setwd("/Users/celestecohen/Downloads/Biofilm\_bioinformatics")

#get the final phenotype files that are in the QTL mapping drive folder

filt<-read.csv(file = "Biofilm\_image\_processing/filtering\_phenotypes.csv", header = TRUE)

wash<-read.csv(file = "Biofilm\_image\_processing/washing\_phenotypes.csv")

#the parentals are plotted on top of the segregants so we can see their colours

wash[57:58,]=wash[1:2,]

wash=wash[-(1:2),]

filt[57:58,]=filt[1:2,]

filt=filt[-(1:2),]

colours=c(rep("royalblue",54),"red","orange")

plot(filt$X.flocc~wash$ratio,col=colours,pch=16,cex=1, xlab="Washing results", ylab="Filtering results",cex.lab=1.5,cex.axis=1)

summary(lm(filt$X.flocc~wash$ratio))

#colour parentals

abline(lm(filt$X.flocc~wash$ratio))