Set repository:

```
library(ggplot2)
#setwd("../meisam_yousefi/OneDrive - National University of Singapore/Lab_Meisam/Results/Scripts/DENV-T
```

Read data:

```
Metabolome <- read.csv(file ="MetabolitesRaw.csv",header = T,quote="")
Metabolome <- Metabolome[,1:10]
Metabolome_mat <- as.matrix(Metabolome[,-1])
class(Metabolome_mat) <- "numeric"
#row.names(Metabolome) <- Metabolome[,1]
#Metabolome <- Metabolome[,-1]
```

PCA:

```
PCAmet <- prcomp(Metabolome_mat)
PCArot <- data.frame(PCAmet$rotation)
PCArot$Group <- c("WT","WT","WT","TMEM41B KO","TMEM41B KO","TMEM41B KO","VMP1 KO","VMP1 KO","VMP1 KO")
#Summary(PCAmet)
```

Plotting:

```
ggplot(PCArot, aes(PC1,PC2,color=Group)) + geom_point(size=4) + theme_bw()
```