

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

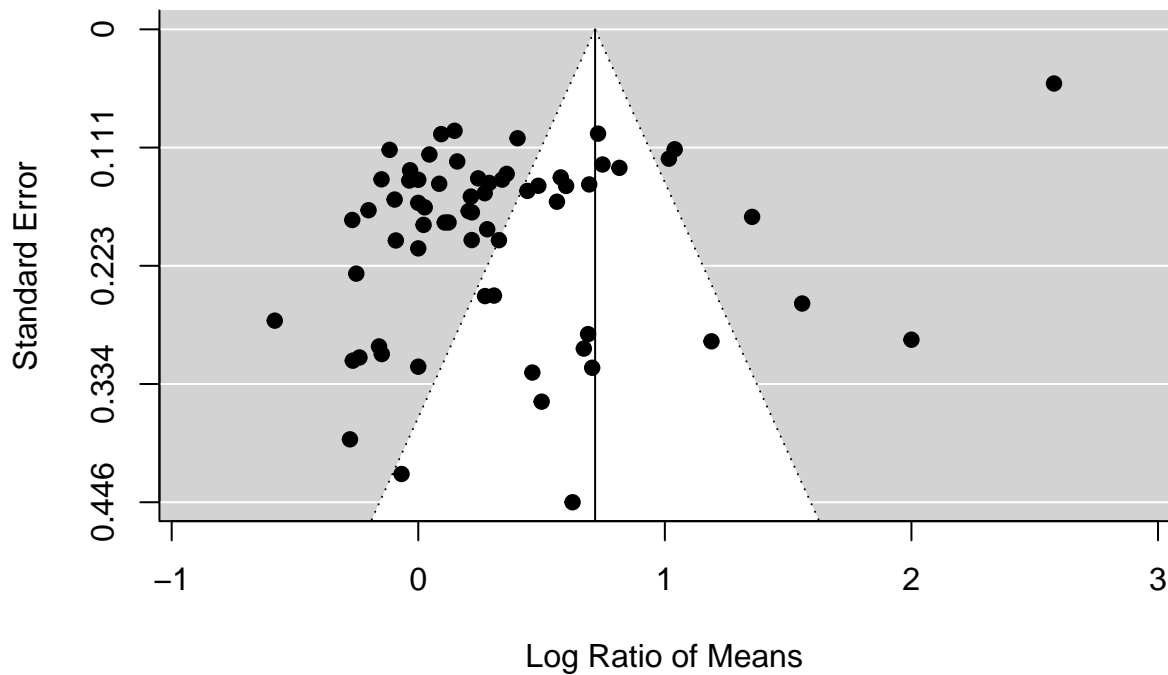
```
#Overall analysis, not split
```

```
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
## -21.9638   43.9275   51.9275   60.5631   52.6055
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.6663  0.8163     10     no  Paper_ID
## sigma^2.2  0.0547  0.2339     25     no  Cohort_ID
## sigma^2.3  0.0212  0.1457     65     no    ES_ID
##
## Test for Heterogeneity:
## Q(df = 64) = 2075.5744, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##   0.7172   0.2690   2.6659   0.0077   0.1899   1.2445   **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Adiposity_overall_lnRR_Omods)
```



#Tibble of overall results

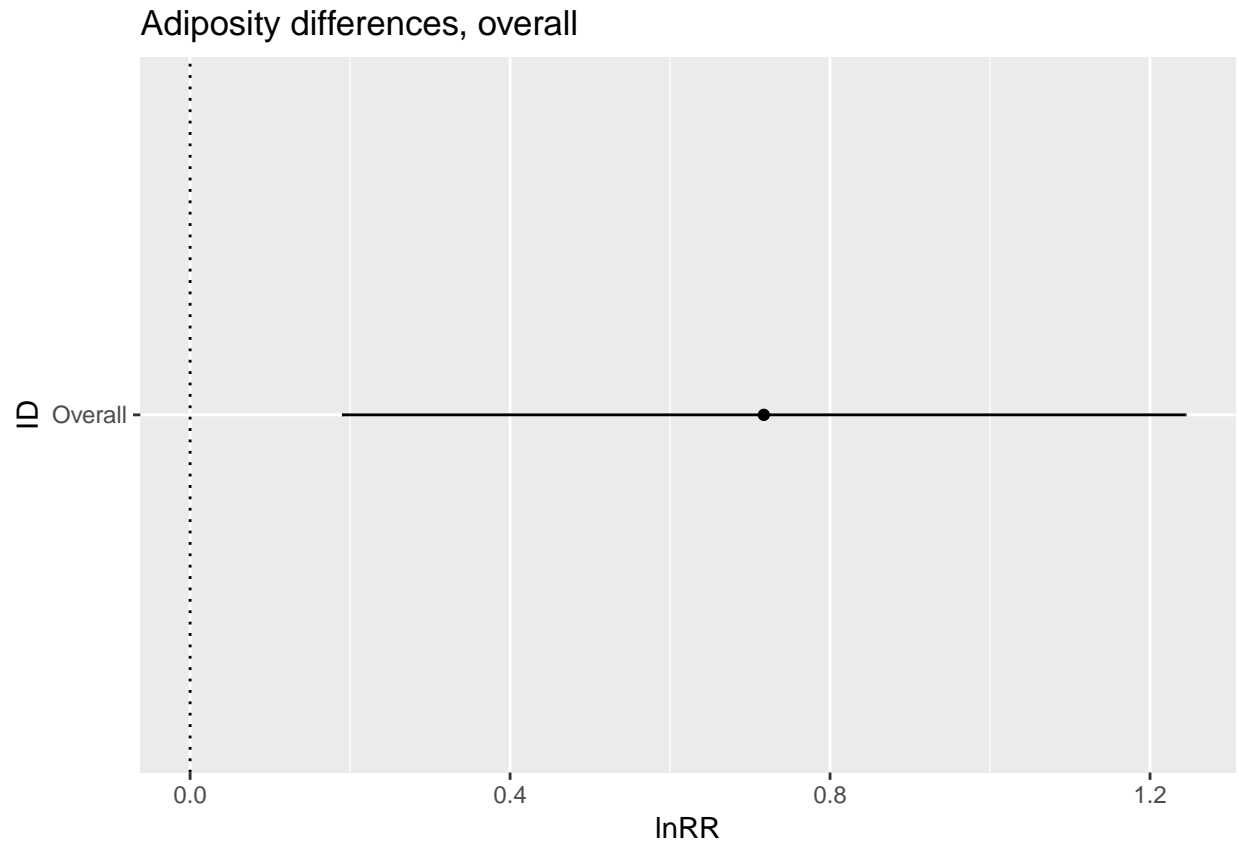
```
Adiposity_overall_lnRR <- tibble(  
  ID = "Overall",  
  lnRR = 0.7172,  
  ci.lb = 0.1899,  
  ci.ub = 1.2445  
)
```

Warning: `list_len()` is deprecated as of rlang 0.2.0.

Please use `new_list()` instead.

This warning is displayed once per session.

```
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
```



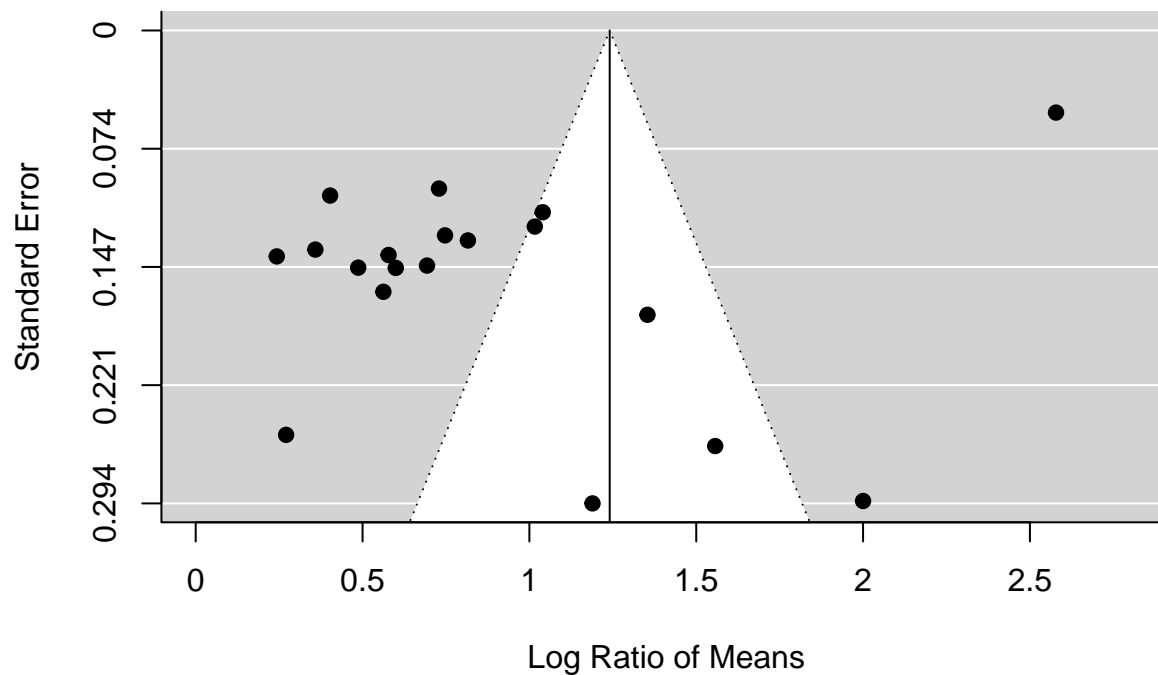
Splitting by exposure type

```
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
## -10.6610   21.3221   29.3221   32.8836   32.3990
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.6268  0.7917     6    no   Paper_ID
## sigma^2.2  0.0000  0.0000     9    no   Cohort_ID
## sigma^2.3  0.0654  0.2557    19    no     ES_ID
##
## Test for Heterogeneity:
## Q(df = 18) = 1024.7727, p-val < .0001
##
## Model Results:
```

```
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 1.2407 0.3375 3.6762 0.0002 0.5792 1.9022 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel (Adiposity_overall_lnRR_MG)
```

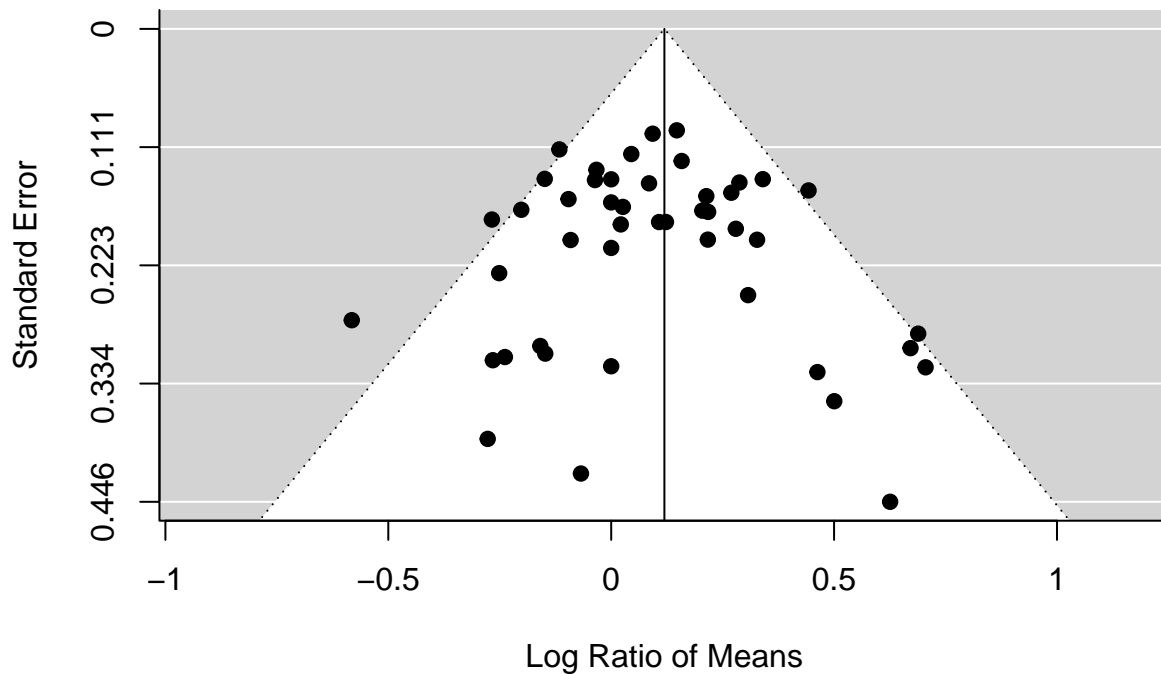


```
Adiposity_overall_lnRR_OF <- rma.mv(yi, vi, random = list(~1|Paper_ID, ~1|Cohort_ID, ~1|ES_ID), data=Adipos)
summary(Adiposity_overall_lnRR_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
## logLik Deviance      AIC      BIC      AICc
## 6.3794 -12.7588 -4.7588 2.4678 -3.7588
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed  factor
## sigma^2.1 0.0040 0.0629     6    no  Paper_ID
## sigma^2.2 0.0304 0.1743    16    no  Cohort_ID
## sigma^2.3 0.0000 0.0000    46    no    ES_ID
```

```
##
## Test for Heterogeneity:
## Q(df = 45) = 64.6623, p-val = 0.0288
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.1194 0.0649 1.8383 0.0660 -0.0079 0.2466 .
##
## ---
## 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(1.2407, 0.1194),
  ci.lb = c(0.5792, -0.0079),
  ci.ub = c(1.9022, 0.2466)
)
```

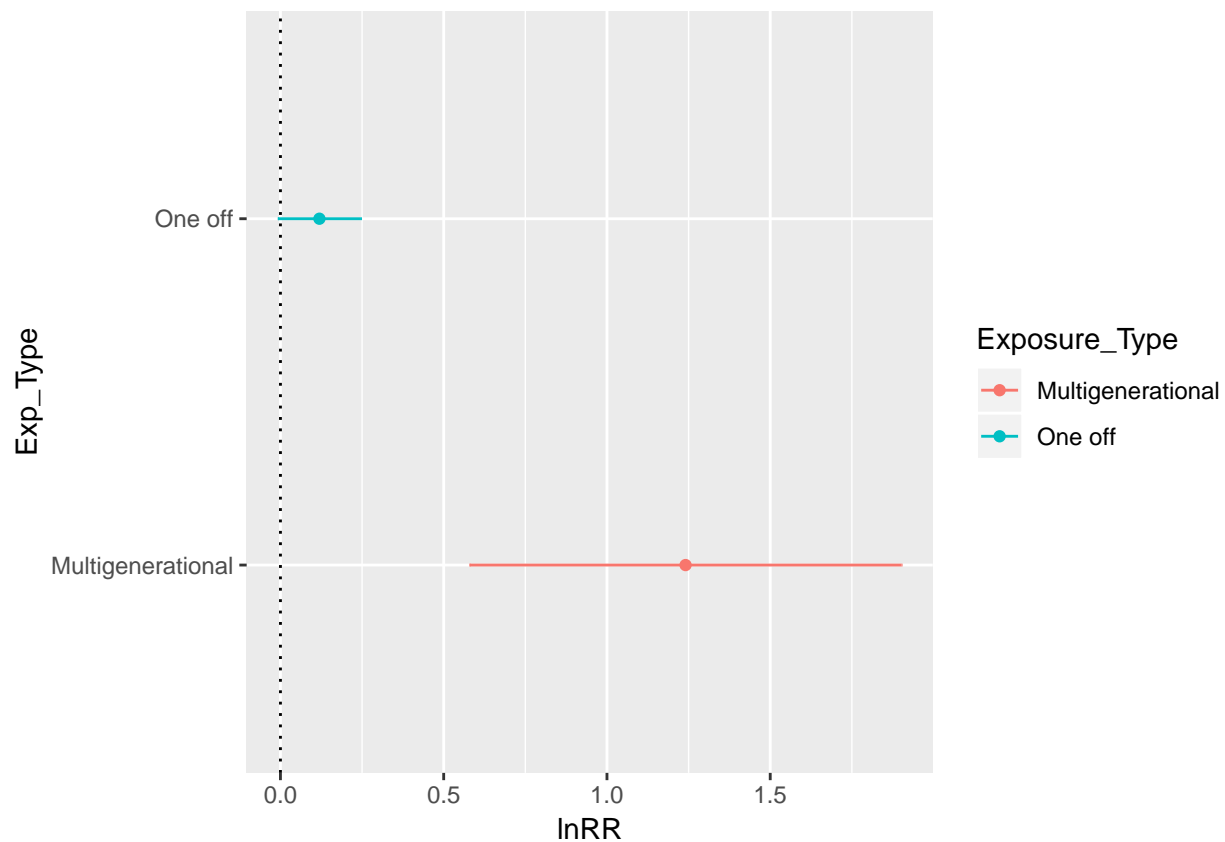
```
Adiposity_Exp_lnRR
```

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

```
##      <chr>          <dbl>   <dbl> <dbl>
## 1 Multigenerational 1.24    0.579 1.90
## 2 One off          0.119 -0.0079 0.247
```

#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, 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|Exposure_Type))
```

```
## 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  0.6981  0.8355     6     no   Paper_ID
## sigma^2.2  0.0000  0.0000     9     no   Cohort_ID
## sigma^2.3  0.0653  0.2555    19     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 17) = 818.7222, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 12.8877, p-val = 0.0016
##
## Model Results:
##
##      estimate      se    zval    pval    ci.lb    ci.ub
## F0_Parent_ExposedFemale  1.3709  0.3911  3.5051  0.0005   0.6043  2.1375
## F0_Parent_ExposedMale    0.6531  0.8420  0.7757  0.4379  -0.9971  2.3034
##
## 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  0.0063  0.0791     6     no   Paper_ID
## sigma^2.2  0.0324  0.1799    16     no   Cohort_ID
## sigma^2.3  0.0000  0.0000    46     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 44) = 61.4679, p-val = 0.0418
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 3.4316, p-val = 0.1798
##
## Model Results:
##
##      estimate      se    zval    pval    ci.lb
## F0_Parent_ExposedFemale  0.1384  0.0747  1.8524  0.0640  -0.0080
```

```
## F0_Parent_ExposedMale      -0.0011  0.2041  -0.0055  0.9956  -0.4012
##                               ci.ub
## F0_Parent_ExposedFemale  0.2849  .
## F0_Parent_ExposedMale      0.3990
##
## ---
## 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)
```

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

```
Adiposity_MG_Sex
```

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.6373  0.7983      6      no  Paper_ID
## sigma^2.2  0.0000  0.0000      9      no  Cohort_ID
## sigma^2.3  0.0701  0.2647     19      no    ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 17) = 845.9961, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 13.6125, p-val = 0.0011
##
## Model Results:
##
##      estimate      se    zval    pval    ci.lb    ci.ub
## SexFemale    1.1890  0.3512  3.3850  0.0007  0.5005  1.8774 ***
## SexMale      1.2919  0.3513  3.6771  0.0002  0.6033  1.9805 ***
##
## ---
## 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)
```

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

```
Adiposity_OF_Sex
```

```
##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
## Variance Components:
```

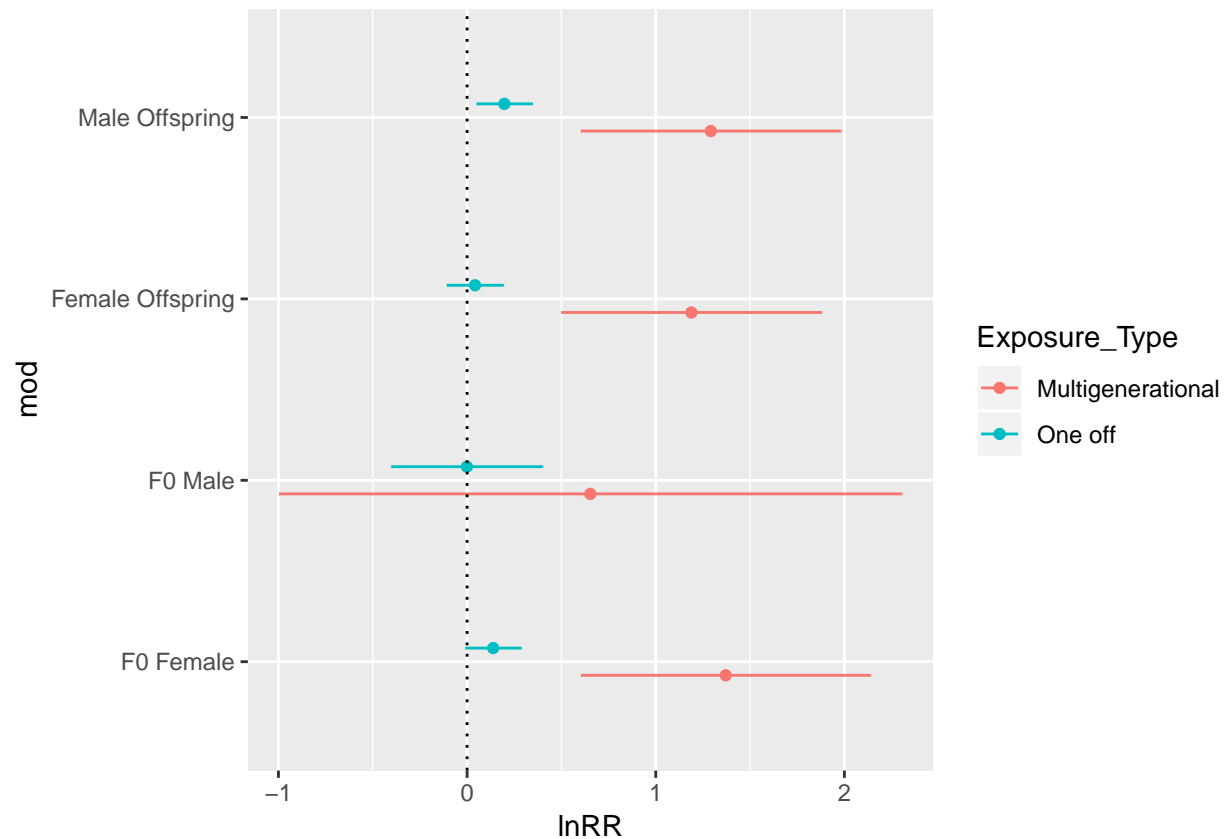


```
##
##          estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0080  0.0892     6     no    Paper_ID
## sigma^2.2 0.0193  0.1388    16     no    Cohort_ID
## sigma^2.3 0.0000  0.0000    46     no      ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 44) = 54.1902, p-val = 0.1396
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 8.1136, p-val = 0.0173
##
## Model Results:
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## SexFemale    0.0423  0.0761  0.5554  0.5786   -0.1069   0.1914
## SexMale      0.1976  0.0746  2.6471  0.0081    0.0513   0.3438  **
##
## ---
## 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",
    mod = c("F0 Female", "F0 Male", "F0 Female", "F0 Male", "Female Offspring", "Male Offspring", "Female Offspring"),
    lnRR = c(1.3709, 0.6531, 0.1384, -0.0011, 1.1890, 1.2919, 0.0423, 0.1976),
    ci.lb = c(0.6043, -0.9971, -0.0080, -0.4012, 0.5005, 0.6033, -0.1069, 0.0513),
    ci.ub = c(2.1375, 2.3034, 0.2849, 0.3990, 1.8774, 1.9805, 0.1914, 0.3438)
)

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

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
## -44.7927  89.5854  97.5854 106.2210  98.2634
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed  factor
```

```
## sigma^2.1 0.0650 0.2549 10 no Paper_ID
## sigma^2.2 0.0348 0.1867 25 no Cohort_ID
## sigma^2.3 0.0000 0.0000 65 no ES_ID
##
## Test for Heterogeneity:
## Q(df = 64) = 84.9840, p-val = 0.0408
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.0529 0.1167 -0.4535 0.6502 -0.2818 0.1759
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#Tibble of overall results

```
Insulin_overall_lnCVR <- tibble(
  ID = "Overall",
  lnCVR = -0.0529,
  ci.lb = -0.2818,
  ci.ub = 0.175
)
```

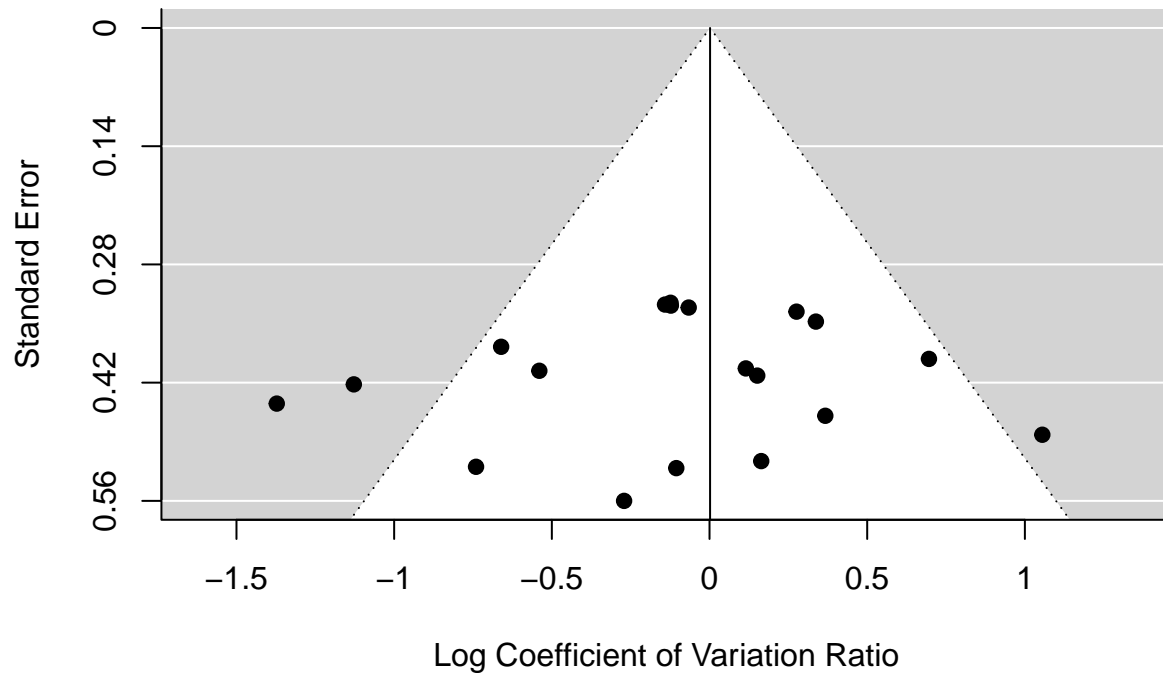
Adiposity lnCVR (split by exposure type)

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

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
##   logLik Deviance      AIC      BIC      AICc
## -15.0157  30.0314  38.0314  41.5929  41.1083
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0000 0.0000     6    no    Paper_ID
## sigma^2.2 0.1139 0.3376     9    no    Cohort_ID
## sigma^2.3 0.0630 0.2510    19    no      ES_ID
##
## Test for Heterogeneity:
## Q(df = 18) = 33.8343, p-val = 0.0132
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##  0.0018 0.1733 0.0101 0.9919 -0.3380 0.3415
##
```

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

```
funnel (Adiposity_overall_lnCVR_MG)
```

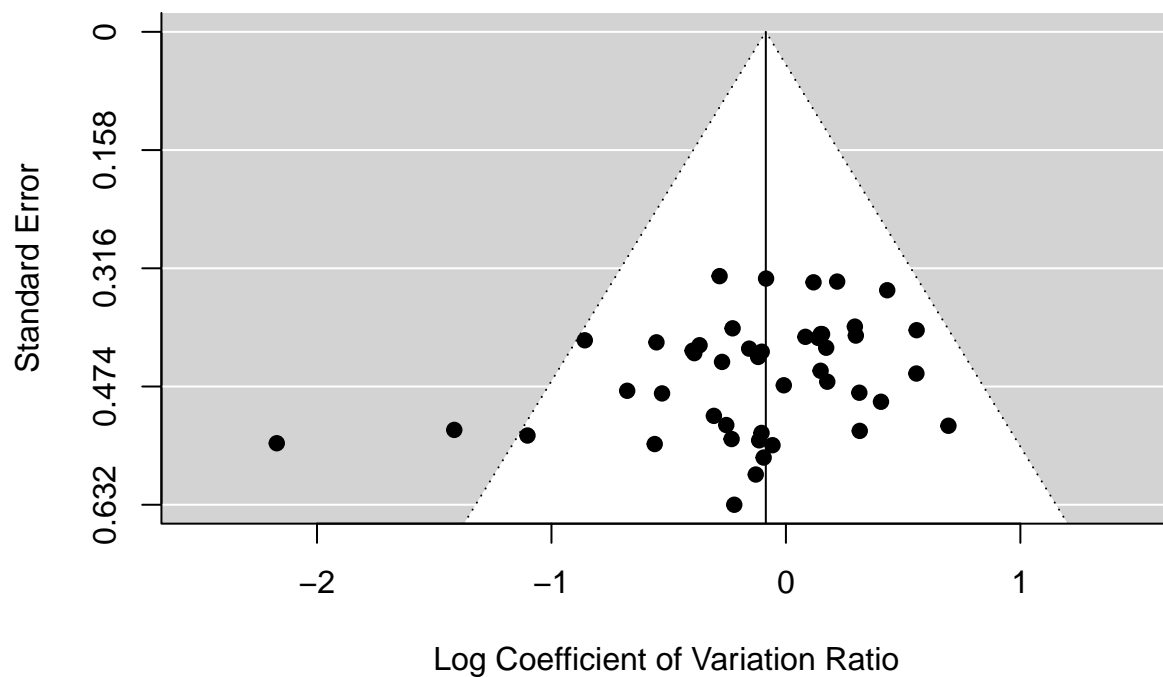


```
Adiposity_overall_lnCVR_OF <- rma.mv(yi, vi, random = list(~1|Paper_ID, ~1|Cohort_ID, ~1|ES_ID), data=Adip
summary(Adiposity_overall_lnCVR_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 46; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -28.5396   57.0791   65.0791   72.3058   66.0791
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed  factor
## sigma^2.1 0.0577 0.2403    6    no  Paper_ID
## sigma^2.2 0.0368 0.1917   16    no  Cohort_ID
## sigma^2.3 0.0000 0.0000   46    no    ES_ID
##
## Test for Heterogeneity:
## Q(df = 45) = 51.1494, p-val = 0.2450
##
```

```
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.0857  0.1430 -0.5992  0.5490 -0.3660  0.1946
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel (Adiposity_overall_lnCVR_OF)
```



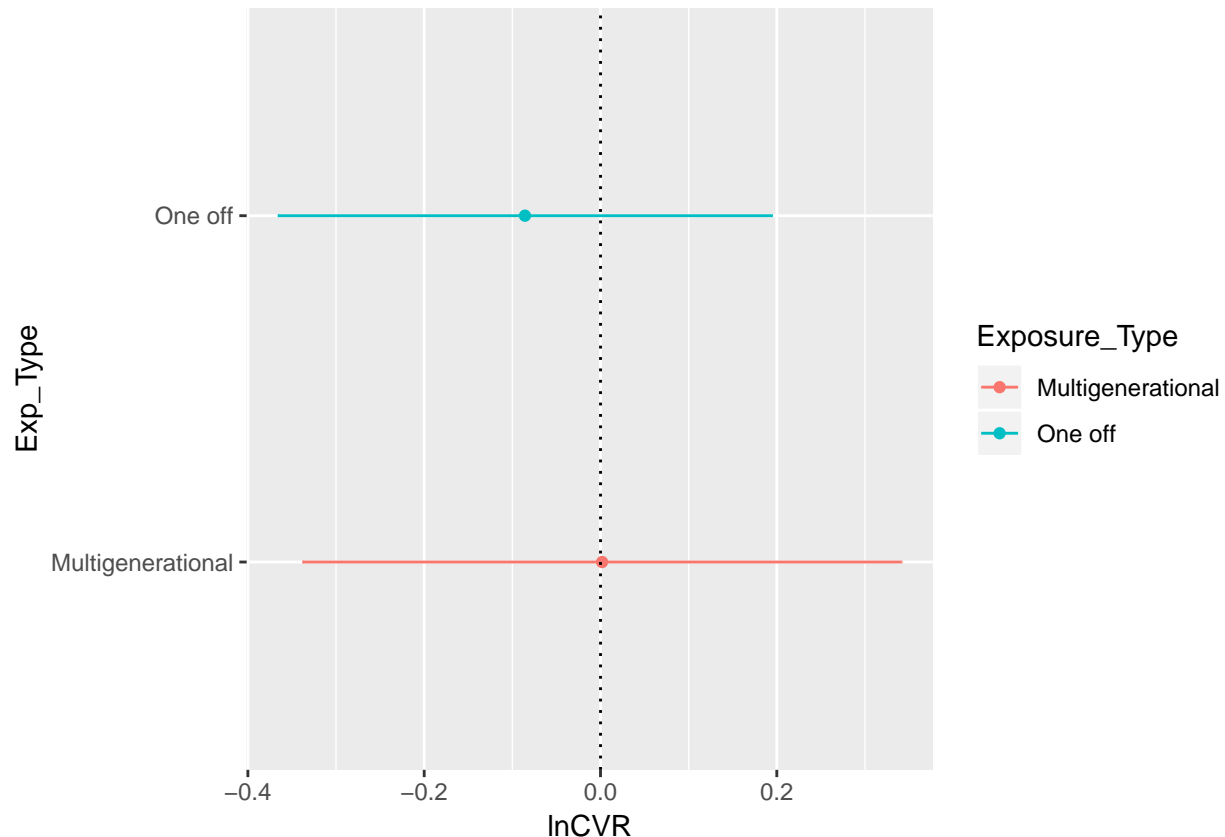
```
Adiposity_Exp_lnCVR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnCVR = c(0.0018, -0.0857),
  ci.lb = c(-0.3380, -0.3660),
  ci.ub = c(0.3415, 0.1946)
)
```

```
Adiposity_Exp_lnCVR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnCVR  ci.lb ci.ub
##   <chr>          <dbl> <dbl> <dbl>
## 1 Multigenerational 0.0018 -0.338 0.342
## 2 One off         -0.0857 -0.366 0.195
```

```
#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  0.0000     6     no   Paper_ID
## sigma^2.2  0.1770  0.4208     9     no   Cohort_ID
## sigma^2.3  0.0597  0.2443    19     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 17) = 33.8068, p-val = 0.0089
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 0.0905, p-val = 0.9557
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb
## F0_Parent_ExposedFemale    0.0503  0.2150   0.2338  0.8152  -0.3711
## F0_Parent_ExposedMale    -0.0858  0.4530  -0.1895  0.8497  -0.9736
##      ci.ub
## F0_Parent_ExposedFemale    0.4717
## F0_Parent_ExposedMale     0.8020
##
## ---
## 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  0.0730  0.2702     6     no   Paper_ID
## sigma^2.2  0.0441  0.2100    16     no   Cohort_ID
## sigma^2.3  0.0000  0.0000    46     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 44) = 49.6318, p-val = 0.2588
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 0.4459, p-val = 0.8002
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb
## F0_Parent_ExposedFemale   -0.1104  0.1705  -0.6478  0.5171  -0.4445
```

```
## F0_Parent_ExposedMale      0.0600  0.3703   0.1619  0.8713  -0.6657
##                               ci.ub
## F0_Parent_ExposedFemale  0.2237
## F0_Parent_ExposedMale      0.7857
##
## ---
## 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  0.1121  0.3347     9     no  Cohort_ID
## sigma^2.3  0.0795  0.2820    19     no    ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 17) = 32.9481, p-val = 0.0114
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 0.0371, p-val = 0.9816
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## SexFemale      0.0267  0.2343   0.1139  0.9093  -0.4326  0.4860
## SexMale       -0.0252  0.2105  -0.1198  0.9046  -0.4377  0.3873
##
## ---
## 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  0.0592  0.2433     6     no  Paper_ID
## sigma^2.2  0.0329  0.1813    16     no  Cohort_ID
## sigma^2.3  0.0000  0.0000    46     no    ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 44) = 49.6421, p-val = 0.2585
```

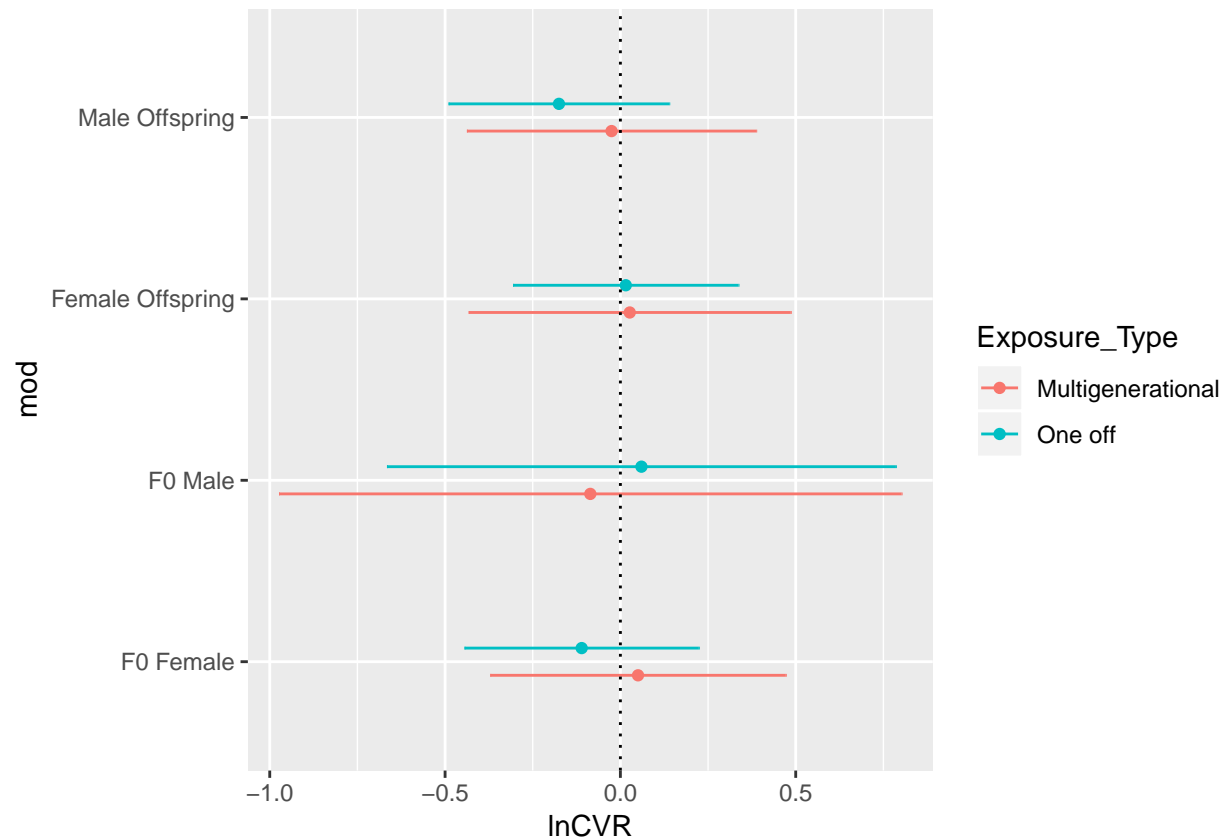


```
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 1.8913, p-val = 0.3884
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## SexFemale    0.0154  0.1640   0.0940  0.9251  -0.3060  0.3368
## SexMale     -0.1752  0.1605  -1.0916  0.2750  -0.4899  0.1394
##
## ---
## 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",
    mod = c("F0 Female", "F0 Male", "F0 Female", "F0 Male", "Female Offspring", "Male Offspring", "Female Of
    lnCVR = c(0.0503, -0.0858, -0.1104, 0.0600, 0.0267, -0.0252, 0.0154, -0.1752),
    ci.lb = c(-0.3711, -0.9736, -0.4445, -0.6657, -0.4326, -0.4377, -0.3060, -0.4899),
    ci.ub = c(0.4717, 0.8020, 0.2237, 0.7857, 0.4860, 0.3873, 0.3368, 0.1394)
)

plot_Adiposity_lnCVR_mods_exp <- ggplot(Adiposity_Exp_mods_lnCVR, aes(x=mod, 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 = mod, y = lnCVR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(x = "mod", y = "lnCVR") +
  coord_flip()

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)

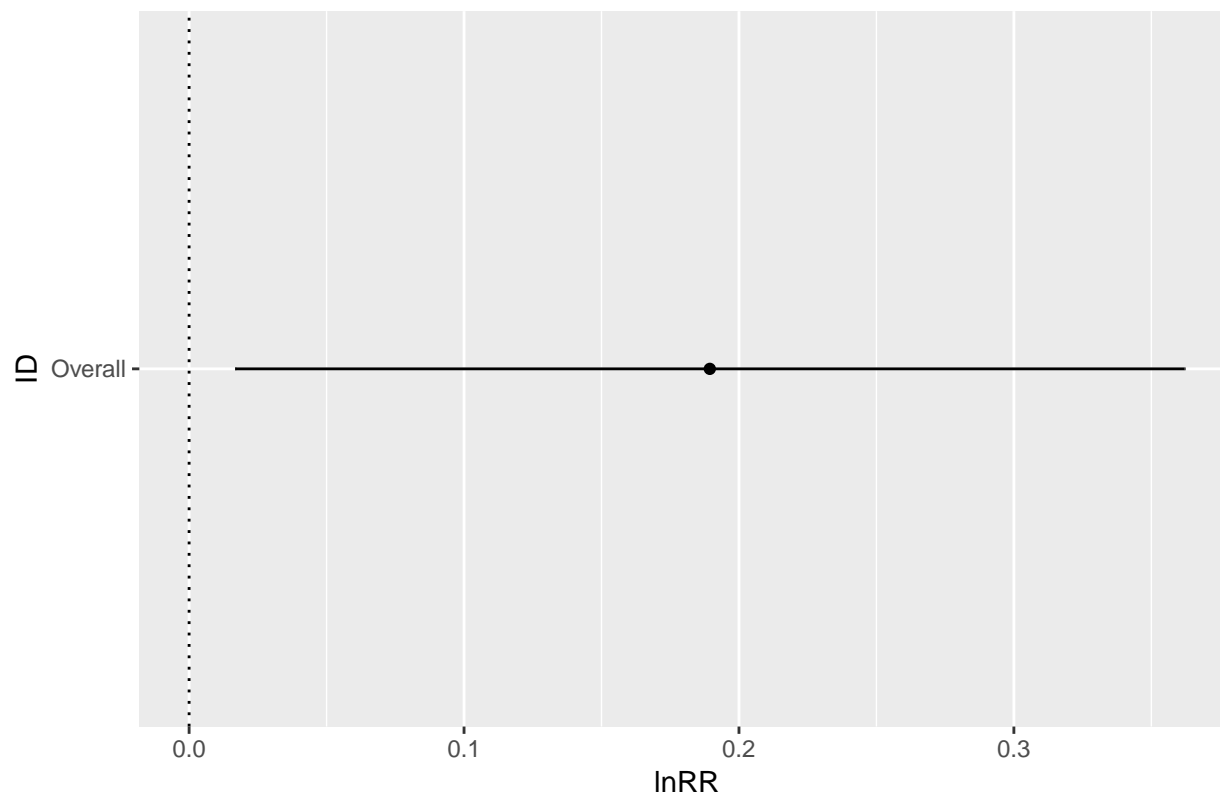
##

```
##   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



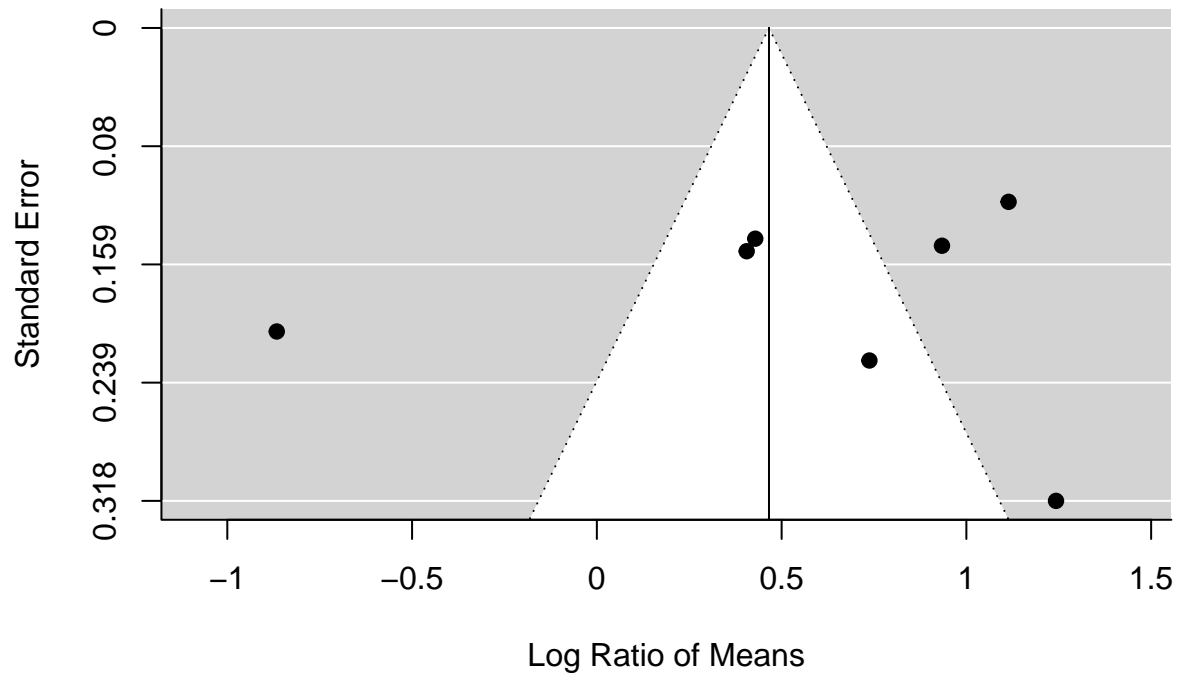
#Triglycerides analysis (split by exposure type)

```
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)
```

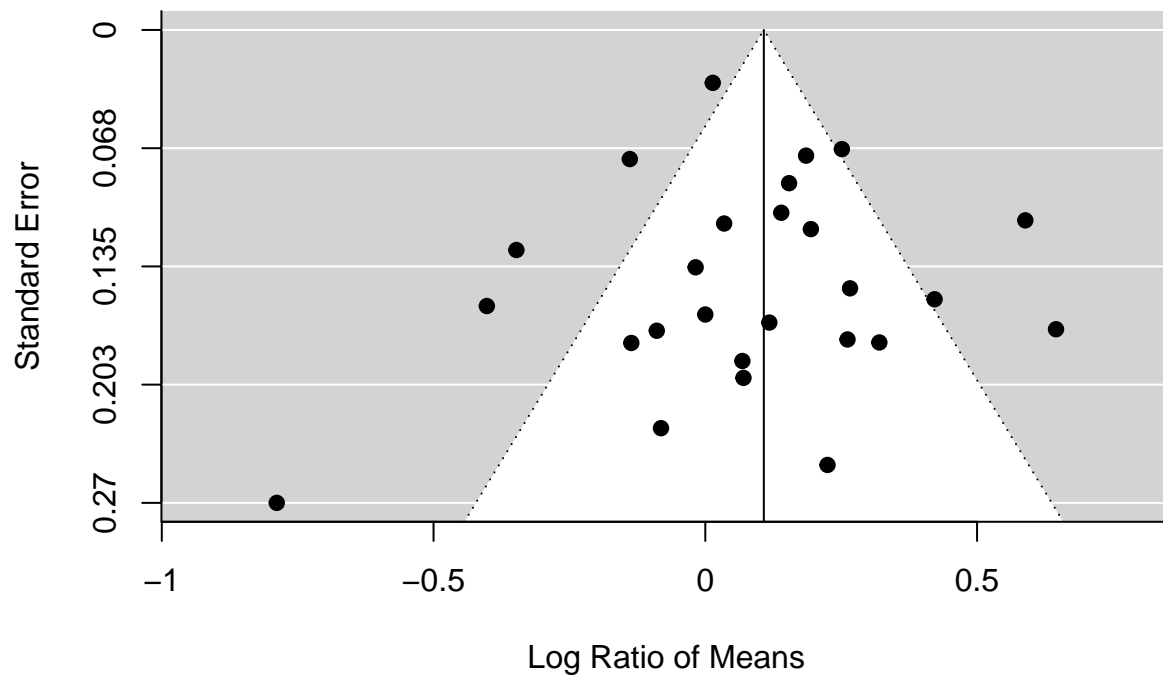


```
Triglycerides_overall_lnRR_OF <- rma.mv(yi, vi, random = list(~1|Cohort_ID, ~1|ES_ID), data=Triglycerides.
summary(Triglycerides_overall_lnRR_OF)
```

```
##
## 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)
```



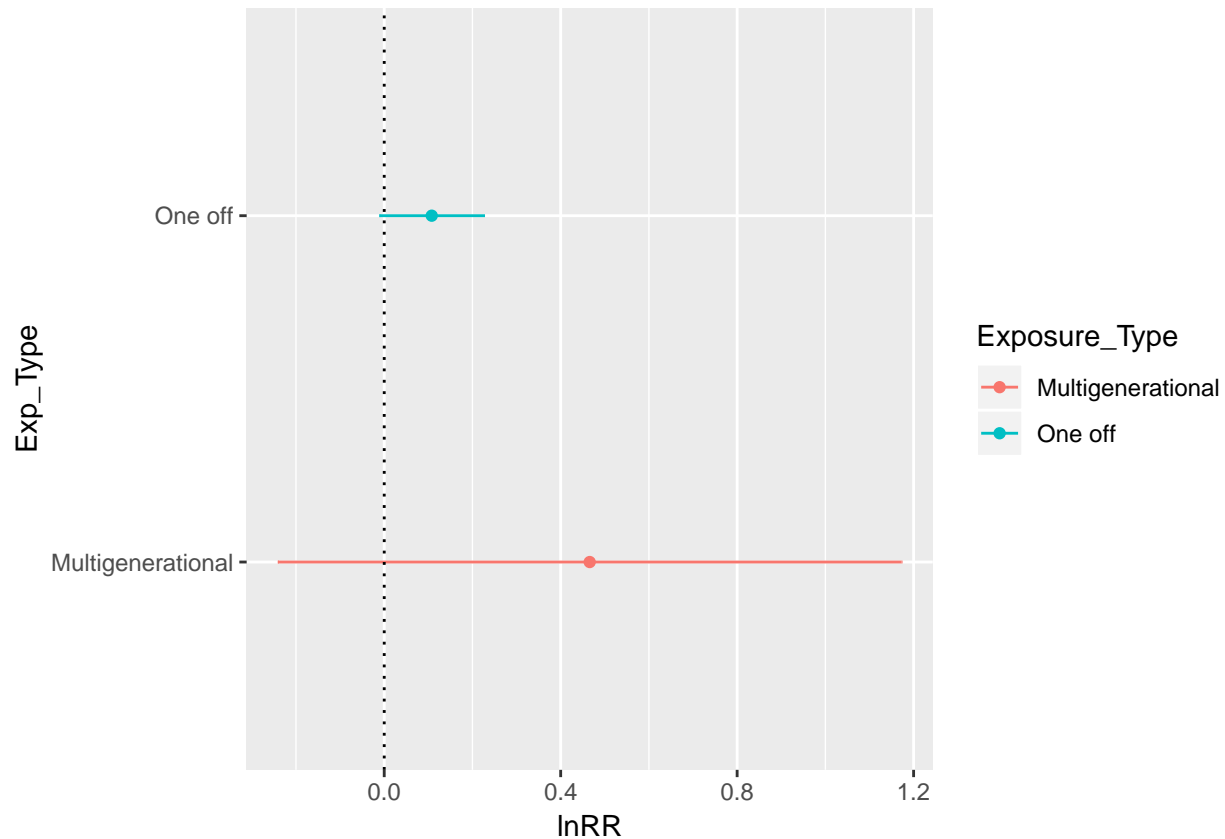
```
Triglycerides_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnRR = c(0.4658, 0.1077),
  ci.lb = c(-0.2411, -0.0109),
  ci.ub = c(1.1727, 0.2262)
)
```

```
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)
```

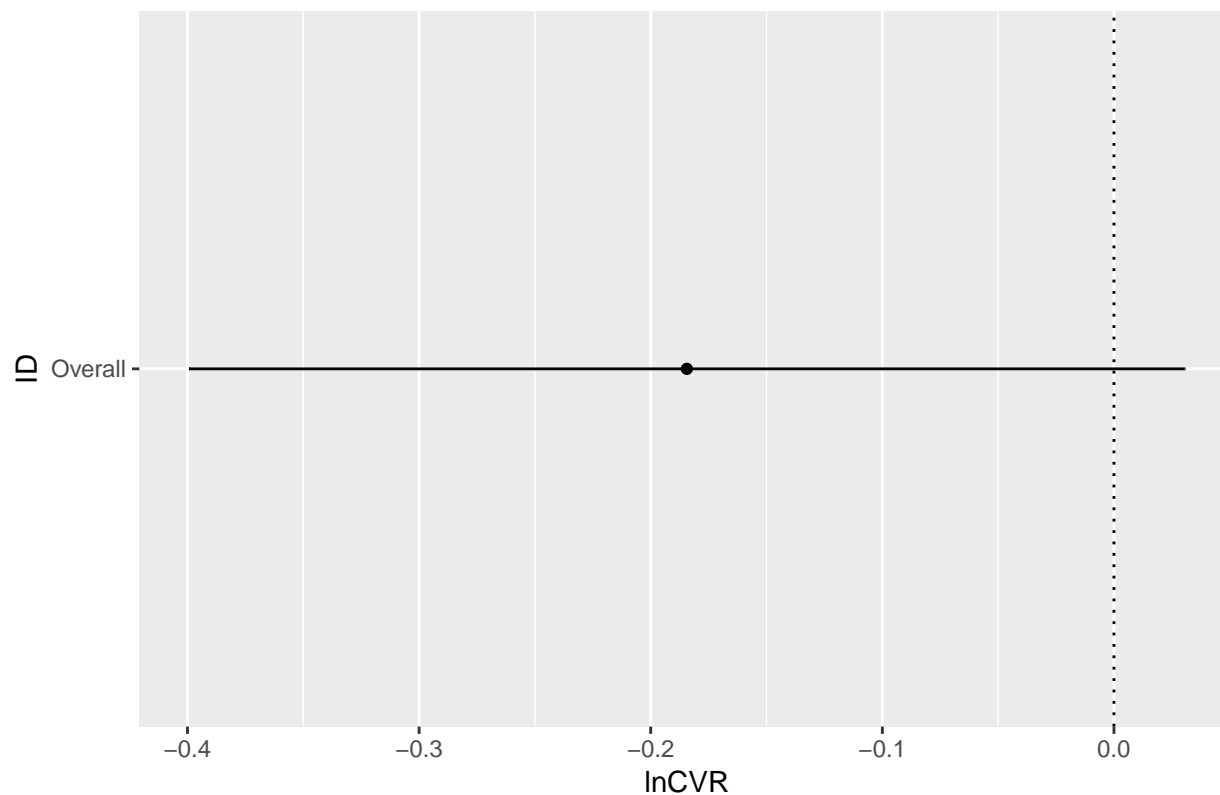
```
##
## Multivariate Meta-Analysis Model (k = 33; method: REML)
##
```

```
##   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



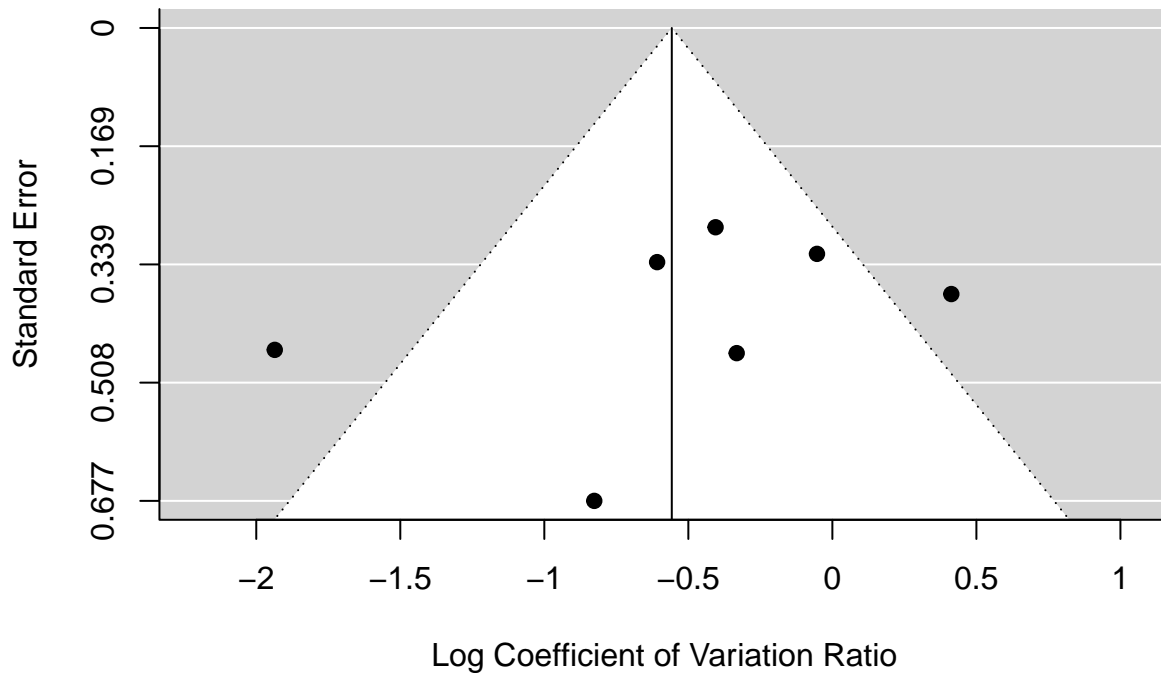
#Triglycerides analysis (split by exposure type)

```
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)
```

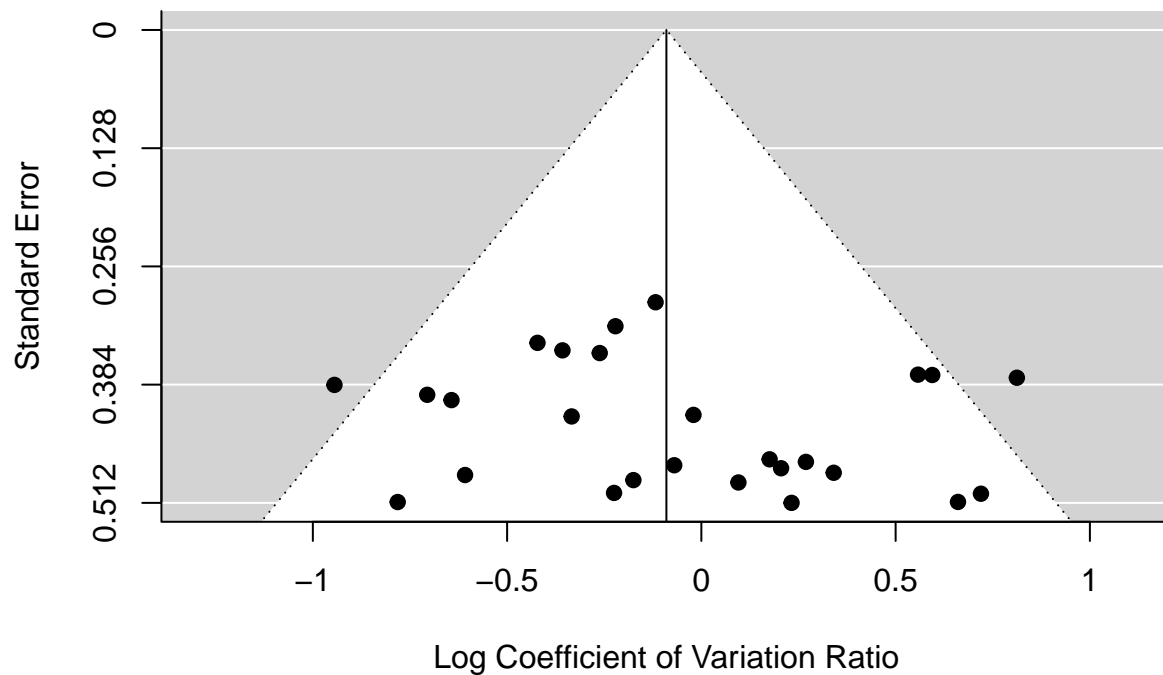


```
Triglycerides_overall_lnCVR_OF <- rma.mv(yi, vi, random = list(~1|Cohort_ID, ~1|ES_ID), data=Triglycerides)
summary(Triglycerides_overall_lnCVR_OF)
```

```
##
## 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
```

