

**Table S2.** R code for phenotype data correction.

```
##### Phenotype Correction #####  
#Session-SWD-choose dirctory  
data=read.csv("5wtc.csv",header = T)#  
dim(data) #  
str(data) #  
head(data) #  
for( i in 1:5) data[,i] = as.factor(data[,i]) #  
data$date5=as.numeric(as.character(data$date5)) #  
str(data)  
summary(data) #  
  
a1=glm(wtc~type+year+quarter+date5,data=data) #  
anova(a1,test="F")###  
a1=glm(wtc~quarter+date5,data=data) #  
bw_adjust=matrix(a1$residuals,ncol=1)#  
head(bw_adjust) #  
#  
colnames(bw_adjust)=c("phe_wtc")  
head(bw_adjust)  
dim(bw_adjust)  
#  
bw_adjust=as.data.frame(cbind(data[,1:8],bw_adjust))  
head(bw_adjust)  
write.csv(bw_adjust,"5wtcj.csv",row.names = F) #
```