#https://cran.r-project.org/web/packages/afex/vignettes/afex\_anova\_example.html

sink(paste(outpath,'Probe\_d5\_tukeytable.txt', sep=''))

lm\_Probe\_d8 <- lm(Probe\_d8 ~ Genotype\*Sex, geno\_combined\_FA)

summary(lm\_Probe\_d5) #gives model test p value

anova(lm\_Probe\_d5) #gives significance of factors

summary(glht(lm\_Probe\_d5, emm(pairwise ~ Genotype\*Sex, contr="sidak"))) #consider save to file #a whole slew of pairwise comparisons

summary(glht(lm\_Probe\_d5, emm(pairwise ~ Genotype\*Sex, contr="sidak", by=NULL)))

#emmeans(lm\_Probe\_d5, ~ Genotype\*Sex, contr="tukey")

summary(as.glht(pairs(Probe\_d5.emm), by = NULL))

summary(as.glht(pairs(Probe\_d5.emm)), test=adjusted("free"))

mypairs<-pairs(Probe\_d5.emm) #\_consider save to file

pairs(Probe\_d5.emm, by="Genotype")

pairs(Probe\_d5.emm, by="Sex")

sink()

#omnibus testing

#https://cran.r-project.org/web/packages/emmeans/vignettes/confidence-intervals.html#adjust

sink()

sink(paste(outpath, "Winding\_ProbeD5\_omnibus.txt"))

test(mypairs, joint = TRUE, adjust = "sidak")

joint\_tests(ref\_grid(lm\_Probe\_d5))

joint\_tests(ref\_grid(lm\_Probe\_d5), by = "Sex", adjust = "sidak")

joint\_tests(ref\_grid(lm\_Probe\_d5), by = "Genotype",adjust = "sidak" )

sink()