**rMVP\_GWAS Script for BAP**

source("https://github.com/xiaolei-lab/rMVP")

install.packages("rMVP")

devtools::install\_github("xiaolei-lab/rMVP")

library(rMVP)

setwd("/zfs/tillers/nkumar2")

setwd("/zfs/tillers/nkumar2/BAP\_rMVP")

df <- read.csv("Yellow.csv", header=T)

write.table(df, file="Yellow.txt", quote=F, row.names = F)

MVP.Data(fileVCF="BAP.final.imputed.vcf",

filePhe="Yellow.csv",

sep.phe = ",",

fileKin=F,

filePC=F,

out="mvp.vcf"

)

genotyp\_dat <- attach.big.matrix("mvp.vcf.geno.desc")

phenotypic\_dat <- read.table("mvp.vcf.phe",head=TRUE)

map\_info <- read.table("mvp.vcf.geno.map", head=TRUE)

GWAS\_imMVP <- MVP(

phe = phenotypic\_dat,

geno=genotyp\_dat,

map=map\_info,

method=c("FarmCPU"),

nPC.FarmCPU=3,

threshold=0.05,

)