**#Set working directory**

setwd("~/")

**#Load libraries**

library("ggplot2", lib.loc="~/R/win-library/3.2")

**#Read in data**

PCA\_data2 <- read.table("PCA\_psycourse\_1KG\_v4.evec", quote="\"")

KG\_psycourse\_pops <- read.delim("KG\_psycourse\_pops.txt")

**#Merge PsyCourse and population data**

KG\_psycourse\_merged <- merge(KG\_psycourse\_pops, PCA\_data2, by.x="sample", by.y="V1")

psycourses <- KG\_psycourse\_merged[KG\_psycourse\_merged$PsyCourse=="PsyCourse",c(1:7)]

**#Create plot**

ggplot(KG\_psycourse\_merged, aes(x=V2, y=V3)) + geom\_point(data=(KG\_psycourse\_merged[KG\_psycourse\_merged$super\_pop!="PsyCourse",]),pch=21, colour="Black", size=5,position = 'jitter',alpha=0.4, aes(fill=super\_pop)) + scale\_fill\_discrete(name="1000 Genomes\nSuper Populations") + theme(legend.text = element\_text(face = "bold")) + geom\_point(data=psycourses, aes(x=V2, y=V3, color=psycourses$PsyCourse), pch=23, size=4, fill="orange",position = 'jitter', stroke=0.2) + scale\_color\_manual(values="black") + guides(color=guide\_legend(title=NULL))+ theme\_light() + xlab("First Principal Component") + ylab("Second Principal Component") + theme(axis.title.y = element\_text(margin=margin(r = 20), size=15, face="bold")) + theme(axis.title.x = element\_text(margin=margin(t = 20), size=16, face="bold"))

ggsave("PsyCourse\_1KG.png", width=8, height=7)