alright so let’s see if we can replicate 2015 paper

library(data.table)  
main\_dir = "/Users/victorpokorny/Library/CloudStorage/GoogleDrive-vpokorny123@gmail.com/My Drive/CAPR Ebbinghaus and Mooney/"  
source(paste0(main\_dir,'R\_scripts/funcs.R')) # big group of functions  
load(file=paste0(main\_dir,"RData/cleaned.RData")) #read in the data

first main finding is reduced misleading index in CHR using 2sd

main\_df <- main\_df[main\_df$phenotype\_final == "chr" | main\_df$phenotype\_final == "hc" ]  
res<-t.test(misleading\_index2SD ~ phenotype\_final, main\_df, alternative = "less",   
 var.equal = TRUE)  
res

##   
## Two Sample t-test  
##   
## data: misleading\_index2SD by phenotype\_final  
## t = -0.86082, df = 433, p-value = 0.1949  
## alternative hypothesis: true difference in means between group hc and group chr is less than 0  
## 95 percent confidence interval:  
## -Inf 1.428438  
## sample estimates:  
## mean in group hc mean in group chr   
## -52.67241 -51.11111

pub\_ready\_stats(res)

## [1] "t(433)=-0.86, p=0.195, Cohen's d=-0.04"