

Insulin

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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")
```

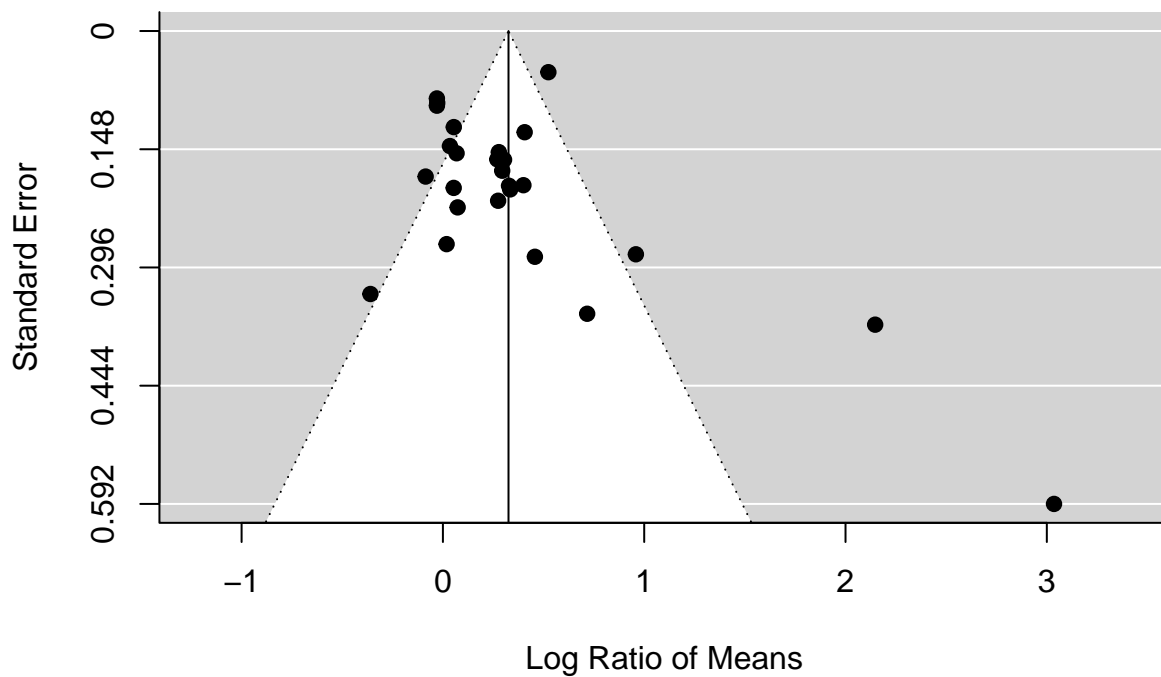
FI Analysis

```
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)
```

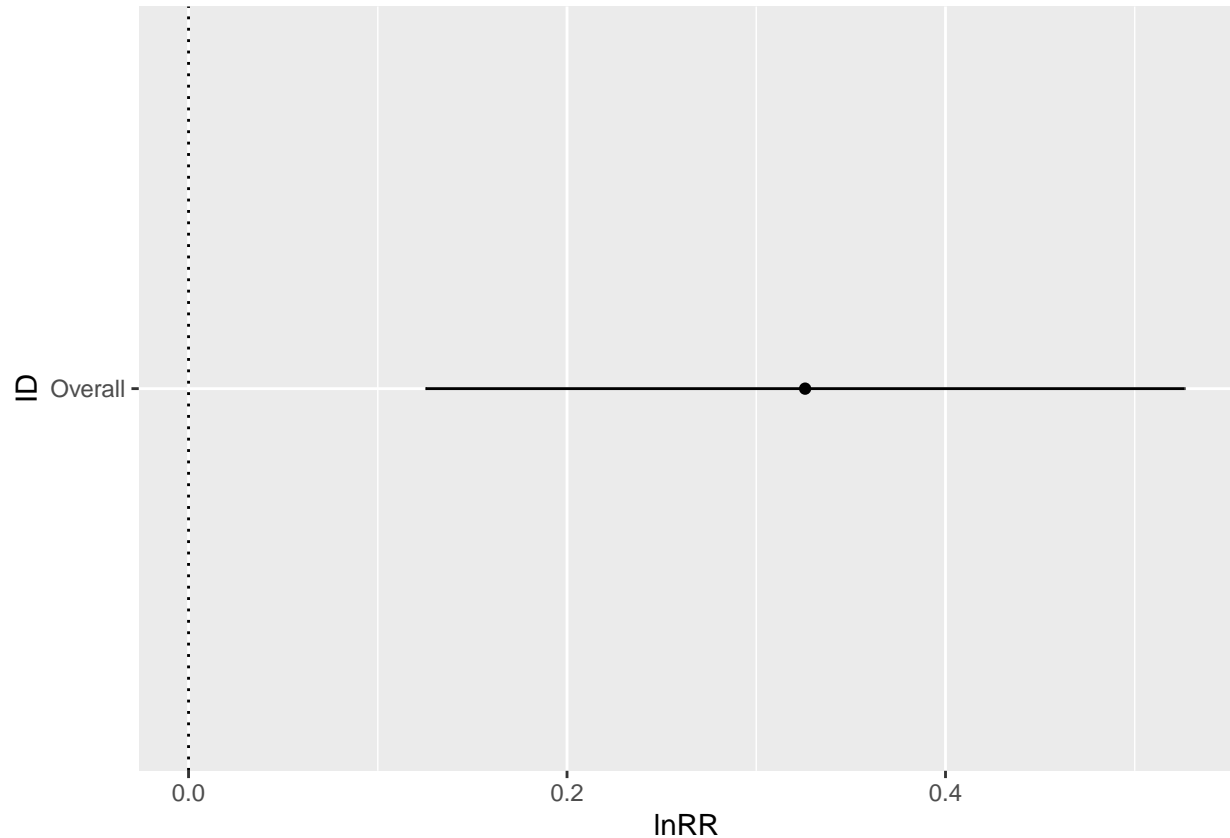


```
#Tibble of overall results
```

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

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
```



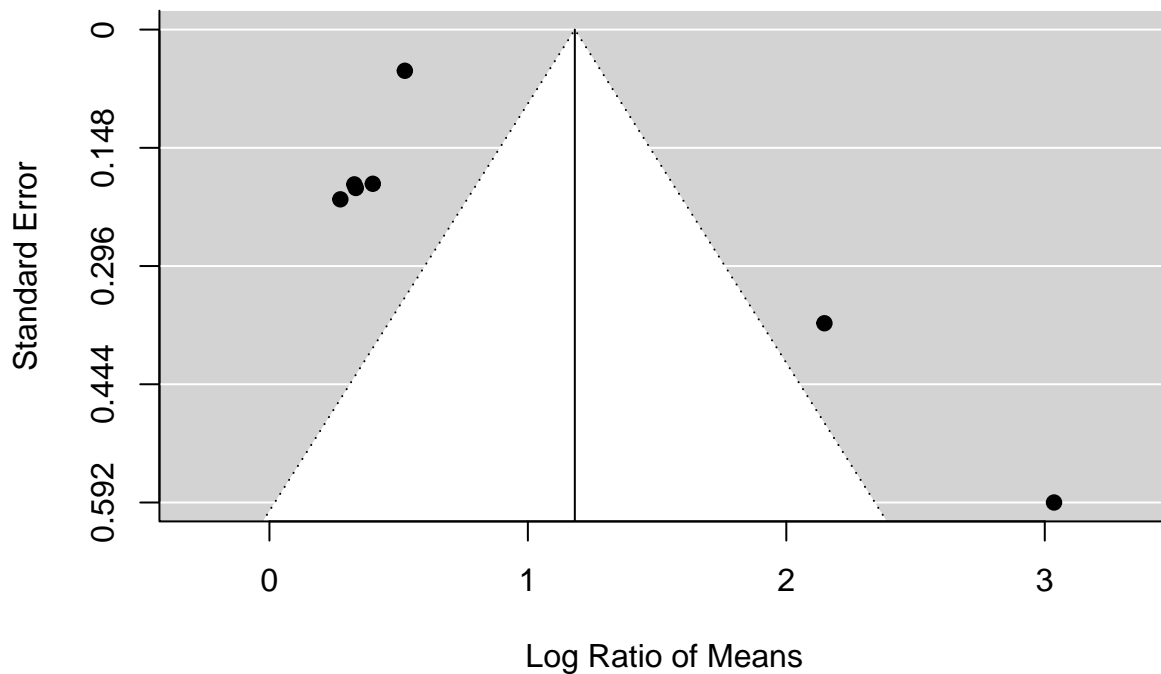
```
#Split by exposure type
```

```
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,
summary(Insulin_overall_lnRR_FI_OF)
```

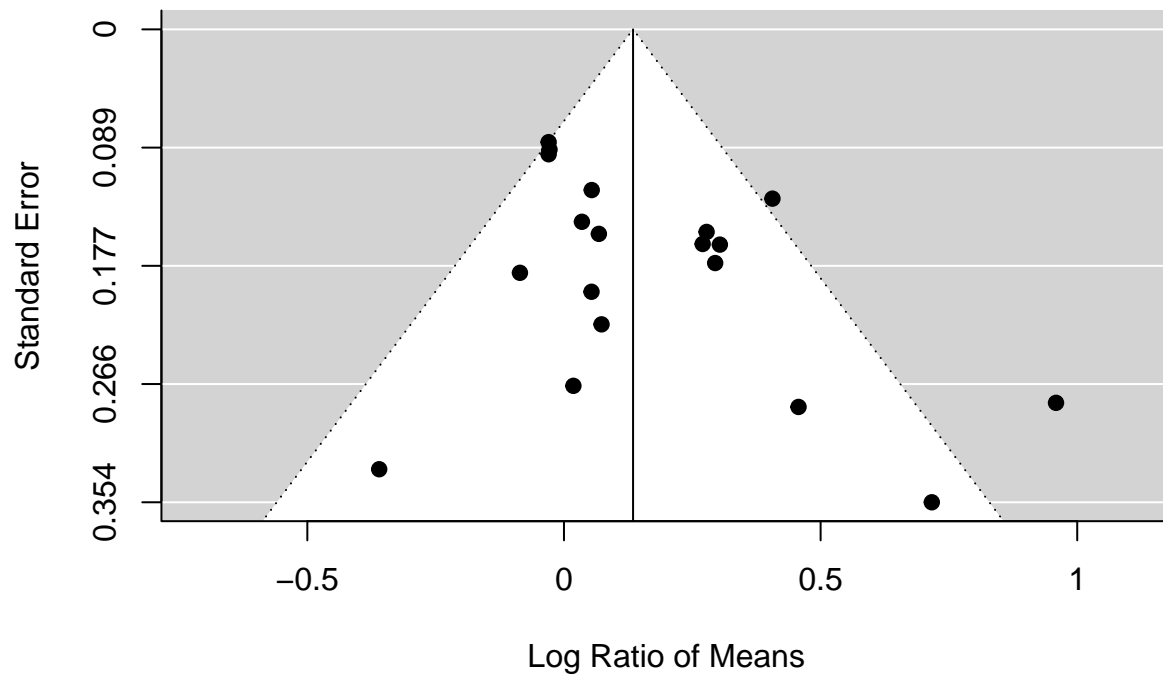
```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
## logLik Deviance      AIC      BIC      AICc
## -0.7398  1.4796  7.4796 10.1507  9.1939
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0088 0.0938    19    no      ES_ID
```

```
## 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
```

```
k_exp <- Insulin_FI_lnRR_OF %>% group_by(Exposure_Type) %>% count()
k_exp
```

```
## # A tibble: 1 x 2
## # Groups:   Exposure_Type [1]
##   Exposure_Type      n
##   <fct>          <int>
## 1 One off          19
```

```
funnel(Insulin_overall_lnRR_FI_OF)
```



```

Insulin_FI_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnRR = c(Insulin_overall_lnRR_FI_MG$b[1], Insulin_overall_lnRR_FI_OF$b[1]),
  ci.lb = c(Insulin_overall_lnRR_FI_MG$ci.lb[1], Insulin_overall_lnRR_FI_OF$ci.lb[1]),
  ci.ub = c(Insulin_overall_lnRR_FI_MG$ci.ub[1], Insulin_overall_lnRR_FI_OF$ci.ub[1])
)

```

```
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

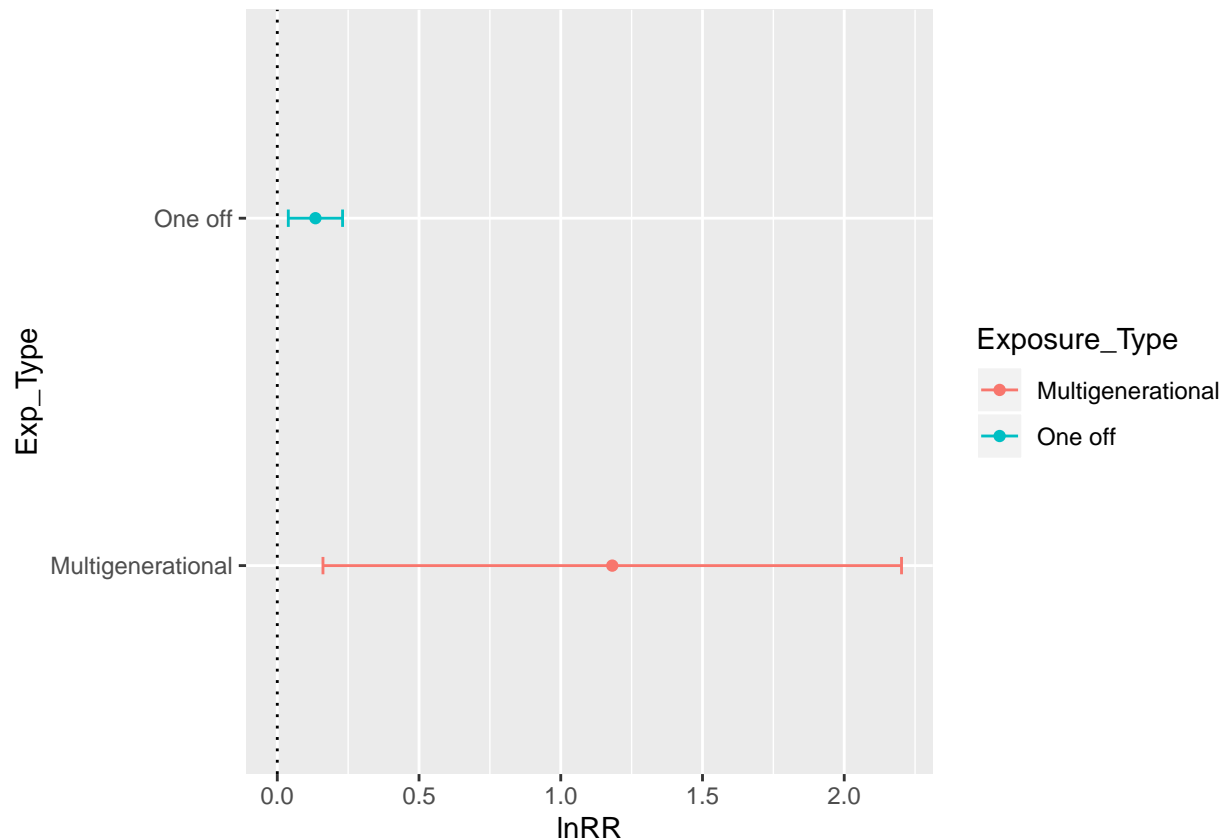
```

#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 = 0.05, 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_Insulin_FI_exp_type

```

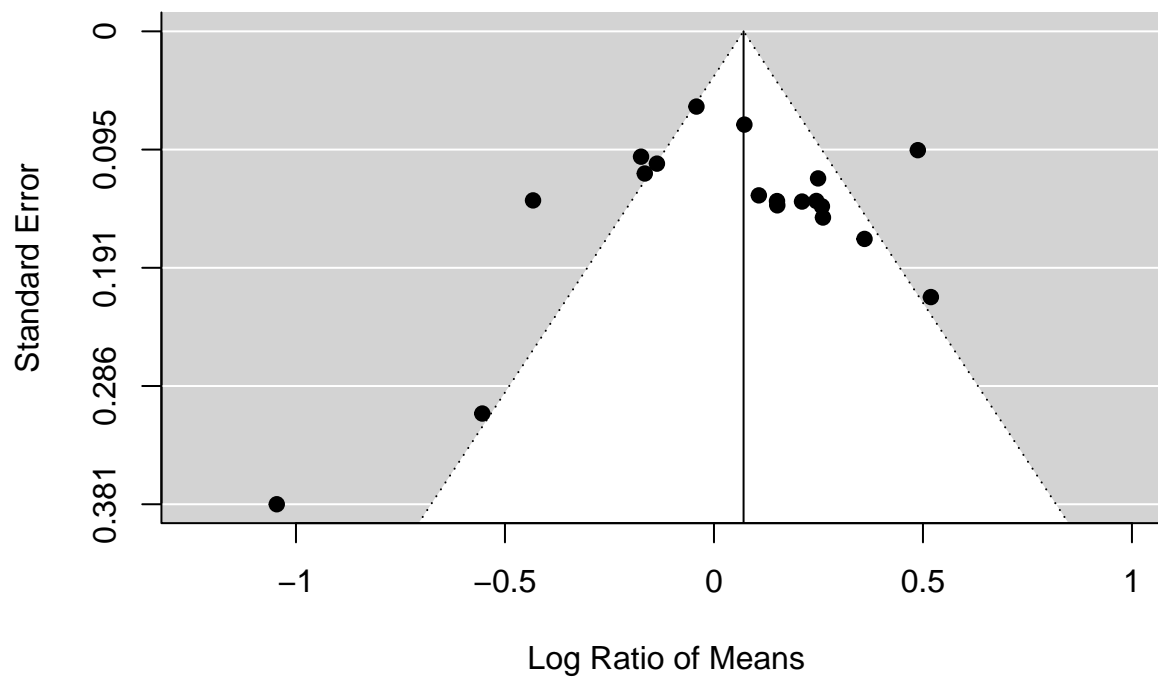


Insulin Tolerance test results

```
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  
## -5.1187  10.2375   16.2375   18.9086   17.9518  
##  
## Variance Components:  
##  
##           estim      sqrt  nlvls  fixed      factor  
## sigma^2.1  0.0282  0.1679     19     no      ES_ID  
## sigma^2.2  0.0282  0.1679     19     no  Cohort_ID  
##  
## Test for Heterogeneity:  
## Q(df = 18) = 78.9554, p-val < .0001  
##  
## Model Results:  
##  
## estimate      se    zval    pval    ci.lb    ci.ub  
##   0.0708  0.0639  1.1091  0.2674  -0.0543  0.1960  
##  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

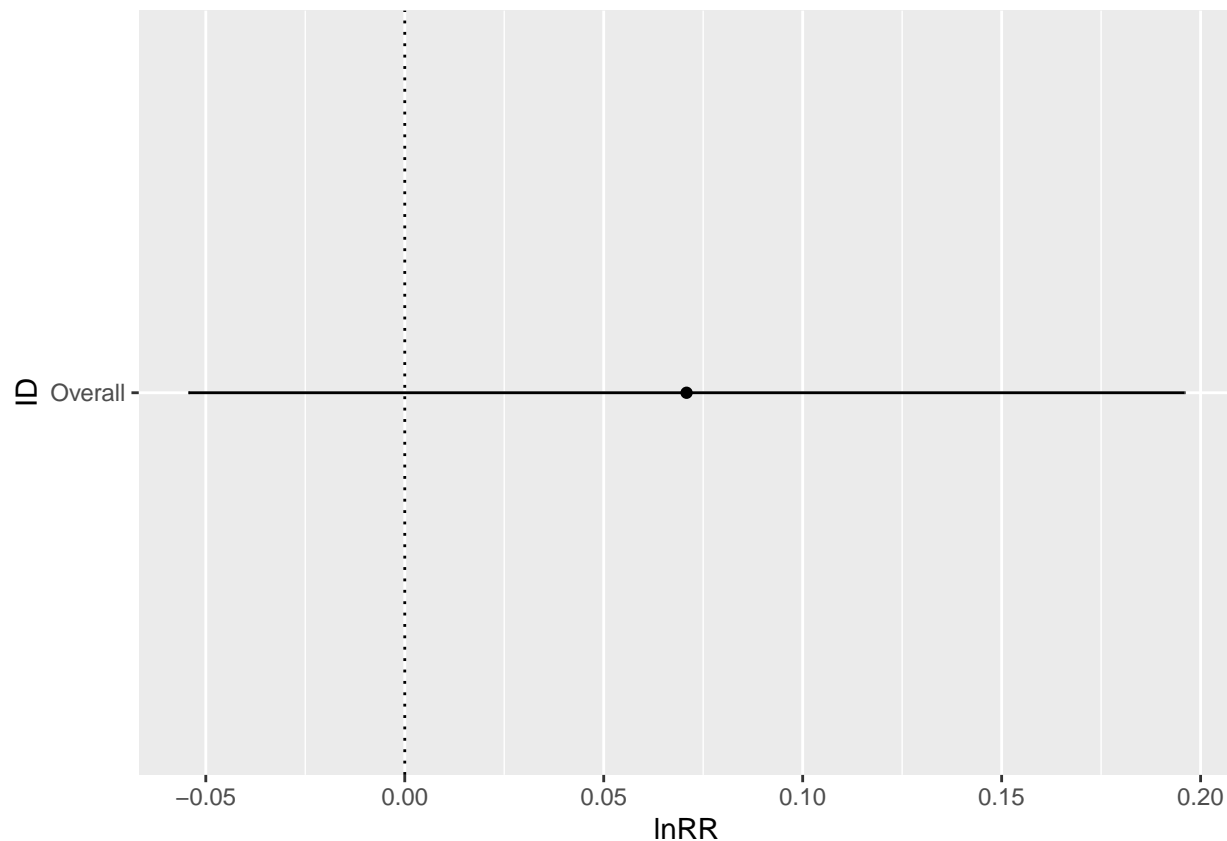
```
funnel(Insulin_lnRR_TT)
```



#Tibble of overall results

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

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
```

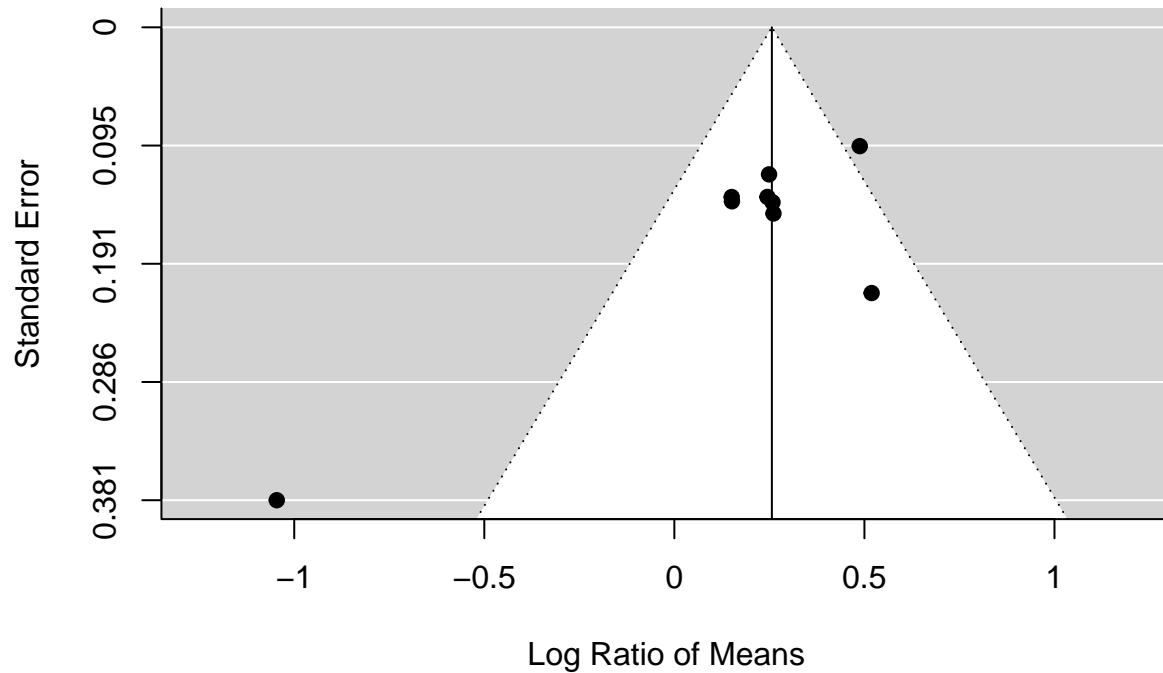
#Split by exposure type

```
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
## -1.9343    3.8685    9.8685   10.1069   15.8685
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0059  0.0769     9    no     ES_ID
## sigma^2.2  0.0059  0.0769     9    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
##  0.2565  0.0611  4.1978 <.0001  0.1368  0.3763 ***
##
```

```
## ---
## 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)
```

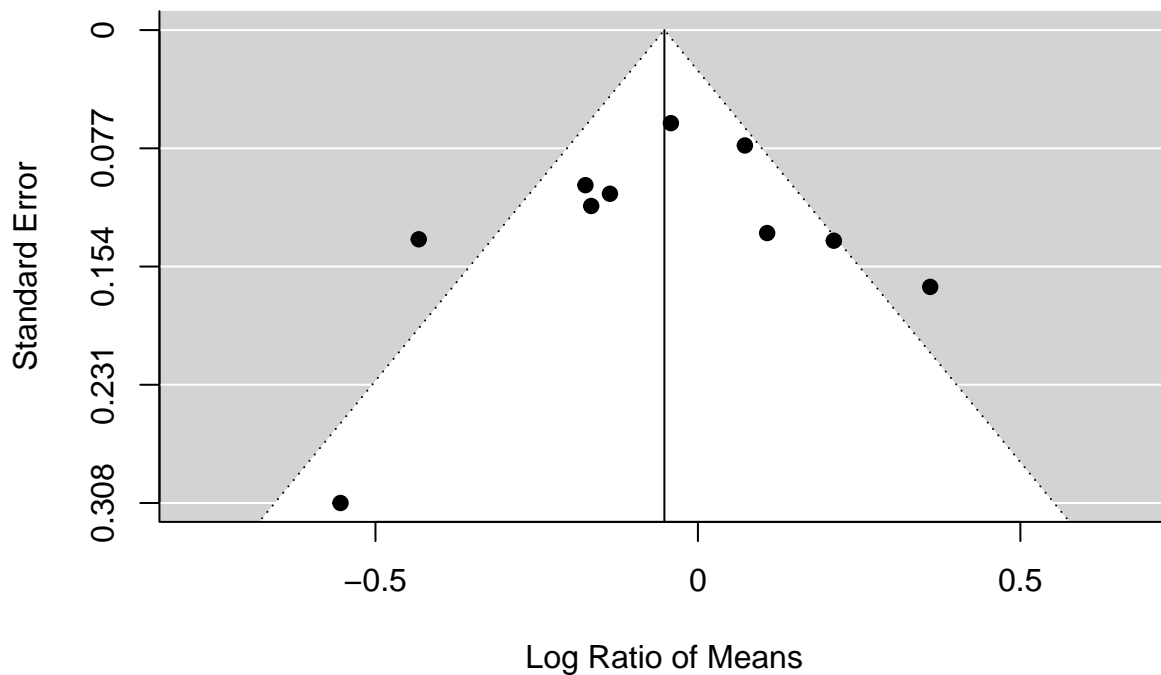
```
##
## Multivariate Meta-Analysis Model (k = 10; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -0.2459    0.4918    6.4918    7.0834    11.2918
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed  factor
## sigma^2.1  0.0161  0.1269    10    no    ES_ID
## sigma^2.2  0.0161  0.1269    10    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
## -0.0520  0.0696  -0.7471   0.4550  -0.1883   0.0844
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
k_exp <- Insulin_TT_lnRR_OF %>% group_by(Exposure_Type) %>% count()
k_exp
```

```
## # A tibble: 1 x 2
## # Groups:   Exposure_Type [1]
##   Exposure_Type      n
##   <fct>          <int>
## 1 One off          10
```

```
funnel(Insulin_overall_lnRR_TT_OF)
```



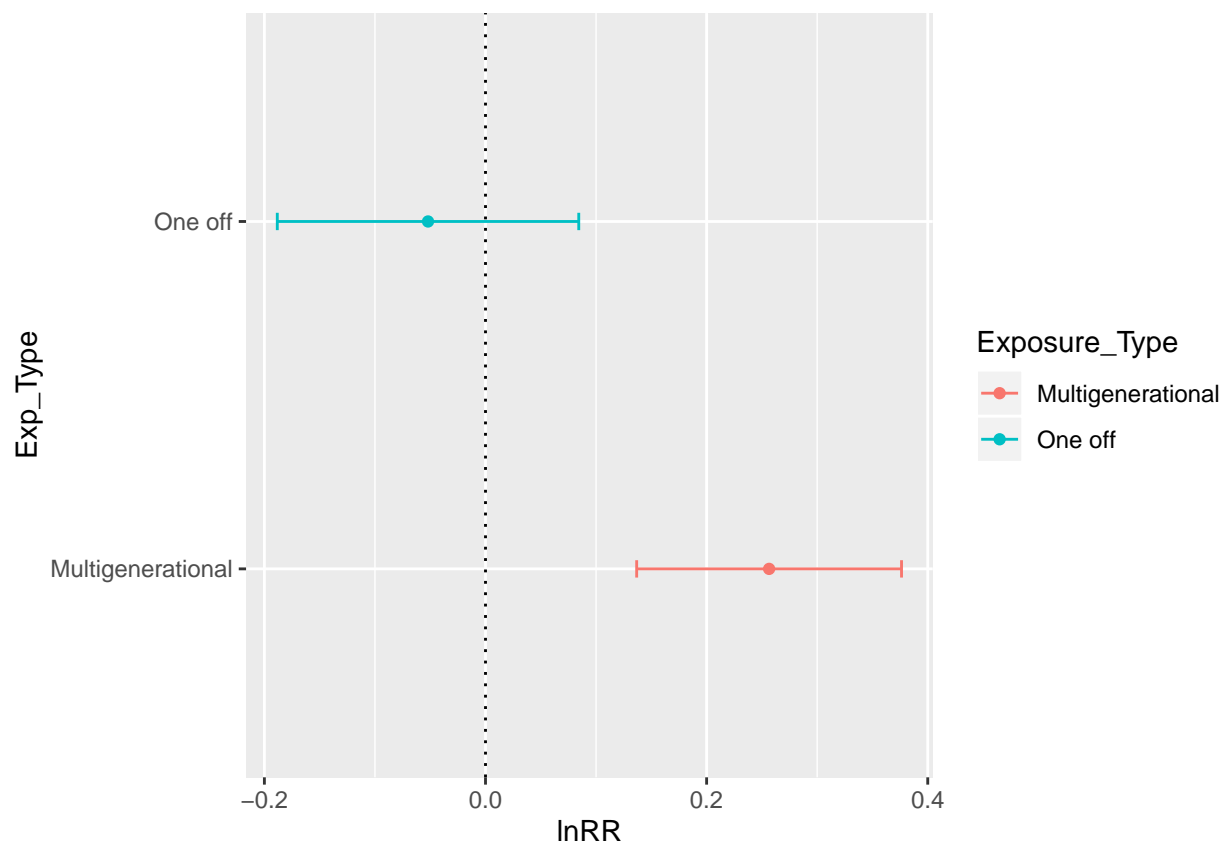
```
Insulin_TT_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnRR = c(Insulin_overall_lnRR_TT_MG$b[1], Insulin_overall_lnRR_TT_OF$b[1]),
  ci.lb = c(Insulin_overall_lnRR_TT_MG$ci.lb[1], Insulin_overall_lnRR_TT_OF$ci.lb[1]),
  ci.ub = c(Insulin_overall_lnRR_TT_MG$ci.ub[1],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

```
Insulin_TT_Exp_lnRR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnRR  ci.lb  ci.ub
##   <chr>          <dbl> <dbl> <dbl>
## 1 Multigenerational  0.257  0.137  0.376
## 2 One off          -0.0520 -0.188  0.0844
```

```
#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 = 0.05, 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_Insulin_TT_exp_type
```

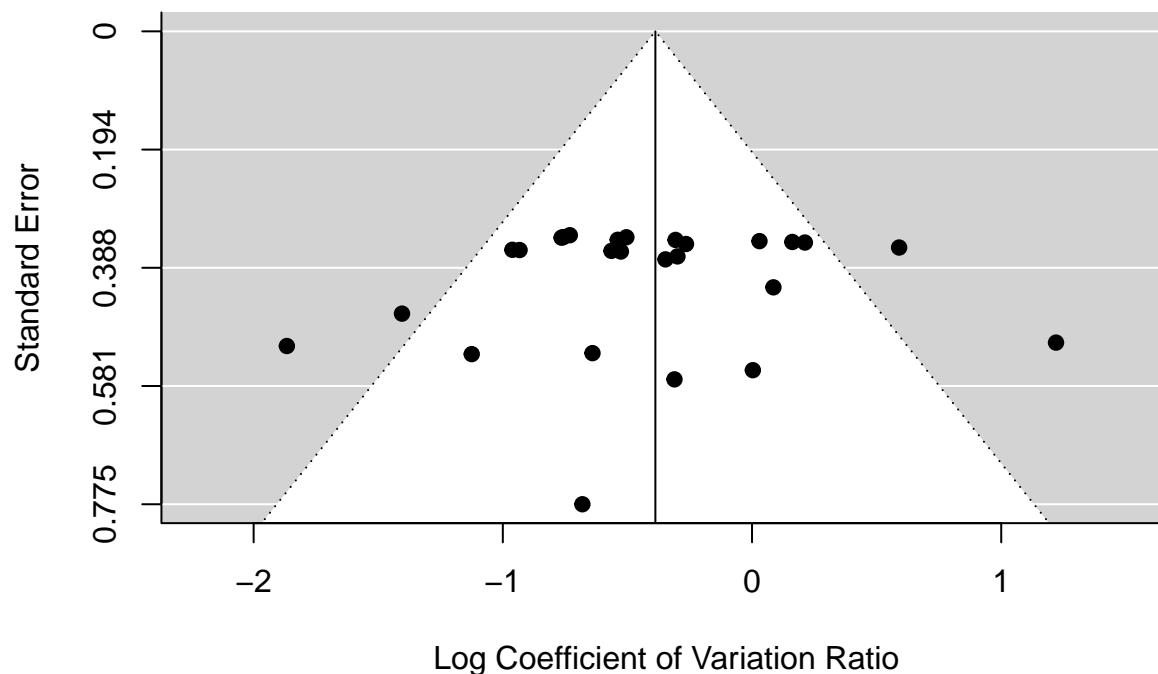


Fasting Insulin analysis (lnCVR)

```
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
```

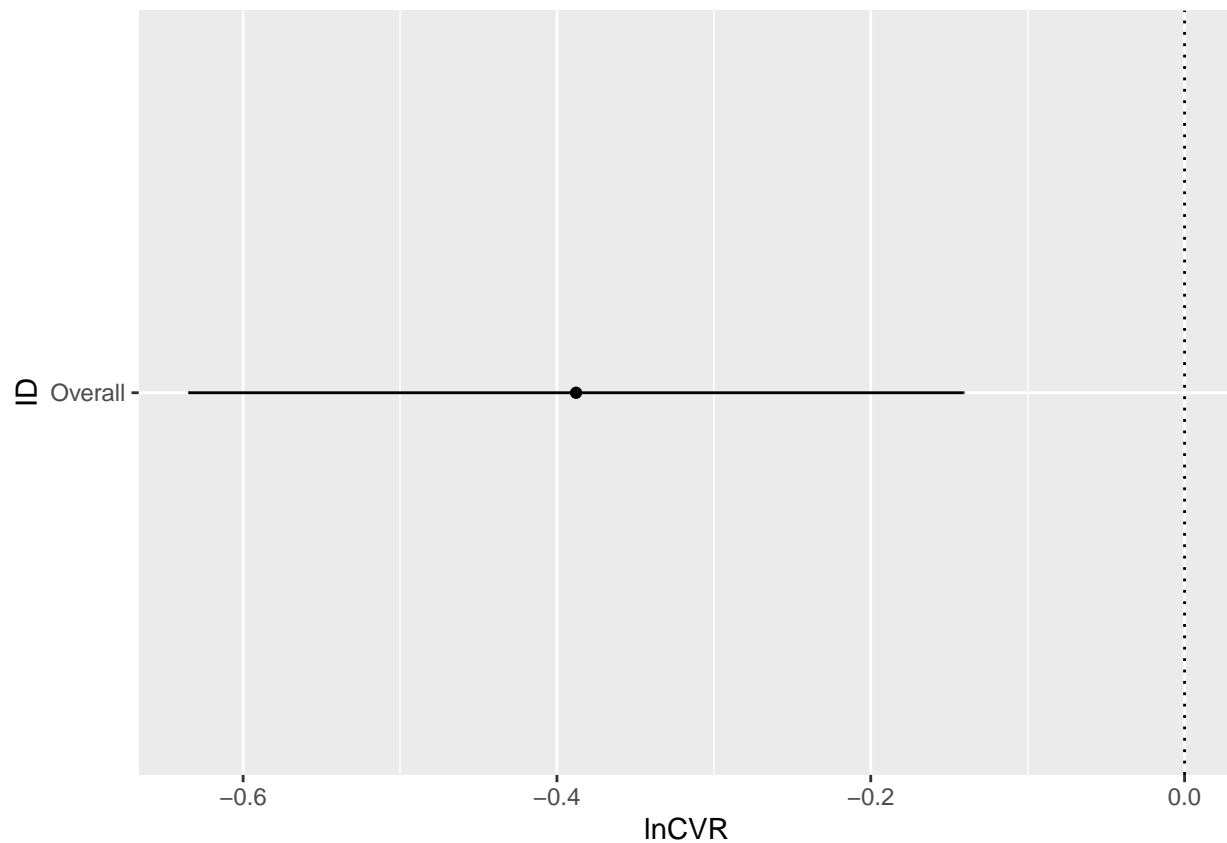
```
funnel(Insulin_lnCVR_FI)
```



#Tibble of overall results

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

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
```



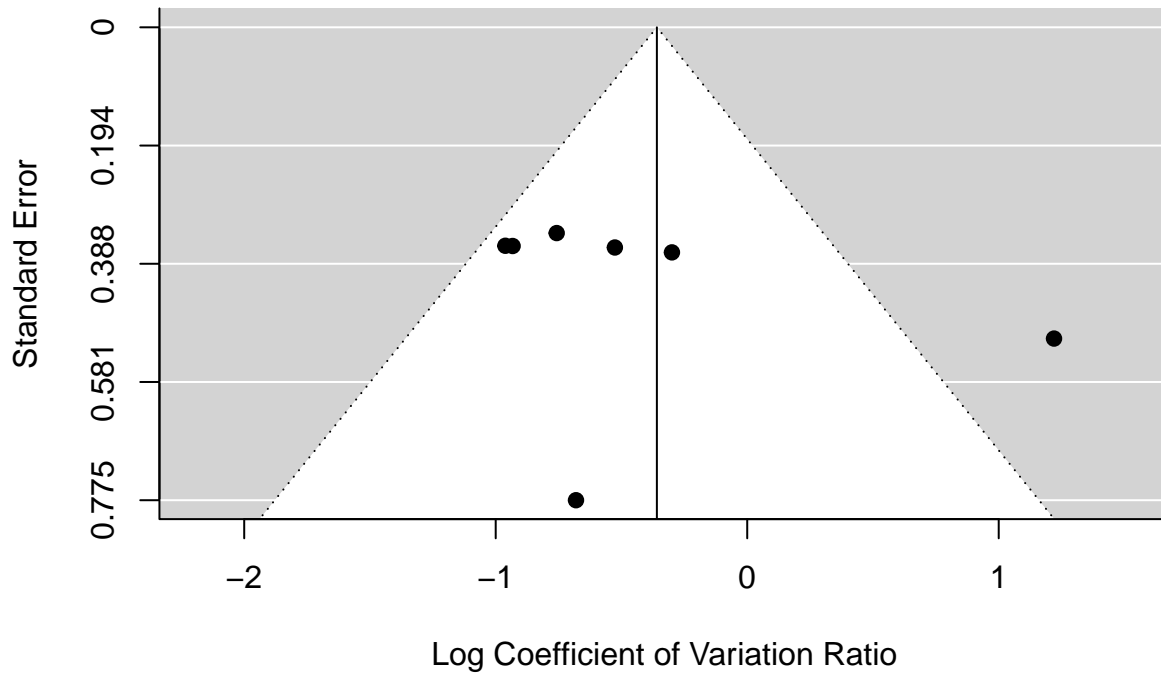
#Split by exposure type

```
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)
```



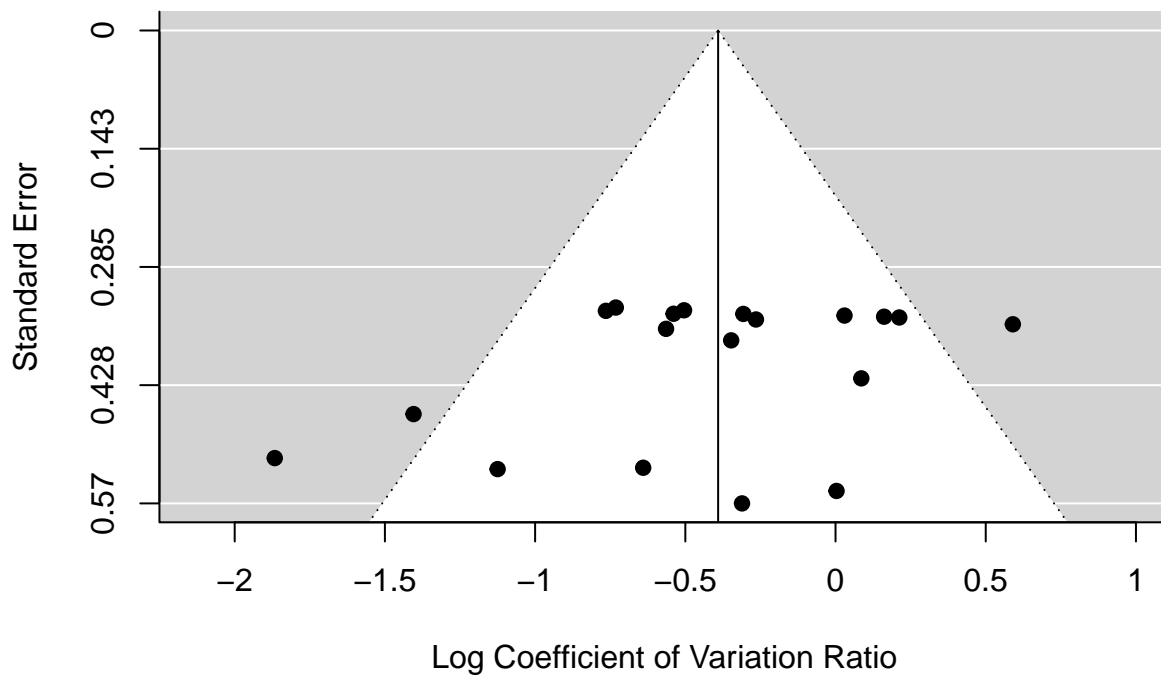
```
Insulin_overall_lnCVR_FI_OF <- rma.mv(yi, vi, random = list(~1|ES_ID,~1|Cohort_ID), data=Insulin_FI_lnCVR_FI_OF)
summary(Insulin_overall_lnCVR_FI_OF)
```

```
##
## 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)
```



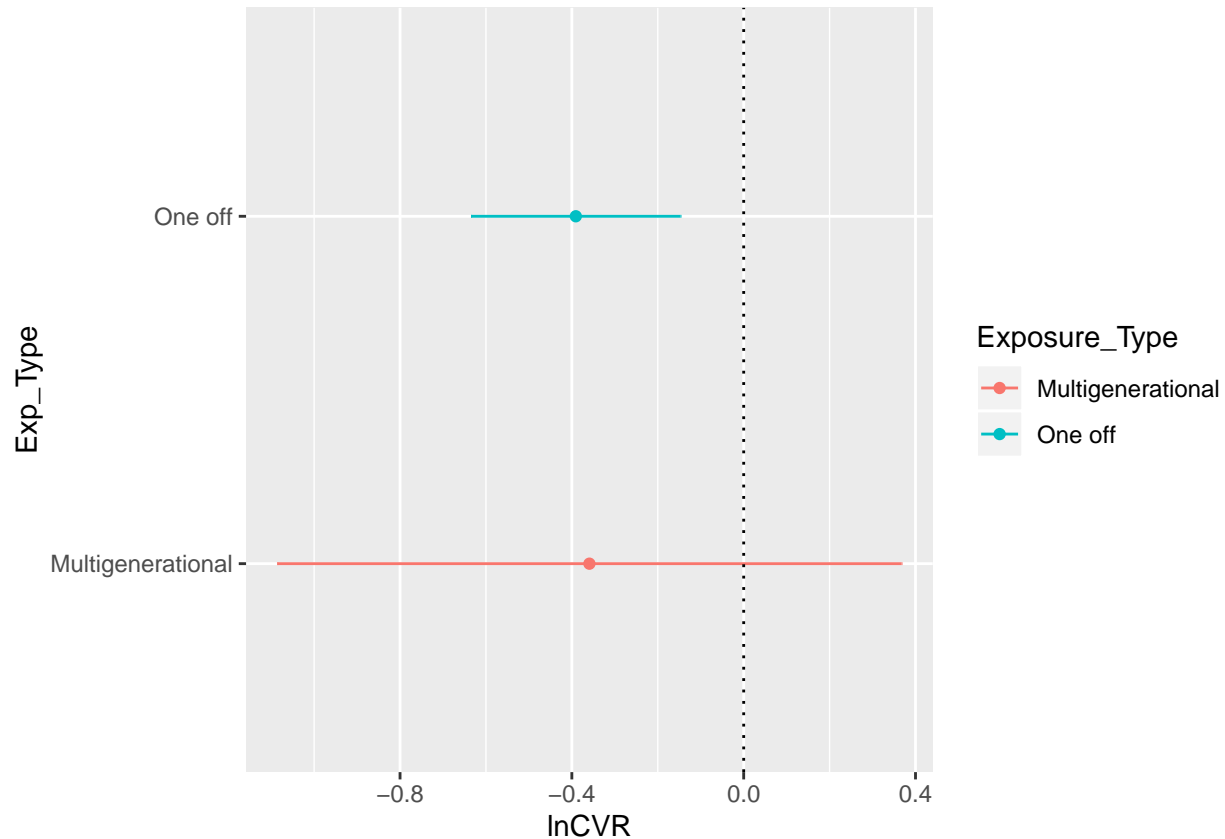
```
Insulin_FI_Exp_lnCVR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnCVR = c(Insulin_overall_lnCVR_FI_MG$b[1], Insulin_overall_lnCVR_FI_OF$b[1]),
  ci.lb = c(Insulin_overall_lnCVR_FI_MG$ci.lb[1], Insulin_overall_lnCVR_FI_OF$ci.lb[1]),
  ci.ub = c(Insulin_overall_lnCVR_FI_MG$ci.ub[1],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

```
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  0.367
## 2 One off          -0.391 -0.635 -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
```



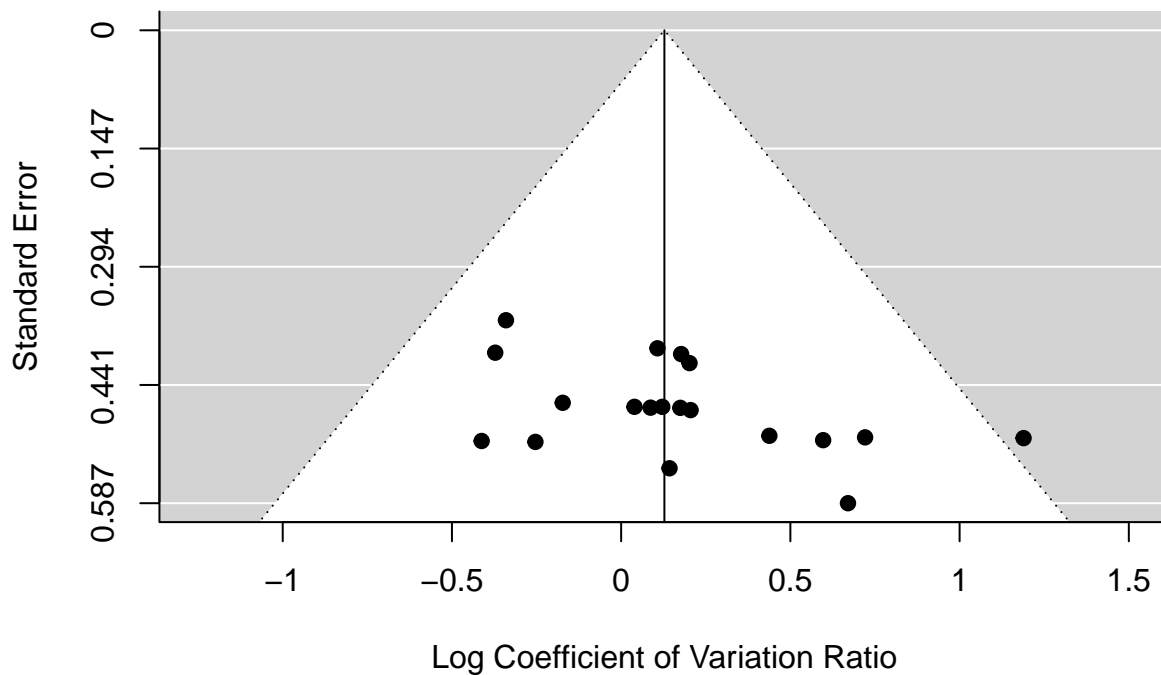
Insulin tolerance test analysis (lnCVR)

```
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    19     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
```

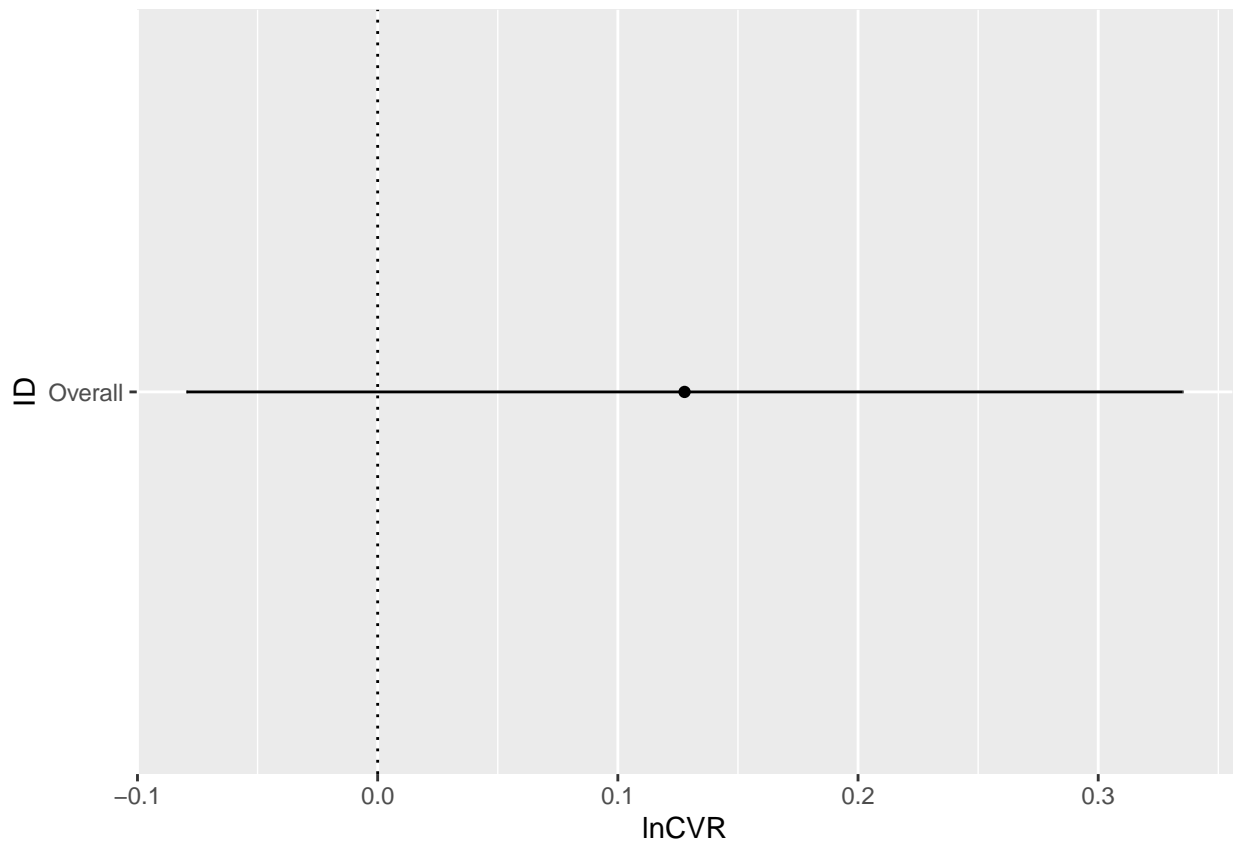
```
Insulin_overall_lnCVR_TT <- tibble(
  ID = "Overall",
  lnCVR = Insulin_lnCVR_TT$b[1],
  ci.lb = Insulin_lnCVR_TT$ci.lb[1],
```

```

    ci.ub = Insulin_lnCVR_TT$ci.ub[1]
  )

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_TT_MG)

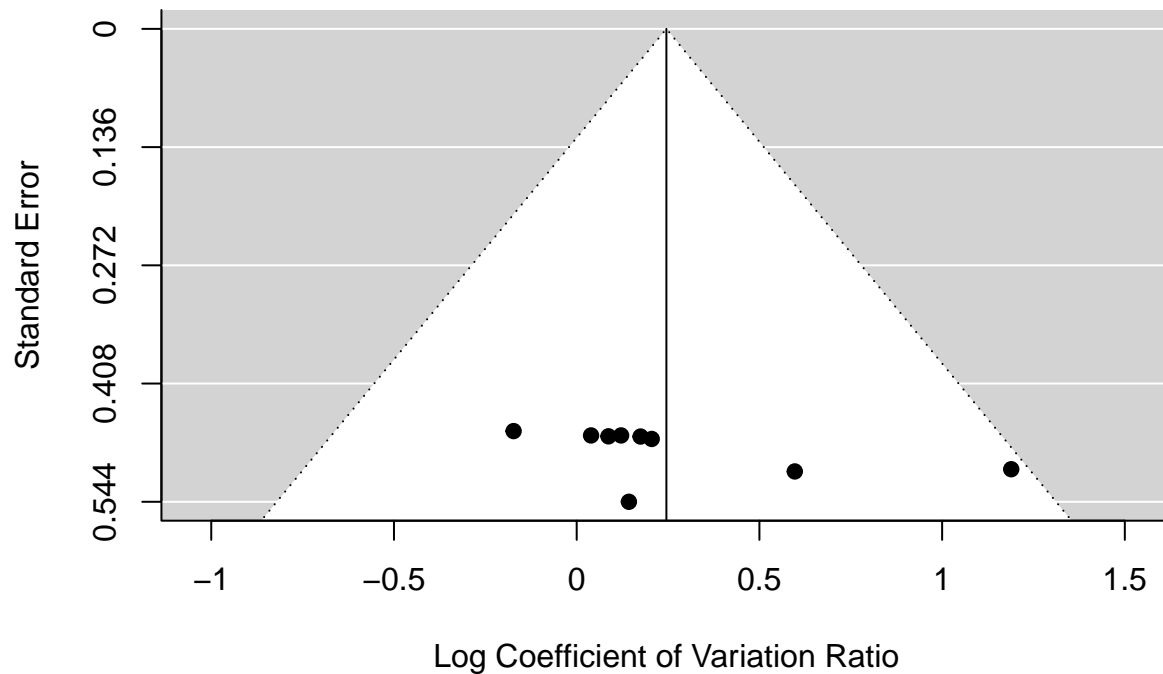
summary(Insulin_overall_lnCVR_TT_MG)

##
## Multivariate Meta-Analysis Model (k = 9; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -4.1615    8.3230   14.3230   14.5614   20.3230
##
## Variance Components:
##

```

```
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000      9     no       ES_ID
## sigma^2.2  0.0000  0.0000      9     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
##    0.2455    0.1611    1.5240    0.1275    -0.0702    0.5612
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Insulin_overall_lnCVR_TT_MG)
```

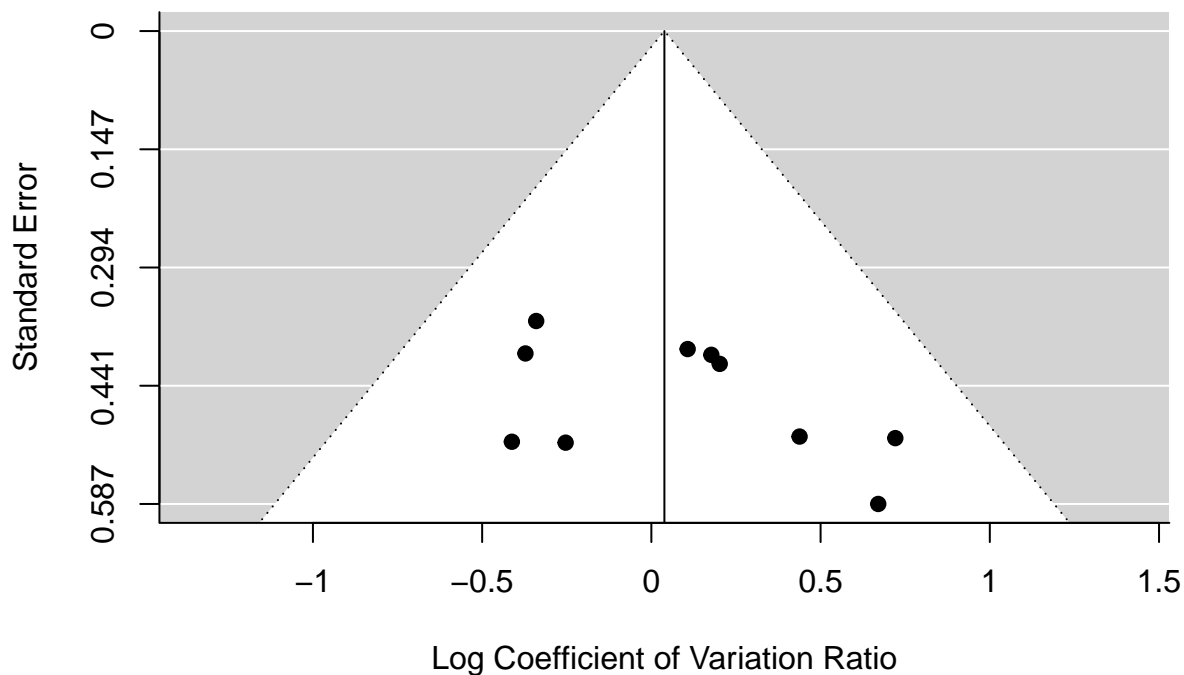


```
Insulin_overall_lnCVR_TT_OF <- rma.mv(yi, vi, random = list(~1|ES_ID, ~1|Cohort_ID), data=Insulin_TT_lnCVR_TT_MG)
summary(Insulin_overall_lnCVR_TT_OF)
```

```
##
## 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    10    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(Insulin_overall_lnCVR_TT_MG$b[1], Insulin_overall_lnCVR_TT_OF$b[1]),
  ci.lb = c(Insulin_overall_lnCVR_TT_MG$ci.lb[1], Insulin_overall_lnCVR_TT_OF$ci.lb[1]),
```

```
ci.ub = c(Insulin_overall_lnCVR_TT_MG$ci.ub[1], Insulin_overall_lnCVR_TT_OF$ci.ub[1])
)
```

```
Insulin_TT_Exp_lnCVR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnCVR   ci.lb ci.ub
##   <chr>          <dbl>   <dbl> <dbl>
## 1 Multigenerational 0.245  -0.0702 0.561
## 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 = 0.05, 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
```

