DMR_583Reg_2_19_2019

Guannan Shen

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Contents

```
## set up workspace
rm(list = ls())
library(data.table)
library(knitr)
library(tidyverse)
library(magrittr)
library(stats)
library(DMRcate)
library(IlluminaHumanMethylation450kanno.ilmn12.hg19)
library(tibble)
library(grid)  # low-level grid functions are required
options(stringsAsFactors = F)
options(dplyr.width = Inf)
getwd()
```

```
## [1] "/home/guanshim/Documents/gitlab/ECCHO_github/DataProcessed/for_obesity"
```

```
## not in function
"%nin%" <- Negate("%in%")

# ######## clean memory ###################### rm(list =
# ls()) gc() ls() slotNames(x) getSlots(x)
```

0.1 DMR analysis

formula_log2 <- ~as.numeric(log2pfoa) + Race

formula_ln <- ~as.numeric(lnpfoa) + Race

Race is binary. It turns out, log2 pfoa and ln (natural log) pfoa have the same results.

```
## need
c("clindat_f", "clindat_m", "which has log2pfoa, lnpfoa, Race",
  "mval_f", "mval_m",
  "formula_log2", "formula_ln")
```

```
## [1] "clindat_f"                        "clindat_m"
## [3] "which has log2pfoa, lnpfoa, Race" "mval_f"
## [5] "mval_m"                           "formula_log2"
## [7] "formula_ln"
```

```
## must put pfoa at the first place
formula_log2 <-  ~as.numeric(log2pfoa) + Race
formula_ln <-  ~as.numeric(lnpfoa) + Race
```

```
## read in data

mval <- fread(file = "/home/guanshim/Documents/gitlab/ECCHO_github/DataRaw/dmr/forGuannan/HS_450K_CB_Mva

# cpg name as row name
rnames <- mval$V1
mval <- as.matrix(mval[, -1])
rownames(mval) <- rnames
## Read in clinical data (log2 transformed PFOA)
clindat <- fread(file = "/home/guanshim/Documents/gitlab/ECCHO_github/DataRaw/dmr/forGuannan/clindat.cs
                 header = T)
## Filter subjects based on clinical data (N = 583)
mval <- mval[, which(colnames(mval) %in% clindat$pid)]
## Filter CpGs based on data from Weiming(N = 433360)
## GUANNAN: I DID NOT DO THIS HERE, SO DO NOT FORGET THIS STEP ##
# read in Filter CpGs based on data from Weiming(N = 433360)
filtered_cpg <- fread("/home/guanshim/Documents/gitlab/ECCHO_github/DataRaw/MeanBeta_ExtremePFOA_M/Mean
                      header = F)
dim(filtered_cpg)
```

```
## [1] 433360      4
```

```
f_cpg <- filtered_cpg$V1
mval <- mval[which(rownames(mval) %in% f_cpg ), ]
dim(mval)
```

```
## [1] 433360    583
```

```
## gender id race
clindat_f <-  fread("~/Documents/gitlab/ECCHO_github/DataProcessed/for_obesity/clindat_f.csv", header =
clindat_m <-  fread("~/Documents/gitlab/ECCHO_github/DataProcessed/for_obesity/clindat_m.csv", header =

mval_f <- mval[, which(colnames(mval) %in% clindat_f$pid )]
mval_m <- mval[, which(colnames(mval) %in% clindat_m$pid )]




################ function wrapper for DMR analysis ##################
DMRcate_wrapper <- function(formula, clindat, mval){
  ## dataset use , female or male, log2pfoa or lnpfoa ##
  gender1 = unlist(strsplit( deparse(substitute(clindat)), "_"))[2]
  gender2 = unlist(strsplit( deparse(substitute(mval)), "_"))[2]
  if(gender1 != gender2)
    stop("should use the same gender data")
  ## the type of pfoa
  log = unlist(strsplit( deparse(substitute(formula)), "_"))[2]
  prefix_name = paste(gender1,"_",log, "pfoa",sep = "")
  ### build design matrix ###
  str(model <- model.frame(formula, clindat))
  design = model.matrix(formula, model)

  ######## DMR analysis ########
  ## Build cpg anno object
  cpganno = cpg.annotate("array",
                          ## female
```

```
                        mval,
                        what = "M",
                        arraytype = "450K",
                        analysis.type = "differential",
                        ## female
                        design = design,
                        ## only have the intercept and the pfoa concentration
                        ##  it will still be coef = 2.
                        ## We are telling DMRcate that we are interested in the log transformed pfoa.
                        coef = 2)
## get results ##
dmrcoutput = dmrcate(cpganno,
                      lambda=1000,
                      c=2,
                      p.adjust.method="BH",
                      consec=FALSE,
                      pcutoff=0.05)
#######################################
# Get list of significant DMRs and CpGs
# associated with those DMRs
#######################################
#get annotation;
anno = as.data.frame(getAnnotation(IlluminaHumanMethylation450kanno.ilmn12.hg19))

#get probes in DMR regions;
getDMRprobes = function(a, anno){
  chr = sapply(strsplit(as.character(a[1]), split=":", fixed=TRUE), "[[", 1)
  start =  as.numeric(sapply(strsplit(sapply(strsplit(as.character(a[1]), split=":", fixed=TRUE), "[[
  stop =  as.numeric(sapply(strsplit(as.character(a[1]), split="-", fixed=TRUE), "[[", 2))

  anno.chr = anno[which(anno$chr==chr),]
  anno2 = as.data.frame(anno.chr[which(anno.chr$pos >= start & anno.chr$pos <= stop),])

  return(anno2)
}
dmr.results = dmrcoutput$results
########### get detailed DMR level results ###############
##Build list of annotation data for probes in each DMR
DMRprobes = list()
for(i in 1:nrow(dmr.results)){
  DMRprobes[[i]] = getDMRprobes(dmr.results[i,], anno)
}

names(DMRprobes) = dmr.results$coord
names(DMRprobes) = gsub(":", "_", names(DMRprobes))
# Write results
readme_sheet = data_frame(
  Columns = c(
    "Annotations for CpGs assocaited with DMR's unadjusted p-value < 0.05",
    "", colnames(DMRprobes[[1]])
  ))

readme_sheet = list(README = readme_sheet)
```

```r
  names(readme_sheet) = "README"
  openxlsx::write.xlsx(c(readme_sheet,
                         DMRprobes),
                       paste("/home/guanshim/Documents/gitlab/ECCHO_github/DataProcessed/dmr/",  prefix_
                             Sys.Date(),"_DMR", ".xlsx", sep= ""))

  ############# get individual cpgs level results data frame ################
  n_cpg = sum(dmrcoutput$results$no.cpgs)
  cpg_sum = (data.frame(matrix(NA, 0,4)))
  ## generate summary table
  for(i in 1:nrow(dmr.results)){
    cpg_sum  = rbind(cpg_sum,
                     cbind(dmr.results[i,1],
                           dmrcoutput$input [dmrcoutput$input$ID %in% getDMRprobes(dmr.results[i,], anno
  }
  colnames(cpg_sum)[c(1,4)] = c("DMR_Identifier", "raw_p")
  if(nrow(cpg_sum) != n_cpg)
    stop("wrong total number of cpgs")
  cpg_min = cpg_sum %>% group_by(DMR_Identifier) %>% filter(raw_p == min(raw_p))
  if(nrow(cpg_min) != nrow(dmr.results))
    stop("wrong number of top1 cpgs in each dmr")
  write.csv(cpg_sum,
            row.names = F,
            paste("/home/guanshim/Documents/gitlab/ECCHO_github/DataProcessed/dmr/",  prefix_name,"_",
                  Sys.Date(),"_DMR_allCpGs", ".csv", sep= ""))
  write.csv(cpg_min,
            row.names = F,
            paste("/home/guanshim/Documents/gitlab/ECCHO_github/DataProcessed/dmr/",  prefix_name,"_",
                  Sys.Date(),"_DMR_top1_CpG", ".csv", sep= ""))
}

########## use the wrapper ############
DMRcate_wrapper(formula_log2, clindat_f, mval_f)
```

```
## 'data.frame':    278 obs. of  2 variables:
##  $ as.numeric(log2pfoa): num  1.07 0.926 0.766 1.585 1.263 ...
##  $ Race                : chr  "All others" "Non-Hispanic white" "All others" "Non-
Hispanic white" ...
##  - attr(*, "terms")=Classes 'terms', 'formula'  language ~as.numeric(log2pfoa) + Race
##   .. ..- attr(*, "variables")= language list(as.numeric(log2pfoa), Race)
##   .. ..- attr(*, "factors")= int [1:2, 1:2] 1 0 0 1
##   .. .. ..- attr(*, "dimnames")=List of 2
##   .. .. .. ..$ : chr [1:2] "as.numeric(log2pfoa)" "Race"
##   .. .. .. ..$ : chr [1:2] "as.numeric(log2pfoa)" "Race"
##   .. ..- attr(*, "term.labels")= chr [1:2] "as.numeric(log2pfoa)" "Race"
##   .. ..- attr(*, "order")= int [1:2] 1 1
##   .. ..- attr(*, "intercept")= int 1
##   .. ..- attr(*, "response")= int 0
##   .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
##   .. ..- attr(*, "predvars")= language list(as.numeric(log2pfoa), Race)
##   .. ..- attr(*, "dataClasses")= Named chr [1:2] "numeric" "character"
##   .. .. ..- attr(*, "names")= chr [1:2] "as.numeric(log2pfoa)" "Race"
```

```
DMRcate_wrapper(formula_log2, clindat_m, mval_m)
```

```
## 'data.frame':    305 obs. of  2 variables:
##  $ as.numeric(log2pfoa): num  1.379 -0.152 0.926 0.678 1.585 ...
##  $ Race                : chr  "Non-Hispanic white" "Non-Hispanic white" "All others" "All others" ..
##  - attr(*, "terms")=Classes 'terms', 'formula'  language ~as.numeric(log2pfoa) + Race
##   .. ..- attr(*, "variables")= language list(as.numeric(log2pfoa), Race)
##   .. ..- attr(*, "factors")= int [1:2, 1:2] 1 0 0 1
##   .. .. ..- attr(*, "dimnames")=List of 2
##   .. .. .. ..$ : chr [1:2] "as.numeric(log2pfoa)" "Race"
##   .. .. .. ..$ : chr [1:2] "as.numeric(log2pfoa)" "Race"
##   .. ..- attr(*, "term.labels")= chr [1:2] "as.numeric(log2pfoa)" "Race"
##   .. ..- attr(*, "order")= int [1:2] 1 1
##   .. ..- attr(*, "intercept")= int 1
##   .. ..- attr(*, "response")= int 0
##   .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
##   .. ..- attr(*, "predvars")= language list(as.numeric(log2pfoa), Race)
##   .. ..- attr(*, "dataClasses")= Named chr [1:2] "numeric" "character"
##   .. .. ..- attr(*, "names")= chr [1:2] "as.numeric(log2pfoa)" "Race"
```

0.2 Obesity outcome linear regression

lm = lm(outcome ~ CpGdata[,i] + Race + Bcell + CD4T + CD8T + Gran + Mono + NK + nRBC, data = Xs)

```
#################################### No maternal_age ###########

c("Need:", "outcome_f", "CpGdata_f", "Xs_f")
```

```
## [1] "Need:"     "outcome_f" "CpGdata_f" "Xs_f"
```

```
## equal length of outcomes and covariates
cpg_FunRegSim <- function(outcome, CpGdata, Xs, Outcome_name,
    Topn) {
    ## get the gender
    gender1 = unlist(strsplit(deparse(substitute(Xs)), "_", fixed = T))[2]
    gender2 = unlist(strsplit(deparse(substitute(CpGdata)), "_",
        fixed = T))[2]
    if (gender1 != gender2)
        stop("should use the same gender data")
    Gender = ifelse(gender1 == "m", "male", "female")
    ## number of CpG to test, also the number of multiple test
    n_cpg = ncol(CpGdata)
    ## outcome lm
    outcome_lm = lapply(1:n_cpg, function(i) {
        lm = lm(outcome ~ CpGdata[, i] + Race + Bcell + CD4T +
            CD8T + Gran + Mono + NK + nRBC, data = Xs)
        coef = summary(lm)$coefficients[2, ]
        return(coef)
    })
    outcome_lm = data.frame(matrix(unlist(outcome_lm), ncol = 4,
        byrow = TRUE, dimnames = list(c(colnames(CpGdata)), c("Estimate",
            "Std.Error", "t.statistic", "p.value"))))
    # adjusted p-value
    outcome_lm = outcome_lm %>% mutate(FDR = p.adjust(p.value,
        "BH", n_cpg), names = colnames(CpGdata)) %>% mutate(Estimate = round(Estimate,
        4), Std.Error = round(Std.Error, 4), t.statistic = round(t.statistic,
        4)) %>% select(names, everything())
    # sort by p.value
    outcome_lm = outcome_lm[order(outcome_lm$p.value), ]
    outcome_lm = data.frame(outcome_lm)

    ## sample size
    size = length(outcome) - sum(is.na(outcome))
    ## save results per outcome
    fwrite(outcome_lm, row.names = F, paste("~/Documents/gitlab/ECCHO_github/DataProcessed/for_obesity/
        Gender, "_", Outcome_name, "_", Sys.Date(), "_", ".csv",
        sep = ""))
    ## summary table
    kable(head(outcome_lm, Topn), caption = paste("Top CpGs from ",
        n_cpg, " CpGs", " for Outcome: ", Outcome_name, " of ",
        Gender, " (Sample Size = ", size, ") ", sep = "", collapse = ""))
}

## read in data
pfas_cell_583 <- read.csv("~/Documents/gitlab/ECCHO_github/DataProcessed/for_obesity/11_05_pfas_cell_58
Outcomes <- colnames(pfas_cell_583)[5:13]
Outcomes
```

```
## [1] "birth_weight"          "ipv3_pp_fm_pct"        "Chol_IPV3"
## [4] "FFA_IPV3"              "Gluc_IPV3"             "HDL_IPV3"
## [7] "Insu_IPV3"             "Trig_IPV3"             "Leptin_actual__ng_ml_"
```

```
## check gender specific data gender mval mval_f gender top
## cpgs
f_dmr_top1cpg <- read.csv("~/Documents/gitlab/ECCHO_github/DataProcessed/for_obesity/f_log2pfoa_2019-02
m_dmr_top1cpg <- read.csv("~/Documents/gitlab/ECCHO_github/DataProcessed/for_obesity/m_log2pfoa_2019-02
dim(f_dmr_top1cpg)
```

```
## [1] 34  4
```

```
dim(m_dmr_top1cpg)
```

```
## [1] 78  4
```

```
CpGdata_f <- mval_f[rownames(mval_f) %in% f_dmr_top1cpg$ID, ]
dim(CpGdata_f)
```

```
## [1]  34 278
```

```
CpGdata_m <- mval_m[rownames(mval_m) %in% m_dmr_top1cpg$ID, ]
dim(CpGdata_m)
```

```
## [1]  78 305
```

```
## clinical outcomes and race and 7 cell types
sum(clindat_f$pid %nin% colnames(CpGdata_f))
```

```
## [1] 0
```

```
sum(clindat_m$pid %nin% colnames(CpGdata_m))
```

```
## [1] 0
```

```
outcome_f <- pfas_cell_583[pfas_cell_583$pid %in% clindat_f$pid,
    ]
outcome_m <- pfas_cell_583[pfas_cell_583$pid %in% clindat_m$pid,
    ]

########
CpGdata_m <- t(CpGdata_m)
CpGdata_f <- t(CpGdata_f)
## # the regression summary table for log10 outcomes
lapply(Outcomes, function(x) {
    cpg_FunRegSim(log10(outcome_m[, x]), CpGdata_m, outcome_m,
        x, 5)
})
```

```
## [[1]]
##
##
## Table: Top CpGs from 78 CpGs for Outcome: birth_weight of male (Sample Size = 305)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 51   cg05214460     -0.0673      0.0278       -2.4246   0.0159265   0.5485946
## 12   cg08773314      0.0217      0.0092        2.3453   0.0196736   0.5485946
## 14   cg11555926      0.0438      0.0205        2.1386   0.0332929   0.5485946
## 19   cg14972155     -0.0216      0.0101       -2.1296   0.0340365   0.5485946
## 55   cg24112091      0.0300      0.0142        2.1162   0.0351663   0.5485946
##
## [[2]]
##
##
## Table: Top CpGs from 78 CpGs for Outcome: ipv3_pp_fm_pct of male (Sample Size = 292)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 58   cg02308988      0.2457      0.0902        2.7250   0.0068321   0.2509146
## 51   cg05214460     -0.2980      0.1107       -2.6921   0.0075249   0.2509146
## 68   cg22018815     -0.1671      0.0641       -2.6059   0.0096506   0.2509146
## 46   cg06878548     -0.1043      0.0417       -2.4989   0.0130287   0.2540599
## 39   cg27448433     -0.1200      0.0528       -2.2706   0.0239281   0.3168033
##
## [[3]]
##
##
## Table: Top CpGs from 78 CpGs for Outcome: Chol_IPV3 of male (Sample Size = 287)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 24   cg10219192      0.0961      0.0321        2.9918   0.0030232   0.2358086
## 34   cg02692313      0.0234      0.0107        2.1895   0.0293961   0.8687082
## 39   cg27448433     -0.0601      0.0281       -2.1367   0.0335005   0.8687082
## 16   cg01411366      0.0479      0.0238        2.0181   0.0445491   0.8687082
## 72   cg27366766      0.0217      0.0117        1.8576   0.0642911   0.9451191
##
## [[4]]
##
##
## Table: Top CpGs from 78 CpGs for Outcome: FFA_IPV3 of male (Sample Size = 265)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 11   cg23330385      0.2861      0.0948        3.0179   0.0028030   0.1660818
## 57   cg24946795      0.1218      0.0422        2.8843   0.0042585   0.1660818
## 41   cg01270001     -0.0774      0.0355       -2.1791   0.0302418   0.7655474
## 49   cg10530889      0.1562      0.0765        2.0422   0.0421611   0.7655474
## 76   cg06729532     -0.1246      0.0688       -1.8100   0.0714685   0.7655474
##
## [[5]]
##
##
## Table: Top CpGs from 78 CpGs for Outcome: Gluc_IPV3 of male (Sample Size = 295)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 51   cg05214460      0.1109      0.0516        2.1516   0.0322659   0.9060537
## 4    cg20930618      0.0746      0.0408        1.8264   0.0688380   0.9060537
## 31   cg19048176      0.0570      0.0316        1.8023   0.0725553   0.9060537
## 35   cg04904815     -0.0462      0.0283       -1.6315   0.1038944   0.9060537
## 23   cg10208897     -0.0163      0.0101       -1.6167   0.1070386   0.9060537
##
## [[6]]
##
##
## Table: Top CpGs from 78 CpGs for Outcome: HDL_IPV3 of male (Sample Size = 261)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 24   cg10219192      0.1022      0.0311        3.2865   0.0011594   0.0904337
## 28   cg12433575     -0.0882      0.0368       -2.3961   0.0173036   0.5671134
## 46   cg06878548     -0.0512      0.0222       -2.3080   0.0218121   0.5671134
## 59   cg22780612      0.0472      0.0226        2.0878   0.0378249   0.6212652
## 26   cg08873424      0.0417      0.0212        1.9673   0.0502507   0.6212652
##
## [[7]]
##
##
## Table: Top CpGs from 78 CpGs for Outcome: Insu_IPV3 of male (Sample Size = 282)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 7    cg08944170     -0.0362      0.0108       -3.3562   0.0009030   0.0704345
## 18   cg21492882      0.1491      0.0687        2.1694   0.0309211   0.7884356
## 22   cg00232827      0.1143      0.0552        2.0690   0.0394916   0.7884356
## 47   cg13764991      0.1934      0.0950        2.0355   0.0427728   0.7884356
## 48   cg16128766      0.1327      0.0718        1.8484   0.0656260   0.7884356
```

```
##
## [[8]]
##
##
## Table: Top CpGs from 78 CpGs for Outcome: Trig_IPV3 of male (Sample Size = 284)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 28   cg12433575      0.1758      0.0669        2.6273   0.0090917   0.7091550
## 36   cg03110795     -0.0902      0.0448       -2.0154   0.0448413   0.9575694
## 11   cg23330385      0.1552      0.0882        1.7600   0.0795282   0.9575694
## 29   cg06132876      0.1536      0.0881        1.7429   0.0824713   0.9575694
## 73   cg21459643     -0.1190      0.0707       -1.6824   0.0936336   0.9575694
##
## [[9]]
##
##
## Table: Top CpGs from 78 CpGs for Outcome: Leptin_actual__ng_ml_ of male (Sample Size = 252)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 29   cg06132876      0.5090      0.1779        2.8618   0.0045805   0.3572811
## 17   cg10745272      0.1757      0.0777        2.2604   0.0246876   0.9606840
## 63   cg03287936     -0.1820      0.0893       -2.0383   0.0426050   0.9606840
## 12   cg08773314     -0.1385      0.0701       -1.9762   0.0492658   0.9606840
## 68   cg22018815     -0.2225      0.1266       -1.7581   0.0799870   0.9745699
```

```r
lapply(Outcomes, function(x) {
    cpg_FunRegSim(log10(outcome_f[, x]), CpGdata_f, outcome_f,
        x, 5)
})
```

```
## [[1]]
##
##
## Table: Top CpGs from 34 CpGs for Outcome: birth_weight of female (Sample Size = 278)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 27   cg01538731     -0.0404      0.0080       -5.0191   0.0000009   0.0000322
## 28   cg00463732      0.0401      0.0153        2.6174   0.0093640   0.1591880
## 33   cg17414107     -0.0349      0.0155       -2.2495   0.0252914   0.2230146
## 18   cg13809095     -0.0325      0.0151       -2.1501   0.0324437   0.2230146
## 29   cg02286380      0.0214      0.0100        2.1457   0.0327963   0.2230146
##
## [[2]]
##
##
## Table: Top CpGs from 34 CpGs for Outcome: ipv3_pp_fm_pct of female (Sample Size = 271)
##
##      names         Estimate   Std.Error   t.statistic     p.value        FDR
## ---  -----------  ---------  ----------  ------------  ----------  ---------
## 10   cg12626589      0.0768      0.0439        1.7508   0.0811622   0.856275
## 32   cg05308117     -0.0839      0.0606       -1.3846   0.1673651   0.856275
## 13   cg04155485     -0.1277      0.0925       -1.3816   0.1682827   0.856275
## 21   cg03416628     -0.0674      0.0488       -1.3798   0.1688275   0.856275
## 15   cg01022670     -0.0826      0.0614       -1.3455   0.1796260   0.856275
##
## [[3]]
##
##
## Table: Top CpGs from 34 CpGs for Outcome: Chol_IPV3 of female (Sample Size = 257)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 10   cg12626589      0.0570      0.0264        2.1550   0.0321255   0.6620813
## 20   cg12762089      0.1243      0.0599        2.0758   0.0389460   0.6620813
## 15   cg01022670      0.0649      0.0370        1.7549   0.0805214   0.6662994
## 23   cg06989610      0.0694      0.0421        1.6471   0.1008059   0.6662994
## 11   cg08209711     -0.0472      0.0291       -1.6228   0.1058972   0.6662994
##
## [[4]]
##
##
## Table: Top CpGs from 34 CpGs for Outcome: FFA_IPV3 of female (Sample Size = 237)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 14   cg07890238     -0.1977      0.0850       -2.3249   0.0209578   0.4602326
## 10   cg12626589     -0.0958      0.0485       -1.9778   0.0491556   0.4602326
## 21   cg03416628      0.1087      0.0553        1.9653   0.0506033   0.4602326
## 13   cg04155485      0.1913      0.1000        1.9135   0.0569396   0.4602326
## 23   cg06989610      0.1378      0.0769        1.7917   0.0745152   0.4602326
##
## [[5]]
##
##
## Table: Top CpGs from 34 CpGs for Outcome: Gluc_IPV3 of female (Sample Size = 263)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 12   cg09221482      0.0763      0.0375        2.0327   0.0431309   0.8064372
## 29   cg02286380      0.0273      0.0168        1.6269   0.1050004   0.8064372
## 16   cg04084786     -0.0212      0.0148       -1.4299   0.1539740   0.8064372
## 5    cg17660833      0.0237      0.0170        1.3905   0.1655943   0.8064372
## 4    cg08621673      0.0332      0.0253        1.3119   0.1907516   0.8064372
##
## [[6]]
##
##
## Table: Top CpGs from 34 CpGs for Outcome: HDL_IPV3 of female (Sample Size = 242)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 30   cg11738485     -0.0073      0.0037       -1.9801   0.0488774   0.6054321
## 32   cg05308117     -0.0697      0.0356       -1.9614   0.0510254   0.6054321
## 9    cg06893296     -0.0602      0.0310       -1.9414   0.0534205   0.6054321
## 6    cg23486067     -0.0270      0.0165       -1.6343   0.1035594   0.7320227
## 26   cg14823973      0.0479      0.0313        1.5276   0.1279831   0.7320227
```

```
##
## [[7]]
##
##
## Table: Top CpGs from 34 CpGs for Outcome: Insu_IPV3 of female (Sample Size = 255)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 29   cg02286380      0.1004      0.0455        2.2076   0.0282003   0.9588099
## 24   cg10773745     -0.0936      0.0578       -1.6185   0.1068514   0.9878332
## 5    cg17660833      0.0687      0.0463        1.4820   0.1396350   0.9878332
## 7    cg18728025     -0.0664      0.0524       -1.2675   0.2061921   0.9878332
## 16   cg04084786      0.0496      0.0396        1.2545   0.2108457   0.9878332
##
## [[8]]
##
##
## Table: Top CpGs from 34 CpGs for Outcome: Trig_IPV3 of female (Sample Size = 252)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 29   cg02286380     -0.1109      0.0371       -2.9895   0.0030824   0.0827014
## 27   cg01538731      0.0886      0.0312        2.8421   0.0048648   0.0827014
## 15   cg01022670      0.0974      0.0596        1.6340   0.1035636   0.8601866
## 23   cg06989610      0.1043      0.0693        1.5040   0.1338885   0.8601866
## 20   cg12762089      0.1362      0.0972        1.4003   0.1627001   0.8601866
##
## [[9]]
##
##
## Table: Top CpGs from 34 CpGs for Outcome: Leptin_actual__ng_ml_ of female (Sample Size = 226)
##
##      names         Estimate   Std.Error   t.statistic     p.value         FDR
## ---  -----------  ---------  ----------  ------------  ----------  ----------
## 17   cg04769618      0.1531      0.0922        1.6602   0.0983169   0.9150444
## 23   cg06989610     -0.2036      0.1317       -1.5463   0.1234865   0.9150444
## 14   cg07890238      0.2123      0.1375        1.5445   0.1239351   0.9150444
## 16   cg04084786     -0.0942      0.0619       -1.5217   0.1295374   0.9150444
## 21   cg03416628     -0.1089      0.0919       -1.1850   0.2373342   0.9150444
```