

Glucose_Analysis

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Meta-regression Glucose

```
load(file="Effect_Size_All_Traits.RData")
load(file="Effect_Size_All_Traits_lnCVR.RData")
#lnRR
Glucose_FBG_lnRR <- subset(Effect_Size_All_Traits, Effect_Size_All_Traits$Trait == "Glucose_FBG")
Glucose_TT_lnRR<- subset(Effect_Size_All_Traits, Effect_Size_All_Traits$Trait == "Glucose_TT")

Glucose_FBG_lnRR_MG <- subset(Glucose_FBG_lnRR, Glucose_FBG_lnRR$Exposure_Type == "Multigenerational")
Glucose_TT_lnRR_MG <- subset(Glucose_TT_lnRR, Glucose_TT_lnRR$Exposure_Type == "Multigenerational")

Glucose_FBG_lnRR_OF <- subset(Glucose_FBG_lnRR, Glucose_FBG_lnRR$Exposure_Type == "One off")
Glucose_TT_lnRR_OF <- subset(Glucose_TT_lnRR, Glucose_TT_lnRR$Exposure_Type == "One off")

#lnCVR
Glucose_FBG_lnCVR <- subset(Effect_Size_All_Traits_lnCVR, Effect_Size_All_Traits_lnCVR$Trait == "Glucose_FBG")
Glucose_TT_lnCVR<- subset(Effect_Size_All_Traits_lnCVR, Effect_Size_All_Traits_lnCVR$Trait == "Glucose_TT")

Glucose_FBG_lnCVR_MG <- subset(Glucose_FBG_lnCVR, Glucose_FBG_lnCVR$Exposure_Type == "Multigenerational")
Glucose_TT_lnCVR_MG <- subset(Glucose_TT_lnCVR, Glucose_TT_lnCVR$Exposure_Type == "Multigenerational")

Glucose_FBG_lnCVR_OF <- subset(Glucose_FBG_lnCVR, Glucose_FBG_lnCVR$Exposure_Type == "One off")
Glucose_TT_lnCVR_OF <- subset(Glucose_TT_lnCVR, Glucose_TT_lnCVR$Exposure_Type == "One off")
```

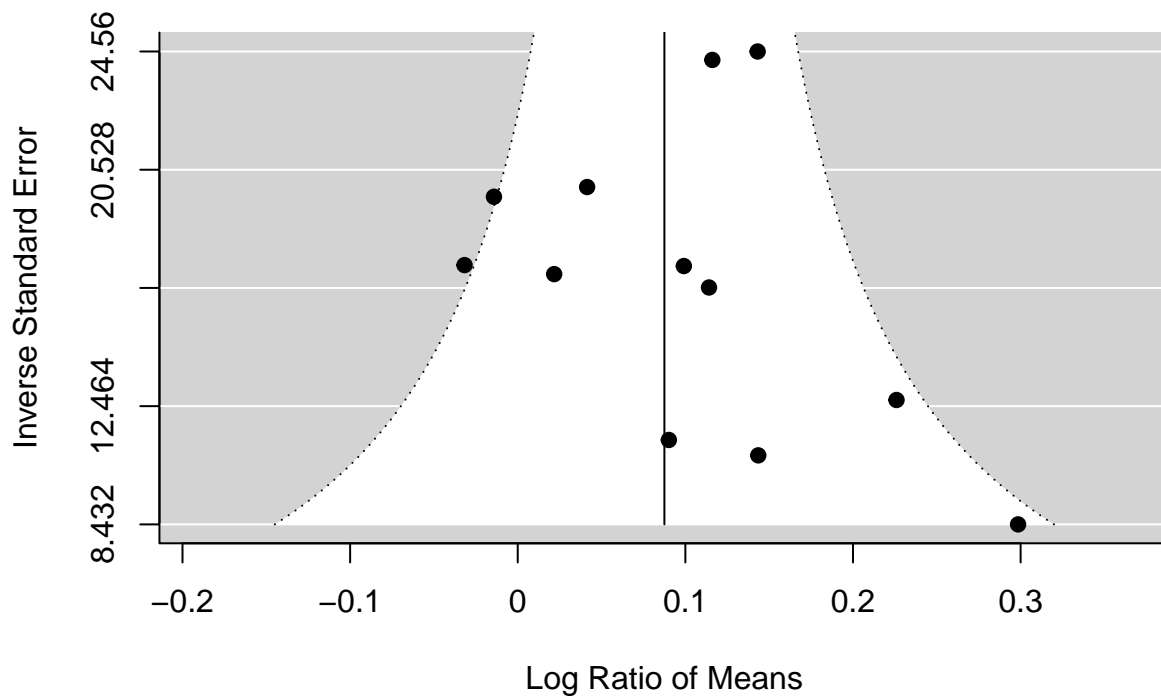
FBG Analysis (Overall and then split by exposure type)

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

```
##
## Multivariate Meta-Analysis Model (k = 12; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##  12.1477  -24.2955  -18.2955  -17.1018  -14.8669
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000     12    no      ES_ID
## sigma^2.2  0.0029  0.0537      9    no  Cohort_ID
##
```

```
## Test for Heterogeneity:
## Q(df = 11) = 19.4840, p-val = 0.0529
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.0875 0.0262 3.3447 0.0008 0.0362 0.1388 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Glucose_overall_lnRR_FBG,yaxis="seinv")
```



```
#Tibble of overall results
```

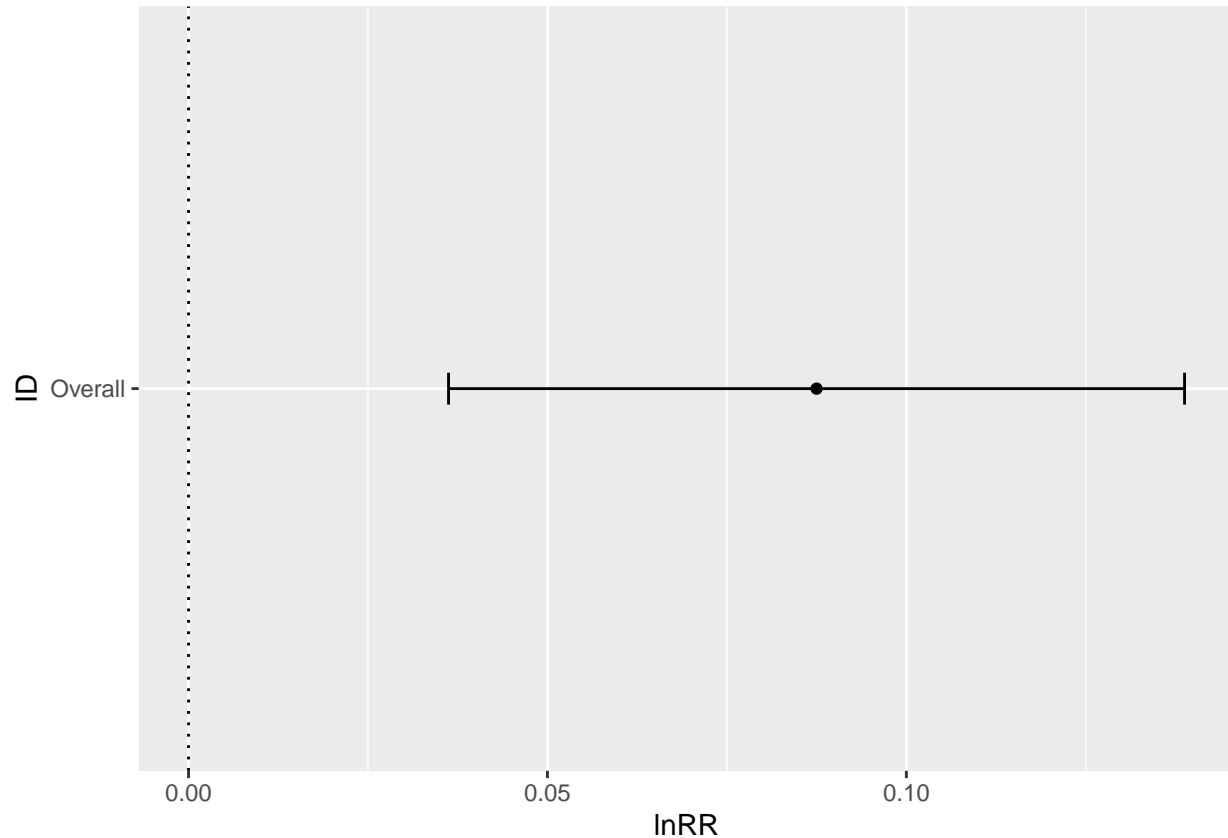
```
Glucose_overall_lnRR_FBG <- tibble(
  ID = "Overall",
  lnRR = Glucose_overall_lnRR_FBG$b[1],
  ci.lb = Glucose_overall_lnRR_FBG$ci.lb[1],
  ci.ub = Glucose_overall_lnRR_FBG$ci.ub[1]
)

plot_Glucose_overall_FBG <- ggplot(Glucose_overall_lnRR_FBG, aes(x=ID, y=lnRR)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0.05, 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_Glucose_overall_FBG

```



#Split by exposure type

```

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

```

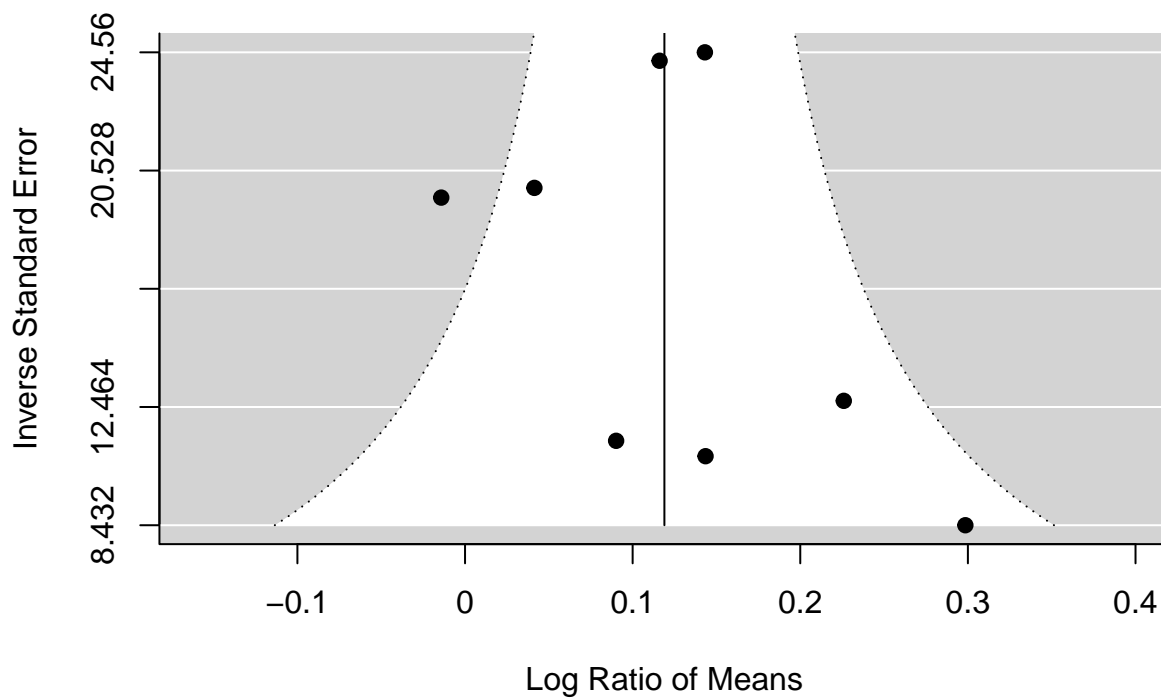
```

##
## Multivariate Meta-Analysis Model (k = 8; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   7.7052 -15.4104  -9.4104  -9.5727  -1.4104
##
## Variance Components:
##
##          estim  sqrt  nlvls  fixed  factor
## sigma^2.1  0.0000  0.0000    8    no    ES_ID
## sigma^2.2  0.0041  0.0641    5    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 7) = 13.2152, p-val = 0.0670

```

```
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.1189 0.0385 3.0854 0.0020 0.0434 0.1945 **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Glucose_overall_lnRR_FBG_MG,yaxis="seinv")
```

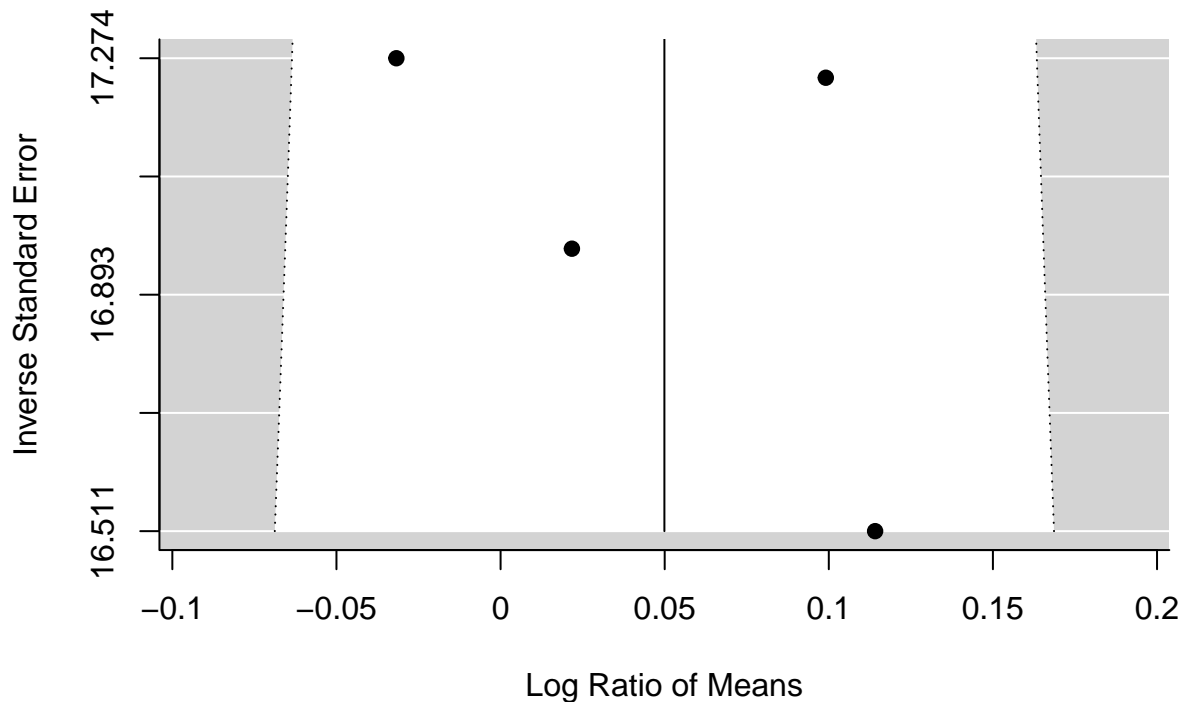


```
Glucose_overall_lnRR_FBG_OF <- rma.mv(yi, vi, random = list(~1|ES_ID,~1|Cohort_ID), data=Glucose_FBG_lnRR)
summary(Glucose_overall_lnRR_FBG_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 4; method: REML)
##
## logLik Deviance      AIC      BIC      AICc
## 3.7895 -7.5791 -1.5791 -4.2832 22.4209
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0006 0.0248     4     no      ES_ID
```

```
## sigma^2.2  0.0006  0.0248      4      no Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 3) = 4.0610, p-val = 0.2550
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb    ci.ub
##  0.0499  0.0343  1.4568  0.1452  -0.0172  0.1171
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Glucose_overall_lnRR_FBG_OF,yaxis="seinv")
```



```
k_exp <- Glucose_FBG_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         4
```

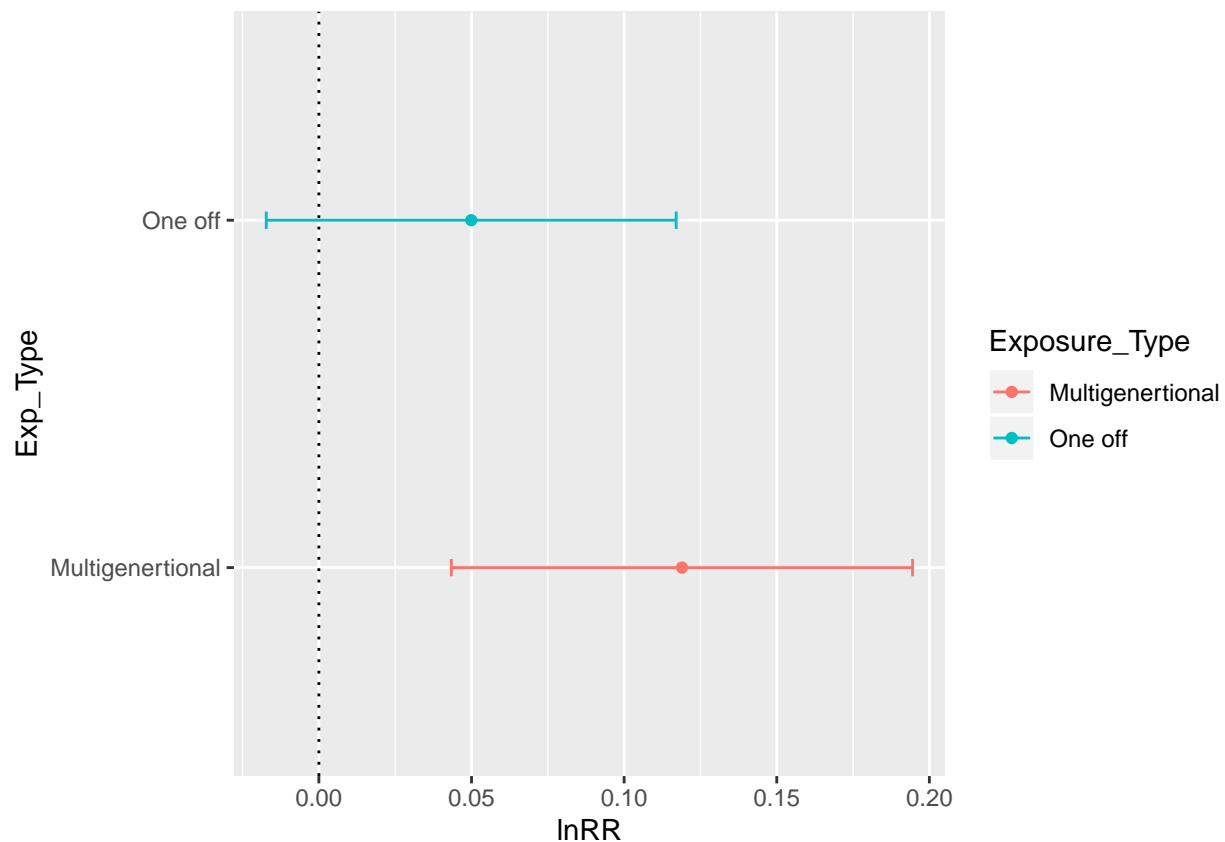
```
Glucose_FBG_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenertional", "One off"),
  lnRR = c(Glucose_overall_lnRR_FBG_MG$b[1], Glucose_overall_lnRR_FBG_OF$b[1]),
  ci.lb = c(Glucose_overall_lnRR_FBG_MG$ci.lb[1], Glucose_overall_lnRR_FBG_OF$ci.lb[1]),
  ci.ub = c(Glucose_overall_lnRR_FBG_MG$ci.ub[1], Glucose_overall_lnRR_FBG_OF$ci.ub[1])
)
```

```
Glucose_FBG_Exp_lnRR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnRR    ci.lb ci.ub
##   <chr>          <dbl>   <dbl> <dbl>
## 1 Multigenertional 0.119    0.0434 0.194
## 2 One off         0.0499 -0.0172 0.117
```

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

```
plot_Glucose_FBG_exp_type <- ggplot(Glucose_FBG_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_Glucose_FBG_exp_type
```

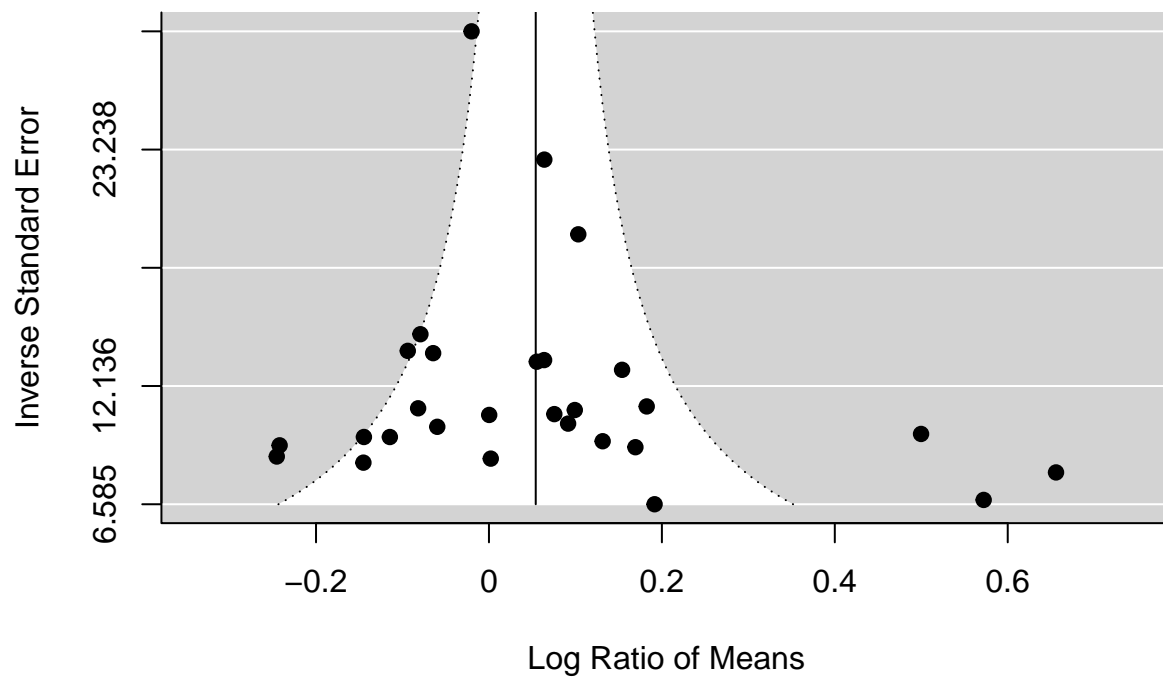


Tolerance test analysis (Overall and then split by exposure type)

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

```
##
## Multivariate Meta-Analysis Model (k = 28; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   4.7126   -9.4253   -3.4253    0.4623   -2.3818
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000    28     no      ES_ID
## sigma^2.2  0.0300  0.1731    27     no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 27) = 105.0308, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##   0.0541  0.0378  1.4301  0.1527  -0.0200  0.1283
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

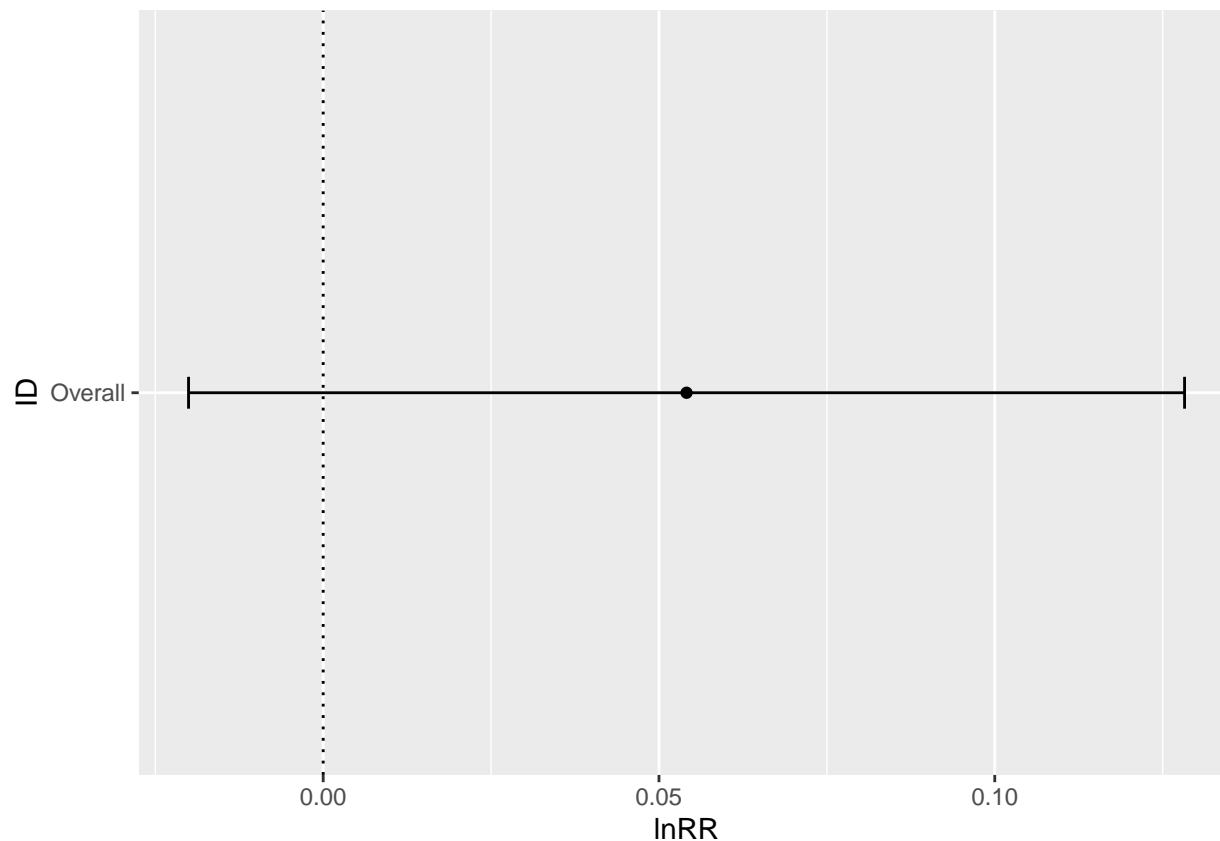
```
funnel(Glucose_overall_lnRR_TT,yaxis="seinv")
```



#Tibble of overall results

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

plot_Glucose_overall_TT <- ggplot(Glucose_overall_lnRR_TT, aes(x=ID, y=lnRR)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0.05, 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_Glucose_overall_TT
```

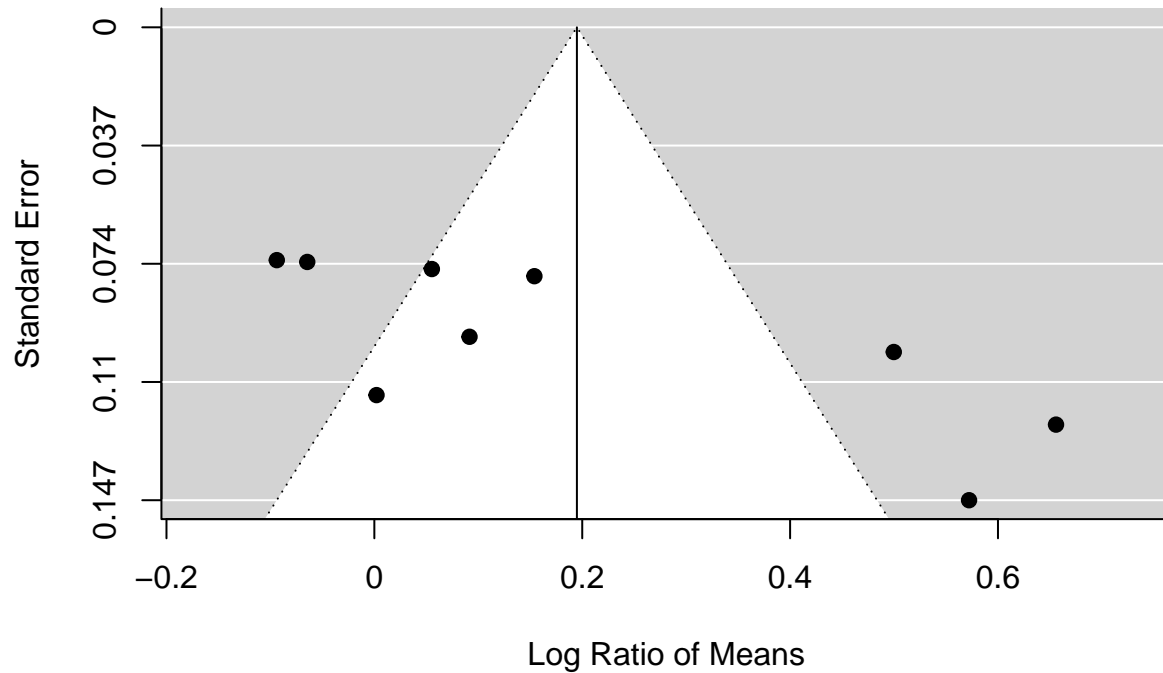
#Split by exposure type

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

```
##
## Multivariate Meta-Analysis Model (k = 9; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -1.2829    2.5658    8.5658    8.8041    14.5658
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0341  0.1846     9    no     ES_ID
## sigma^2.2  0.0341  0.1846     9    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 8) = 59.3958, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval   ci.lb   ci.ub
##   0.1949  0.0931  2.0929  0.0364  0.0124  0.3774 *
```

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

```
funnel(Glucose_overall_lnRR_TT_MG)
```



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

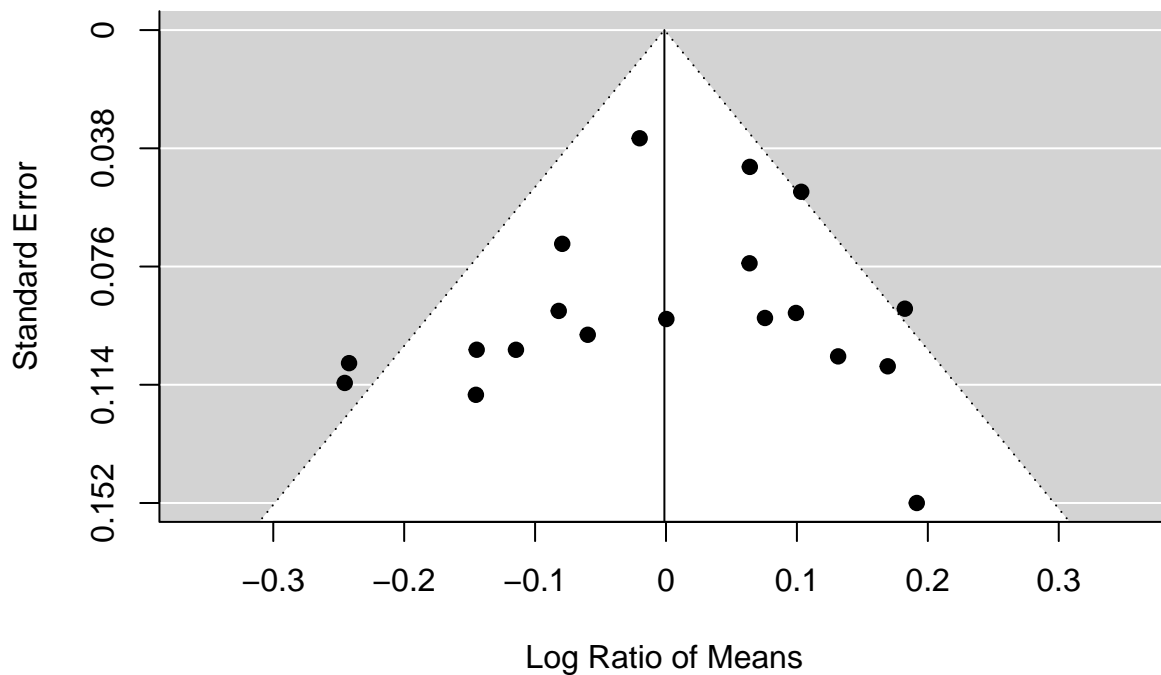
```
##
## Multivariate Meta-Analysis Model (k = 19; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## 11.8580 -23.7160 -17.7160 -15.0448 -16.0017
##
## Variance Components:
##
##          estim  sqrt  nlvls  fixed  factor
## sigma^2.1  0.0000  0.0000   19    no    ES_ID
## sigma^2.2  0.0064  0.0801   18    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 18) = 35.5344, p-val = 0.0081
##
## Model Results:
```

```
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.0012  0.0276  -0.0446  0.9645  -0.0552  0.0528
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
k_exp <- Glucose_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          19
```

```
funnel(Glucose_overall_lnRR_TT_OF)
```



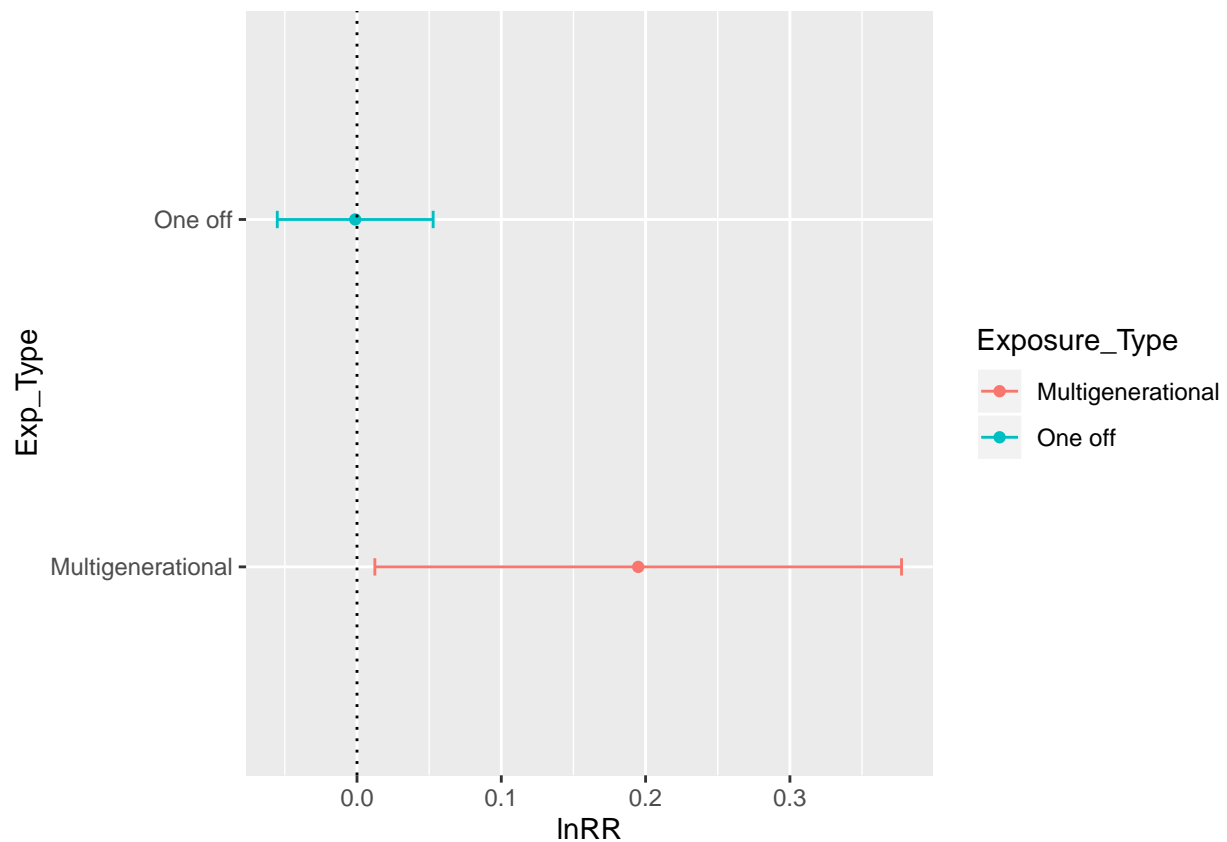
```
Glucose_TT_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnRR = c(Glucose_overall_lnRR_TT_MG$b[1], Glucose_overall_lnRR_TT_OF$b[1]),
  ci.lb = c(Glucose_overall_lnRR_TT_MG$ci.lb[1], Glucose_overall_lnRR_TT_OF$ci.lb[1]),
  ci.ub = c(Glucose_overall_lnRR_TT_MG$ci.ub[1],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

```
Glucose_TT_Exp_lnRR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnRR    ci.lb    ci.ub
##   <chr>          <dbl>    <dbl>    <dbl>
## 1 Multigenerational  0.195    0.0124  0.377
## 2 One off          -0.00123 -0.0552  0.0528
```

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

```
plot_Glucose_TT_exp_type <- ggplot(Glucose_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_Glucose_TT_exp_type
```

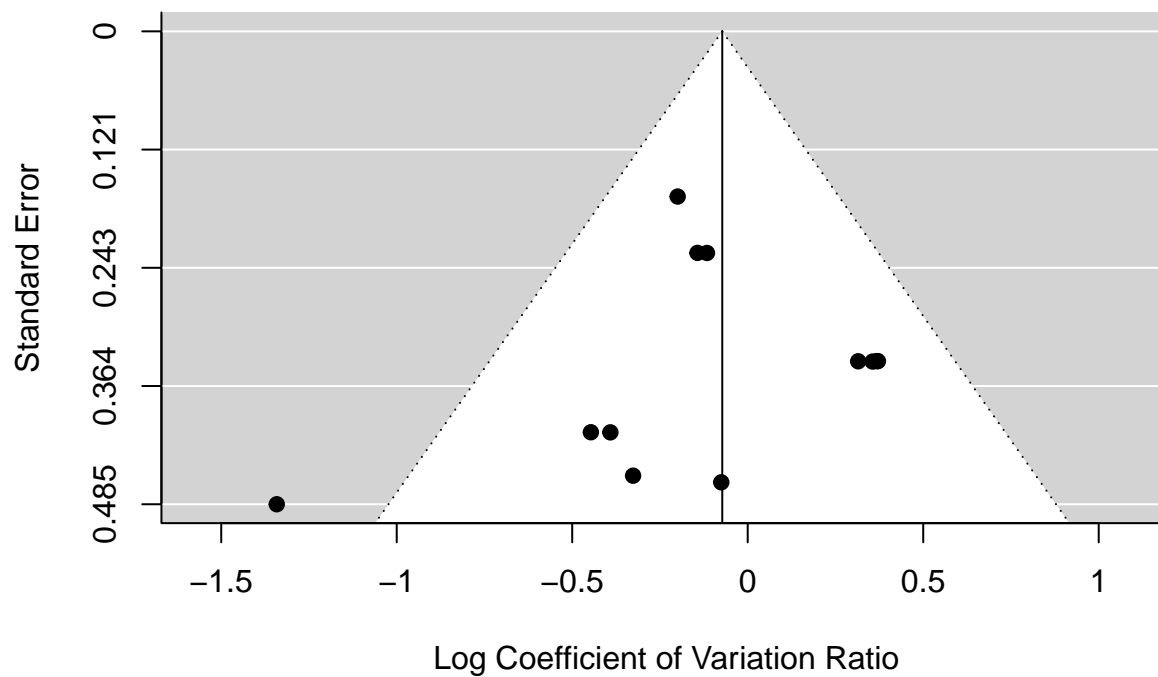


FBG Analysis (lnCVR)

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

```
##
## Multivariate Meta-Analysis Model (k = 12; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -5.8607    11.7215    17.7215    18.9152    21.1501
##
## Variance Components:
##
##              estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000     12     no      ES_ID
## sigma^2.2  0.0401  0.2003      9     no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 11) = 15.5523, p-val = 0.1586
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.0725  0.1162  -0.6243  0.5324  -0.3003  0.1552
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

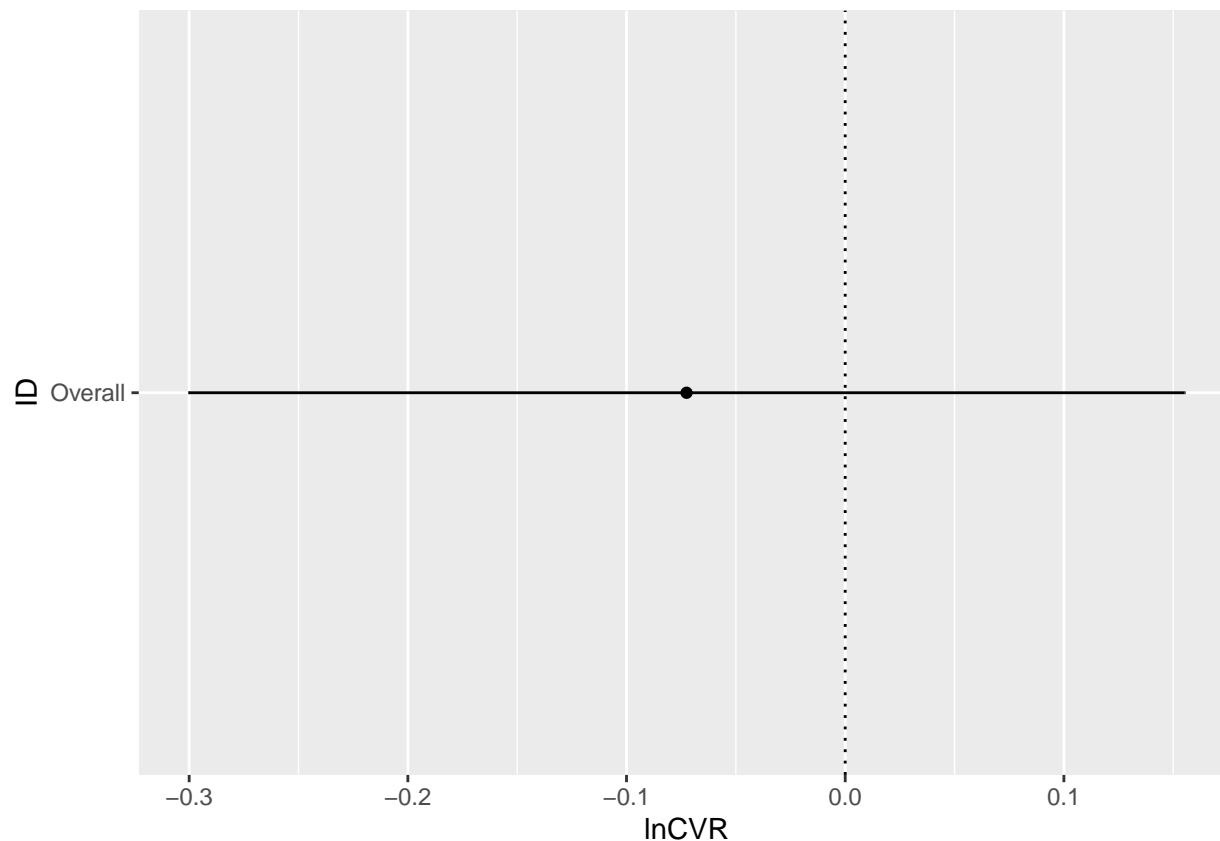
```
funnel(Glucose_overall_lnCVR_FBG)
```



#Tibble of overall results

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

plot_Glucose_overall_FBG_lnCVR <- ggplot(Glucose_overall_lnCVR_FBG, 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_Glucose_overall_FBG_lnCVR
```



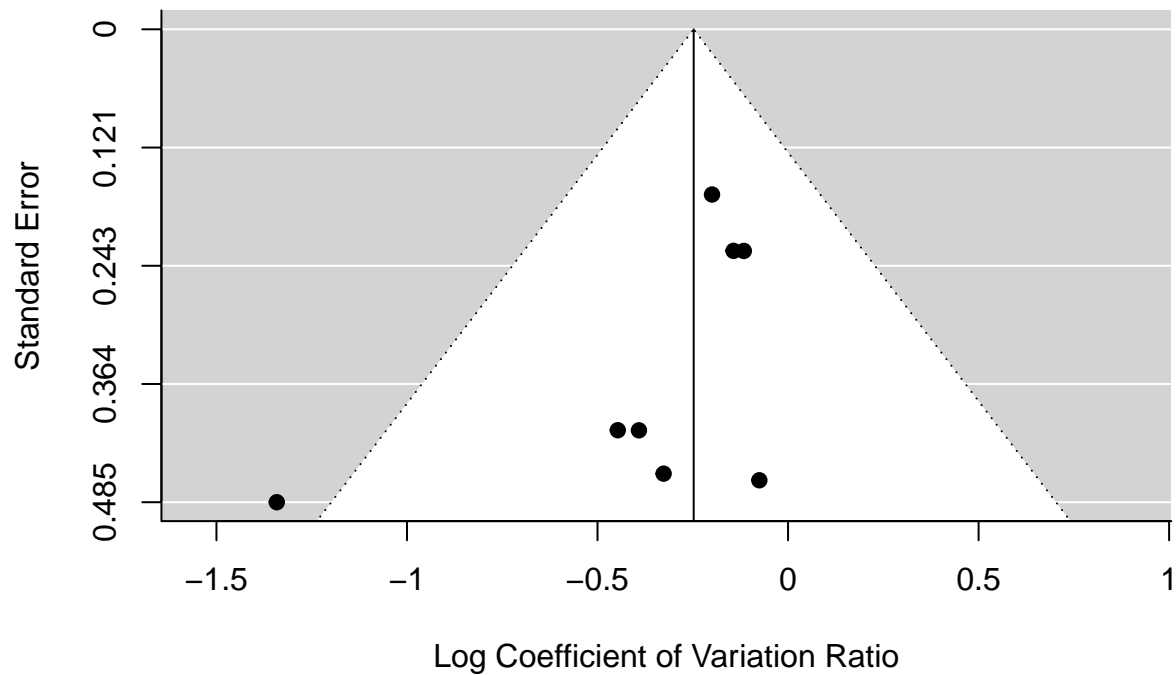
#Split by exposure type

```
Glucose_overall_lnCVR_FBG_MG <- rma.mv(yi, vi, random = list(~1|ES_ID,~1|Cohort_ID), data=Glucose_FBG_1
summary(Glucose_overall_lnCVR_FBG_MG)
```

```
##
## Multivariate Meta-Analysis Model (k = 8; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -2.0156    4.0313   10.0313    9.8690   18.0313
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0000  0.0000     8    no     ES_ID
## sigma^2.2  0.0000  0.0000     5    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 7) = 6.2373, p-val = 0.5123
##
## Model Results:
##
## estimate      se      zval    pval    ci.lb    ci.ub
## -0.2477  0.1005  -2.4652  0.0137  -0.4446  -0.0508 *
```

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

```
funnel(Glucose_overall_lnCVR_FBG_MG)
```



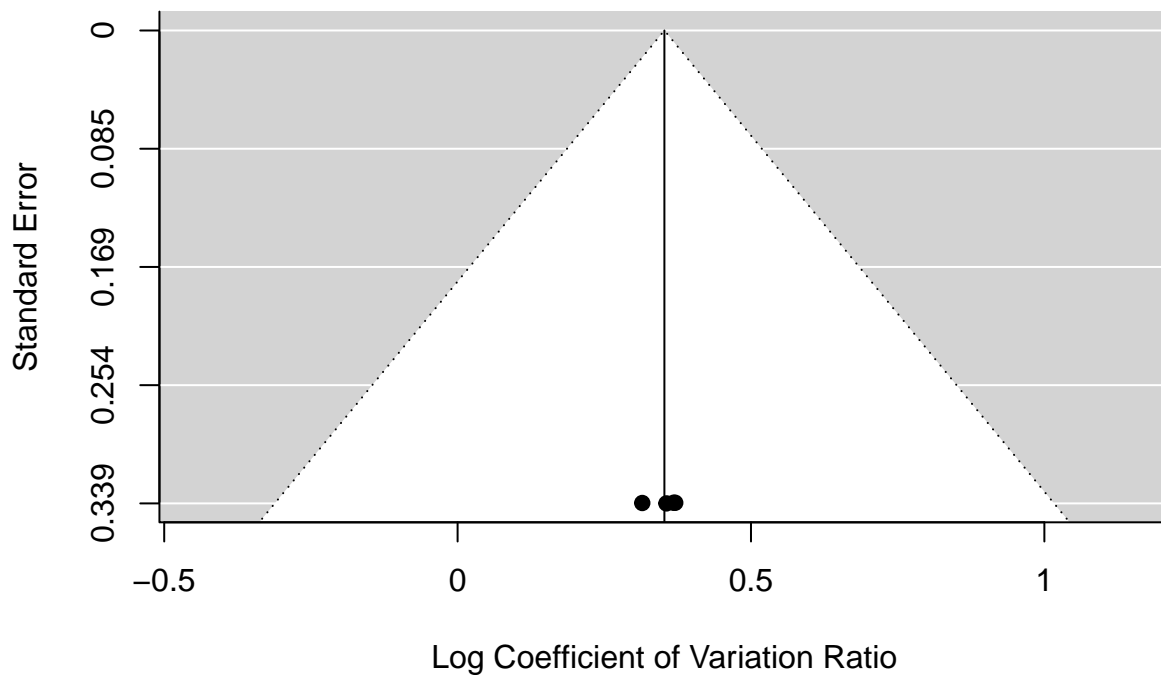
```
Glucose_overall_lnCVR_FBG_OF <- rma.mv(yi, vi, random = list(~1|ES_ID,~1|Cohort_ID), data=Glucose_FBG_l
summary(Glucose_overall_lnCVR_FBG_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 4; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   0.4841  -0.9683    5.0317    2.3276    29.0317
##
## Variance Components:
##
##          estim  sqrt  nlvls  fixed  factor
## sigma^2.1  0.0000  0.0000    4    no    ES_ID
## sigma^2.2  0.0000  0.0000    4    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 3) = 0.0177, p-val = 0.9994
##
## Model Results:
```



```
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.3524 0.1692 2.0825 0.0373 0.0207 0.6842 *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Glucose_overall_lnCVR_FBG_OF)
```



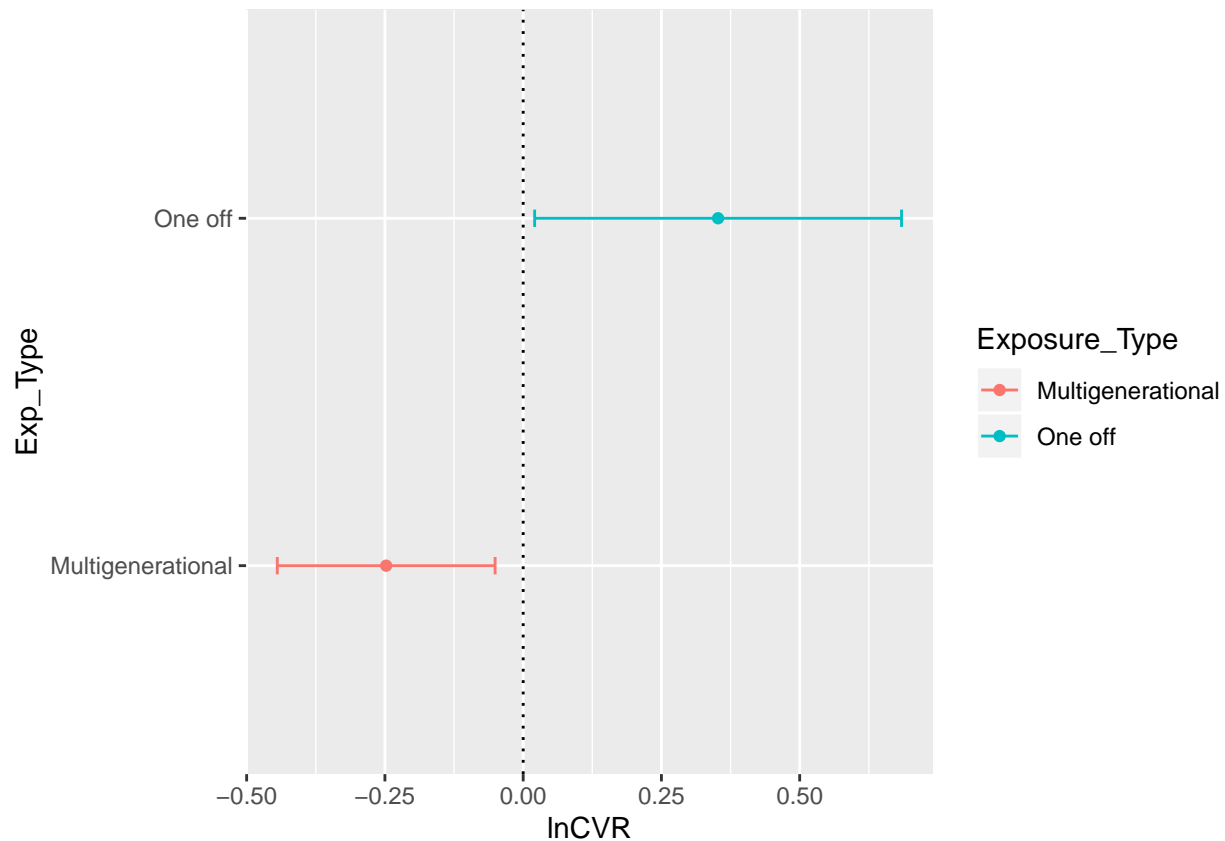
```
Glucose_FBG_Exp_lnCVR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnCVR = c(Glucose_overall_lnCVR_FBG_MG$b[1], Glucose_overall_lnCVR_FBG_OF$b[1]),
  ci.lb = c(Glucose_overall_lnCVR_FBG_MG$ci.lb[1], Glucose_overall_lnCVR_FBG_OF$ci.lb[1]),
  ci.ub = c(Glucose_overall_lnCVR_FBG_MG$ci.ub[1],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

```
Glucose_FBG_Exp_lnCVR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnCVR    ci.lb    ci.ub
##   <chr>          <dbl>    <dbl>    <dbl>
## 1 Multigenerational -0.248 -0.445 -0.0508
## 2 One off           0.352  0.0207  0.684
```

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

```
plot_Glucose_FBG_exp_type_lnCVR <- ggplot(Glucose_FBG_Exp_lnCVR, aes(x=Exposure_Type, y=lnCVR, colour =  
  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_Glucose_FBG_exp_type_lnCVR
```



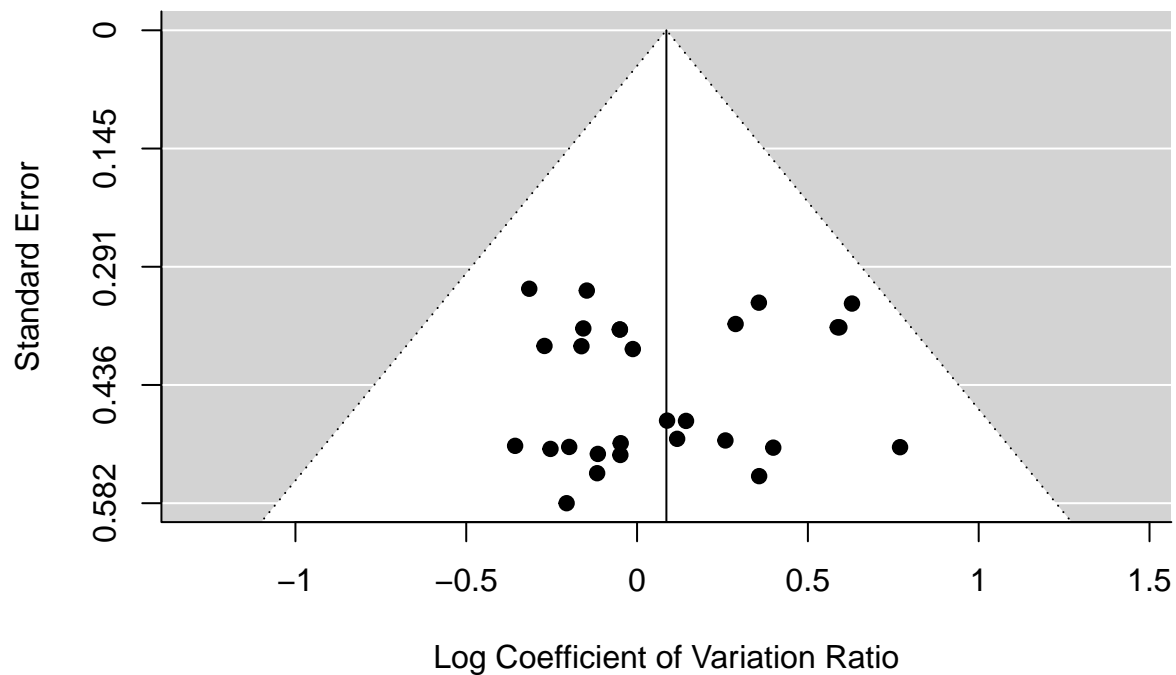
Tolerance test analysis (lnCVR)

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

```
##  
## Multivariate Meta-Analysis Model (k = 28; method: REML)  
##  
##   logLik  Deviance      AIC      BIC      AICc  
## -10.5642  21.1283  27.1283  31.0158  28.1718  
##
```

```
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000    28    no      ES_ID
## sigma^2.2  0.0000  0.0000    27    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 27) = 16.2263, p-val = 0.9485
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    0.0859  0.0795  1.0805  0.2799  -0.0699  0.2416
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Glucose_overall_lnCVR_TT)
```



```
#Tibble of overall results
```

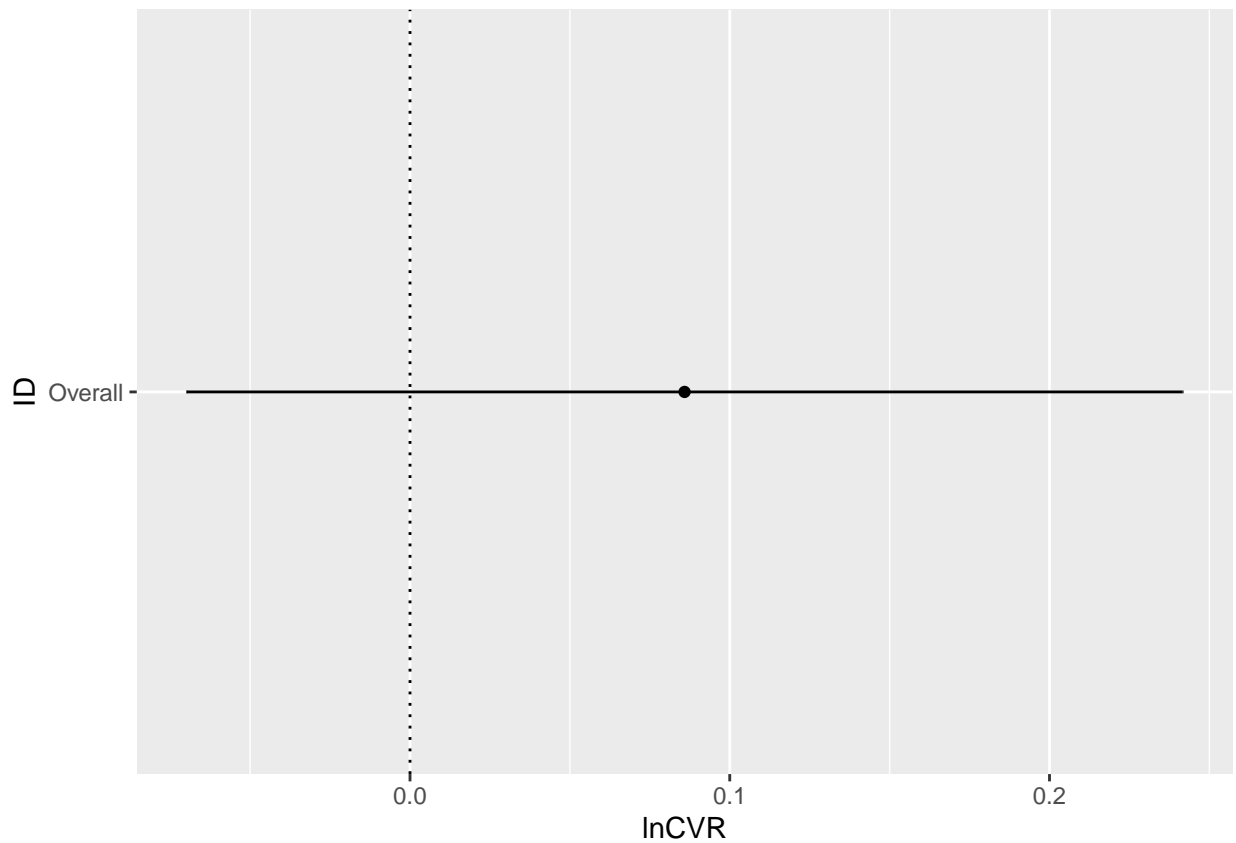
```
Glucose_overall_lnCVR_TT <- tibble(
  ID = "Overall",
  lnCVR = Glucose_overall_lnCVR_TT$b[1],
  ci.lb = Glucose_overall_lnCVR_TT$ci.lb[1] ,
```

```

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

plot_Glucose_overall_TT_lnCVR <- ggplot(Glucose_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_Glucose_overall_TT_lnCVR

```



```

#Split by exposure type

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

summary(Glucose_overall_lnCVR_TT_MG)

```

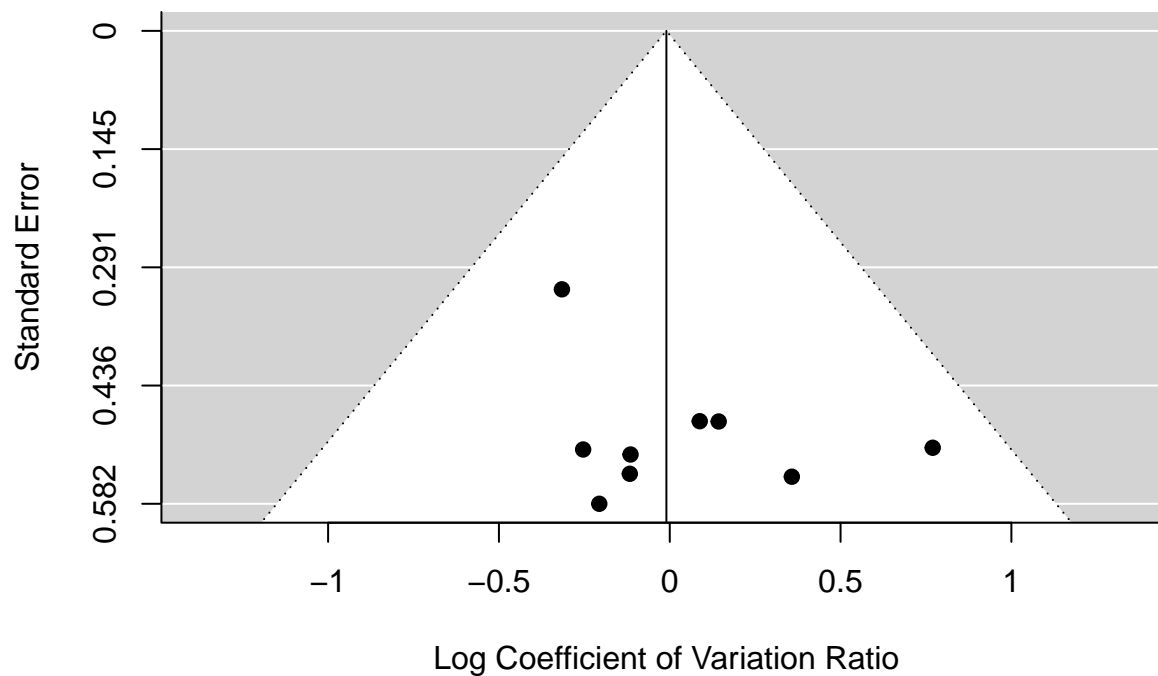
```

##
## Multivariate Meta-Analysis Model (k = 9; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   -3.8680    7.7360   13.7360   13.9744   19.7360
##
## 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) = 4.2413, p-val = 0.8347
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.0098  0.1592  -0.0615   0.9509   -0.3219   0.3023
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Glucose_overall_lnCVR_TT_MG)
```

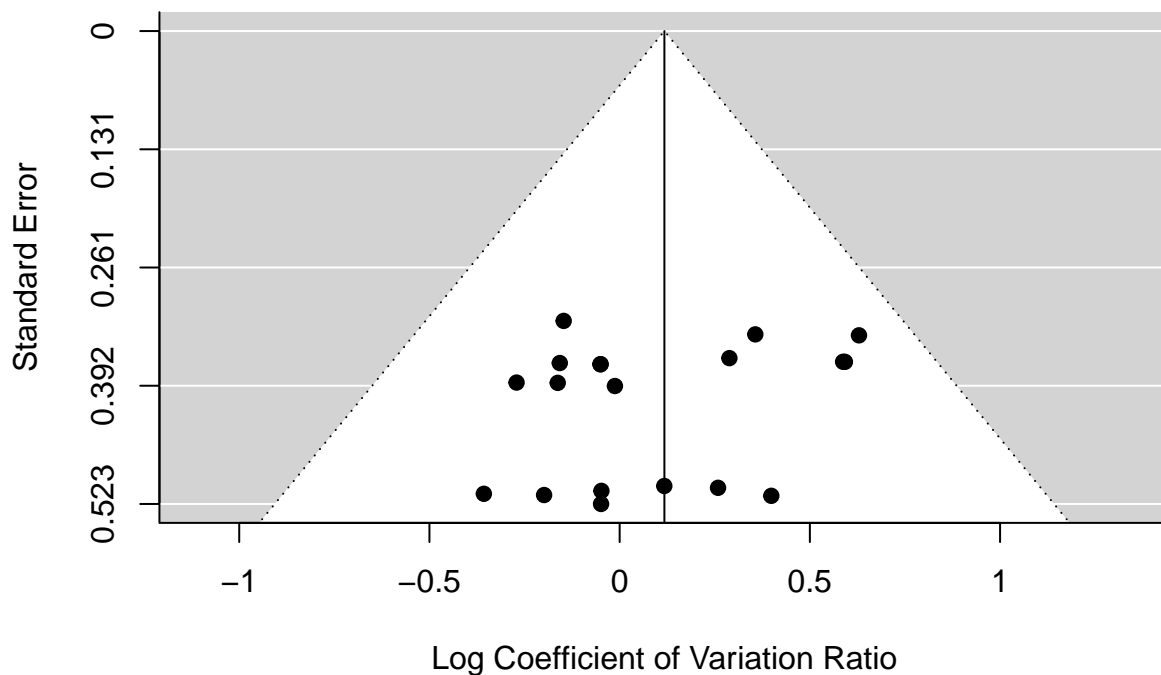


```
Glucose_overall_lnCVR_TT_OF <- rma.mv(yi, vi, random = list(~1|ES_ID, ~1|Cohort_ID), data=Glucose_TT_lnCVR_TT_MG)
summary(Glucose_overall_lnCVR_TT_OF)
```

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

```
## -6.3263 12.6526 18.6526 21.3237 20.3669
##
## 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    18    no  Cohort_ID
##
## Test for Heterogeneity:
## Q(df = 18) = 11.5042, p-val = 0.8717
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.1176  0.0917  1.2824  0.1997  -0.0621  0.2973
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Glucose_overall_lnCVR_TT_OF)
```



```
Glucose_TT_Exp_lnCVR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnCVR = c(Glucose_overall_lnCVR_TT_MG$b[1], Glucose_overall_lnCVR_TT_OF$b[1]),
  ci.lb = c(Glucose_overall_lnCVR_TT_MG$ci.lb[1], Glucose_overall_lnCVR_TT_OF$ci.lb[1]),
```

```
ci.ub = c(Glucose_overall_lnCVR_TT_MG$ci.ub[1],Glucose_overall_lnCVR_TT_OF$ci.ub[1])
)
```

```
Glucose_TT_Exp_lnCVR
```

```
## # A tibble: 2 x 4
##   Exposure_Type      lnCVR   ci.lb ci.ub
##   <chr>          <dbl>   <dbl> <dbl>
## 1 Multigenerational -0.00980 -0.322  0.302
## 2 One off          0.118   -0.0621 0.297
```

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

```
plot_Glucose_TT_exp_type_lnCVR <- ggplot(Glucose_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_Glucose_TT_exp_type_lnCVR
```

