**Supplementary Code 1. R code example to calculate DNAm age using NEOage clocks.**

library(minfi) # logit2

# logit transformed DNA methylation data (datM; columns: samples, rows: CpGs)

datM = logit2(datM)

# PMA EPIC

## reading in clock CpGs with coefficients

NEOage\_EPIC\_PMA\_clock=read.csv("05-13-2021\_PMA-EPIC.csv", header = T)

## subset and transform DNAm data to selected CpGs

dataClock = data.frame(t(datM[NEOage\_EPIC\_PMA\_clock$ID[-1],]))

## calculate NEOage

NEOage\_EPIC\_PMA = as.numeric(NEOage\_EPIC\_PMA\_clock[1,2] + as.numeric(as.matrix(dataClock) %\*% as.numeric(NEOage\_EPIC\_PMA\_clock$coef[-1])))

# PMA 450k

## reading in clock CpGs with coefficients

NEOage\_450k\_PMA\_clock=read.csv("05-13-2021\_PMA-450k.csv", header = T)

## subset and transform DNAm data to selected CpGs

dataClock = data.frame(t(datM[NEOage\_450k\_PMA\_clock$ID[-1],]))

## calculate NEOage

NEOage\_450k\_PMA = as.numeric(NEOage\_450k\_PMA\_clock[1,2] + as.numeric(as.matrix(dataClock) %\*% as.numeric(NEOage\_450k\_PMA\_clock$coef[-1])))

# PNA EPIC

## reading in clock CpGs with coefficients

NEOage\_EPIC\_PNA\_clock=read.csv("05-13-2021\_PNA-EPIC.csv", header = T)

## subset and transform DNAm data to selected CpGs

dataClock = data.frame(t(datM[NEOage\_EPIC\_PNA\_clock$ID[-1],]))

## calculate NEOage

NEOage\_EPIC\_PNA = as.numeric(NEOage\_EPIC\_PNA\_clock[1,2] + as.numeric(as.matrix(dataClock) %\*% as.numeric(NEOage\_EPIC\_PNA\_clock$coef[-1])))

# PNA 450k

## reading in clock CpGs with coefficients

NEOage\_450k\_PNA\_clock=read.csv("05-13-2021\_PNA-450k.csv", header = T)

## subset and transform DNAm data to selected CpGs

dataClock = data.frame(t(datM[NEOage\_450k\_PNA\_clock$ID[-1],]))

## calculate NEOage

NEOage\_450k\_PNA = as.numeric(NEOage\_450k\_PNA\_clock[1,2] + as.numeric(as.matrix(dataClock) %\*% as.numeric(NEOage\_450k\_PNA\_clock$coef[-1])))