```
p <- subset(sample.info,Type=='PLEASE-T1' | Type=='COMBO',
            select=c(Disease,Cluster,Human.Per,Fungi.Per)) %>%
na.omit() %>%
ggplot(aes(log10(Human.Per),log10(Fungi.Per))) +
geom_point(aes(colour = Cluster,shape= Disease),size=5) +
  scale_color_manual(values=c("#0066CC", "#FF3333"),name="") +
  scale_shape_manual(values=c(20,1),name="") +
  #scale_size_area(range = c(1, 10))+
  #scale_size_continuous(range = c(3, 10)) +
  #labs(title = 'Ordination bacterial taxa') +
  #stat_smooth_func(geom="text",method="lm",hjust=0,parse=TRUE) +
  geom_smooth(method="lm",se=FALSE) +
  theme_classic()
print(p)
```