#-----------------------------------------------------------------------------------------------------#

# Manifest add

#-----------------------------------------------------------------------------------------------------#

source("C:/DATA\_STORAGE/Projects/PRS-multi-trait/Scripts/.Main/Settings.R")

f\_getManifest(1)

f\_addGWAStoManifest(

short=c("ASD"),

n=c(10000), # default 10,000? @RRR discuss

filename=c("D:/DATA\_STORAGE/GWAS/Autism\_Spectrum\_Disorder\_2019/ASD\_2019\_70.txt"),

year=c("2019"),

trait=c("Autism\_Spectrum\_Disorder\_2019"),

DOI=c("?"),

genomeBuild = c("?"),

traitType = c("CAT"),

rawSNPs = c("?"),

finalModelSNPs = c("?"),

modelRunningTime = c("?"),

usedRefSet = c("?"),

processed=c(0),

FORCE = FALSE)

f\_getManifest(1)

f\_getTraits()

f\_prepareGWAS(trait = "ASD")

f\_calcPGS\_LDAK(Trait = "ASD")

# ADNI

cohort\_name = "ADNI\_QC\_EUR05\_2"

temp\_bfile = paste0("C:/Users/p70072451/Downloads/ADNI/",cohort\_name)

temp\_bfile3 = f\_wslpath(temp\_bfile)

f\_predPRS(bfile = temp\_bfile3, Trait = "ASD")

PGS\_all = f\_collect\_all\_PRS(cohort\_name)

plot(PGS\_all)