**Additional file: code for MR analysis**

library(TwoSampleMR)

MDD\_file <- system.file("extdata/exposure.csv", package="TwoSampleMR")

MDD\_exp\_dat <- read\_exposure\_data( filename = MDD\_file, sep = ",", snp\_col = "SNP",beta\_col = "beta", se\_col = "se",effect\_allele\_col = "effect\_allele",other\_allele\_col = "other\_allele", eaf\_col = "eaf", pval\_col = "P\_value", phenotype\_col = "exposure")

outcome\_dat <-read\_outcome\_data(snps = MDD\_exp\_dat$SNP,filename = "ostomyelitis.csv",sep = ",",snp\_col = "SNP",beta\_col = "beta",se\_col = "se",effect\_allele\_col = "effect\_allele",other\_allele\_col = "other\_allele", eaf\_col = "eaf", pval\_col = "P\_value")

dat <- harmonise\_data(exposure\_dat = MDD\_exp\_dat, outcome\_dat = outcome\_dat)

write.csv(dat,"MDD\_ostomyelitis\_dat.csv")

res <- mr(dat)

res

write.csv(res," MDD\_ostomyelitis\_LSB\_dat1.2\_res.csv")

h <- mr\_heterogeneity(dat)

write.csv(h," MDD\_ostomyelitis\_LSB\_dat1.2\_h.csv")

p <- mr\_pleiotropy\_test(dat)

write.csv(p," MDD\_ostomyelitis LSB\_dat1.2\_p.csv")

res\_single <- mr\_singlesnp(dat)

res\_loo <- mr\_leaveoneout(dat)

res <- mr(dat, method\_list=c("mr\_egger\_regression", "mr\_ivw","mr\_weighted\_median"))

p1 <- mr\_scatter\_plot(res, dat)

p1[[1]]

res\_single <-mr\_singlesnp(

dat,

parameters = default\_parameters(),

single\_method = "mr\_wald\_ratio",

all\_method = "mr\_ivw")

))

p2 <- mr\_forest\_plot(res\_single)

p2[[1]]

res\_loo <- mr\_leaveoneout(dat)

p3 <- mr\_leaveoneout\_plot(res\_loo)

p3[[1]]

p4 <- mr\_funnel\_plot(res\_single)

p4[[1]]

#MR-PRESSO

library(MRPRESSO)

mr\_presso(BetaOutcome = "beta.outcome", BetaExposure = "beta.exposure", SdOutcome = "se.outcome", SdExposure = "se.exposure", OUTLIERtest = TRUE, DISTORTIONtest = TRUE, data = dat, NbDistribution = 10000, SignifThreshold = 0.05,)