

Insulin

Hamza

2 October 2019

Meta-regression Insulin

```
load(file="Effect_Size_All_Traits.RData")
load(file="Effect_Size_All_Traits_lnCVR.RData")
#lnRR
Insulin_FI_lnRR <- subset(Effect_Size_All_Traits, Effect_Size_All_Traits$Trait == "Insulin_FI")
Insulin_TT_lnRR<- subset(Effect_Size_All_Traits, Effect_Size_All_Traits$Trait == "Insulin_TT")

Insulin_FI_lnRR_MG <- subset(Insulin_FI_lnRR, Insulin_FI_lnRR$Exposure_Type == "Multigenerational")
Insulin_TT_lnRR_MG <- subset(Insulin_TT_lnRR, Insulin_TT_lnRR$Exposure_Type == "Multigenerational")

Insulin_FI_lnRR_OF <- subset(Insulin_FI_lnRR, Insulin_FI_lnRR$Exposure_Type == "One off")
Insulin_TT_lnRR_OF <- subset(Insulin_TT_lnRR, Insulin_TT_lnRR$Exposure_Type == "One off")

#lnCVR
Insulin_FI_lnCVR <- subset(Effect_Size_All_Traits_lnCVR, Effect_Size_All_Traits_lnCVR$Trait == "Insulin_FI")
Insulin_TT_lnCVR<- subset(Effect_Size_All_Traits_lnCVR, Effect_Size_All_Traits_lnCVR$Trait == "Insulin_TT")

Insulin_FI_lnCVR_MG <- subset(Insulin_FI_lnCVR, Insulin_FI_lnCVR$Exposure_Type == "Multigenerational")
Insulin_TT_lnCVR_MG <- subset(Insulin_TT_lnCVR, Insulin_TT_lnCVR$Exposure_Type == "Multigenerational")

Insulin_FI_lnCVR_OF <- subset(Insulin_FI_lnCVR, Insulin_FI_lnCVR$Exposure_Type == "One off")
Insulin_TT_lnCVR_OF <- subset(Insulin_TT_lnCVR, Insulin_TT_lnCVR$Exposure_Type == "One off")
```

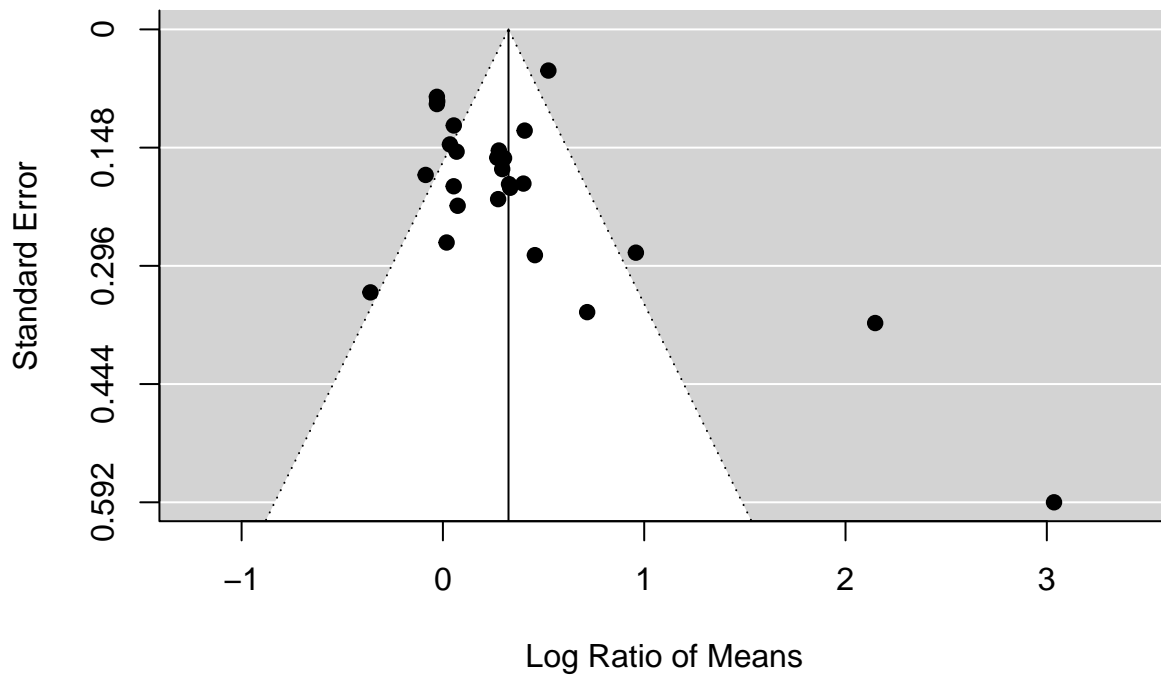
FI Analysis

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

```
##
## Multivariate Meta-Analysis Model (k = 26; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -19.6439   39.2878   45.2878   48.9444   46.4307
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000    26    no      ES_ID
## sigma^2.2  0.1888  0.4345    22    no  Cohort_ID
##
```

```
## Test for Heterogeneity:
## Q(df = 25) = 133.3188, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.3258 0.1023 3.1846 0.0014 0.1253 0.5263 **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Insulin_lnRR_FI)
```

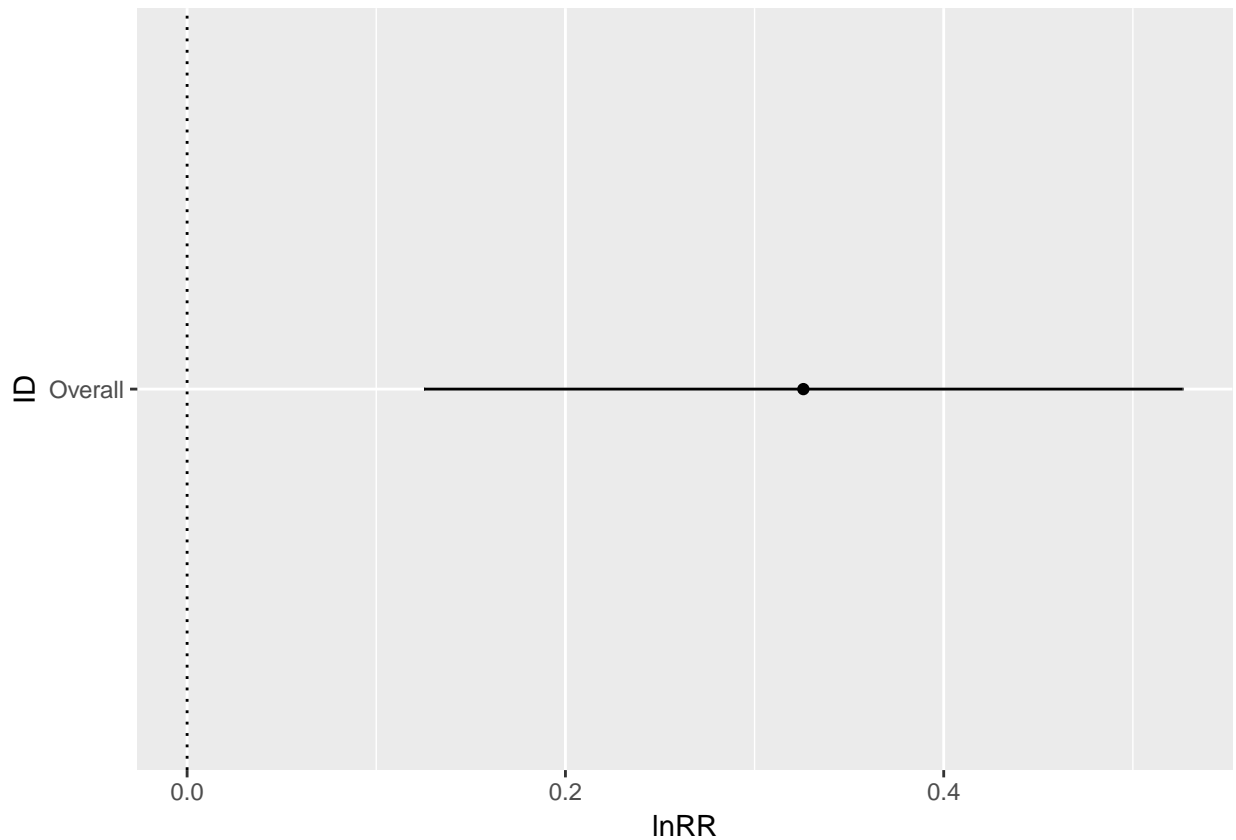


```
#Tibble of overall results
```

```
Insulin_overall_lnRR_FI <- tibble(
  ID = "Overall",
  lnRR = 0.3258,
  ci.lb = 0.1253,
  ci.ub = 0.5263
)
```

```
## Warning: `list_len()` is deprecated as of rlang 0.2.0.
## Please use `new_list()` instead.
## This warning is displayed once per session.
```

```
plot_Insulin_overall_FI <- ggplot(Insulin_overall_lnRR_FI, 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(x = "ID", y = "lnRR") +
  coord_flip()
plot_Insulin_overall_FI
```



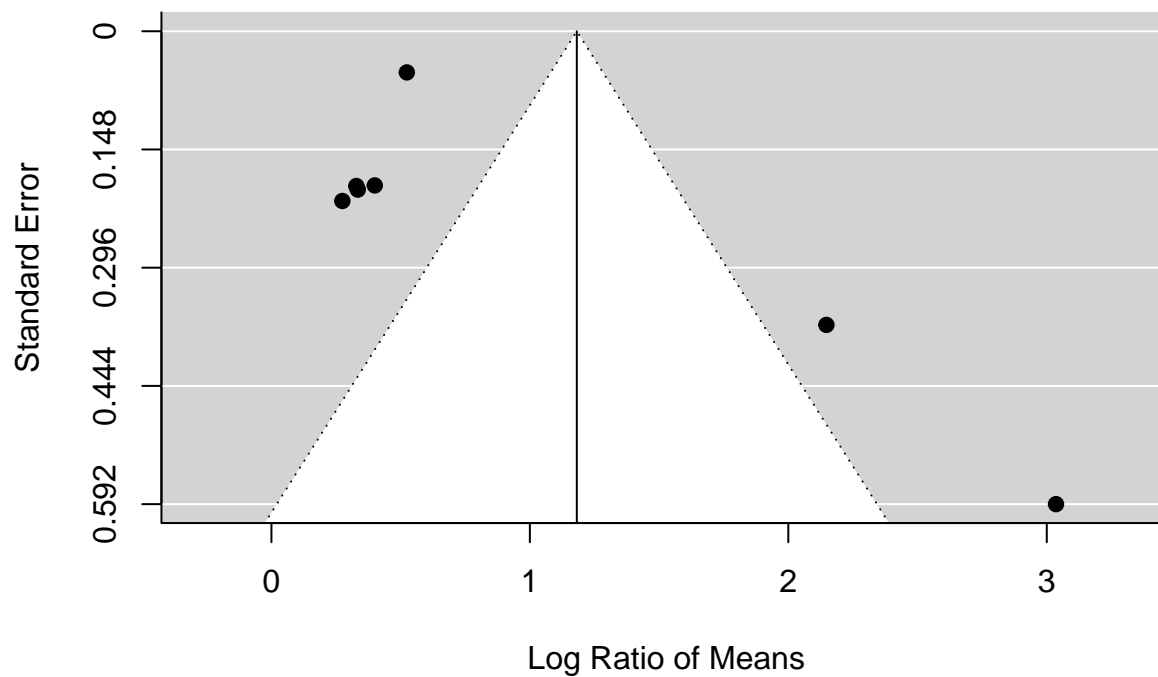
```
#Split by exposure type

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

```
##
## Multivariate Meta-Analysis Model (k = 7; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   -5.6192   11.2385   17.2385   16.6138   29.2385
##
## Variance Components:
##
##          estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0000  0.0000     7    no     ES_ID
## sigma^2.2  1.2613  1.1231     5    no  Cohort_ID
```

```
##
## Test for Heterogeneity:
## Q(df = 6) = 41.1767, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 1.1817 0.5207 2.2695 0.0232 0.1612 2.2022 *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Insulin_overall_lnRR_FI_MG)
```

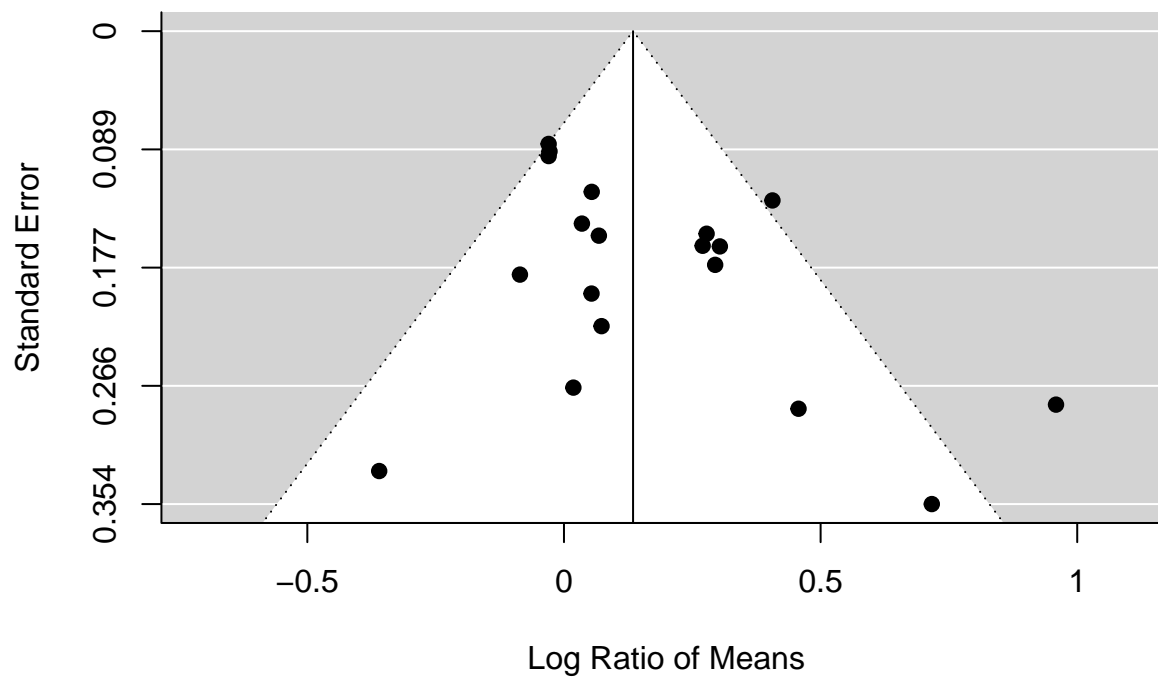


```
Insulin_overall_lnRR_FI_OF <- rma.mv(yi, vi, random = list(~1|ES_ID,~1|Cohort_ID), data=Insulin_FI_lnRR_FI_OF)
summary(Insulin_overall_lnRR_FI_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
## logLik Deviance      AIC      BIC      AICc
## -0.7398  1.4796  7.4796 10.1507  9.1939
##
## Variance Components:
```

```
##
##          estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0088  0.0938    19    no      ES_ID
## sigma^2.2 0.0088  0.0938    19    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 18) = 35.0758, p-val = 0.0092
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    0.1346  0.0488  2.7566  0.0058  0.0389  0.2303  **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Insulin_overall_lnRR_FI_OF)
```



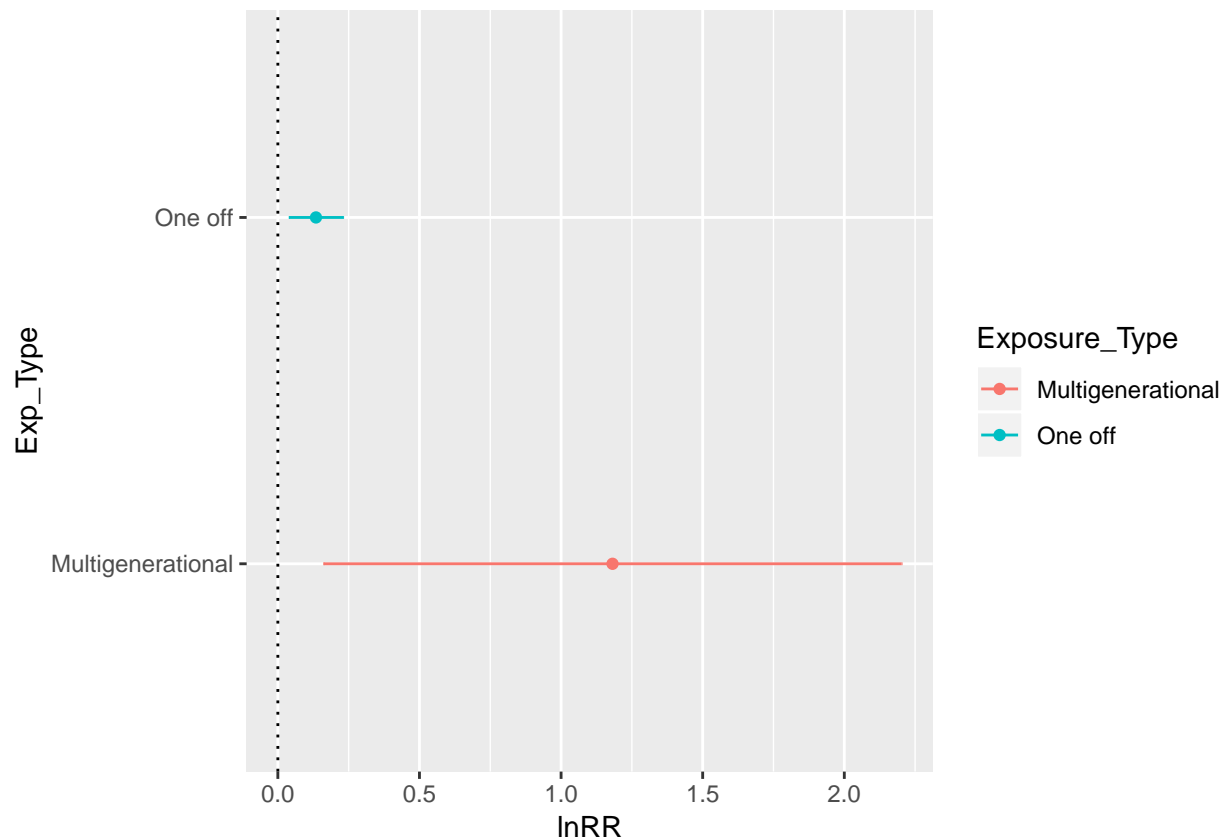
```
Insulin_FI_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnRR = c(1.1817, 0.1346),
  ci.lb = c(0.1612, 0.0389),
  ci.ub = c(2.2022, 0.2303)
)

Insulin_FI_Exp_lnRR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnRR  ci.lb ci.ub
##   <chr>          <dbl> <dbl> <dbl>
## 1 Multigenerational 1.18  0.161  2.20
## 2 One off          0.135 0.0389 0.230
```

#Plotting when split by exp type

```
plot_Insulin_FI_exp_type <- ggplot(Insulin_FI_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_Insulin_FI_exp_type
```

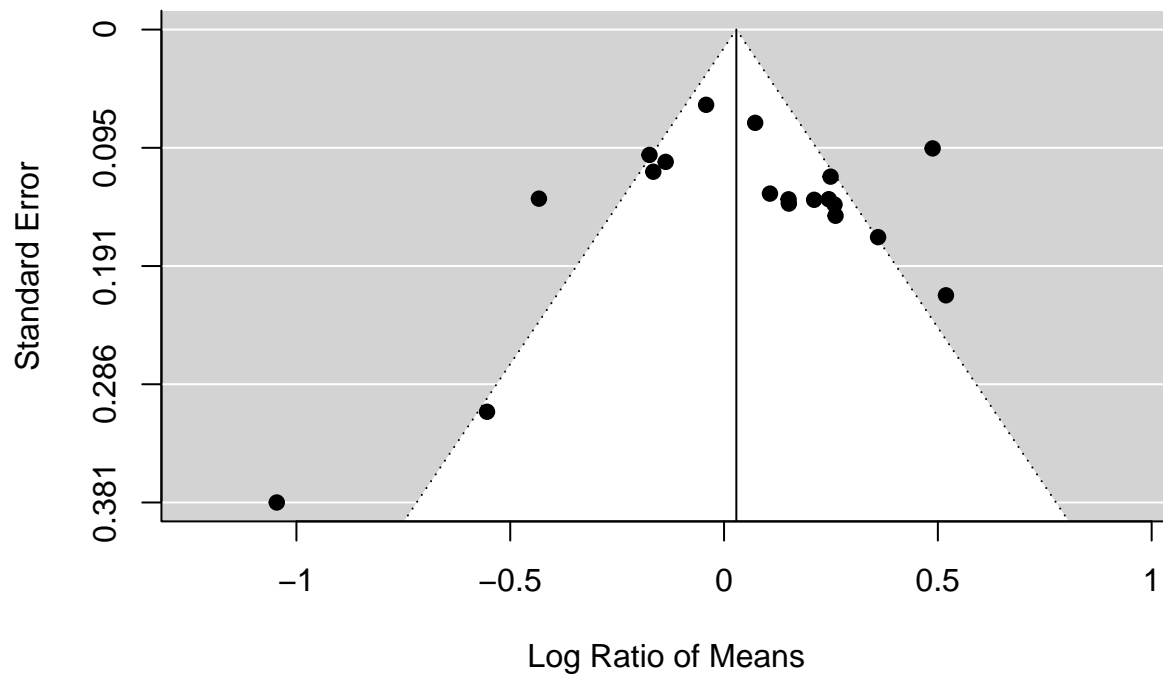


Insulin Tolerance test results

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

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   0.0131  -0.0262    5.9738    8.6449    7.6881
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000     19    no      ES_ID
## sigma^2.2  0.1220  0.3493     11    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 18) = 78.9554, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb    ci.ub
##   0.0288  0.1167  0.2467  0.8051  -0.1999  0.2575
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

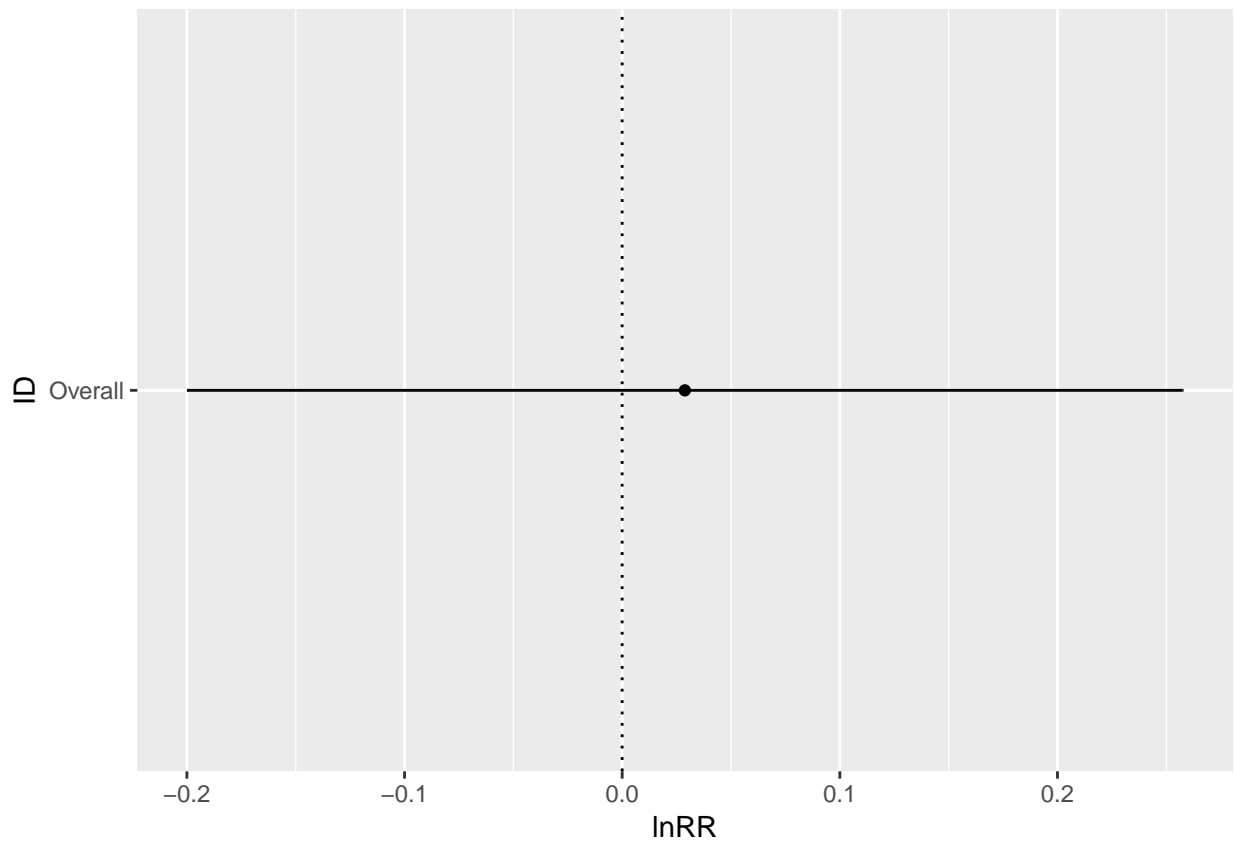
```
funnel(Insulin_lnRR_TT)
```



```
#Tibble of overall results
```

```
Insulin_overall_lnRR_TT <- tibble(  
  ID = "Overall",  
  lnRR = 0.0288,  
  ci.lb = -0.1999,  
  ci.ub = 0.2575  
)
```

```
plot_Insulin_overall_TT <- ggplot(Insulin_overall_lnRR_TT, 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(x = "ID", y = "lnRR") +  
  coord_flip()  
plot_Insulin_overall_TT
```



```
#Split by exposure type
```

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

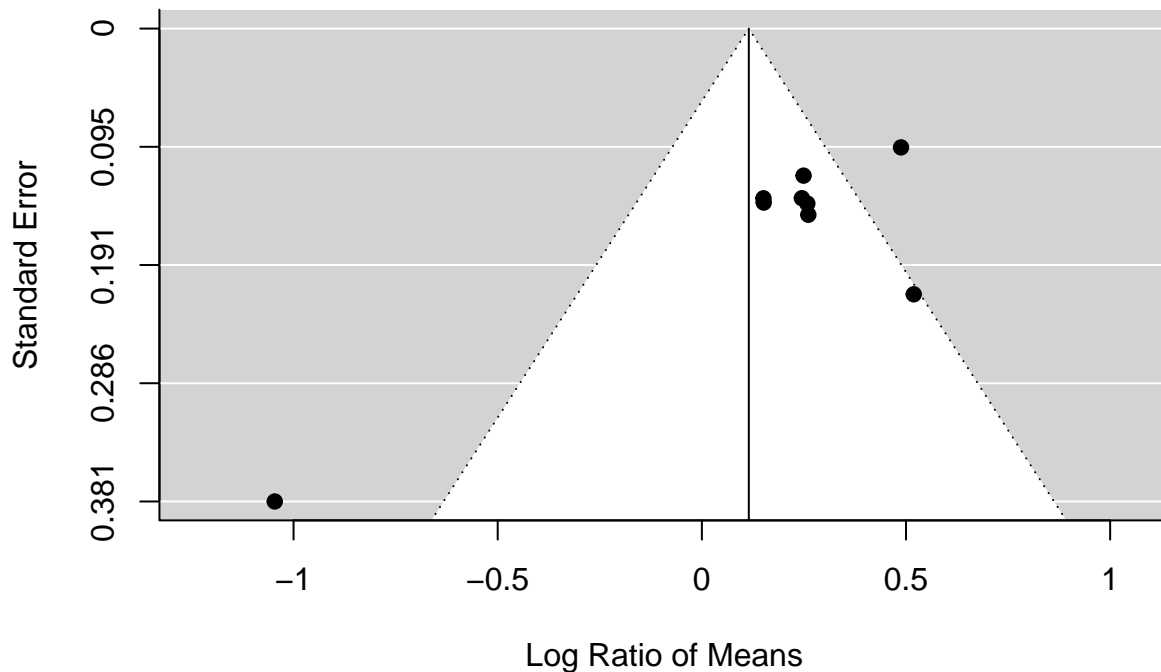
```
##
```

```
## Multivariate Meta-Analysis Model (k = 9; method: REML)
```



```
##
##   logLik  Deviance      AIC      BIC      AICc
##   1.3312  -2.6625    3.3375    3.5758    9.3375
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000     9    no      ES_ID
## sigma^2.2  0.3584  0.5987     4    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 8) = 19.9297, p-val = 0.0106
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    0.1149  0.3171  0.3625  0.7170  -0.5066  0.7365
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

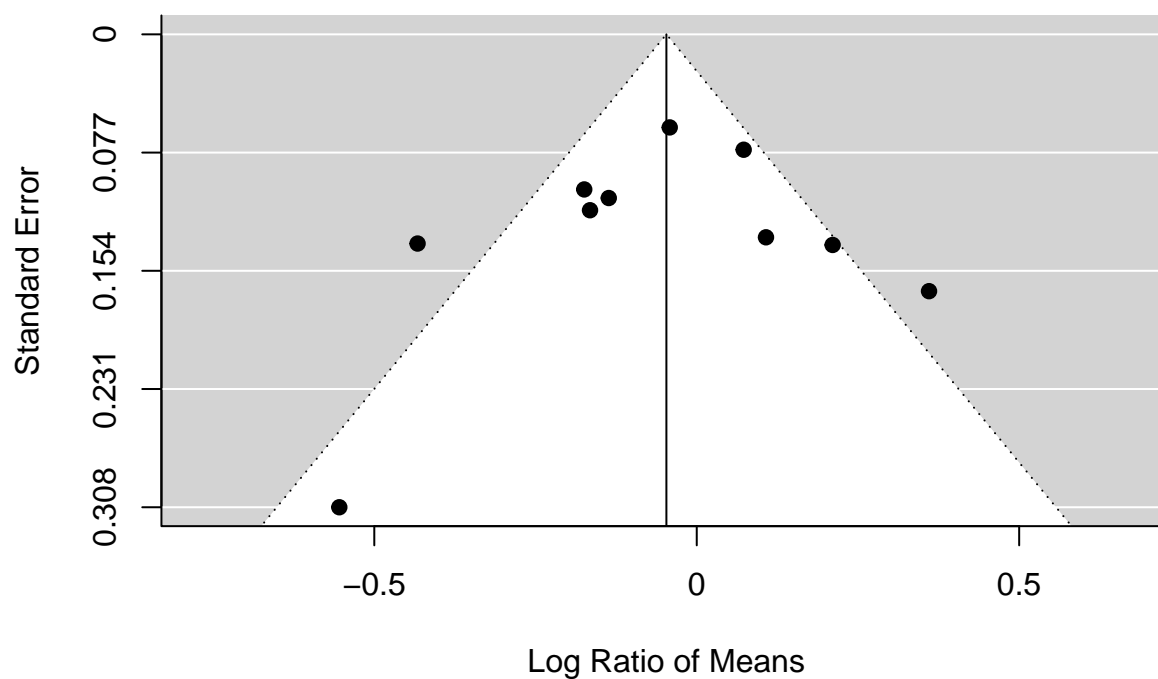
```
funnel(Insulin_overall_lnRR_TT_MG)
```



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

```
##
## Multivariate Meta-Analysis Model (k = 10; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   0.3948  -0.7897    5.2103    5.8020    10.0103
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0047  0.0683     10    no      ES_ID
## sigma^2.2  0.0549  0.2342      7    no    Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 9) = 27.4026, p-val = 0.0012
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.0470  0.1069  -0.4400  0.6599  -0.2566  0.1625
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Insulin_overall_lnRR_TT_OF)
```



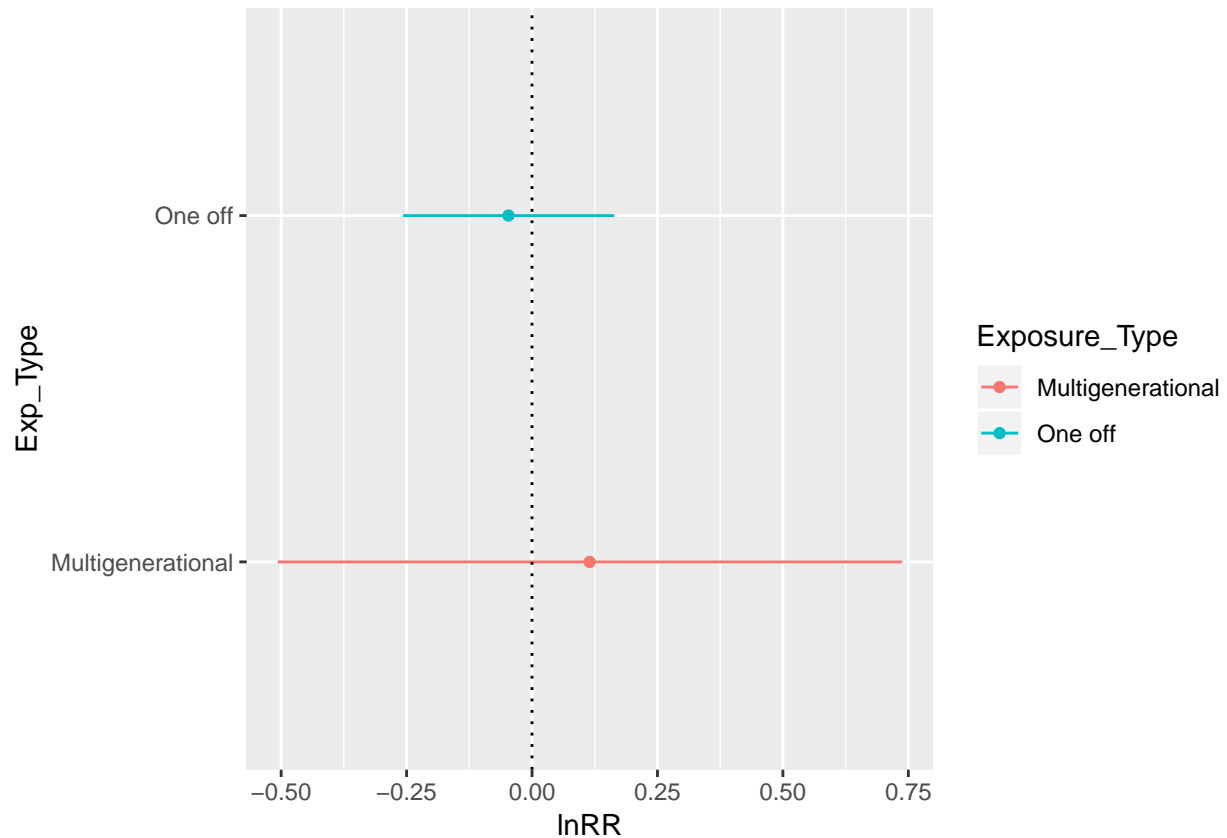
```
Insulin_TT_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnRR = c(0.1149, -0.0470),
  ci.lb = c(-0.5066, -0.2566),
  ci.ub = c(0.7365, 0.1625)
)
```

```
Insulin_TT_Exp_lnRR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnRR  ci.lb ci.ub
##   <chr>            <dbl> <dbl> <dbl>
## 1 Multigenerational  0.115 -0.507 0.736
## 2 One off           -0.047 -0.257 0.162
```

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

```
plot_Insulin_TT_exp_type <- ggplot(Insulin_TT_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_Insulin_TT_exp_type
```

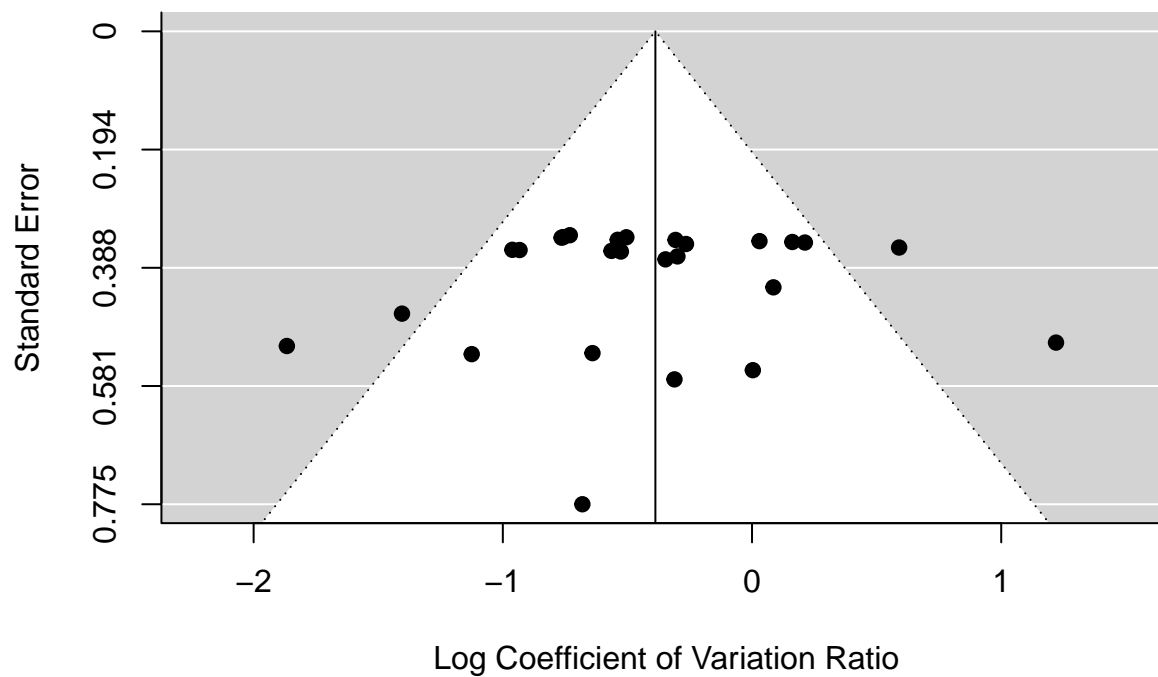


Fasting Insulin analysis (lnCVR)

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

```
##
## Multivariate Meta-Analysis Model (k = 26; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -21.8996  43.7992   49.7992   53.4558   50.9421
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000    26     no      ES_ID
## sigma^2.2  0.1923  0.4385    22     no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 25) = 50.9646, p-val = 0.0016
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##  -0.3878  0.1260  -3.0780  0.0021  -0.6348  -0.1409  **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

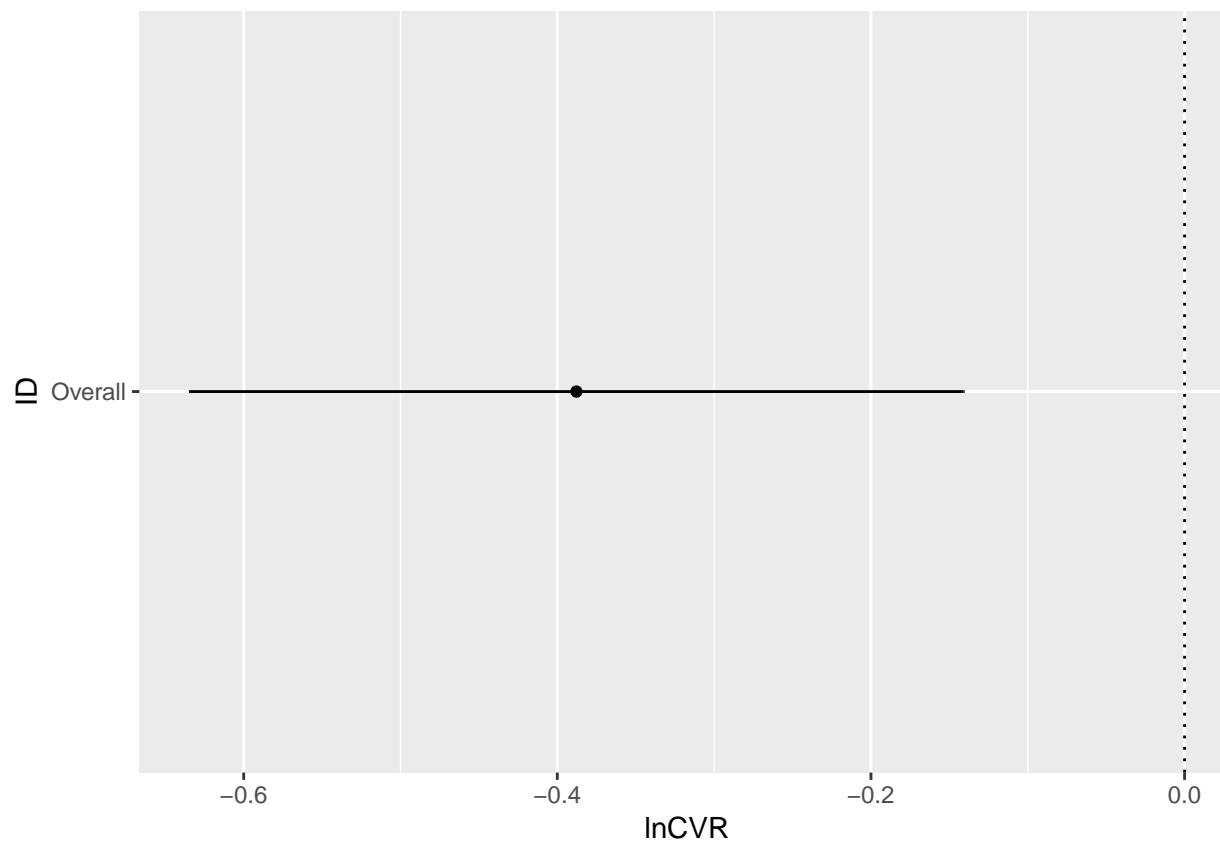
```
funnel(Insulin_lnCVR_FI)
```



#Tibble of overall results

```
Insulin_overall_lnCVR_FI <- tibble(
  ID = "Overall",
  lnCVR = -0.3878,
  ci.lb = -0.6348,
  ci.ub = -0.1409
)

plot_Insulin_overall_FI_lnCVR <- ggplot(Insulin_overall_lnCVR_FI, 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 = "lnCVR") +
  coord_flip()
plot_Insulin_overall_FI_lnCVR
```



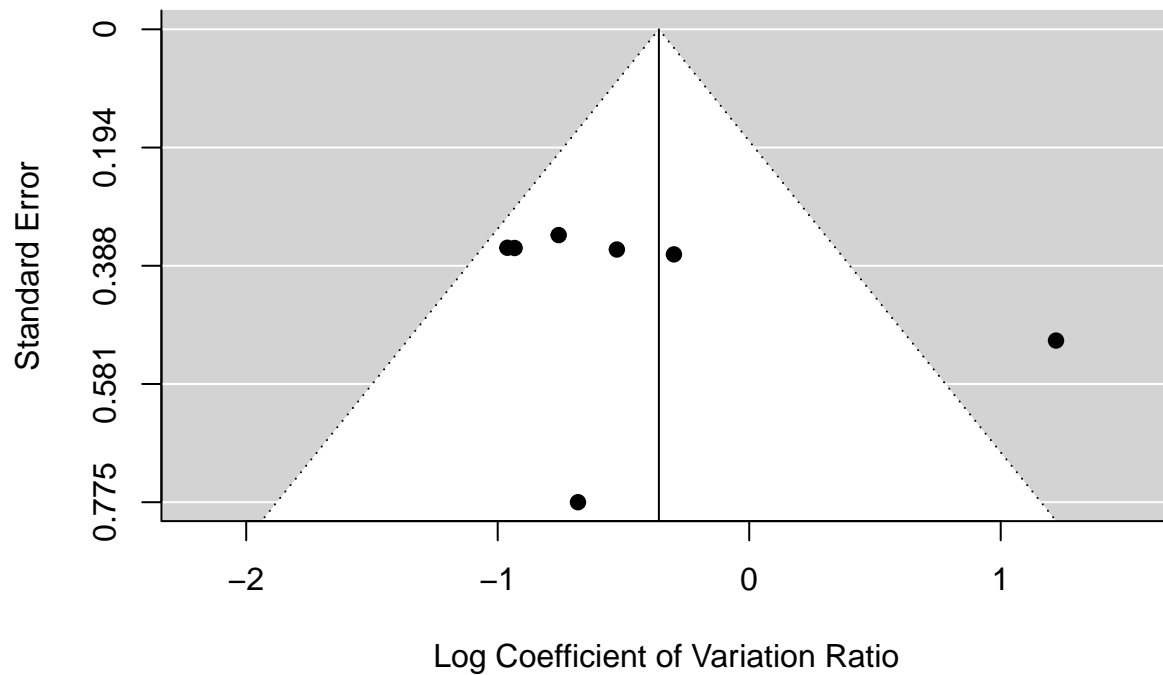
#Split by exposure type

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

```
##
## Multivariate Meta-Analysis Model (k = 7; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -5.5196   11.0392   17.0392   16.4145   29.0392
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0000  0.0000     7    no     ES_ID
## sigma^2.2  0.5102  0.7142     5    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 6) = 15.3613, p-val = 0.0176
##
## Model Results:
##
## estimate      se      zval    pval    ci.lb    ci.ub
## -0.3591  0.3707 -0.9687  0.3327 -1.0858  0.3675
##
```

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

```
funnel(Insulin_overall_lnCVR_FI_MG)
```

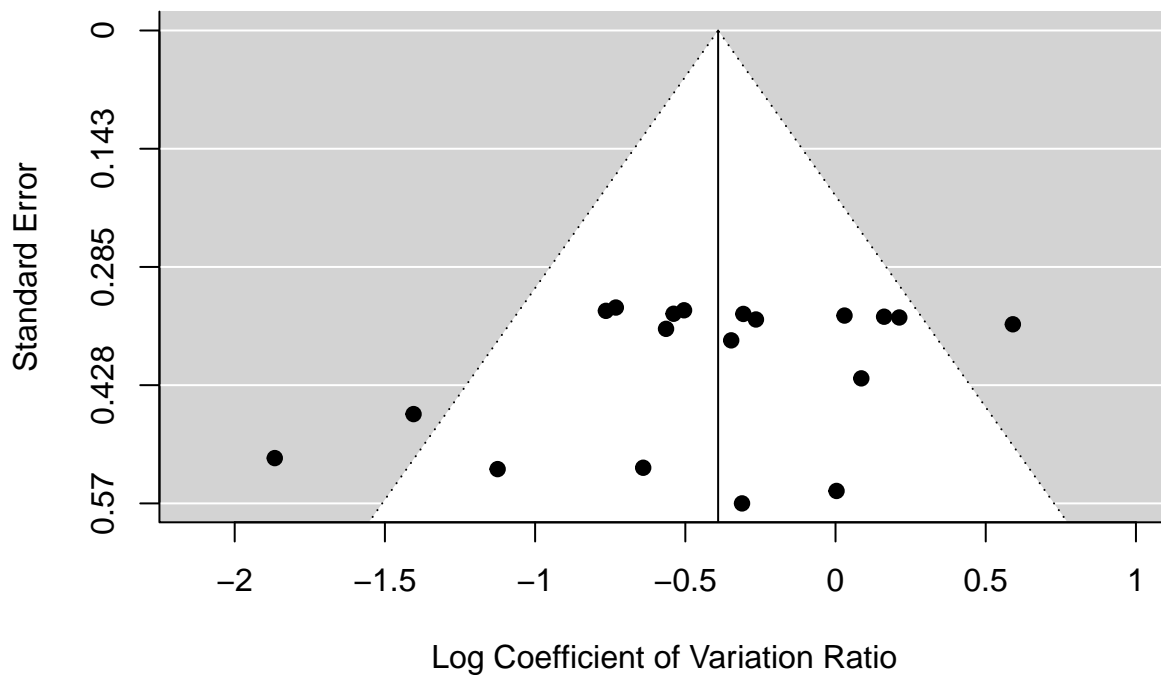


```
Insulin_overall_lnCVR_FI_OF <- rma.mv(yi, vi, random = list(~1|ES_ID,~1|Cohort_ID), data=Insulin_FI_lnCVR_FI_OF)
summary(Insulin_overall_lnCVR_FI_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -15.3824   30.7649   36.7649   39.4360   38.4792
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed  factor
## sigma^2.1  0.0679  0.2605    19    no    ES_ID
## sigma^2.2  0.0679  0.2605    19    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 18) = 34.5939, p-val = 0.0106
##
## Model Results:
```

```
##
## estimate      se      zval    pval    ci.lb    ci.ub
## -0.3908  0.1244  -3.1421  0.0017  -0.6345  -0.1470  **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Insulin_overall_lnCVR_FI_OF)
```



```
Insulin_FI_Exp_lnCVR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnCVR = c(-0.3591, -0.3908),
  ci.lb = c(-1.0858, -0.6345),
  ci.ub = c(0.3675, -0.1470)
)
```

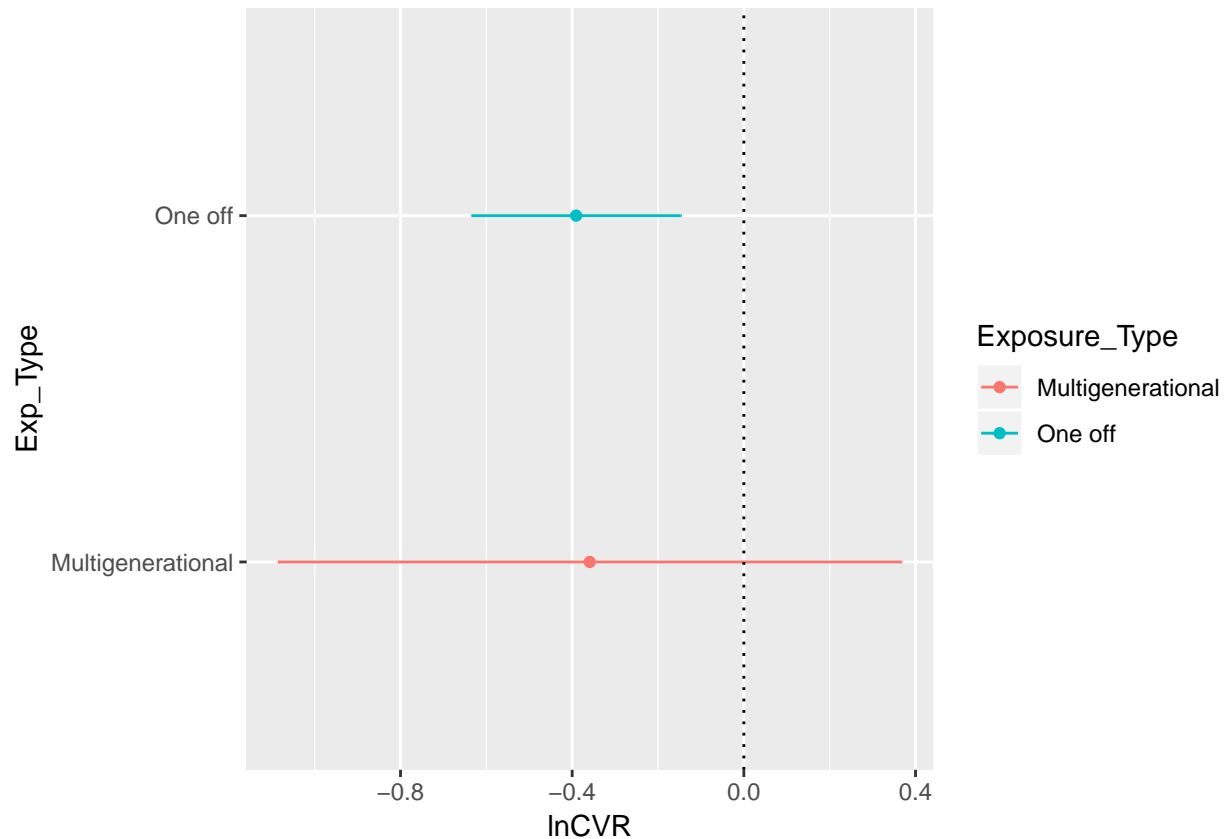
```
Insulin_FI_Exp_lnCVR
```

```
## # A tibble: 2 x 4
##   Exposure_Type    lnCVR  ci.lb  ci.ub
##   <chr>          <dbl> <dbl> <dbl>
## 1 Multigenerational -0.359 -1.09  0.368
## 2 One off          -0.391 -0.634 -0.147
```



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

```
plot_Insulin_FI_exp_type_lnCVR <- ggplot(Insulin_FI_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_Insulin_FI_exp_type_lnCVR
```



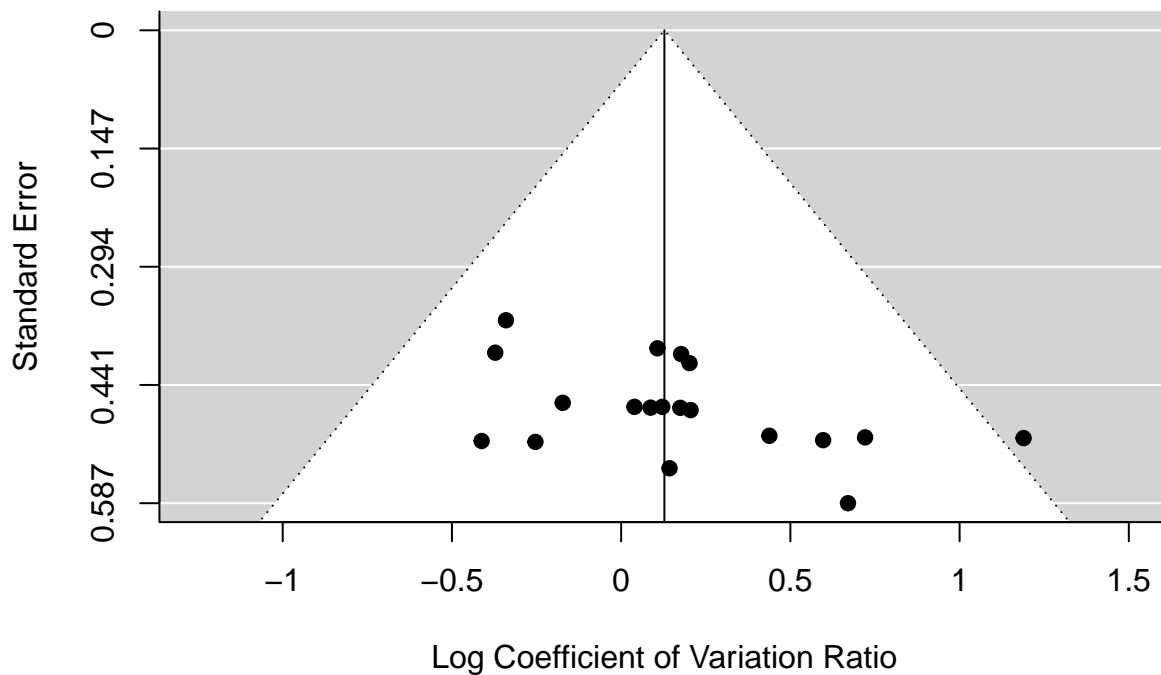
Insulin tolerance test analysis (lnCVR)

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

```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##  -9.5517   19.1034   25.1034   27.7745   26.8177
##
```

```
## Variance Components:
##
##          estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0000  0.0000    19    no      ES_ID
## sigma^2.2 0.0000  0.0000    11    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 18) = 13.3227, p-val = 0.7721
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    0.1278  0.1058  1.2078  0.2271  -0.0796  0.3351
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Insulin_lnCVR_TT)
```



```
#Tibble of overall results
```

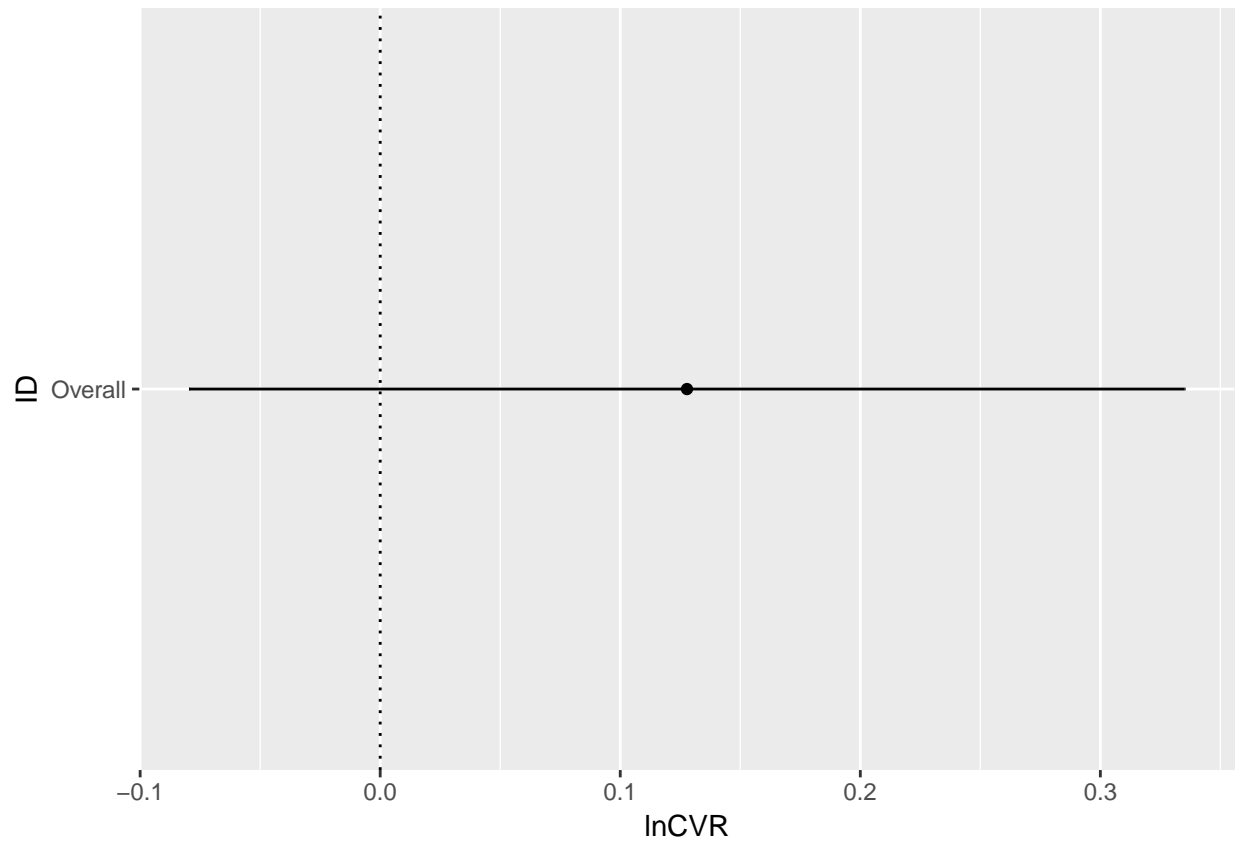
```
Insulin_overall_lnCVR_TT <- tibble(
  ID = "Overall",
  lnCVR = 0.1278,
  ci.lb = -0.0796,
```

```

ci.ub = 0.3351
)

plot_Insulin_overall_TT_lnCVR <- ggplot(Insulin_overall_lnCVR_TT, 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 = "lnCVR") +
  coord_flip()
plot_Insulin_overall_TT_lnCVR

```



```

#Split by exposure type

Insulin_overall_lnCVR_TT_MG <- rma.mv(yi, vi, random = list(~1|ES_ID,~1|Cohort_ID), data=Insulin_TT_lnCVR)

summary(Insulin_overall_lnCVR_TT_MG)

```

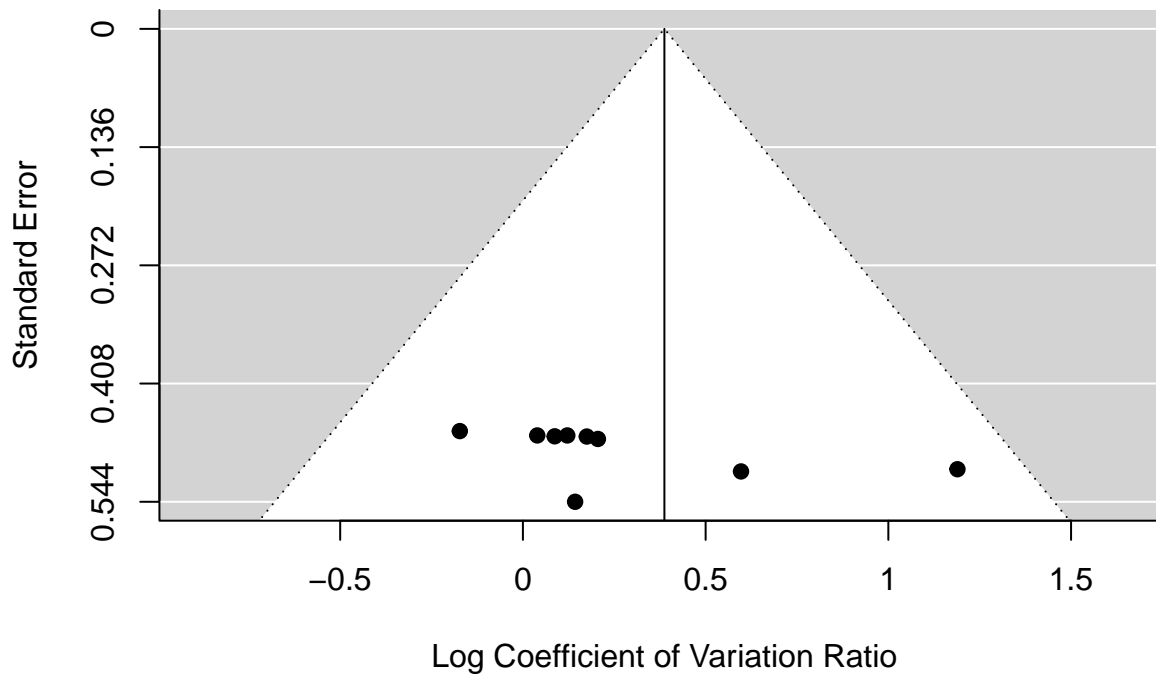
```

##
## Multivariate Meta-Analysis Model (k = 9; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   -3.8409    7.6818  13.6818  13.9202  19.6818
##
## Variance Components:
##

```

```
##          estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0000  0.0000     9    no      ES_ID
## sigma^2.2 0.1078  0.3284     4    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 8) = 5.2075, p-val = 0.7352
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    0.3872  0.2593  1.4933  0.1354  -0.1210  0.8954
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Insulin_overall_lnCVR_TT_MG)
```

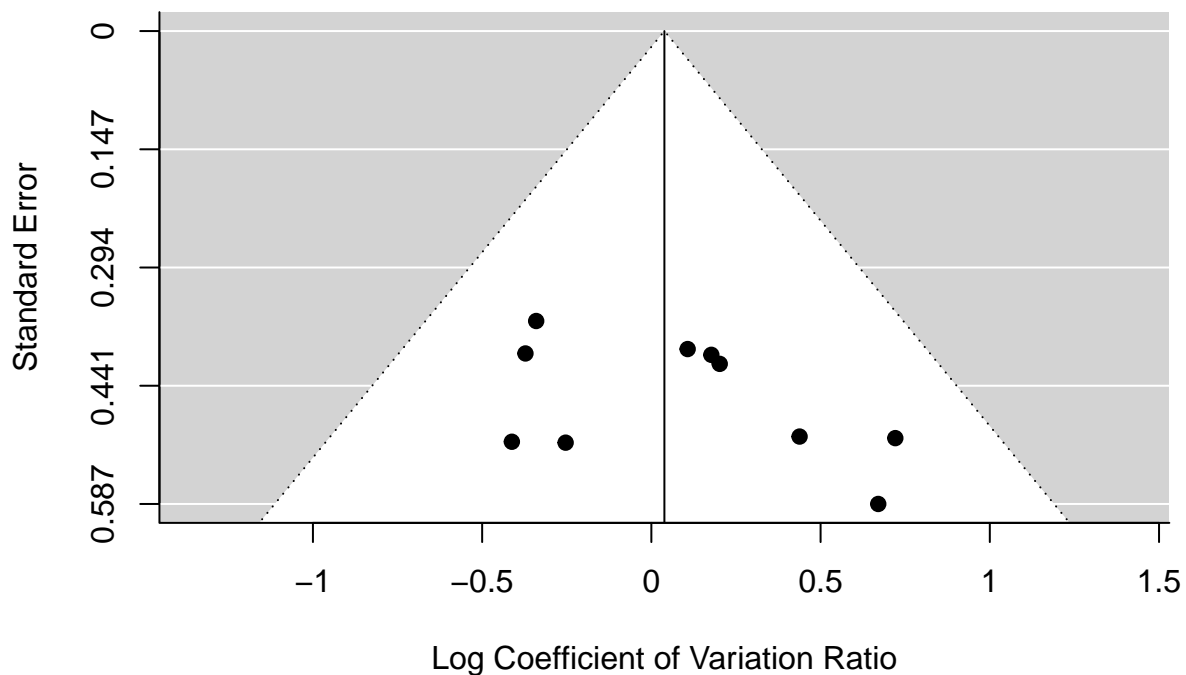


```
Insulin_overall_lnCVR_TT_OF <- rma.mv(yi, vi, random = list(~1|ES_ID, ~1|Cohort_ID), data=Insulin_TT_lnCVR_TT_MG)
summary(Insulin_overall_lnCVR_TT_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 10; method: REML)
##
##    logLik  Deviance      AIC      BIC      AICc
```

```
## -4.7677    9.5354   15.5354   16.1270   20.3354
##
## Variance Components:
##
##          estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0000  0.0000    10    no      ES_ID
## sigma^2.2  0.0000  0.0000     7    no    Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 9) = 7.1761, p-val = 0.6188
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb    ci.ub
##   0.0385  0.1403  0.2744  0.7838  -0.2365  0.3134
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Insulin_overall_lnCVR_TT_OF)
```



```
Insulin_TT_Exp_lnCVR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnCVR = c(0.3872, 0.0385),
  ci.lb = c(-0.1210, -0.2365),
```

```
ci.ub = c(0.8954,0.3134)
)
```

```
Insulin_TT_Exp_lnCVR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnCVR ci.lb ci.ub
##   <chr>          <dbl> <dbl> <dbl>
## 1 Multigenerational 0.387  -0.121 0.895
## 2 One off          0.0385 -0.236 0.313
```

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

```
plot_Insulin_TT_exp_type_lnCVR <- ggplot(Insulin_TT_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_Insulin_TT_exp_type_lnCVR
```

