Appendix S1. Null distributions for phenotypic integration indices.

The objective of this appendix is to demonstrate that the same null distribution may be used to test phenotypic integration indices estimated using both 'pint' and 'pintsc' functions. For that, we generated three random variables (named var1, var2, and var3) drawing 100 numbers between 0 and 1 in a uniform distribution. Then, we calculated the correlation between var1 and var2, the partial correlation controlling by var3, and the difference between both estimates. We repeated this procedure 1000 times and plotted the resulting distributions (script available below). Distributions are identical for both correlation estimates (Fig. S1), and differences follow a normal distribution (Fig. S2). Thus, the partial correlation matrix shows the same pattern as a simple correlation matrix between two random variables, justifying the use of the same null distribution in both cases. However, it is important to note that the null hypothesis is also the same in both cases: correlation between traits and with the control variable are all random. In other words, we assume that the control variable shows no correlation with any of the remaining variables. The script for this demonstration is provided at the end of this appendix.
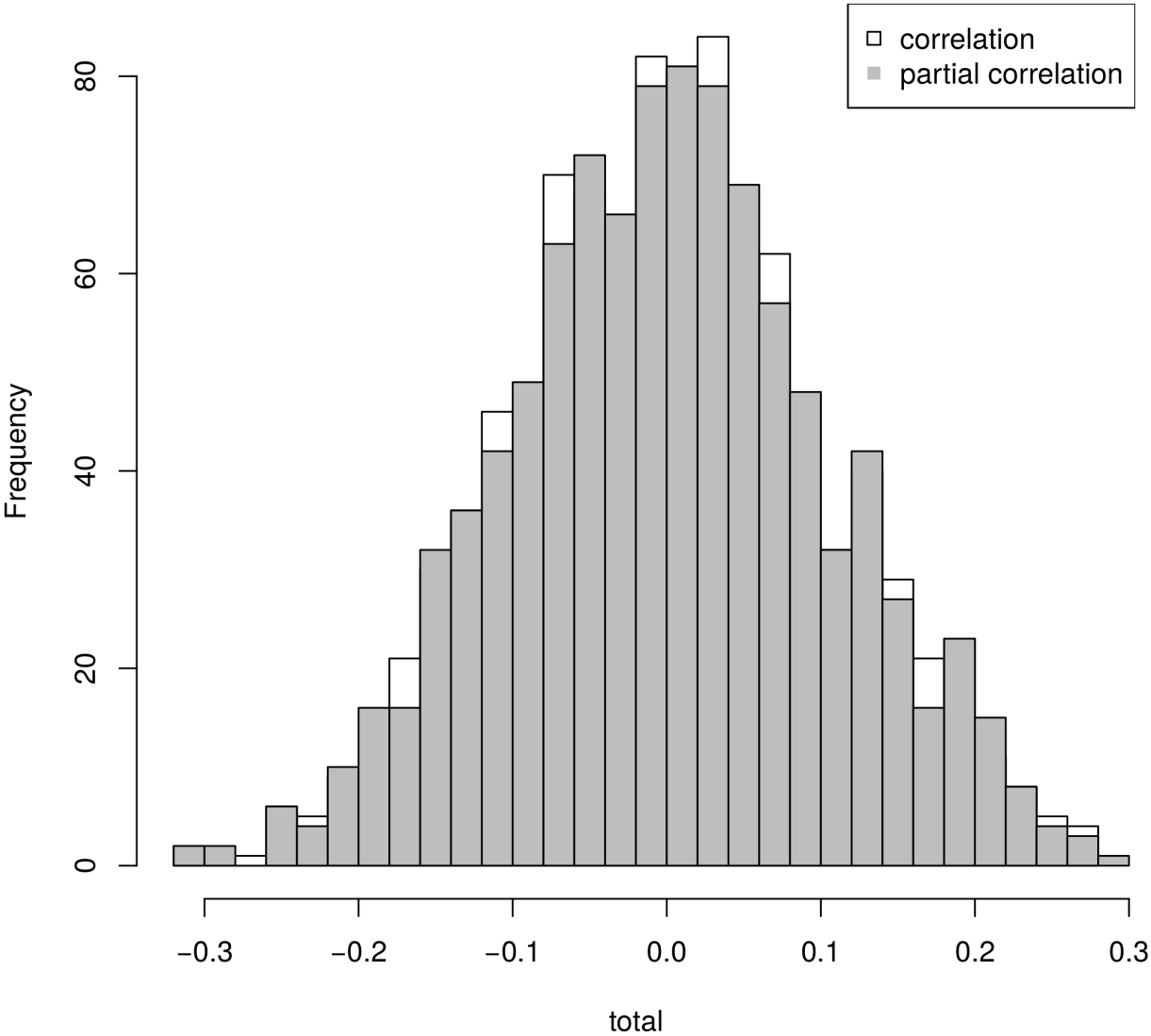
Fig. S1. Distribution of the correlation and partial correlation between simulated variables (based on 1000 simulations).
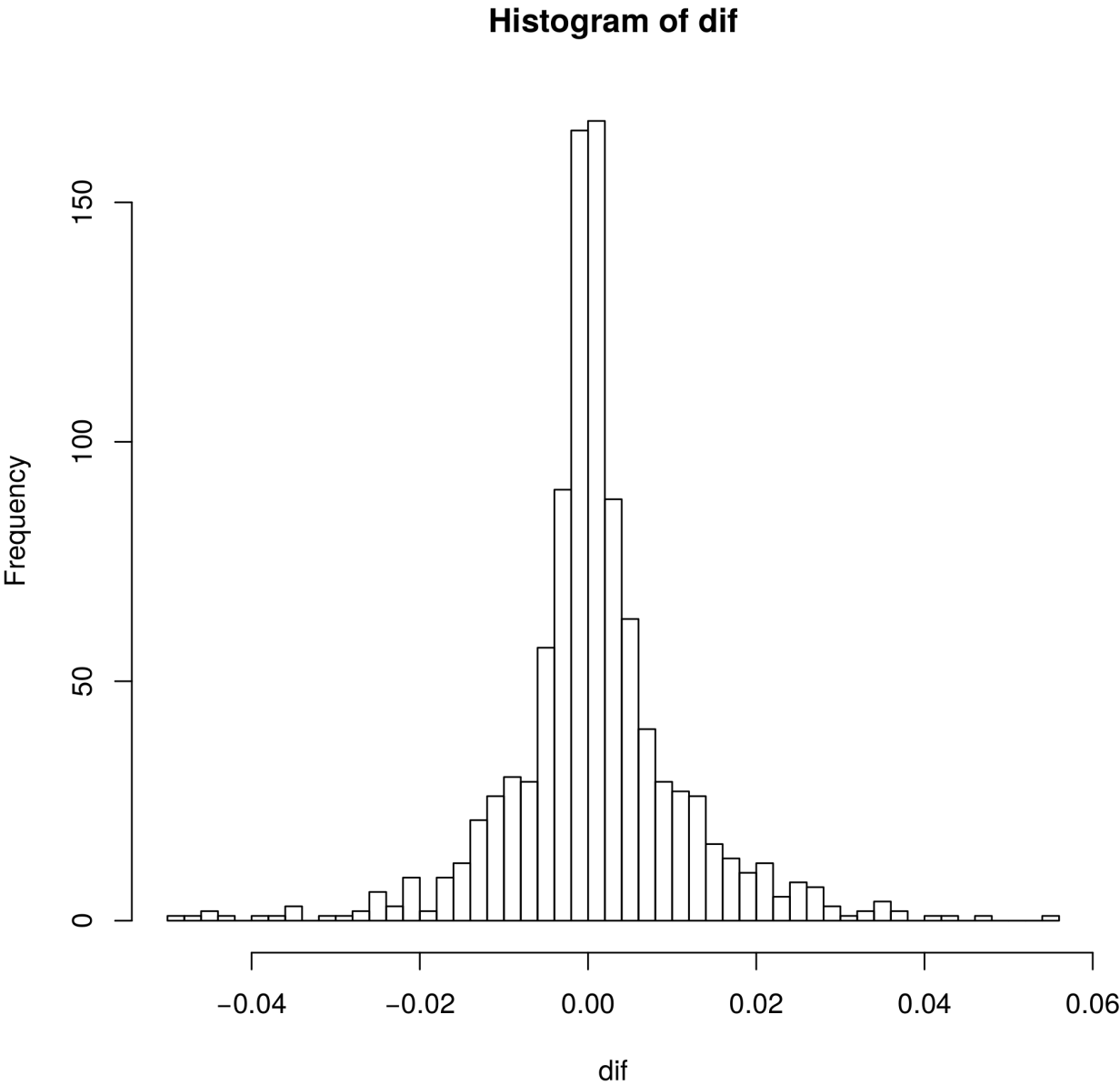
Histogram of dif

Fig. S2. Distribution of the differences between correlation and partial correlation between simulated variables (based on 1000 simulations).

```
#Script


library(PHENIX)
for (i in 1:1000)
{
    var1<-sample(seq(0,1,0.001),100)
    var2<-sample(seq(0,1,0.001),100)
    var3<-sample(seq(0,1,0.001),100)
    TOTAL<-cor(var1,var2)
    PARTIAL<-cor.par(cbind(var1,var2),var3)[1,2]
    if(i==1)
    {dif<-TOTAL-PARTIAL
    total<-TOTAL
    partial<-PARTIAL}
    if(i>1)
    {dif<-c(dif,TOTAL-PARTIAL)
    total<-c(total,TOTAL)
    partial<-c(partial,PARTIAL)}
}
#Distribution of both correlations
hist(total,nclass=40,main="")
hist(partial,nclass=40,add=TRUE,col="grey")

legend("topright",legend=c("correlation","partial
correlation"),pch=c(0,15),col=c("black","grey"))

dev.new()

#Distribution of the difference between correlation and partial
correlation:
hist(dif,nclass=40)
```