

# t test comparing pCR vs RD samples

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```
library(dplyr)

## Warning: package 'dplyr' was built under R version 4.2.3
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(ggplot2)

## Warning: package 'ggplot2' was built under R version 4.2.3

library(reshape2)
library(ggpubr)

## Warning: package 'ggpubr' was built under R version 4.2.3

library(rstatix)

## Warning: package 'rstatix' was built under R version 4.2.3
##
## Attaching package: 'rstatix'
## The following object is masked from 'package:stats':
##
##   filter

library(EnvStats)

## Warning: package 'EnvStats' was built under R version 4.2.3
##
## Attaching package: 'EnvStats'
## The following objects are masked from 'package:stats':
##
##   predict, predict.lm

x<-read.csv("D:/MultiOmics/Data/FeatVal.csv")
rownames(x) <- x[,2]; x <- x[,-1:-2]
```

```

x <- x[, c(names(x)[-which(names(x) == "Response")], "Response")]
x[x=="False"] <- 0
x[x=="True"] <- 1

x$Response <- ifelse(x$Response == 0, "RD", "pCR")
x[x=="NaN"] <- 0

x[,1:93] <- lapply(x[,1:93], as.numeric)

x[,1:93] <- scale(x[,1:93])
x[x=="NaN"] <- 0

x.m <- melt(x)

```

```
## Using Response as id variables
```

```
colnames(x.m) <- c("Response", "Feature", "value")
```

```

t_test <- x.m %>%
  group_by(Feature) %>%
  t_test(value ~ Response) %>%
  adjust_pvalue(method = "bonferroni") %>%
  add_significance("p.adj")

```

```

t_test <- t_test %>%
  add_xy_position(fun = "mean_se", x = "Response")

```

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t_test <- x.m %>%
  group_by(Feature) %>%
  t_test(value ~ Response) %>%
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```

t_test <- t_test %>%
  add_xy_position(fun = "mean_se", x = "Response")

```

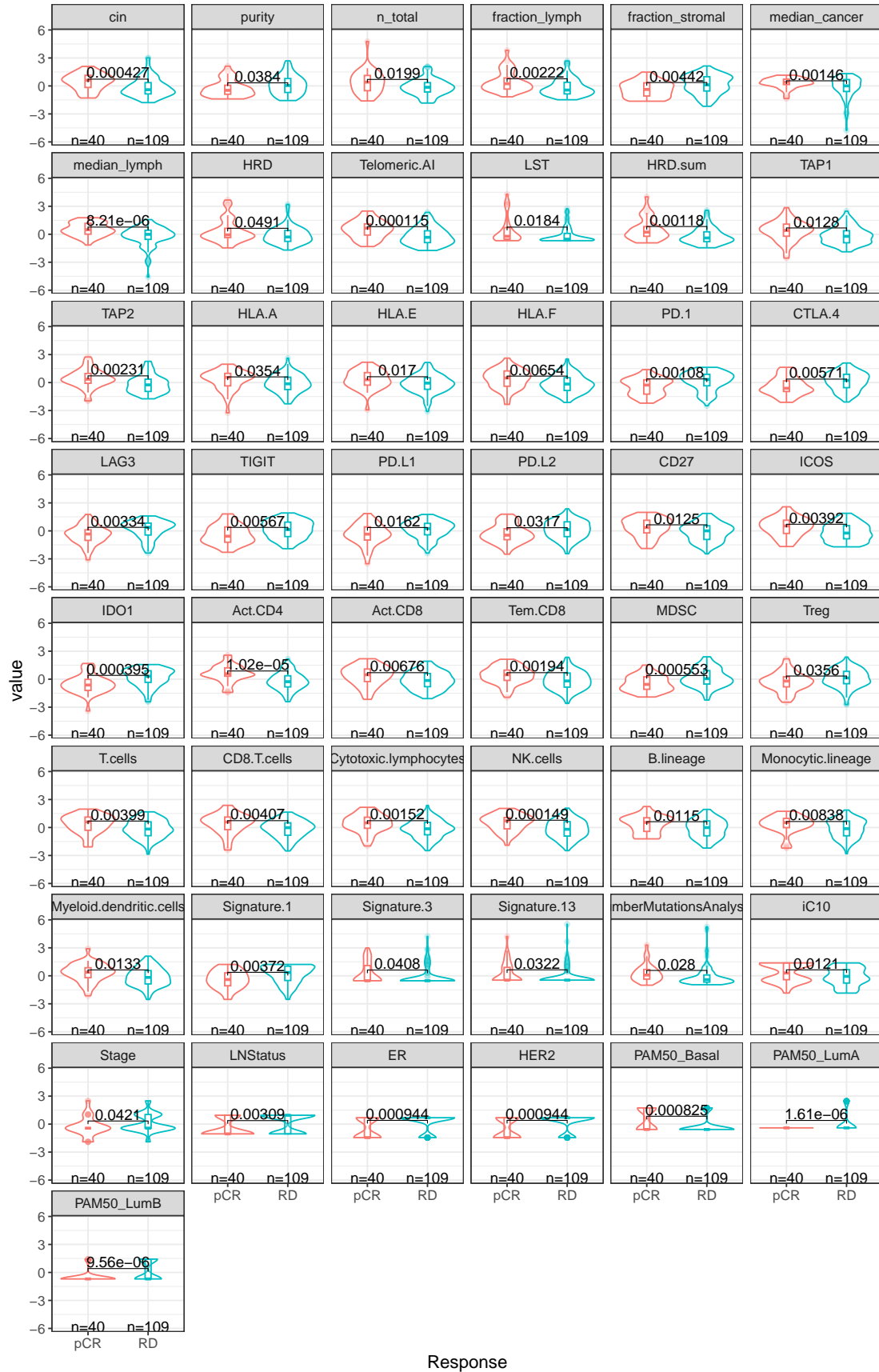
```
t_test <- subset(t_test, t_test$p < 0.05)
```

```
x.m <- subset(x.m, x.m$Feature %in% t_test$Feature)
```

```

ggplot(x.m, aes(x=Response, y=value, color=Response)) +
  geom_violin() +
  geom_boxplot(width=0.1, alpha=0.2) +
  facet_wrap(~Feature, ncol=6) +
  stat_pvalue_manual(t_test, label="p", size=4) +
  stat_n_text(size=4) +
  theme_bw() +
  theme(text=element_text(size=13)) +
  theme(legend.position="none")

```



Showing features with significant differences

```
t_test <- subset(t_test, t_test$p.adj < 0.05)
t_test2 <- t_test

t_test2$statistic2 <- t_test2$statistic / abs(t_test2$statistic)
t_test2$`-Log(p.adj)*Direction` <- -log10(t_test2$p.adj) * t_test2$statistic2
t_test2 <- t_test2[order(-t_test2$`-Log(p.adj)*Direction`),]

t_test2$Feature <- as.character(t_test2$Feature)
t_test2$Feature <- factor(t_test2$Feature, levels=t_test2$Feature)

t_test2 <- t_test2[, c(1, 16, 17)]

ggplot(t_test2, aes(x=Feature, y=`-Log(p.adj)*Direction`, fill=as.factor(statistic2)))+
  geom_bar(stat="identity", width=0.65)+
  scale_color_discrete(name="")+theme(axis.title.y=element_blank())+
  theme_bw()+theme(text=element_text(size=14))+theme(axis.text.x=element_text(angle=90))+
  theme(legend.position="none")+
  ylim(-4, 4)
```

