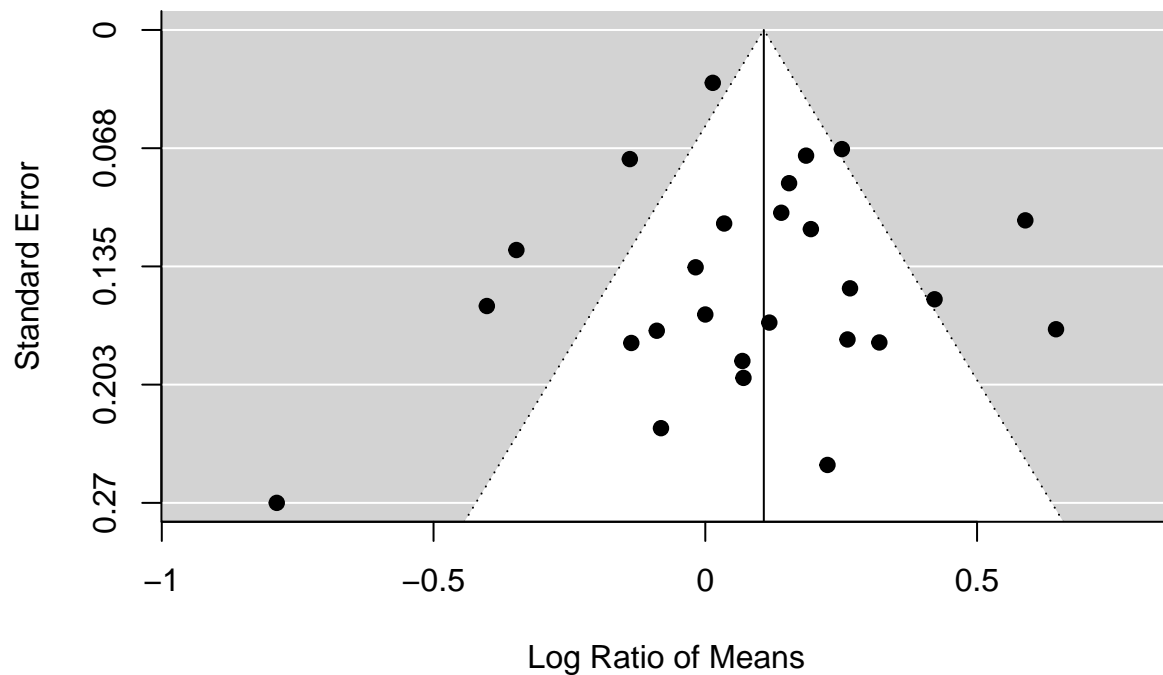


```
Triglycerides_overall_lnRR_OF <- rma.mv(yi, vi, random = list(~1|Cohort_ID, ~1|ES_ID), data=Triglycerides.
summary(Triglycerides_overall_lnRR_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 26; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -2.6854   5.3709  11.3709  15.0275  12.5137
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed  factor
## sigma^2.1  0.0390  0.1974   17    no  Cohort_ID
## sigma^2.2  0.0114  0.1067   26    no    ES_ID
##
## Test for Heterogeneity:
## Q(df = 25) = 101.6759, p-val < .0001
##
## Model Results:
```

```
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.1077 0.0605 1.7797 0.0751 -0.0109 0.2262 .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel (Triglycerides_overall_lnRR_OF)
```



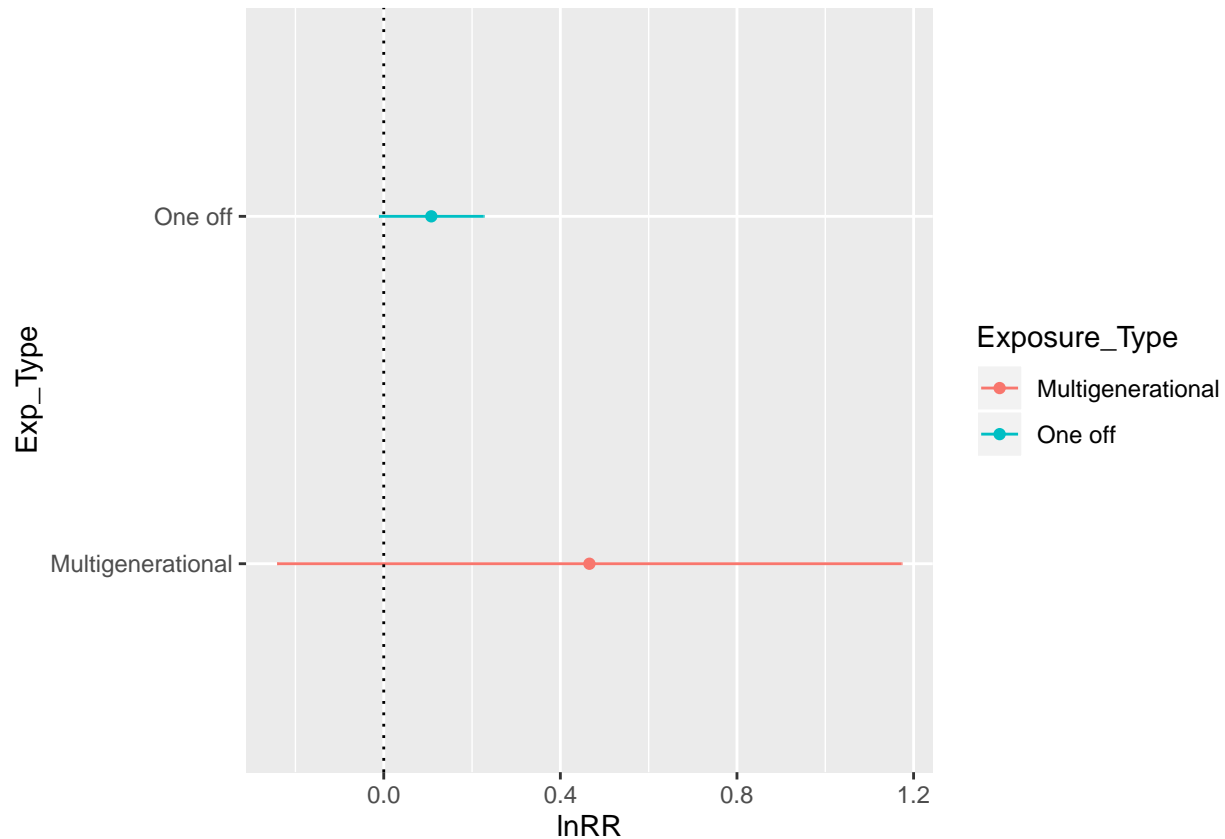
```
Triglycerides_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnRR = c(0.4658, 0.1077),
  ci.lb = c(-0.2411, -0.0109),
  ci.ub = c(1.1727, 0.2262)
)
```

```
Triglycerides_Exp_lnRR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnRR    ci.lb ci.ub
##   <chr>          <dbl>   <dbl> <dbl>
## 1 Multigenerational 0.466 -0.241 1.17
## 2 One off          0.108 -0.0109 0.226
```

```
#Plotting when split by exp type
```

```
plot_Triglycerides_exp_type <- ggplot(Triglycerides_Exp_lnRR, aes(x=Exposure_Type, y=lnRR, colour = Exp
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +
  geom_point(aes(x = Exposure_Type, y = lnRR), position = position_dodge(0.3))+
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(x = "Exp_Type", y = "lnRR") +
  coord_flip()
plot_Triglycerides_exp_type
```



Triglycerides lnCVR

Overall Triglycerides analysis

```
TG_overall_lnCVR_0mods <- rma.mv(yi, vi, random = list(~1|Cohort_ID, ~1|ES_ID), data=Triglycerides_lnCVR,
  summary(TG_overall_lnCVR_0mods)
```

```
##
## Multivariate Meta-Analysis Model (k = 33; method: REML)
##
```

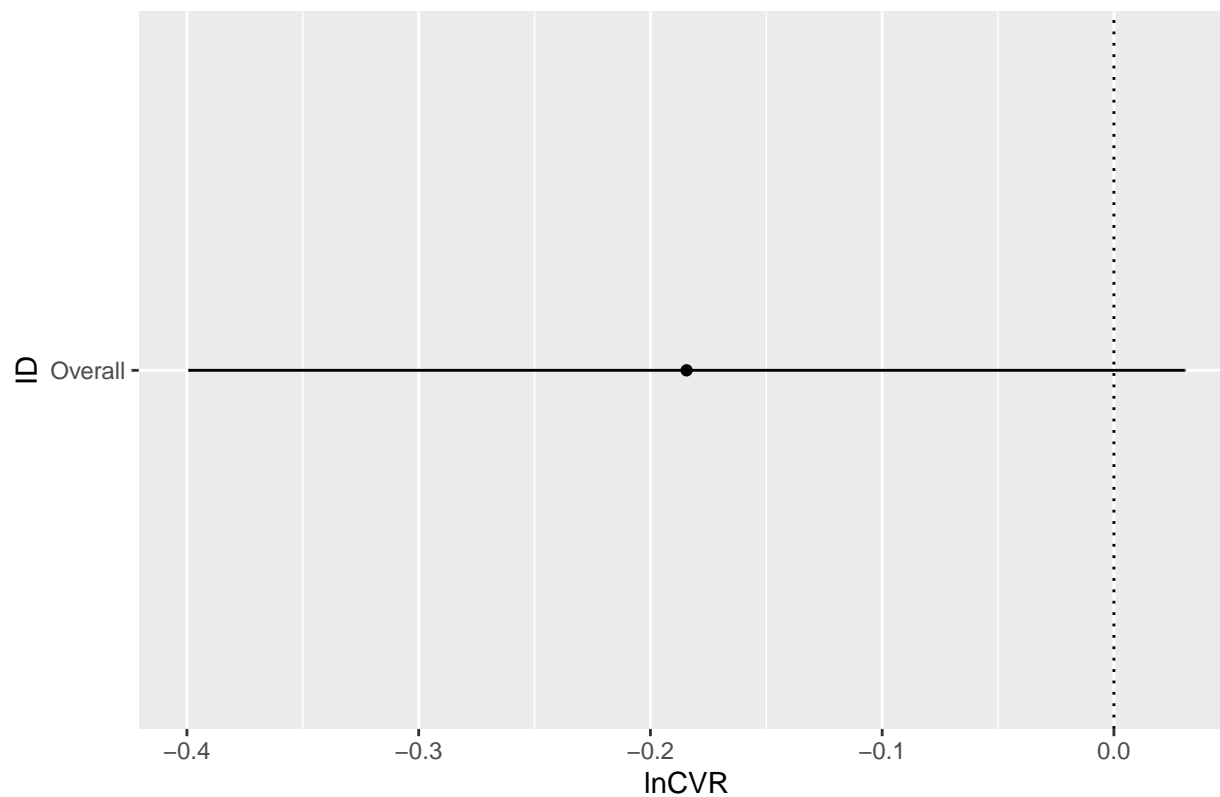


```
##    logLik  Deviance      AIC      BIC      AICc
## -26.2586   52.5171   58.5171   62.9143   59.3743
##
## Variance Components:
##
##          estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.1394  0.3734     22     no Cohort_ID
## sigma^2.2  0.0000  0.0001     33     no      ES_ID
##
## Test for Heterogeneity:
## Q(df = 32) = 56.1655, p-val = 0.0052
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.1844  0.1096  -1.6820  0.0926  -0.3993  0.0305
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TG_overall_lnCVR <- tibble(
  ID = "Overall",
  lnCVR = -0.1844,
  ci.lb = -0.3993,
  ci.ub = 0.0305
)
```

```
plot_tg_overall_lnCVR <- ggplot(TG_overall_lnCVR, aes(x=ID, y=lnCVR)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +
  geom_point(aes(x = ID, y = lnCVR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(title = "TG differences, overall", x = "ID", y = "lnCVR") +
  coord_flip()
plot_tg_overall_lnCVR
```

TG differences, overall



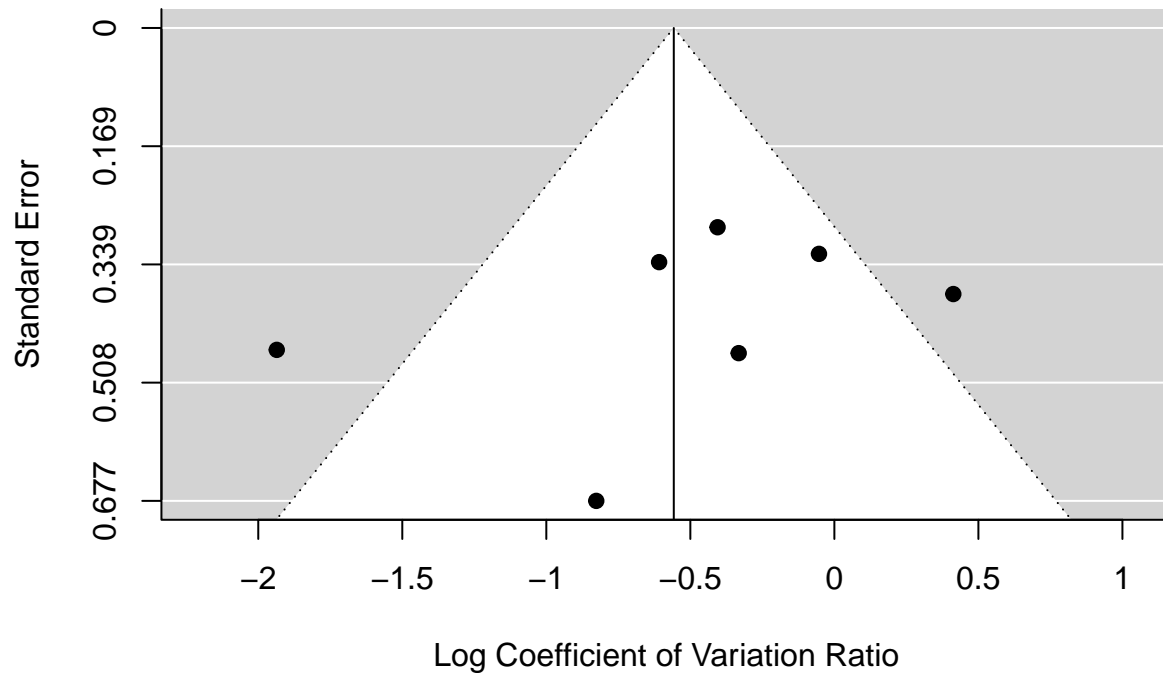
#Triglycerides analysis (split by exposure type)

```
Triglycerides_overall_lnCVR_MG <- rma.mv(yi, vi, random = list(~1|Cohort_ID, ~1|ES_ID), data=Triglycerides)
summary(Triglycerides_overall_lnCVR_MG)
```

```
##
## Multivariate Meta-Analysis Model (k = 7; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   -6.0827   12.1653   18.1653   17.5406   30.1653
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed   factor
## sigma^2.1  0.5408  0.7354     5    no  Cohort_ID
## sigma^2.2  0.0000  0.0000     7    no    ES_ID
##
## Test for Heterogeneity:
## Q(df = 6) = 17.5981, p-val = 0.0073
##
## Model Results:
##
## estimate      se      zval    pval    ci.lb    ci.ub
##   -0.5575  0.3744  -1.4891  0.1365  -1.2913  0.1763
##
```

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

```
funnel (Triglycerides_overall_lnCVR_MG)
```

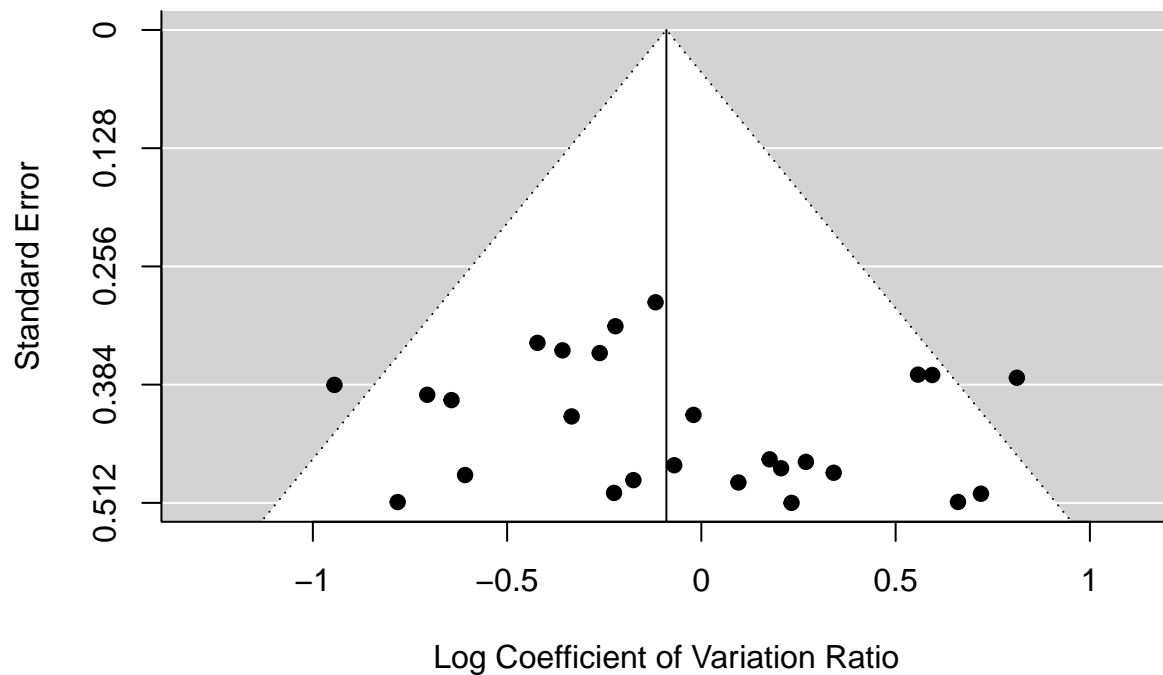


```
Triglycerides_overall_lnCVR_OF <- rma.mv(yi, vi, random = list(~1|Cohort_ID, ~1|ES_ID), data=Triglycerides)
summary(Triglycerides_overall_lnCVR_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 26; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -17.4330   34.8660  40.8660  44.5226  42.0089
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed  factor
## sigma^2.1  0.0712  0.2668    17    no  Cohort_ID
## sigma^2.2  0.0000  0.0000    26    no    ES_ID
##
## Test for Heterogeneity:
## Q(df = 25) = 34.2371, p-val = 0.1029
##
## Model Results:
```

```
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.0900  0.1057 -0.8516  0.3944 -0.2972  0.1171
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel (Triglycerides_overall_lnCVR_OF)
```



```
Triglycerides_Exp_lnCVR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnCVR = c(-0.5575, -0.0900),
  ci.lb = c(-1.2913, -0.2972),
  ci.ub = c(0.1763, 0.1171)
)
```

```
Triglycerides_Exp_lnCVR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnCVR  ci.lb ci.ub
##   <chr>          <dbl> <dbl> <dbl>
## 1 Multigenerational -0.558 -1.29  0.176
## 2 One off          -0.09 -0.297 0.117
```

```
#Plotting when split by exp type
```

```
plot_Triglycerides_exp_type <- ggplot(Triglycerides_Exp_lnCVR, aes(x=Exposure_Type, y=lnCVR, colour = Exposure_Type)) +  
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +  
  geom_point(aes(x = Exposure_Type, y = lnCVR), position = position_dodge(0.3)) +  
  geom_hline(yintercept = 0, lty = "dotted") +  
  labs(x = "Exp_Type", y = "lnCVR") +  
  coord_flip()  
plot_Triglycerides_exp_type
```

