

Supplementary Material – Code

Code for Epigenome-wide Association Analysis

```
#Load libraries
library(lme4)
library(lmerTest)
options(stringsAsFactors=FALSE)
#treat strings in a data frame as characters and not as factors by default

#load data
fulldata <-[Read in file with ID, Predictor, Covariates and Methylation all in columns]
methdata <-[Read in file with ID and Methylation in columns]

#normalise methylation data
normdataC <-function(x){normdat <-qqnorm(x,plot.it=FALSE)
resultnorm <-normdat$x}
normdata <-apply(methdata,2,normdataC)

#linear model function
runlinmod <- function(x){
  y <-normdata[,x]
  h<-lmer(y~[Predictor] +[Covariates],data=fulldata,na.action=na.omit)
  coeff <-summary(h)$coefficients
  result <-c(coeff[2,1],coeff[2,2],coeff[2,4],coeff[2,5])
  return(result)
}

modelres <-do.call(cbind,lapply(1:NCOL(normdata),runlinmod))
rownames(modelres) <-c("estimate","S.error","t value","pvalue")
colnames(modelres) <-colnames(normdata)
```

```
modelresout <-t(modelres)
```

```
write.csv (modelresout, file=[location])
```

Code for mediation analysis

```
diet_input<-[Read in file with diet data, visceral fat, covariates and methylation data]
```

```
M <-diet_input$cg26804336
```

```
Y <-as.numeric(diet_input$VF)
```

```
#model.0 <-lm(Y~X)
```

```
model.0<-lmer(Y~dqii_score + BMI+ as.factor(smokestatus1) + Age+ (1|KCLfam),data=diet_input)
```

```
coeff0 <-summary(model.0)$coefficients
```

```
#model.1 <-lm(M~X)
```

```
meth_model<-lmer(M~dqii_score + BMI+ as.factor(smokestatus1) + Age + (1|KCLfam),  
data=diet_input)
```

```
coeff1 <-summary(meth_model)$coefficients
```

```
#model.Y <-lm(Y~X+M)
```

```
meth_diet_model<-lmer(Y~dqii_score + cg26804336+ BMI+ as.factor(smokestatus1) + Age+  
(1|KCLfam),data=diet_input)
```

```
coeff2 <-summary(meth_diet_model)$coefficients
```

```
library(mediation)
```

```
results <-mediate(meth_model, meth_diet_model,sims =500,treat="dqii_score",  
mediator="cg26804336", boot=FALSE)
```

```
summary(results)
```