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

# Manifest add

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

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

f\_getManifest(1)

f\_addGWAStoManifest(

short=c("BMI"),

n=c(755315), # default 10,000? @RRR discuss

filename=c("D:/DATA\_STORAGE/GWAS/BMI-new\_\_UKBioBank\_34\_2018/BMI\_2018-new\_\_UKBioBank\_34.txt"),

year=c("2018"),

trait=c("BMI"),

DOI=c("?"),

genomeBuild = c("?"),

traitType = c("CONT"),

rawSNPs = c("?"),

finalModelSNPs = c("?"),

modelRunningTime = c("?"),

usedRefSet = c("?"),

processed=c(0),

FORCE = FALSE)

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

f\_getManifest(1)

f\_getTraits()

f\_prepareGWAS(trait = "BMI")

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

f\_calcPGS\_LDAK(Trait = "Height22")

# 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 = "BMI")

f\_predPRS(bfile = temp\_bfile3, Trait = "Height22")

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

plot(PGS\_all)