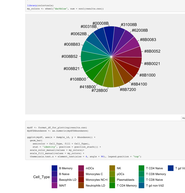
R Notebook

Code ▾

Listing 446

```
library(ggplot2)
setwd("/Users/Admin/Desktop/PhD/Collaborations/Lymphoma_Bone/Scripts/Seurat/")
Sample_id <- read.table("./Sample_id.tsv", header=TRUE)
Cell_Type <- read.table("./Cell_Type.tsv", header=TRUE, sep="\t")
Cell_Type$Sample_id <- Cell_Type$Sample_id[match(Cell_Type$Cell_Barcode,Sample_id$Cell_Barcode,nrow=1)]
Cell_Type$Cell_Type <- factor(Cell_Type$Cell_Type,levels=c("Monocytes C","Monocytes NC+I","Neutrophils L2","Neutrophils L1","Eosinophils L2","Eosinophils L1","B Memory","B Naive","NK","CD4 Memory","CD4 Naive","CD8 Memory","CD8 Naive","pDCs","mDCs","Plasmablasts"))
Cell_Type$Sample_id <- factor(Cell_Type$Sample_id,levels=c("Healthy_001","Healthy_002","Healthy_003","NEG_001","NEG_002","NEG_003","NEG.THC_001","NEG.THC_002","NEG.THC_003","NEG.THC.TIP_001","NEG.THC.TIP_002","NEG.THC.TIP_003","POS_001","POS_002","POS_003"))
Cell_Type$Cohort <- factor(Cell_Type$Cohort,levels=c("Healthy","NEG","NEG.THC","NEG.THC.TIP","POS"))
```

```
# Overall cell proportions
ggplot(Cell_Type,aes(x=Sample_id,fill=Cell_Type))+geom_bar(position="fill")+
theme(axis.text.x=element_text(angle=90))+ylab("Abundance")+
scale_fill_manual(values=c("#FF0000","#0000FF","#00FF00","#00FFFF","#FF00FF","#FFFF00","#000000","#008000","#800080","#008080","#808000","#808080","#00FF80","#FF8000","#0080FF"))
```

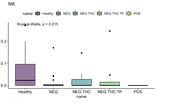



```
# Overall cell proportions - Cohort
ggplot(Cell_Type,aes(x=Cohort,fill=Cell_Type))+geom_bar(position="fill")+
theme(axis.text.x=element_text(angle=90))+ylab("Abundance")+
scale_fill_manual(values=c("#FF0000","#0000FF","#00FF00","#00FFFF","#FF00FF","#FFFF00","#000000","#008000","#800080","#008080","#808000","#808080","#00FF80","#FF8000","#0080FF"))
```

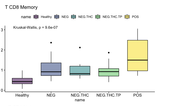
```
# Overall cell proportions - Sample_id
ggplot(Cell_Type,aes(x=Sample_id,fill=Cell_Type))+geom_bar(position="fill")+
theme(axis.text.x=element_text(angle=90))+ylab("Abundance")+
scale_fill_manual(values=c("#FF0000","#0000FF","#00FF00","#00FFFF","#FF00FF","#FFFF00","#000000","#008000","#800080","#008080","#808000","#808080","#00FF80","#FF8000","#0080FF"))
```

```
# Cohort 1 Control
Cohort1_Control <- Cohort1[Cohort1$Cohort=="Control",]
Cohort1_Control$Cell_Type <- factor(Cohort1_Control$Cell_Type,levels=c("Monocytes C","Monocytes NC+I","Neutrophils L2","Neutrophils L1","Eosinophils L2","Eosinophils L1","B Memory","B Naive","NK","CD4 Memory","CD4 Naive","CD8 Memory","CD8 Naive","pDCs","mDCs","Plasmablasts"))
Cohort1_Control$Sample_id <- factor(Cohort1_Control$Sample_id,levels=c("Healthy_001","Healthy_002","Healthy_003"))
Cohort1_Control$Cohort <- factor(Cohort1_Control$Cohort,levels=c("Healthy"))
Cohort1_Control$Cell_Barcode <- Cohort1_Control$Cell_Barcode[Cohort1_Control$Cell_Barcode %in% Cell_Type$Cell_Barcode]
```

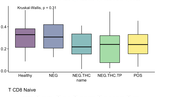
NK



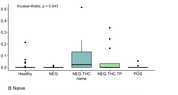
T CD8 Memory



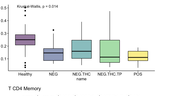
T CD4 Naive



T CD8 Naive



B Naive



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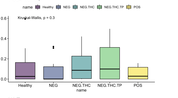
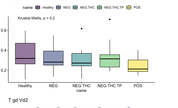
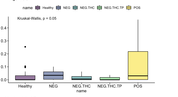


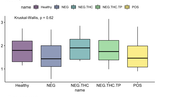
MAIT



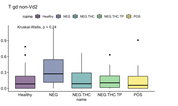
T gd Vd2



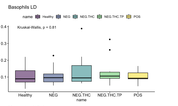
Neutrophils LD



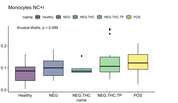
T gd non-Vd2



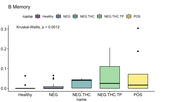
Basophils LD



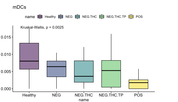
Monocytes NC+I



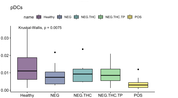
B Memory



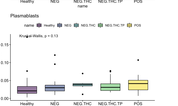
mDCs



pDCs

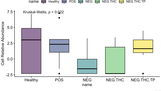


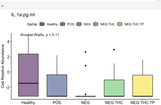
Plasmablasts

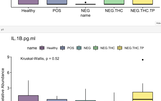


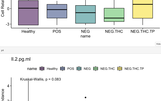
Print boxplots

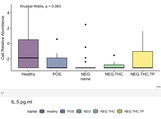
```
sel_phyloseq
sel_phyloseq_df <- data.frame(
  TRC_count=sum(sel_phyloseq@otu_table)/
  sample_sums(sel_phyloseq),
  sel_phyloseq@sam_data,
  sel_phyloseq@otu_table/sel_phyloseq@otu_table[,
  "OTU_1"]
)
ggplot(ggplot_plot_subset$d, ggplot_plot_subset$d$
       .
       .
       .
```

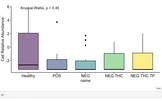


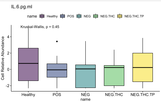


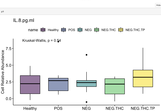


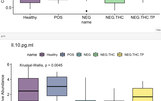


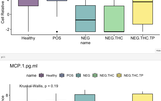


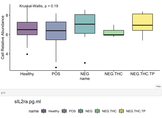


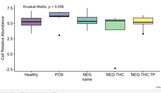


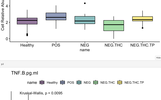


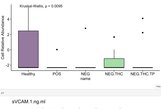


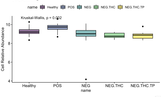


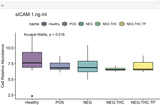


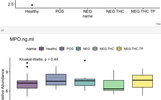


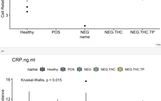


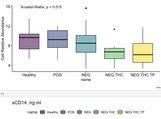


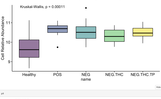


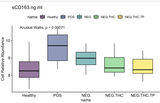












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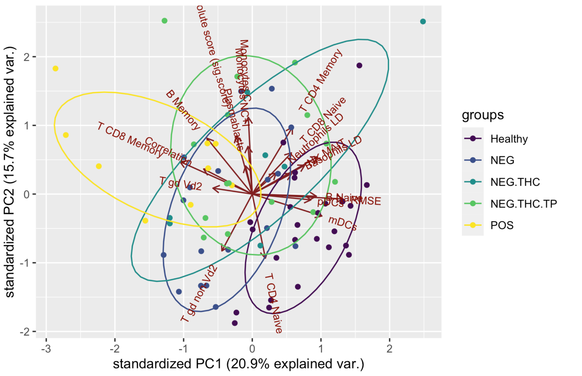
```
type.abdab.csx <- results.csx[, keep]

# Generate vector with group names
my_names <- colnames(type.abdab.csx)
my_names[which(my_names %in% hth)] <- "Healthy"
my_names[which(my_names %in% pos)] <- "POS"
my_names[which(my_names %in% neg)] <- "NEG"
my_names[which(my_names %in% negt)] <- "NEG.THC"
my_names[which(my_names %in% negtp)] <- "NEG.THC.TP"

# Remove all-zero rows
type.abdab.csx <- type.abdab.csx[rowSums(type.abdab.csx) > 0,]

# Transpose table
type.abdab.csx.t <- t(type.abdab.csx)

# Calculate PCA
type.abdab.csx.pca <- prcomp(type.abdab.csx.t, center = TRUE,scale. = TRUE)
summary(type.abdab.csx.pca)
```

```
Importance of components:
                          PC1    PC2    PC3     PC4     PC5     PC6     PC7     PC8
Standard deviation     2.0428 1.7738 1.5472 1.23845 1.09597 1.03290 1.00019 0.95245
Proportion of Variance 0.2087 0.1573 0.1197 0.07669 0.06006 0.05334 0.05002 0.04536
Cumulative Proportion  0.2087 0.3660 0.4857 0.56236 0.62242 0.67576 0.72578 0.77114
                           PC9    PC10    PC11    PC12    PC13    PC14    PC15    PC16
Standard deviation     0.88570 0.83208 0.77599 0.7042 0.69240 0.6357 0.57176 0.56133
Proportion of Variance 0.03922 0.03462 0.03011 0.0248 0.02397 0.0202 0.01635 0.01575
Cumulative Proportion  0.81036 0.84498 0.87509 0.8999 0.92386 0.9441 0.96041 0.97616
                          PC17    PC18    PC19      PC20
Standard deviation     0.49529 0.44739 0.17697 3.228e-15
Proportion of Variance 0.01207 0.01001 0.00157 0.000e+00
Cumulative Proportion  0.98843 0.99843 1.00000 1.000e+00
```

Hide

```
library(ggbiplot)
ggbiplot(type.abdab.csx.pca, groups = my_names, ellipse = T) +
  scale_fill_viridis(discrete = TRUE, alpha=0.6, ) +
  scale_colour_viridis_d()
```



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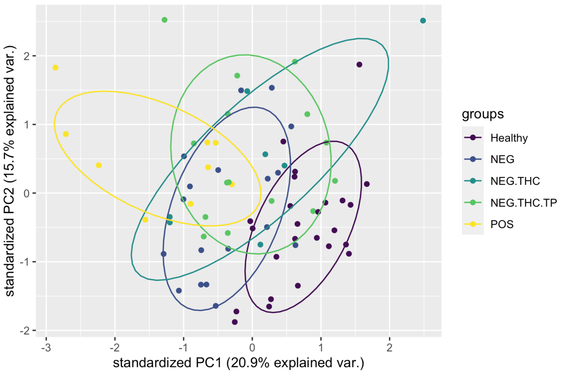
```
ggbiplot(type.abdab.csx.pca, groups = my_names, ellipse = T, var.axes = F) +
  scale_fill_viridis(discrete = TRUE, alpha=0.6, ) +
  scale_colour_viridis_d()
```



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```
yunhua.raw.abis <- read.csv("for_Hernan/data/CellTypeDeconvolution.txt", header = T, row.names = 1, sep = "\t")
```

```
pandoc: CIBERSORTx.utf8.md: openBinaryFile: does not exist (No such file or directory)
```

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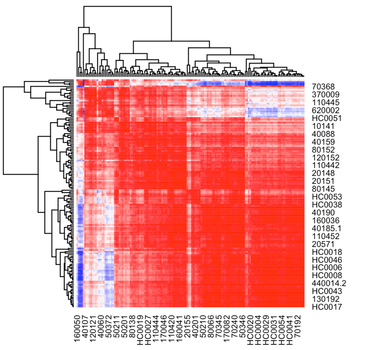
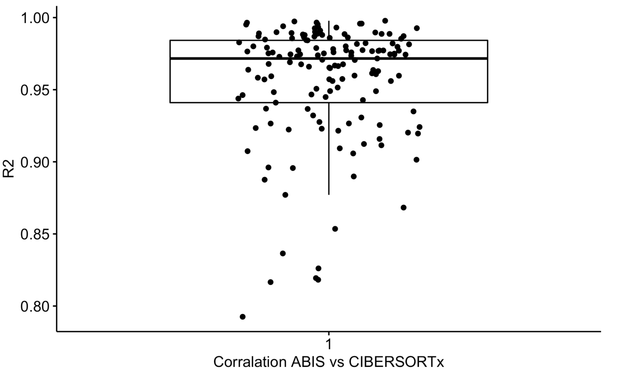
```
x <- gsub("X","",colnames(yunhua.raw.abis))
colnames(yunhua.raw.abis) <- x

# Format cibersortx results
x <- gsub(" ","_",rownames(results.csx))
results.frm.csx <- as.data.frame(results.csx)
rownames(results.frm.csx) <- x

# Run correlation analysis
my_correlation <- cor(yunhua.raw.abis, results.frm.csx)

col<- colorRampPalette(c("blue", "white", "red"))(20)
heatmap(x = my_correlation, col = col, symm = TRUE)
```



Hide

```
correl_vector <- c()
for (i in 1:ncol(my_correlation)){
    correl_vector<- c(correl_vector, my_correlation[i,i])
}

# Calculate R2
correl_vector_r2 <- correl_vector * correl_vector

# Plot correlations
ggboxplot(correl_vector_r2, add = "jitter", ylab = "R2", xlab = "Corralation ABIS vs CIBERSORTx")
```