

Retrospective and Prospective Study of the Interleukin-28B and Endogenous Interferon with Hepatitis-C Virus and/ or Schistosoma mansoni

Mona Maher

August 25, 2019

```
library(tinytex)
```

```
## Warning: package 'tinytex' was built under R version 3.5.3
```

```
options(tinytex.verbose = TRUE)
IFN<-read.csv(file.choose(), header = T)
attach(IFN)
View(IFN)
```

Demonstration the demographic data *AGE*

```
options(tinytex.verbose = TRUE)
summary(IFN$age..yr.)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  30.00   38.00   43.00   43.84   46.50   81.00
```

```
library(finalfit)
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 3.5.3
```

```
##
```

```
## 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
```

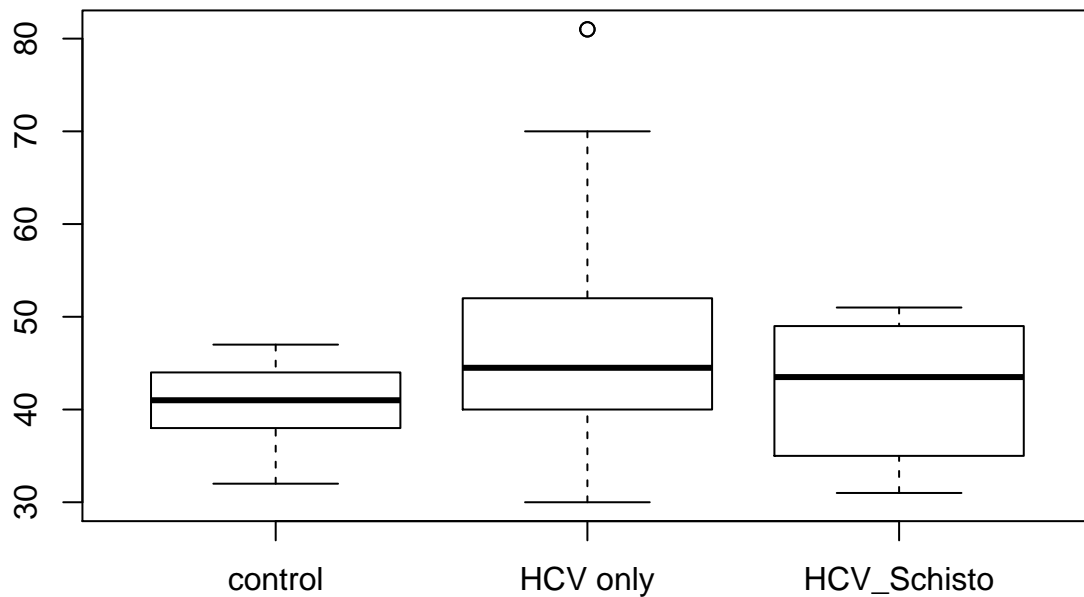
```
table1<-as.data.frame(IFN%>%summary_factorlist("age..yr.", "Patient.Group", p = F, add_dependent_label = T))
```

```
## Warning in summary_factorlist(., "age..yr.", "Patient.Group", p = F,
## add_dependent_label = T, : Dependent is not a factor and will be treated as
## a continuous variable
```

```
table1
```

```
##      Dependent: age..yr.      Mean (sd)
## 1      Patient.Group      control 40.5 (4.3)
## 2                      HCV only 46.9 (11.3)
## 3                      HCV_Schisto 42.3 (7.2)
```

```
boxplot(age..yr.~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$age..yr.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$age..yr.
## W = 0.86666, p-value = 2.288e-08
  • p-value is less than 0.05 so reject null hypothesis
  • The age is not normally distributed
```

```
options(tinytex.verbose = TRUE)
kruskal.test(age..yr.~Patient.Group, data = IFN)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  age..yr. by Patient.Group
## Kruskal-Wallis chi-squared = 8.4174, df = 2, p-value = 0.01487
```

```
library(FSA)
```

```
## Warning: package 'FSA' was built under R version 3.5.3
## ## FSA v0.8.24. See citation('FSA') if used in publication.
## ## Run fishR() for related website and fishR('IFAR') for related book.
```

```
dunnTest(age..yr.~Patient.Group, data = IFN)
```

```
## Dunn (1964) Kruskal-Wallis multiple comparison
```

```
## p-values adjusted with the Holm method.
##           Comparison      Z    P.unadj    P.adj
## 1 control - HCV only -2.877020 0.004014505 0.01204352
## 2 control - HCV_Schisto -1.041659 0.297569646 0.29756965
## 3 HCV only - HCV_Schisto 1.370589 0.170503248 0.34100650
```

```
library(ggplot2)
```

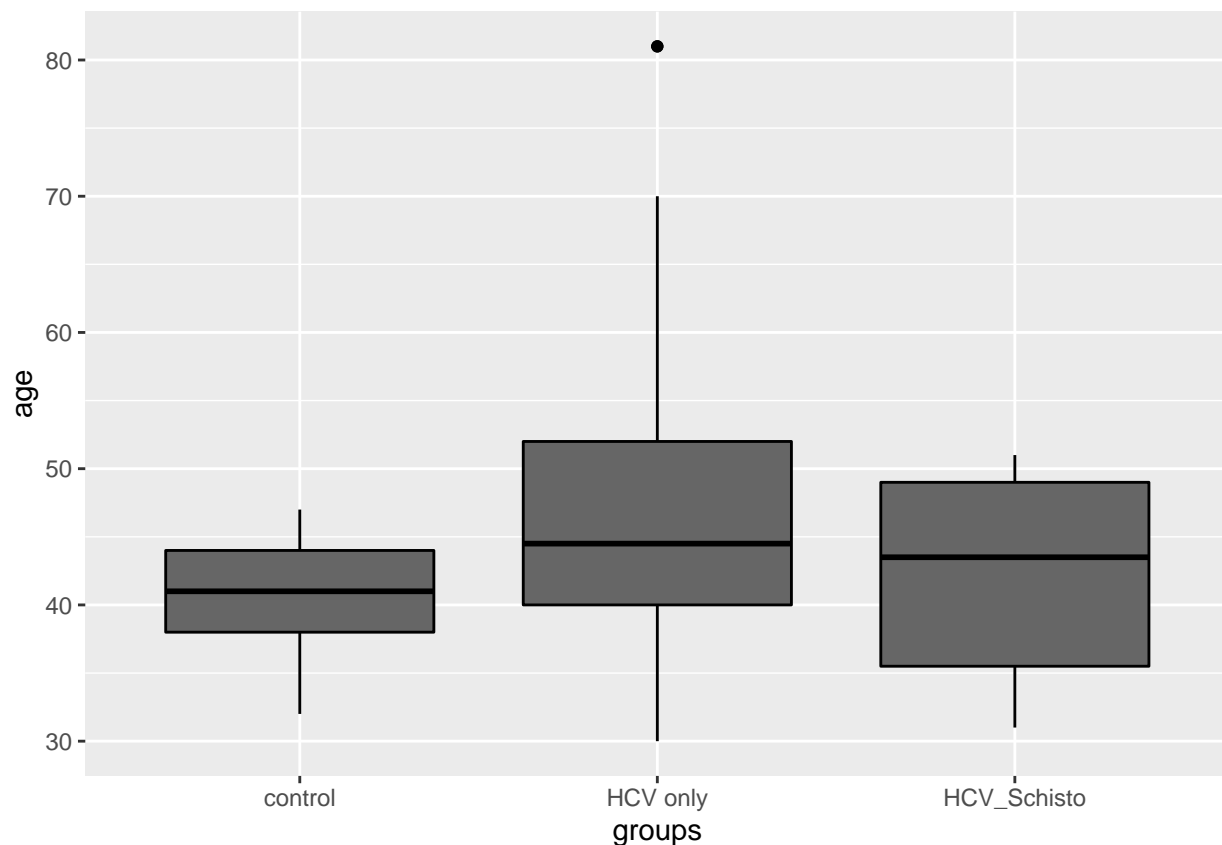
```
## Warning: package 'ggplot2' was built under R version 3.5.3
```

```
library(tidyr)
```

```
## Warning: package 'tidyr' was built under R version 3.5.3
```

```
##
## Attaching package: 'tidyr'
## The following object is masked _by_ '.GlobalEnv':
##
## table1
```

```
ggplot(IFN, aes(x= Patient.Group, y= age..yr.)) +
  geom_boxplot(fill = "grey40", color = "black") +
  scale_x_discrete() + labs(x = "groups", y = "age")
```



```
conf1<-diff(tapply(IFN$age..yr.,IFN$Patient.Group,mean))
quantile(conf1,prob = 0.025)
```

```
## 2.5%
```

```
## -4.287201
```

```
quantile(conf1,prob = 0.975)
```

```
## 97.5%
```

```
## 6.14824
```

- There is a significant difference only between control and HCV groups in ages
- Confidence interval shows that no difference in means of age between groups

gender

```
options(tinytex.verbose = TRUE)
```

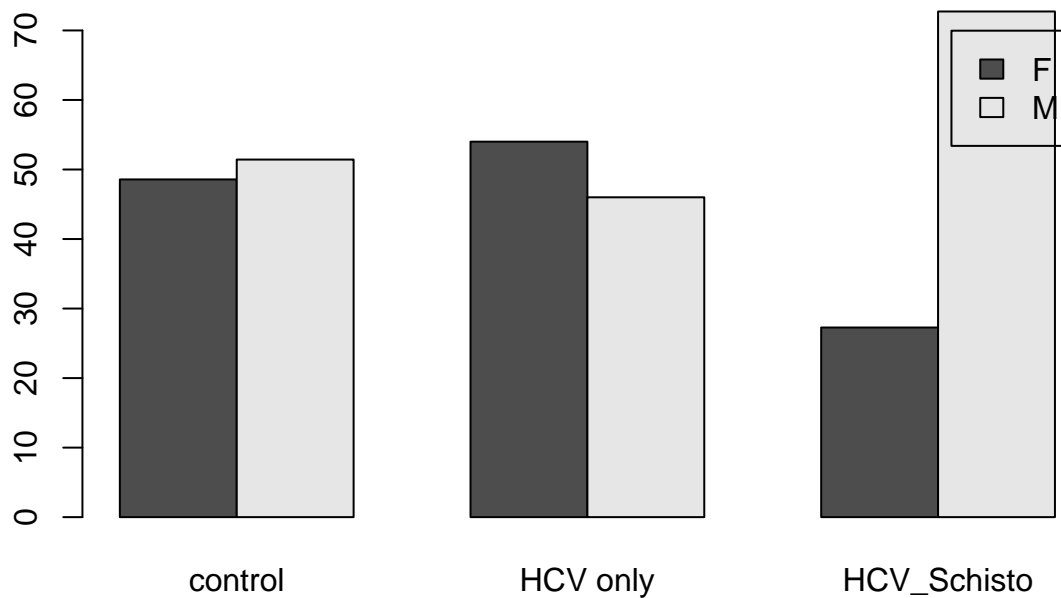
```
table2<-as.data.frame(IFN%>%summary_factorlist("gender", "Patient.Group", p = F, add_dependent_label = T))
table2
```

```
## Dependent: gender          F          M
## 1 Patient.Group control 17 (48.6) 18 (51.4)
## 2           HCV only 27 (54.0) 23 (46.0)
## 3           HCV_Schisto 6 (27.3) 16 (72.7)
```

```
tab00<-table(IFN$Patient.Group, IFN$gender)
```

```
tab0<- prop.table(tab00,1)*100
```

```
barplot(t(tab0), beside = T, legend.text = colnames(tab0))
```

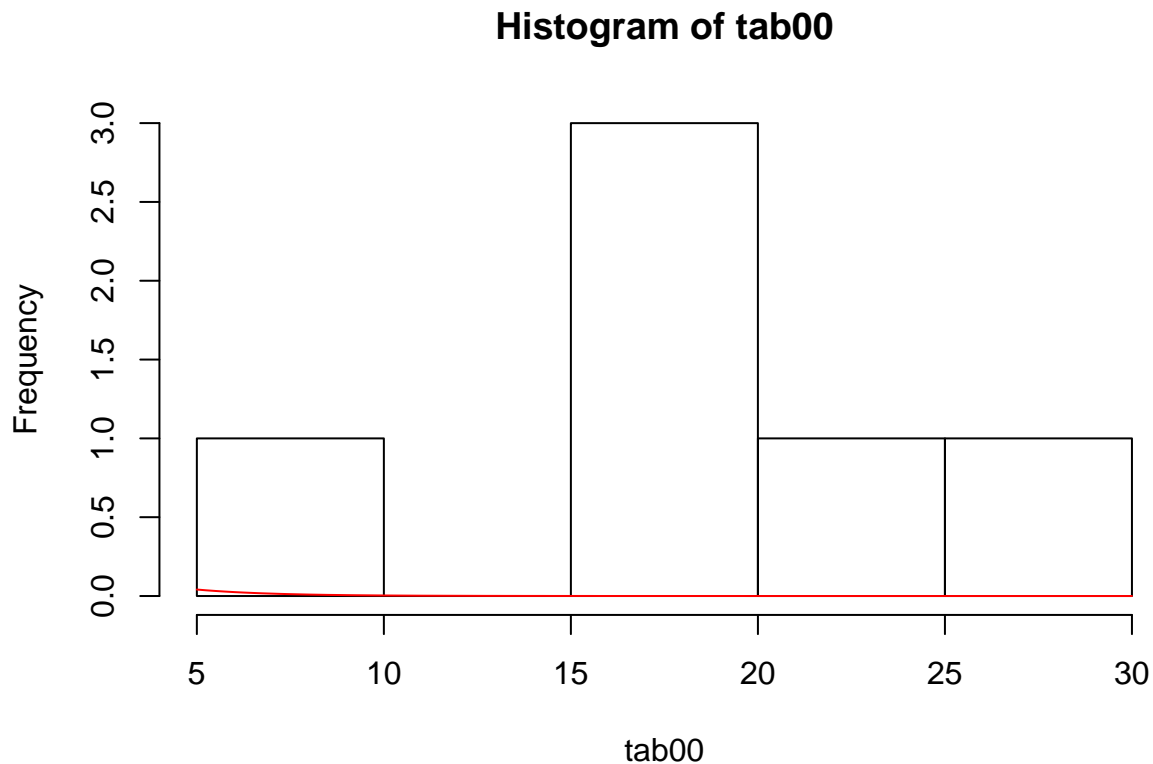


```
options(tinytex.verbose = TRUE)
```

```
chisq.test(tab00)
```

```
##
```

```
## Pearson's Chi-squared test
##
## data:  tab00
## X-squared = 4.4551, df = 2, p-value = 0.1078
x<-hist(tab00)
curve(dchisq(x, 2), col= "red", add = T)
```



-p-value is more than 0.05 so fail to reject null hypothesis - There is no significant difference in gender between groups

residence

```
options(tinytex.verbose = TRUE)
table3<-as.data.frame(IFN%>%summary_factorlist("residence", "Patient.Group", p = F, add_dependent_label
```

```
## Warning in chisq.test(tab, correct = FALSE): Chi-squared approximation may
## be incorrect
```

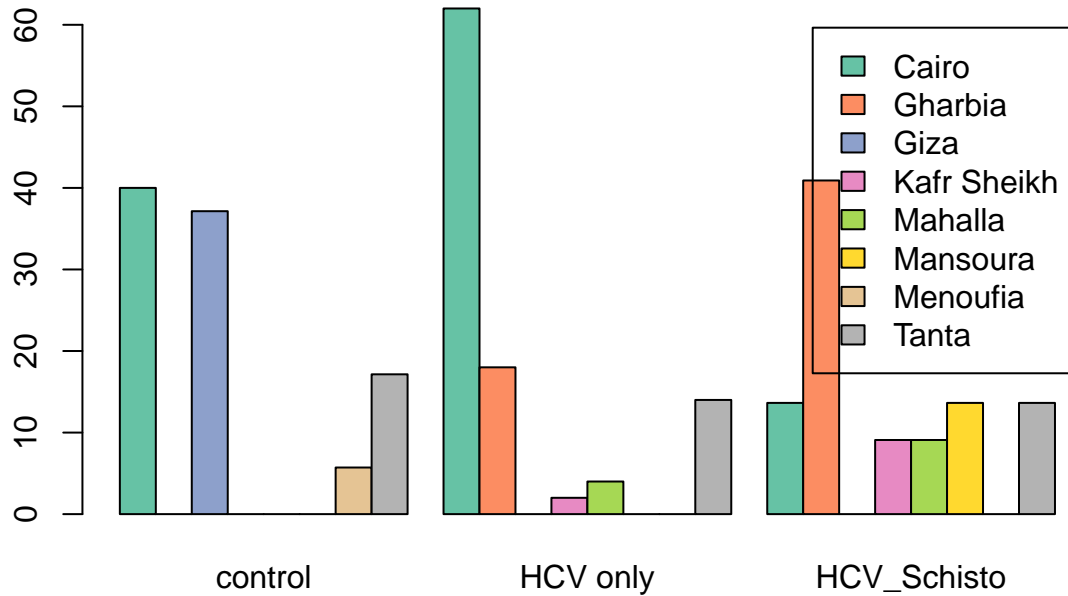
table3

```
##   Dependent: residence      Cairo  Gharbia    Giza
## 1   Patient.Group    control 14 (40.0)  0 (0.0) 13 (37.1)
## 2                HCV only 31 (62.0)  9 (18.0)  0 (0.0)
## 3                HCV_Schisto  3 (13.6)  9 (40.9)  0 (0.0)
##   Kafr Sheikh Mahalla Mansoura Menoufia    Tanta
## 1    0 (0.0) 0 (0.0)  0 (0.0)  2 (5.7)  6 (17.1)
## 2    1 (2.0) 2 (4.0)  0 (0.0)  0 (0.0)  7 (14.0)
## 3    2 (9.1) 2 (9.1)  3 (13.6)  0 (0.0)  3 (13.6)
```

```

tabb<-table(IFN$Patient.Group, IFN$residence)
tab<- prop.table(tabb,1)*100
library(RColorBrewer)
col<-brewer.pal(8, "Set2")
barplot(t(tab), beside = T, legend.text = colnames(tab), col = col)

```



- The plot showed that Cairo has the highest HCV only infection level and Garbia has the highest HCV with schistosoma infection level.

```

options(tinytex.verbose = TRUE)
chisq.test(tabb)

```

```
## Warning in chisq.test(tabb): Chi-squared approximation may be incorrect
```

```
##
```

```
## Pearson's Chi-squared test
```

```
##
```

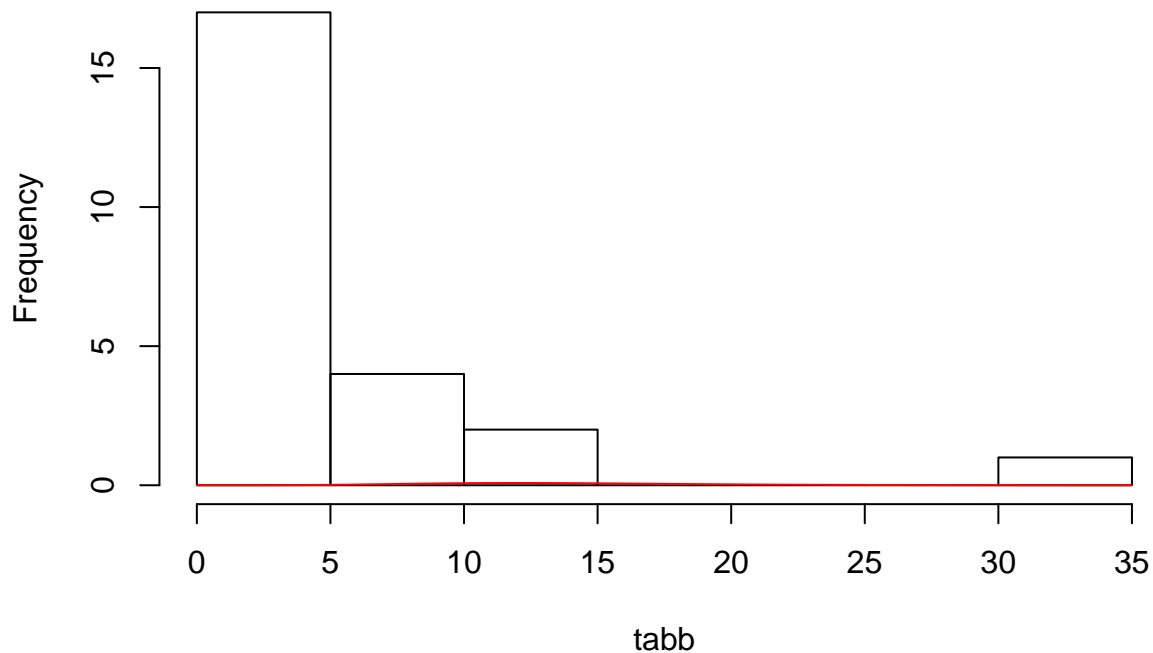
```
## data: tabb
```

```
## X-squared = 71.574, df = 14, p-value = 9.997e-10
```

```
x<-hist(tabb)
```

```
curve(dchisq(x, 14), col= "red", add = T)
```

Histogram of tabb



- p-value is less than 0.05 so reject null hypothesis - There is a significant difference in residence between groups

occupation

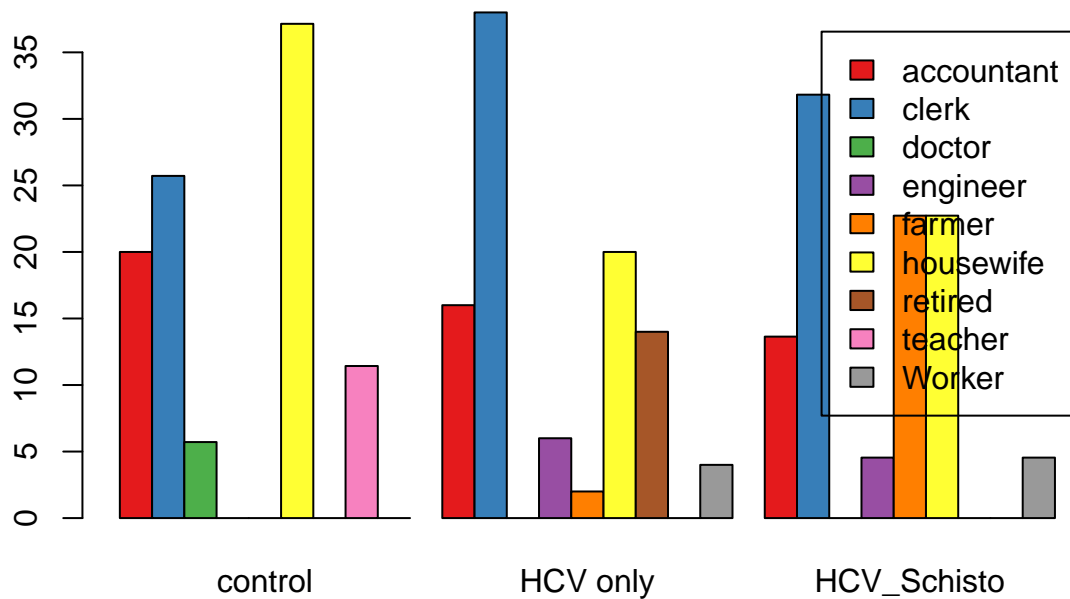
```
options(tinytex.verbose = TRUE)
table4<-as.data.frame(IFN%>%summary_factorlist("occupation", "Patient.Group", p = F, add_dependent_label = TRUE))
```

```
## Warning in chisq.test(tab, correct = FALSE): Chi-squared approximation may
## be incorrect
```

```
table4
```

```
##   Dependent: occupation      accountant      clerk  doctor engineer
## 1      Patient.Group      control    7 (20.0)  9 (25.7) 2 (5.7)  0 (0.0)
## 2                      HCV only    8 (16.0) 19 (38.0) 0 (0.0)  3 (6.0)
## 3                      HCV_Schisto  3 (13.6)  7 (31.8) 0 (0.0)  1 (4.5)
##   farmer housewife retired  teacher  Worker
## 1  0 (0.0) 13 (37.1)  0 (0.0)  4 (11.4)  0 (0.0)
## 2  1 (2.0) 10 (20.0)  7 (14.0)  0 (0.0)  2 (4.0)
## 3  5 (22.7)  5 (22.7)  0 (0.0)  0 (0.0)  1 (4.5)
```

```
tab11<-table(IFN$Patient.Group, IFN$occupation)
tab1<- prop.table(tab11,1)*100
col1<-brewer.pal(9, "Set1")
barplot(t(tab1), beside = T, legend.text = colnames(tab1), col = col1)
```



```
options(tinytex.verbose = TRUE)
chisq.test(tab11)
```

```
## Warning in chisq.test(tab11): Chi-squared approximation may be incorrect
```

```
##
```

```
## Pearson's Chi-squared test
```

```
##
```

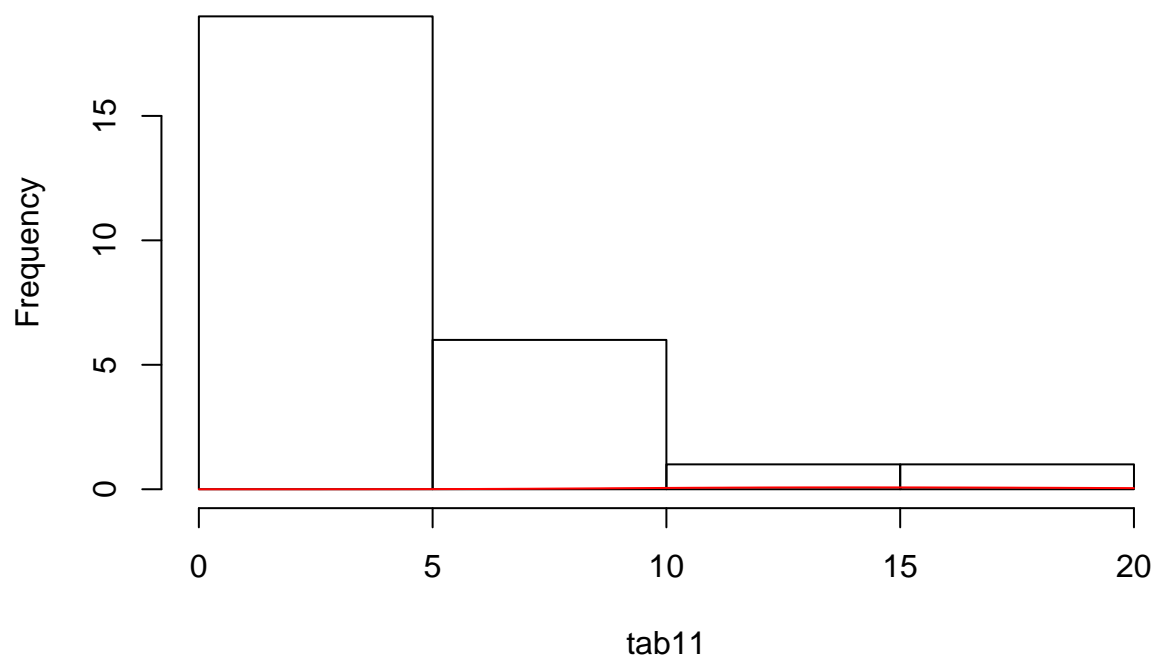
```
## data: tab11
```

```
## X-squared = 42.207, df = 16, p-value = 0.0003675
```

```
x<-hist(tab11)
```

```
curve(dchisq(x, 16), col= "red", add = T)
```


Histogram of tab11



- p-value is less than 0.05 so reject null hypothesis - There is a significant difference in occupation between groups

primary outcome

peg-IFN

```
table5<-as.data.frame(IFN%>%summary_factorlist("IFN...IU.ml.", "Patient.Group", p = F, add_dependent_l
```

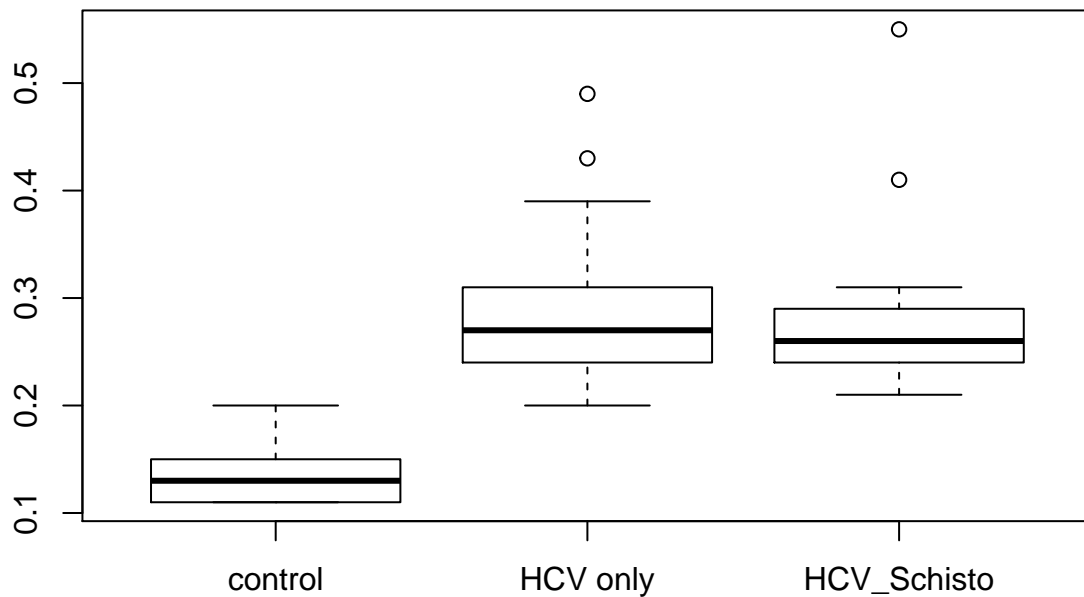
```
## Warning in summary_factorlist(., "IFN...IU.ml.", "Patient.Group", p = F, :
```

```
## Dependent is not a factor and will be treated as a continuous variable
```

```
table5
```

```
##   Dependent: IFN...IU.ml.      Mean (sd)
## 1      Patient.Group      control 0.1 (0.0)
## 2                      HCV only 0.3 (0.1)
## 3                      HCV_Schisto 0.3 (0.1)
```

```
boxplot(IFN...IU.ml. ~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$IFN....IU.ml.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$IFN....IU.ml.
## W = 0.93809, p-value = 8.545e-05
• p-value is less than 0.05 so reject null hypothesis
• IFN is not normally distributed
```

```
options(tinytex.verbose = TRUE)
kruskal.test(IFN....IU.ml.~Patient.Group, data = IFN)
```

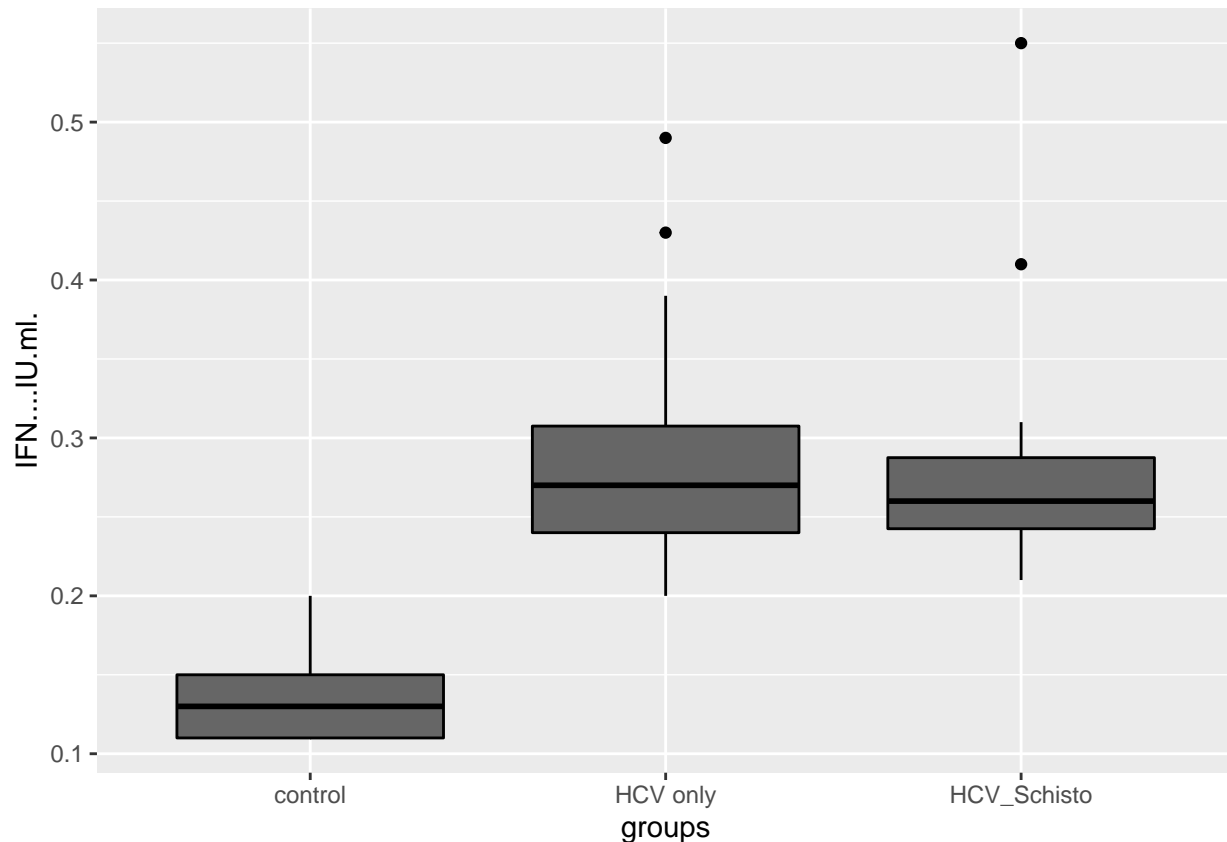
```
##
##  Kruskal-Wallis rank sum test
##
## data:  IFN....IU.ml. by Patient.Group
## Kruskal-Wallis chi-squared = 70.216, df = 2, p-value = 5.66e-16
```

```
library(FSA)
dunnTest(IFN....IU.ml.~Patient.Group, data = IFN)
```

```
## Dunn (1964) Kruskal-Wallis multiple comparison
##  p-values adjusted with the Holm method.
##
##      Comparison      Z      P.unadj      P.adj
## 1      control - HCV only -7.977664 1.491285e-15 4.473854e-15
```

```
## 2 control - HCV_Schisto -6.055239 1.402089e-09 2.804179e-09
## 3 HCV only - HCV_Schisto 0.432688 6.652414e-01 6.652414e-01
```

```
library(ggplot2)
library(tidyr)
ggplot(IFN, aes(x= Patient.Group, y= IFN....IU.ml.)) +
  geom_boxplot(fill = "grey40", color = "black") +
  scale_x_discrete() + labs(x = "groups", y = "IFN....IU.ml.")
```



```
conf2<-diff(tapply(IFN$IFN....IU.ml.,IFN$Patient.Group,mean))
quantile(conf2,prob = 0.025)
```

```
##          2.5%
## 0.0001387013
```

```
quantile(conf2,prob = 0.975)
```

```
##          97.5%
## 0.1429003
```

- p-value of control-HCV and control-HCV_Schisto is less than 0.05 so reject null hypothesis
- p-value of HCV only-HCV_Schisto is more than 0.05 so fail to reject null hypothesis
- There is a highly significant difference between control-HCV and control-HCV_Schisto but no significant difference between HCV only-HCV_Schisto in PEG-IFN
- Confidence interval shows that there is a difference in means of PEG-IFN between groups
- SO we conclude that IFN level is increased in HCV and HCV with Schistosoma co-infection

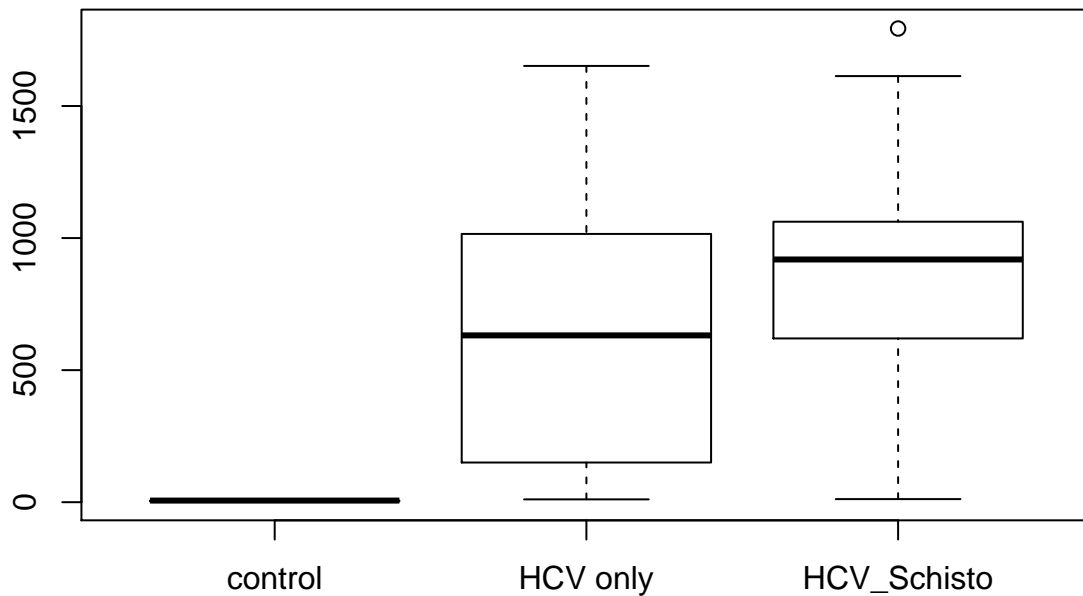
- We conclude also that Schistosoma infection don't significantly affect on PEG-IFN level in patients with HCV

IL-28B

```
options(tinytex.verbose = TRUE)
table6<-as.data.frame(IFN%>%summary_factorlist("IL.28B..pg.ml.", "Patient.Group", p = F, add_dependent_

## Warning in summary_factorlist(., "IL.28B..pg.ml.", "Patient.Group", p =
## F, : Dependent is not a factor and will be treated as a continuous variable
table6

##   Dependent: IL.28B..pg.ml.          Mean (sd)
## 1      Patient.Group      control      5.7 (1.9)
## 2                        HCV only 631.2 (478.1)
## 3                        HCV_Schisto 893.9 (393.0)
boxplot(IL.28B..pg.ml.~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$IL.28B..pg.ml.)

##
##  Shapiro-Wilk normality test
##
## data:  IFN$IL.28B..pg.ml.
## W = 0.84712, p-value = 3.931e-09
```

- p-value is less than 0.05 so reject null hypothesis
- IL-28B is not normally distributed

```

options(tinytex.verbose = TRUE)
kruskal.test(IL.28B..pg.ml.~Patient.Group, data = IFN)

##
## Kruskal-Wallis rank sum test
##
## data: IL.28B..pg.ml. by Patient.Group
## Kruskal-Wallis chi-squared = 71.899, df = 2, p-value = 2.44e-16

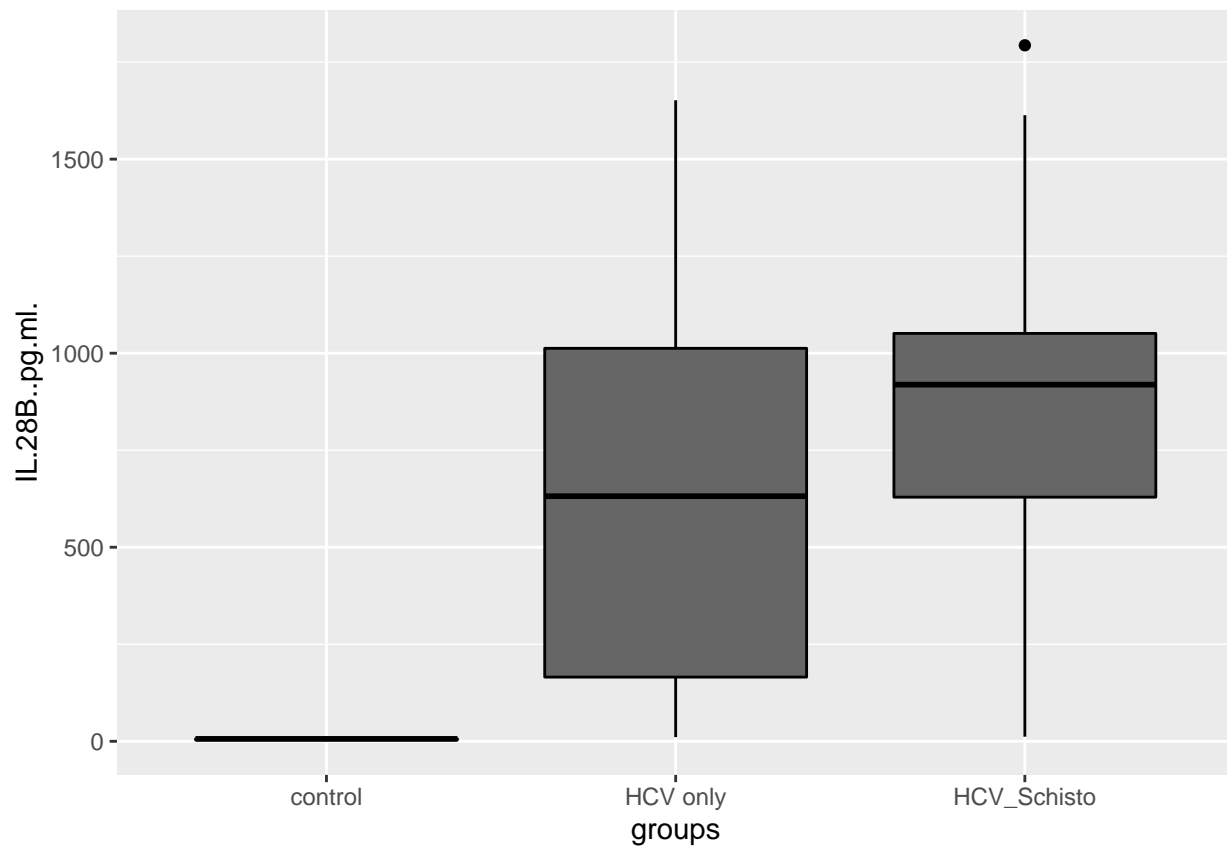
library(FSA)
dunnTest(IL.28B..pg.ml.~Patient.Group, data = IFN)

## Dunn (1964) Kruskal-Wallis multiple comparison
## p-values adjusted with the Holm method.

##           Comparison      Z      P.unadj      P.adj
## 1 control - HCV only -7.338475 2.160418e-13 6.481255e-13
## 2 control - HCV_Schisto -7.231474 4.777786e-13 9.555571e-13
## 3 HCV only - HCV_Schisto -1.368811 1.710583e-01 1.710583e-01

ggplot(IFN, aes(x= Patient.Group, y= IL.28B..pg.ml.)) +
  geom_boxplot(fill = "grey40", color = "black") +
  scale_x_discrete() + labs(x = "groups", y = "IL.28B..pg.ml.")

```



```

conf3<-diff(tapply(IFN$IL.28B..pg.ml.,IFN$Patient.Group,mean))
quantile(conf3,prob = 0.025)

```

```
## 2.5%
```

```
## 271.7832
```

```
quantile(conf3,prob = 0.975)
```

```
## 97.5%
```

```
## 616.4539
```

- p-value of control-HCV and control-HCV_Schisto is less than 0.05 so reject null hypothesis
- p-value of HCV only-HCV_Schisto is more than 0.05 so fail to reject null hypothesis
- There is a highly significant difference between control-HCV and control-HCV_Schisto but no significant difference between HCV only-HCV_Schisto in IL-28B
- Confidence interval shows that there is a difference in means of IL-28B between groups
- SO we conclude that IL-28B level is increased in HCV and HCV with Schistosoma co-infection
- We conclude also that Schistosoma infection don't significantly affect on IL-28B level in patients with HCV

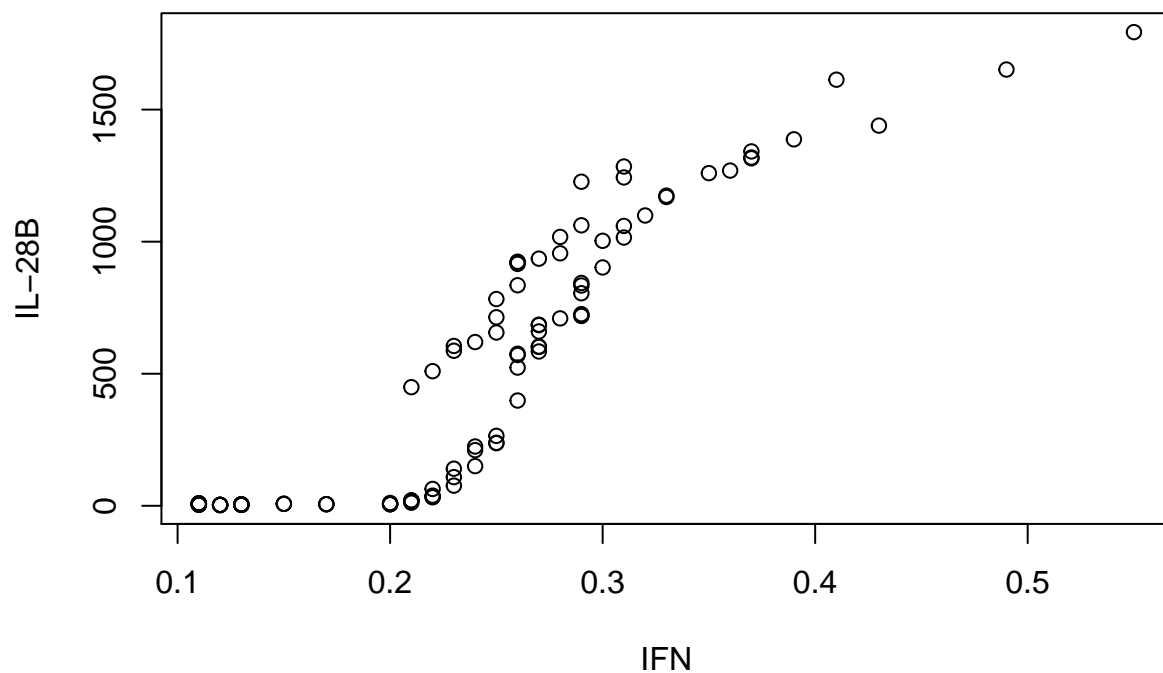
To investigate correlation between PEG-IFN and IL-28

```
options(tinytex.verbose = TRUE)
```

```
cor(IFN$IFN....IU.ml.,IFN$IL.28B..pg.ml., method = "spearman")
```

```
## [1] 0.9455703
```

```
plot(IFN$IFN....IU.ml.,IFN$IL.28B..pg.ml., xlab = "IFN", ylab = "IL-28B")
```



- It's positive strong linear relationship between IFN and IL-28B

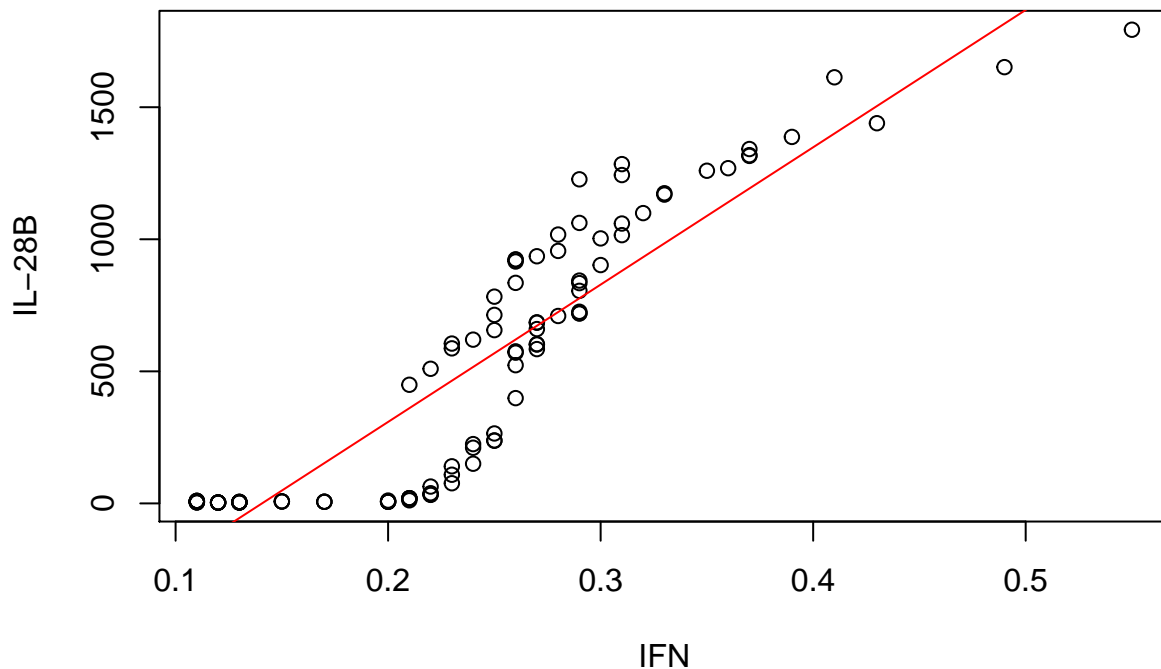
```

options(tinytex.verbose = TRUE)
model<-lm(IL.28B..pg.ml.~ IFN...IU.ml., data = IFN)
model

##
## Call:
## lm(formula = IL.28B..pg.ml. ~ IFN...IU.ml., data = IFN)
##
## Coefficients:
## (Intercept)  IFN...IU.ml.
##      -731.2      5198.8

plot(IFN$IFN...IU.ml.,IFN$IL.28B..pg.ml., xlab = "IFN", ylab = "IL-28B")
abline(model, col=2)

```



```

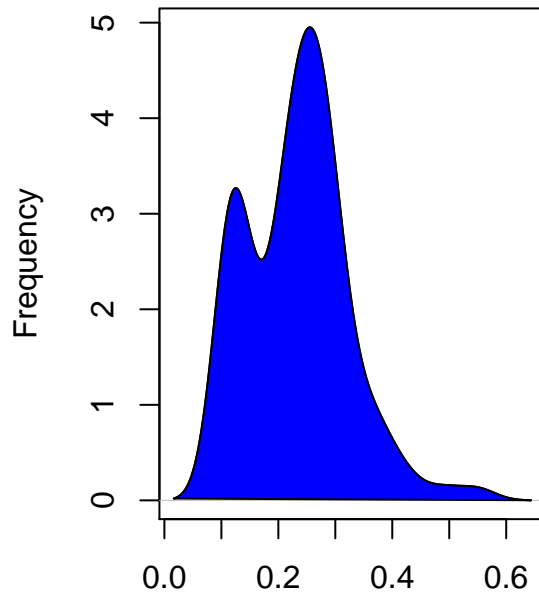
library(e1071)

## Warning: package 'e1071' was built under R version 3.5.3

par(mfrow=c(1, 2))
plot(density(IFN$IFN...IU.ml.), main="Density Plot: IFN", ylab="Frequency")
polygon(density(IFN$IFN...IU.ml.), col="blue")
plot(density(IFN$IL.28B..pg.ml.), main="Density Plot: IL-28B", ylab="Frequency")
polygon(density(IFN$IL.28B..pg.ml.), col="blue")

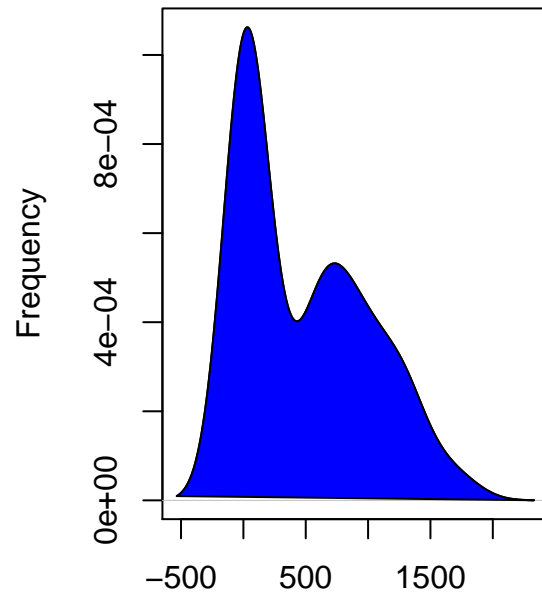
```

Density Plot: IFN



N = 107 Bandwidth = 0.03121

Density Plot: IL-28B

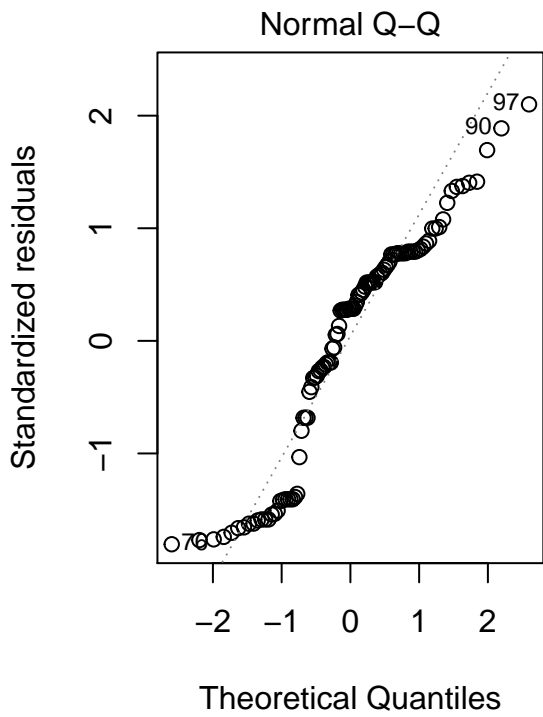
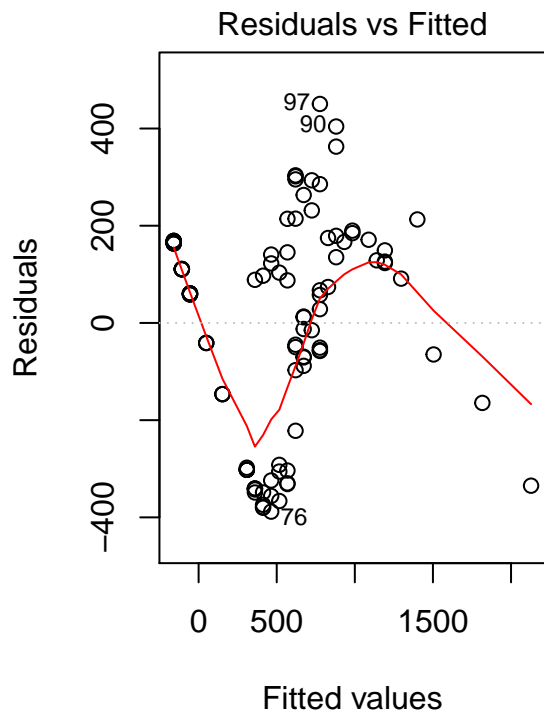


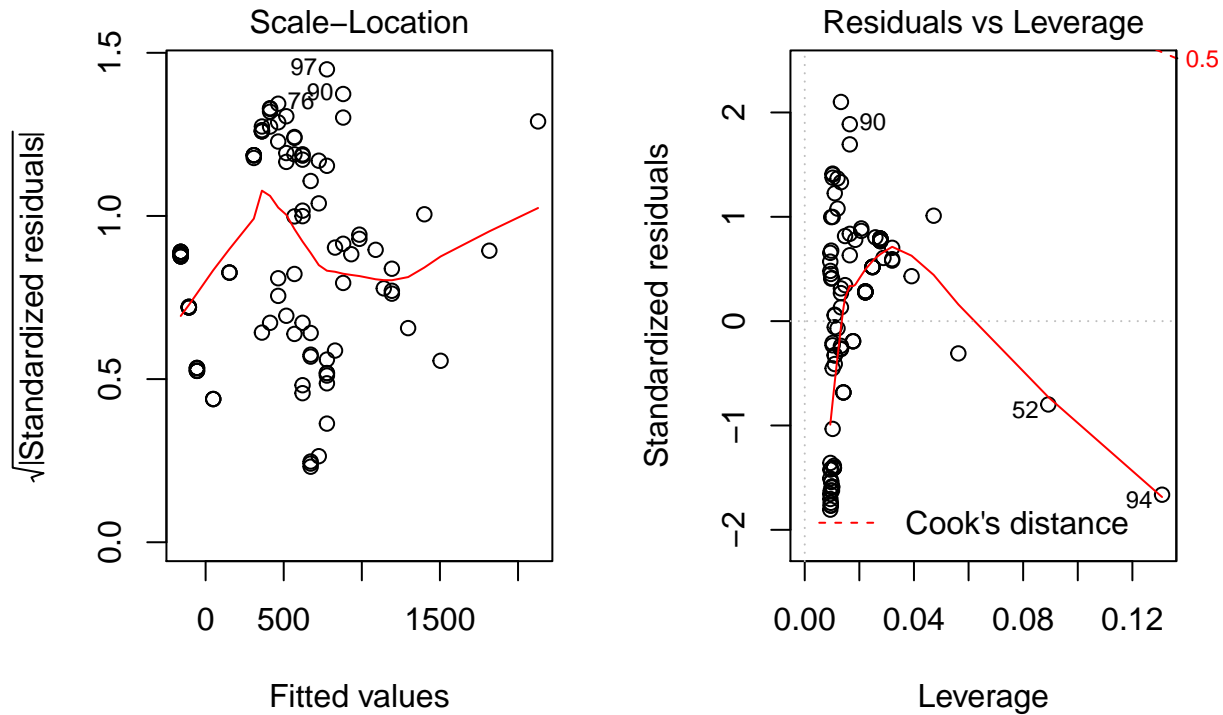
N = 107 Bandwidth = 179.2

```
summary(model)
```

```
##
## Call:
## lm(formula = IL.28B.pg.ml. ~ IFN....IU.ml., data = IFN)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -388.17 -146.44   60.85  164.52  450.48
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -731.18     59.16  -12.36  <2e-16 ***
## IFN....IU.ml.  5198.80    237.48   21.89  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 215.9 on 105 degrees of freedom
## Multiple R-squared:  0.8203, Adjusted R-squared:  0.8186
## F-statistic: 479.2 on 1 and 105 DF, p-value: < 2.2e-16
```

```
plot(model)
```



```
confint(model)
```

```
##                2.5 %    97.5 %
## (Intercept)  -848.4719 -613.8792
## IFN....IU.ml. 4727.9213 5669.6708
```

-The variability of IL-28B is 82% with IFN, there is a highly significant difference between observation and errors. -From confidence interval mu don't equal zero so the mean of IFN don't equal the mean of IL-28B

Secondary outcome

ALT

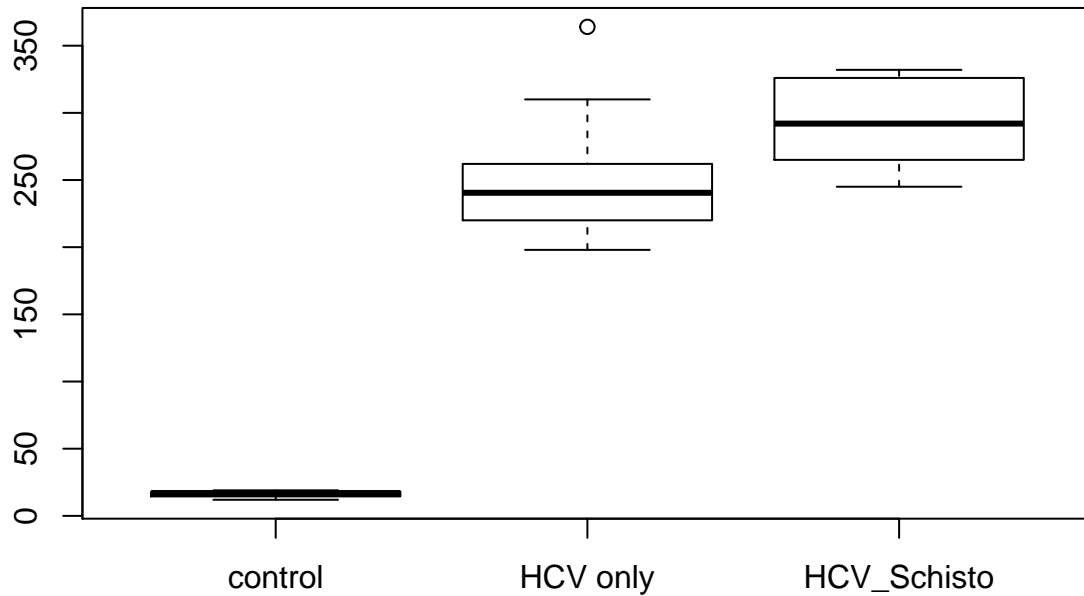
```
options(tinytex.verbose = TRUE)
library(finalfit)
library(dplyr)
table7<-as.data.frame(IFN%>%summary_factorlist("ALT..IU.L.", "Patient.Group", p = F, add_dependent_label = T))
```

```
## Warning in summary_factorlist(., "ALT..IU.L.", "Patient.Group", p = F,
## add_dependent_label = T, : Dependent is not a factor and will be treated as
## a continuous variable
```

```
table7
```

```
##   Dependent: ALT..IU.L.      Mean (sd)
## 1   Patient.Group    control  16.2 (1.9)
## 2                   HCV only 243.9 (32.1)
## 3                   HCV_Schisto 294.3 (28.2)
```

```
boxplot(ALT..IU.L.~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$ALT..IU.L.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$ALT..IU.L.
## W = 0.79652, p-value = 7.366e-11
```

- p-value is less than 0.05 so reject null hypothesis
- ALT is not normally distributed

```
options(tinytex.verbose = TRUE)
kruskal.test(ALT..IU.L.~Patient.Group, data = IFN)
```

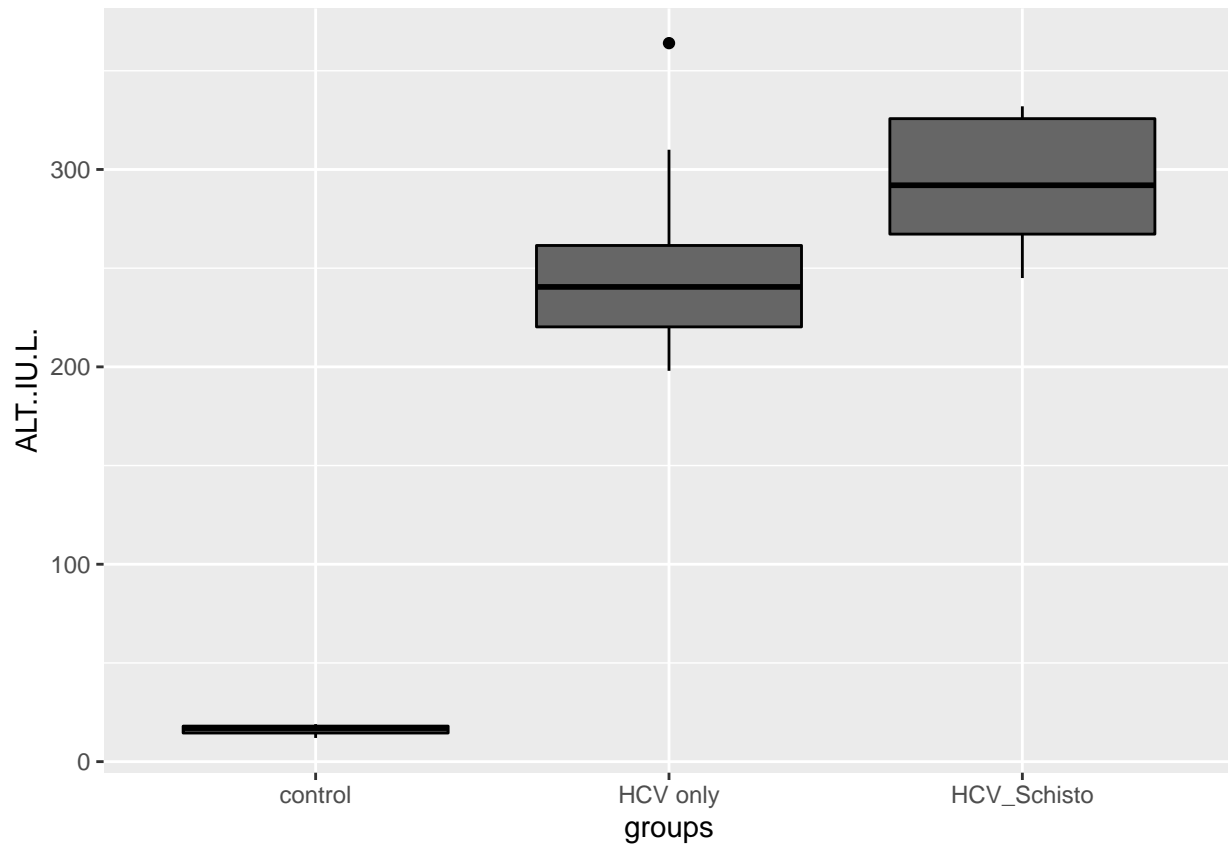
```
##
##  Kruskal-Wallis rank sum test
##
## data:  ALT..IU.L. by Patient.Group
## Kruskal-Wallis chi-squared = 82.856, df = 2, p-value < 2.2e-16
```

```
library(FSA)
library(ggplot2)
dunnTest(ALT..IU.L.~Patient.Group, data = IFN)
```

```
## Dunn (1964) Kruskal-Wallis multiple comparison
##  p-values adjusted with the Holm method.
```

```
##           Comparison      Z      P.unadj      P.adj
## 1   control - HCV only -6.560785 5.352537e-11 1.070507e-10
## 2 control - HCV_Schisto -8.673447 4.192309e-18 1.257693e-17
## 3 HCV only - HCV_Schisto -3.572222 3.539654e-04 3.539654e-04
```

```
ggplot(IFN, aes(x= Patient.Group, y= ALT..IU.L.)) +
  geom_boxplot(fill = "grey40", color = "black") +
  scale_x_discrete() + labs(x = "groups", y = "ALT..IU.L.")
```



```
conf4<-diff(tapply(IFN$ALT..IU.L.,IFN$Patient.Group,mean))
quantile(conf4,prob = 0.025)
```

```
##      2.5%
## 54.88823
```

```
quantile(conf4,prob = 0.975)
```

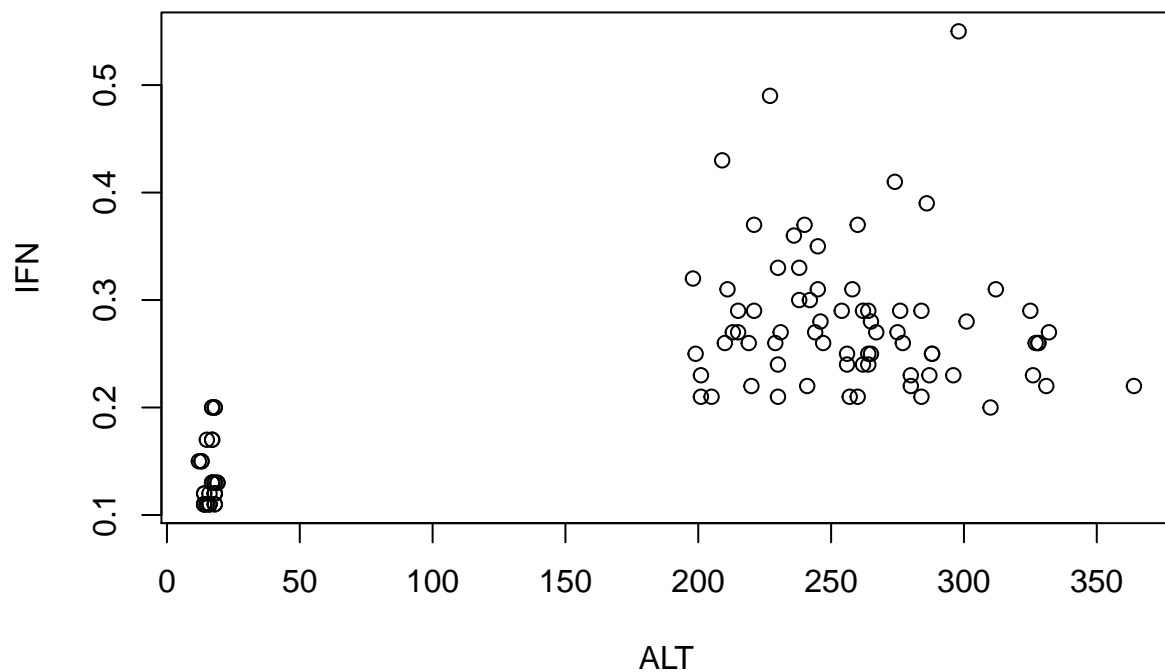
```
##      97.5%
## 223.23
```

- p-value of all groups is less than 0.05 so reject null hypothesis
- Confidence interval shows that there is a difference in means of ALT between groups
- There is a significant difference in ALT between groups

```
cor(IFN$ALT..IU.L., IFN$IFN....IU.ml., method = "spearman")
```

```
## [1] 0.6196662
```

```
plot(IFN$ALT..IU.L., IFN$IFN....IU.ml., xlab = "ALT", ylab = "IFN")
```



There is a positive moderate linear relationship between PEG-IFN and ALT level.

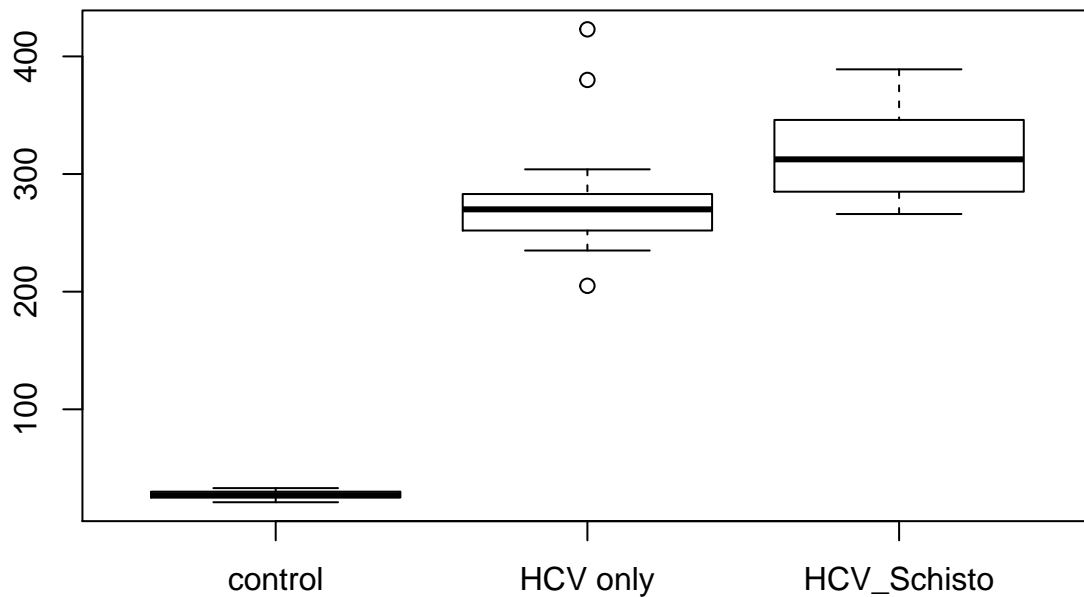
AST

```
options(tinytex.verbose = TRUE)
table8<-as.data.frame(IFN%>%summary_factorlist("AST..IU.L.", "Patient.Group", p = F, add_dependent_label=T))

## Warning in summary_factorlist(., "AST..IU.L.", "Patient.Group", p = F,
## add_dependent_label = T, : Dependent is not a factor and will be treated as
## a continuous variable
table8
```

##	Dependent: AST..IU.L.		Mean (sd)
## 1	Patient.Group	control	27.5 (3.5)
## 2		HCV only	272.9 (33.8)
## 3		HCV_Schisto	315.3 (35.5)

```
boxplot(AST..IU.L.~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$AST..IU.L.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$AST..IU.L.
## W = 0.7906, p-value = 4.84e-11
• p-value is less than 0.05 so reject null hypothesis
• AST is not normally distributed
```

```
kruskal.test(AST..IU.L.~Patient.Group, data = IFN)
```

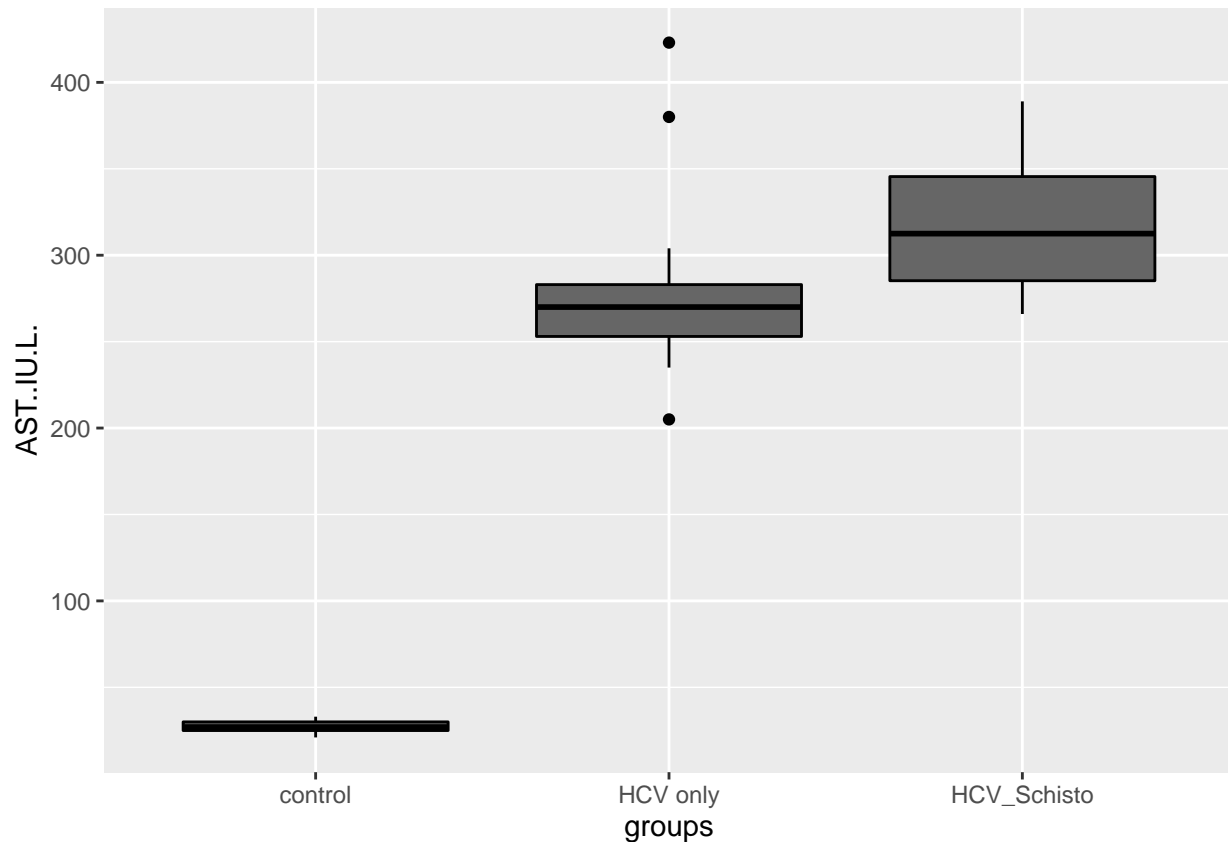
```
##
##  Kruskal-Wallis rank sum test
##
## data:  AST..IU.L. by Patient.Group
## Kruskal-Wallis chi-squared = 80.003, df = 2, p-value < 2.2e-16
```

```
dunnTest(AST..IU.L.~Patient.Group, data = IFN)
```

```
## Dunn (1964) Kruskal-Wallis multiple comparison
##  p-values adjusted with the Holm method.
```

```
##           Comparison      Z      P.unadj      P.adj
## 1    control - HCV only -6.706491 1.993598e-11 3.987196e-11
## 2    control - HCV_Schisto -8.398797 4.510752e-17 1.353226e-16
## 3    HCV only - HCV_Schisto -3.154625 1.607043e-03 1.607043e-03
```

```
ggplot(IFN, aes(x= Patient.Group, y= AST..IU.L.)) +
  geom_boxplot(fill = "grey40", color = "black") +
  scale_x_discrete() + labs(x = "groups", y = "AST..IU.L.")
```



```
conf5<-diff(tapply(IFN$AST..IU.L.,IFN$Patient.Group,mean))
quantile(conf5,prob = 0.025)
```

```
##      2.5%
## 47.42977
```

```
quantile(conf5,prob = 0.975)
```

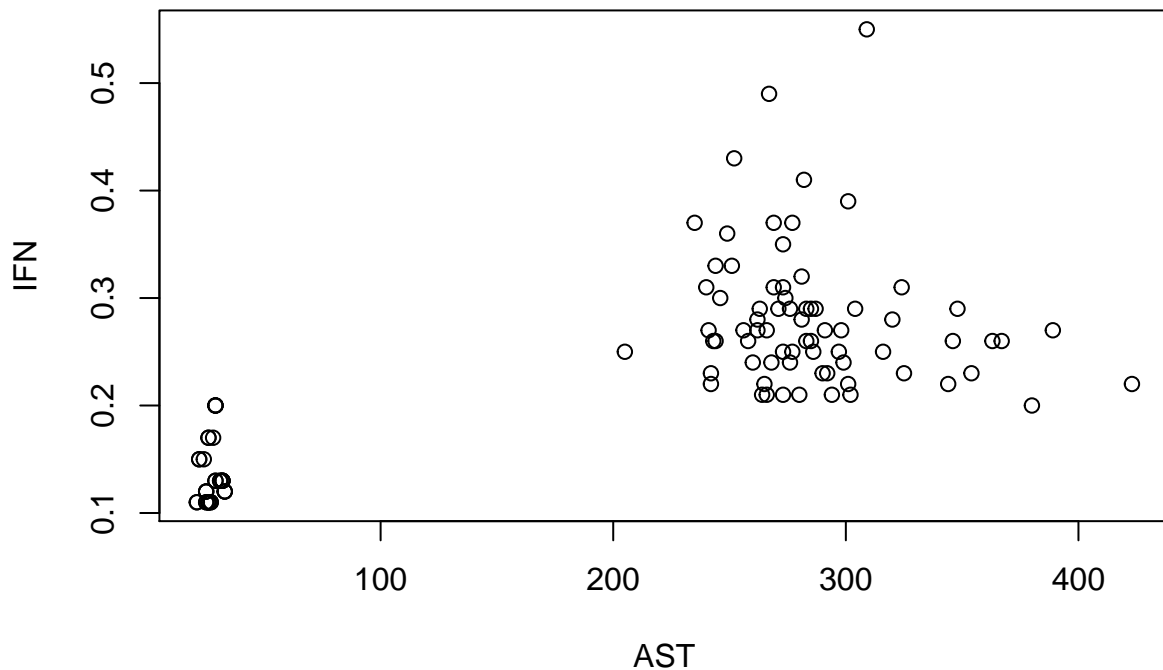
```
##      97.5%
## 240.3572
```

- p-value of all groups is less than 0.05 so reject null hypothesis
- Confidence interval shows that there is a difference in means of AST between groups
- There is a significant difference in AST between groups

```
cor(IFN$AST..IU.L., IFN$IFN....IU.ml., method = "spearman")
```

```
## [1] 0.604152
```

```
plot(IFN$AST..IU.L., IFN$IFN....IU.ml., xlab = "AST", ylab = "IFN")
```



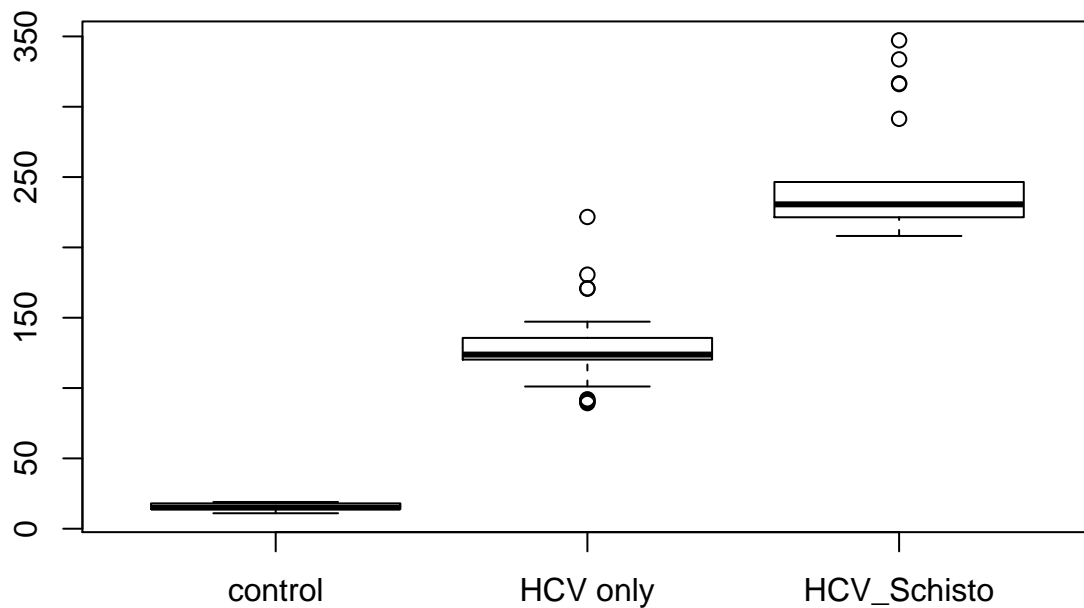
- There is a positive strong linear relationship between PEG-IFN and AST

GGT

```
options(tinytex.verbose = TRUE)
table9<-as.data.frame(IFN%>%summary_factorlist("GGT..IU.L.", "Patient.Group", p = F, add_dependent_label = T))

## Warning in summary_factorlist(., "GGT..IU.L.", "Patient.Group", p = F,
## add_dependent_label = T, : Dependent is not a factor and will be treated as
## a continuous variable
table9

##   Dependent: GGT..IU.L.      Mean (sd)
## 1 Patient.Group control  15.5 (2.5)
## 2                HCV only 128.3 (22.6)
## 3                HCV_Schisto 248.5 (42.4)
boxplot(GGT..IU.L. ~ Patient.Group, data= IFN)
```

```
shapiro.test(IFN$GGT..IU.L.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$GGT..IU.L.
## W = 0.89482, p-value = 3.932e-07
• p-value is less than 0.05 so reject null hypothesis
• GGT is not normally distributed
```

```
options(tinytex.verbose = TRUE)
kruskal.test(GGT..IU.L.~Patient.Group, data = IFN)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  GGT..IU.L. by Patient.Group
## Kruskal-Wallis chi-squared = 90.195, df = 2, p-value < 2.2e-16
```

```
dunnTest(GGT..IU.L.~Patient.Group, data = IFN)
```

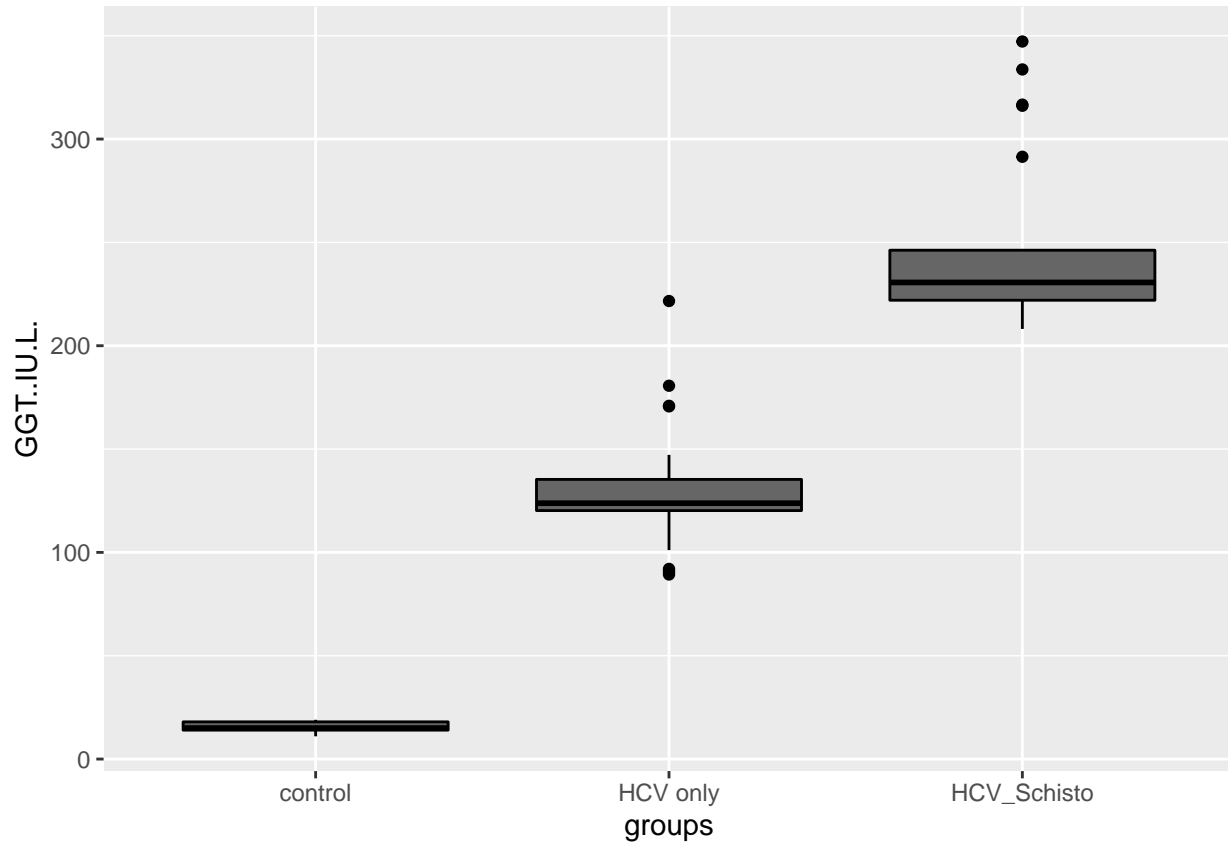
```
## Dunn (1964) Kruskal-Wallis multiple comparison
```

```
##  p-values adjusted with the Holm method.
```

```
##           Comparison      Z      P.unadj      P.adj
## 1    control - HCV only -6.234512 4.531885e-10 9.063771e-10
## 2    control - HCV_Schisto -9.269271 1.874223e-20 5.622670e-20
```

```
## 3 HCV only - HCV_Schisto -4.486919 7.226041e-06 7.226041e-06
```

```
ggplot(IFN, aes(x= Patient.Group, y= GGT..IU.L.)) +  
geom_boxplot(fill = "grey40", color = "black") +  
scale_x_discrete() + labs(x = "groups", y = "GGT..IU.L.")
```



```
conf6<-diff(tapply(IFN$GGT..IU.L.,IFN$Patient.Group,mean))  
quantile(conf6,prob = 0.025)
```

```
## 2.5%
```

```
## 112.897
```

```
quantile(conf6,prob = 0.975)
```

```
## 97.5%
```

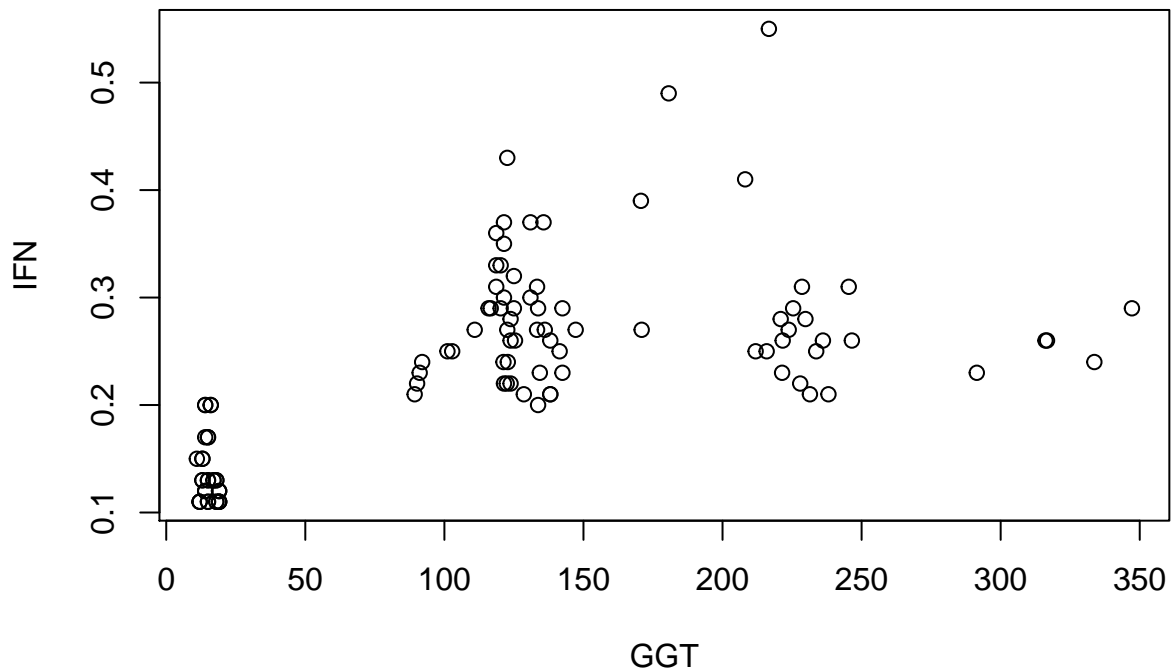
```
## 120.042
```

- p-value of all groups is less than 0.05 so reject null hypothesis
- Confidence interval shows that there is a difference in means of GGT between groups
- There is a significant difference in GGT between groups

```
cor(IFN$GGT..IU.L., IFN$IFN....IU.ml., method = "spearman")
```

```
## [1] 0.6347158
```

```
plot(IFN$GGT..IU.L., IFN$IFN...IU.ml., xlab = "GGT", ylab = "IFN")
```



-There is a positive moderate linear relationship between PEG-IFN and GGT.

ALP

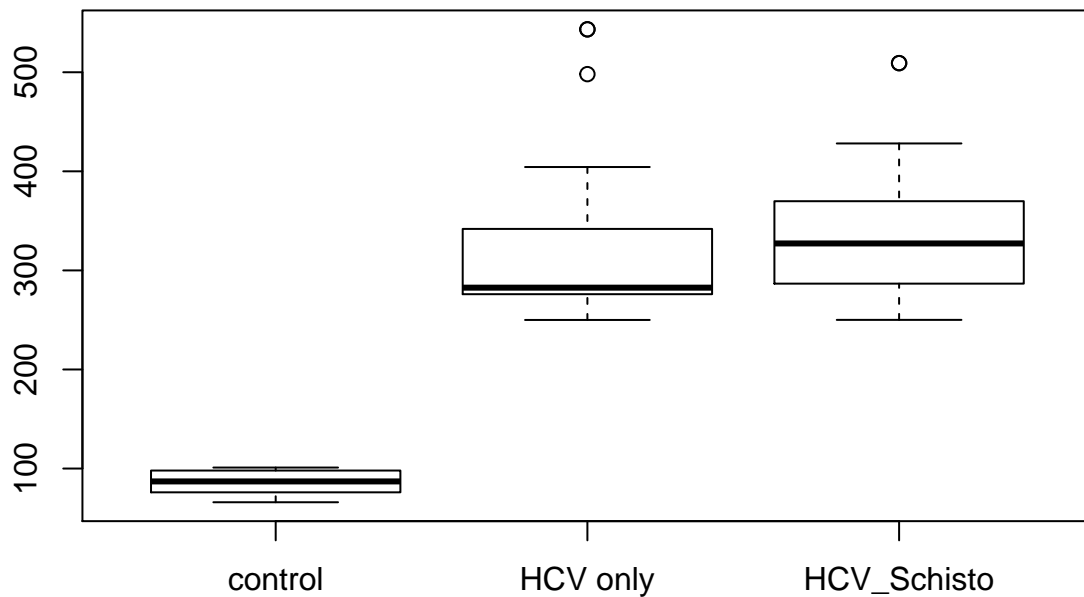
```
options(tinytex.verbose = TRUE)
table10<-as.data.frame(IFN%>%summary_factorlist("ALP..IU.L.", "Patient.Group", p = F, add_dependent_label = T))
```

```
## Warning in summary_factorlist(., "ALP..IU.L.", "Patient.Group", p = F,
## add_dependent_label = T, : Dependent is not a factor and will be treated as
## a continuous variable
```

```
table10
```

```
##   Dependent: ALP..IU.L.      Mean (sd)
## 1      Patient.Group      control 86.9 (12.4)
## 2                      HCV only 313.9 (67.5)
## 3                      HCV_Schisto 341.2 (72.4)
```

```
boxplot(ALP..IU.L. ~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$ALP..IU.L.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$ALP..IU.L.
## W = 0.89246, p-value = 3.048e-07
• p-value is less than 0.05 so reject null hypothesis
• ALP is not normally distributed
```

```
options(tinytex.verbose = TRUE)
kruskal.test(ALP..IU.L.~Patient.Group, data = IFN)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  ALP..IU.L. by Patient.Group
## Kruskal-Wallis chi-squared = 71.618, df = 2, p-value = 2.807e-16
```

```
dunnTest(ALP..IU.L.~Patient.Group, data = IFN)
```

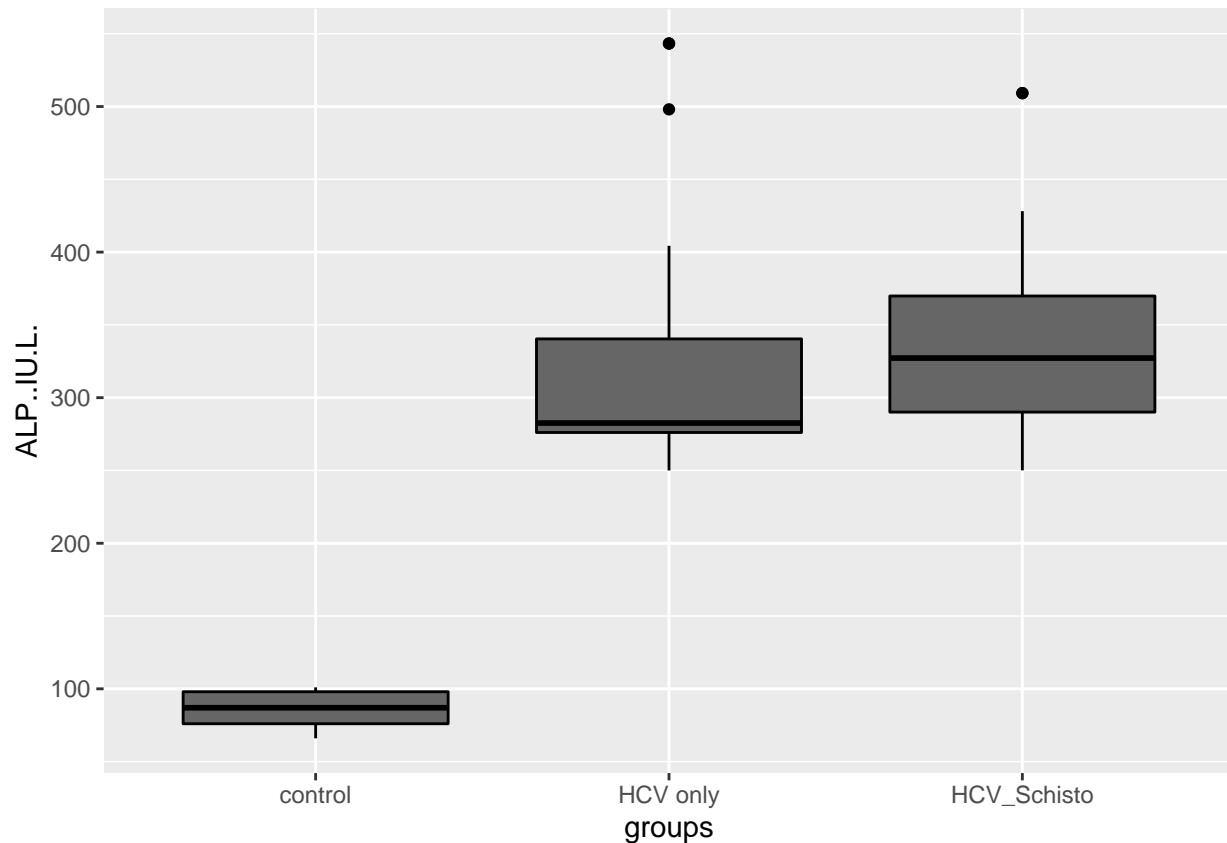
```
## Dunn (1964) Kruskal-Wallis multiple comparison
```

```
##  p-values adjusted with the Holm method.
```

```
##           Comparison      Z      P.unadj      P.adj
## 1    control - HCV only -7.376570 1.624194e-13 4.872581e-13
## 2    control - HCV_Schisto -7.161545 7.977277e-13 1.595455e-12
```

```
## 3 HCV only - HCV_Schisto -1.261628 2.070828e-01 2.070828e-01
```

```
ggplot(IFN, aes(x= Patient.Group, y= ALP..IU.L.)) +  
geom_boxplot(fill = "grey40", color = "black") +  
scale_x_discrete() + labs(x = "groups", y = "ALP..IU.L.")
```



```
conf7<-diff(tapply(IFN$ALP..IU.L.,IFN$Patient.Group,mean))  
quantile(conf7,prob = 0.025)
```

```
##      2.5%
```

```
## 32.29572
```

```
quantile(conf7,prob = 0.975)
```

```
##      97.5%
```

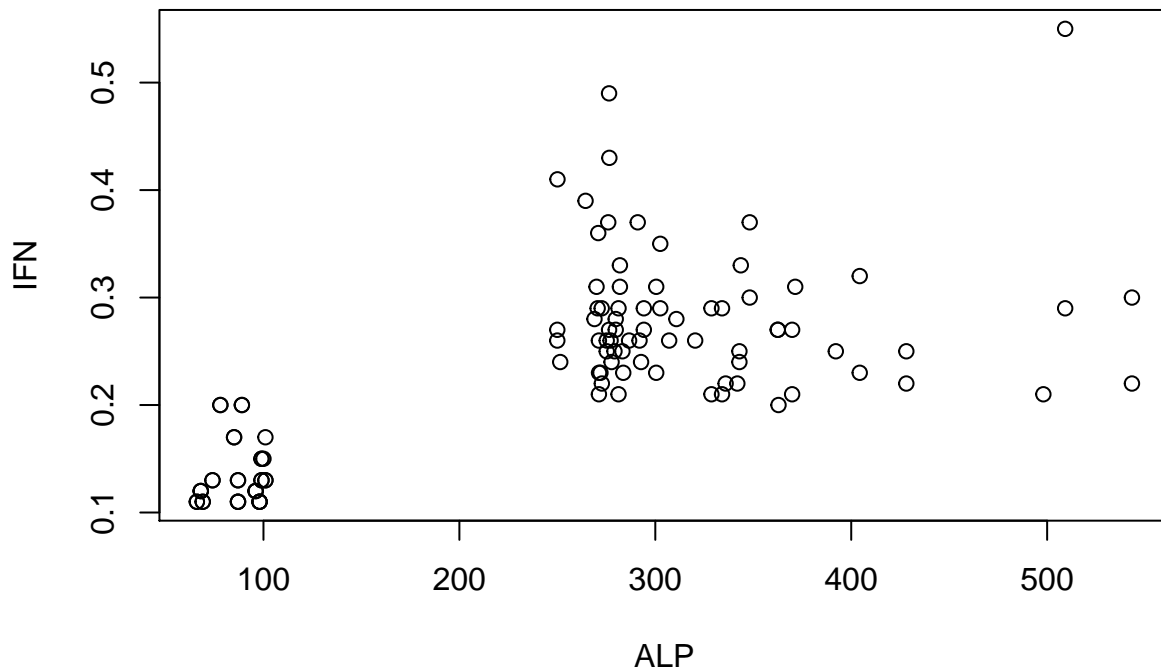
```
## 222.0721
```

- p-value of control-HCV and control-HCV_Schisto is less than 0.05 so reject null hypothesis
- p-value of HCV only-HCV_Schisto is more than 0.05 so fail to reject null hypothesis
- There is a highly significant difference between control-HCV and control-HCV_Schisto but no significant difference between HCV only-HCV_Schisto in ALP
- Confidence interval shows that there is a difference in means of ALP between groups
- We conclude that Schistosoma infection don't significantly affect on ALP level in patients with HCV

```
cor(IFN$ALP..IU.L., IFN$IFN....IU.ml., method = "spearman")
```

```
## [1] 0.6262072
```

```
plot(IFN$ALP..IU.L., IFN$IFN...IU.ml., xlab = "ALP", ylab = "IFN")
```



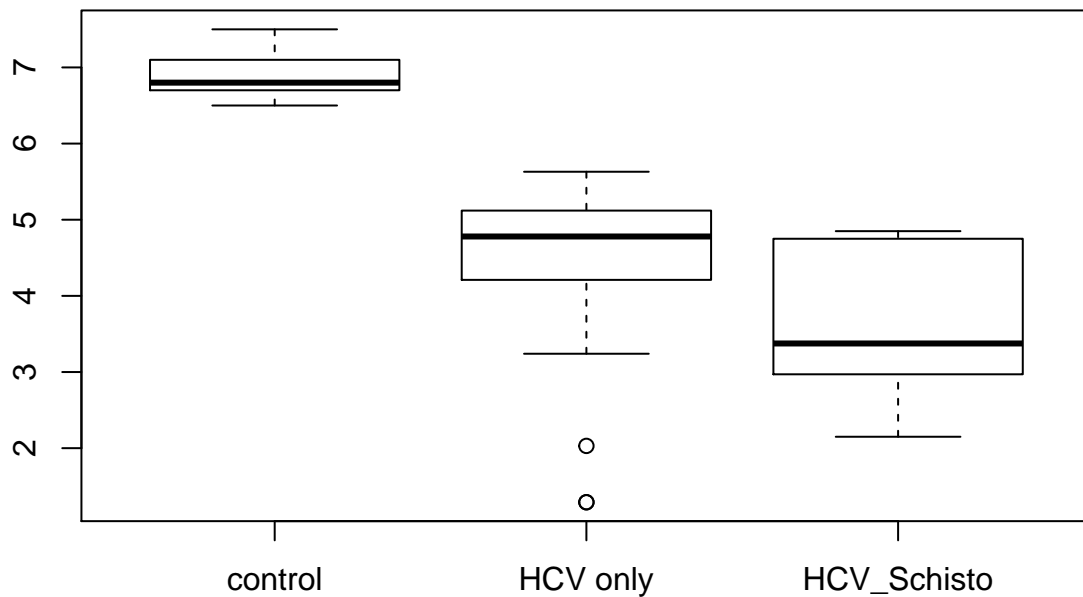
-There is a positive moderate linear relationship between PEG-IFN and ALP.

Total protein

```
options(tinytex.verbose = TRUE)
table11<-as.data.frame(IFN%>%summary_factorlist("TP..g.dL.", "Patient.Group", p = F, add_dependent_label = T))

## Warning in summary_factorlist(., "TP..g.dL.", "Patient.Group", p = F,
## add_dependent_label = T, : Dependent is not a factor and will be treated as
## a continuous variable
table11

##   Dependent: TP..g.dL.      Mean (sd)
## 1 Patient.Group control 6.9 (0.3)
## 2 Patient.Group HCV only 4.5 (1.0)
## 3 Patient.Group HCV_Schisto 3.6 (1.0)
boxplot(TP..g.dL.~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$TP..g.dL.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$TP..g.dL.
## W = 0.95157, p-value = 0.0006587
# p-value is less than 0.05 so reject null hypothesis
# TP is not normally distributed
```

```
options(tinytex.verbose = TRUE)
kruskal.test(TP..g.dL.~Patient.Group, data = IFN)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  TP..g.dL. by Patient.Group
## Kruskal-Wallis chi-squared = 76.079, df = 2, p-value < 2.2e-16
```

```
dunnTest(TP..g.dL.~Patient.Group, data = IFN)
```

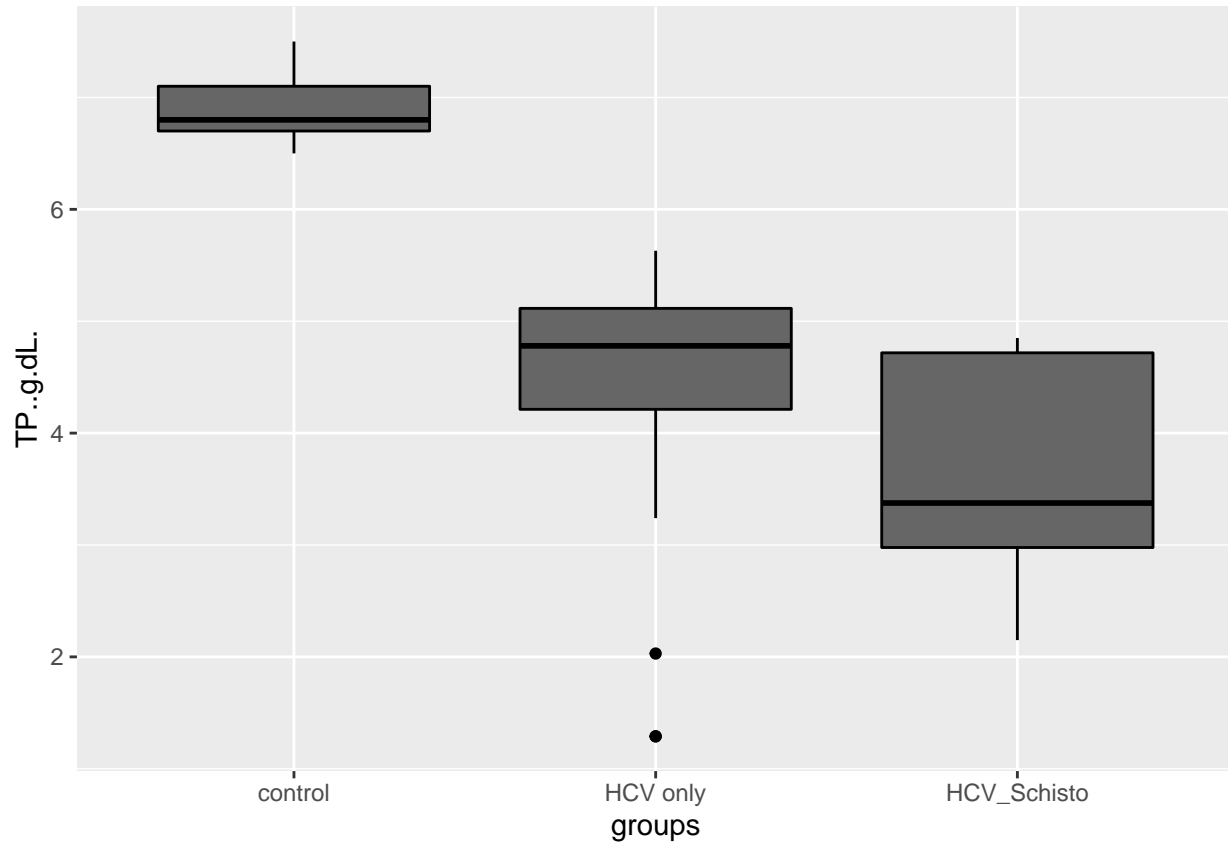
```
## Dunn (1964) Kruskal-Wallis multiple comparison
```

```
##  p-values adjusted with the Holm method.
```

```
##           Comparison      Z      P.unadj      P.adj
## 1    control - HCV only 6.957892 3.454006e-12 6.908013e-12
## 2    control - HCV_Schisto 7.939791 2.025230e-15 6.075691e-15
```

```
## 3 HCV only - HCV_Schisto 2.449924 1.428863e-02 1.428863e-02
```

```
ggplot(IFN, aes(x= Patient.Group, y= TP..g.dL.)) +  
geom_boxplot(fill = "grey40", color = "black") +  
scale_x_discrete() + labs(x = "groups", y = "TP..g.dL.")
```



```
conf8<-diff(tapply(IFN$TP..g.dL., IFN$Patient.Group, mean))  
quantile(conf8, prob = 0.025)
```

```
##      2.5%  
## -2.331123
```

```
quantile(conf8, prob = 0.975)
```

```
##      97.5%  
## -0.9460847
```

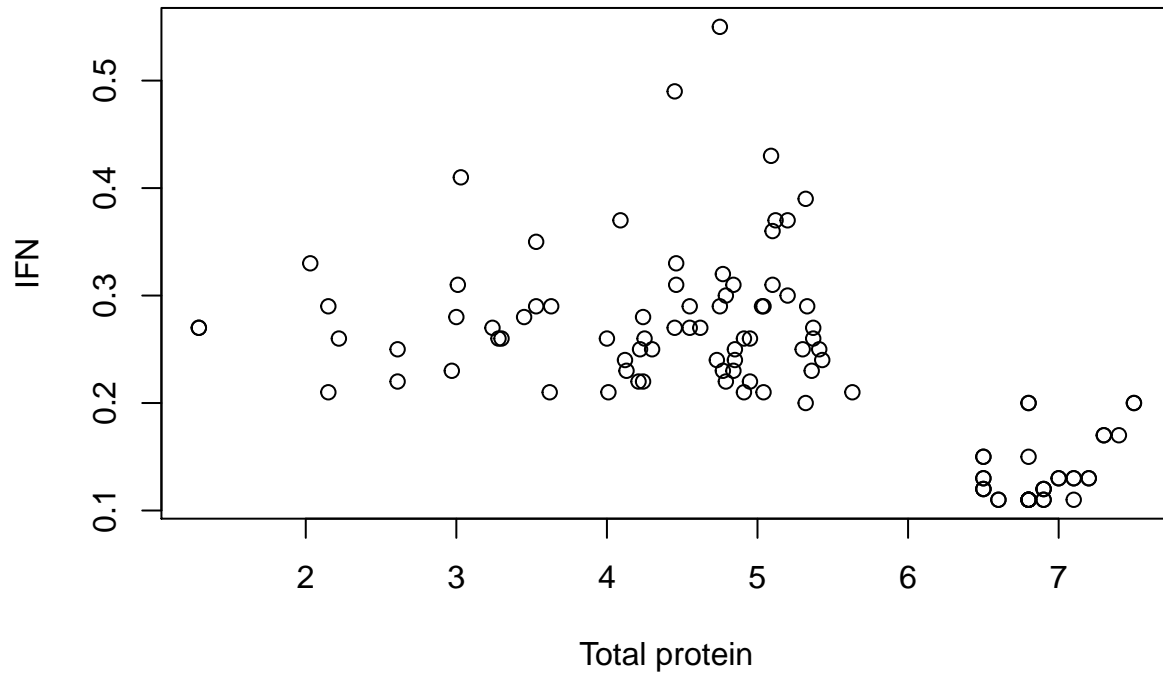
- p-value of all groups is less than 0.05 so reject null hypothesis
- Confidence interval shows that there is a difference in means of TP between groups
- There is a significant difference in TP between groups

```
cor(IFN$TP..g.dL., IFN$IFN....IU.ml., method = "spearman")
```

```
## [1] -0.6515043
```



```
plot(IFN$TP..g.dL., IFN$IFN....IU.ml., xlab = "Total protein", ylab = "IFN")
```



-There is a negative moderate linear relationship between PEG-IFN and TP.

Albumin

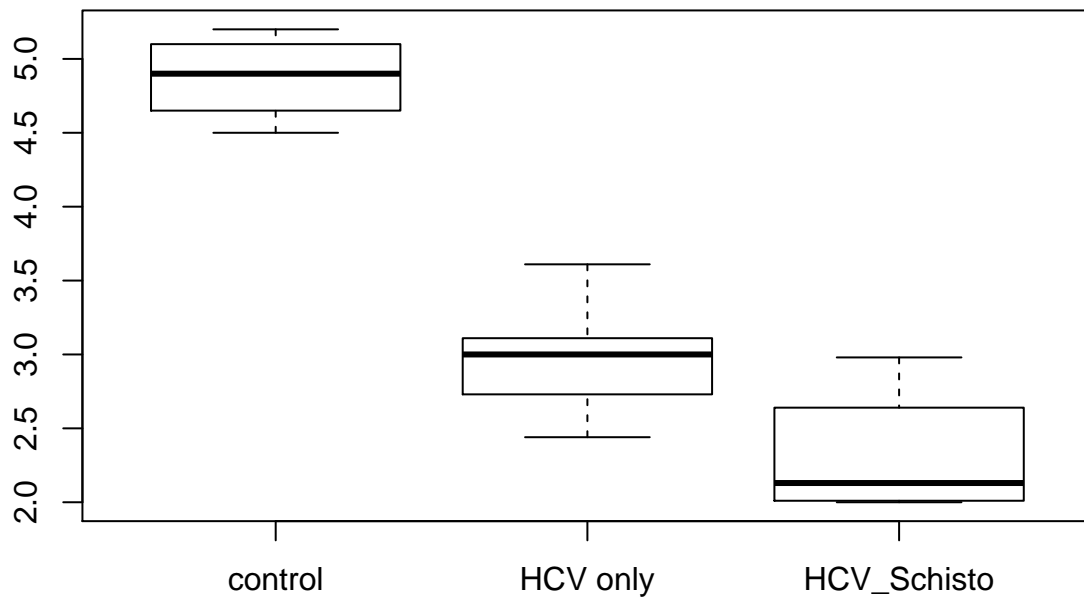
```
table12<-as.data.frame(IFN%>%summary_factorlist("Alb...g.dL.", "Patient.Group", p = F, add_dependent_la
```

```
## Warning in summary_factorlist(., "Alb...g.dL.", "Patient.Group", p = F, :  
## Dependent is not a factor and will be treated as a continuous variable
```

```
table12
```

```
##   Dependent: Alb...g.dL.           Mean (sd)  
## 1      Patient.Group      control 4.9 (0.2)  
## 2              HCV only 2.9 (0.3)  
## 3      HCV_Schisto 2.3 (0.3)
```

```
boxplot(Alb...g.dL. ~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$Alb...g.dL.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$Alb...g.dL.
## W = 0.86679, p-value = 2.317e-08
  • p-value is less than 0.05 so reject null hypothesis
  • Albumin is not normally distributed
```

```
options(tinytex.verbose = TRUE)
kruskal.test(Alb...g.dL.~Patient.Group, data = IFN)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  Alb...g.dL. by Patient.Group
## Kruskal-Wallis chi-squared = 84.933, df = 2, p-value < 2.2e-16
```

```
dunnTest(Alb...g.dL.~Patient.Group, data = IFN)
```

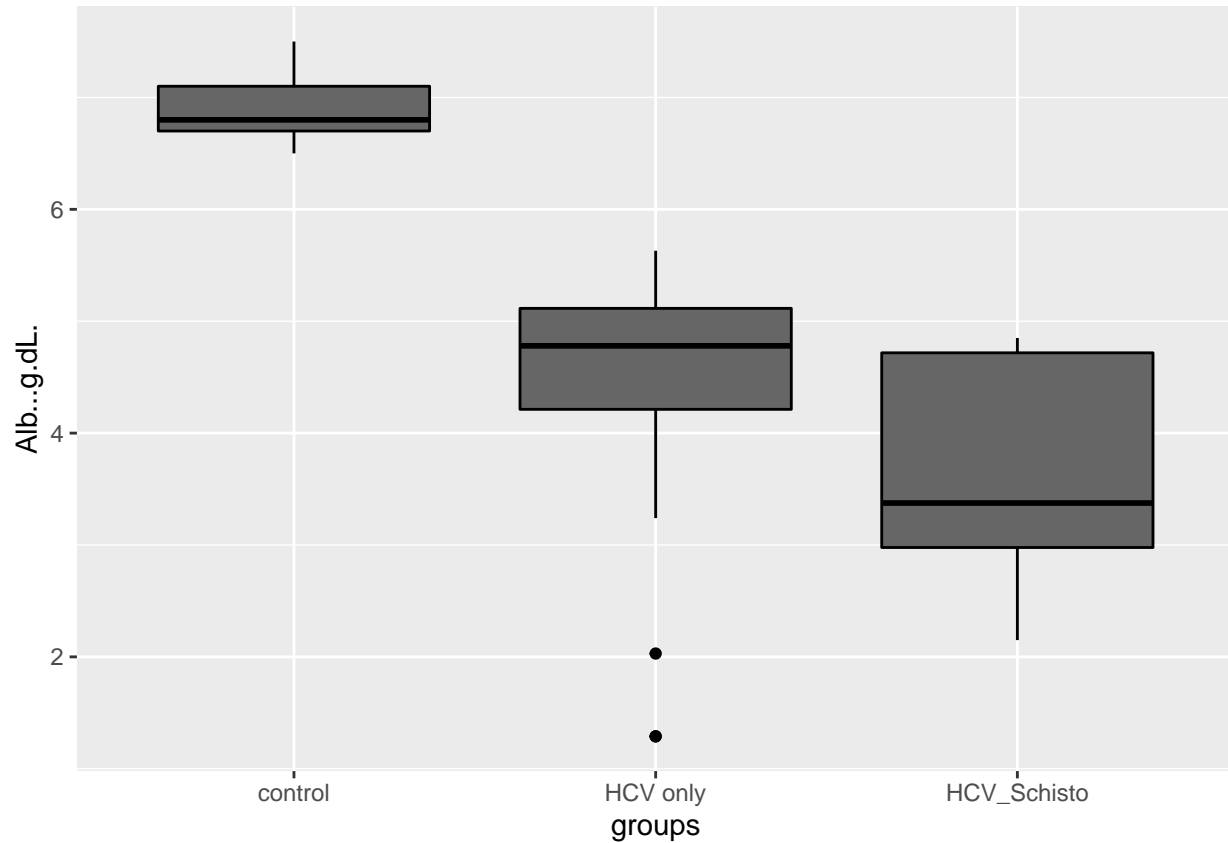
```
## Dunn (1964) Kruskal-Wallis multiple comparison
```

```
##  p-values adjusted with the Holm method.
```

```
##           Comparison      Z      P.unadj      P.adj
## 1    control - HCV only 6.471779 9.685576e-11 1.937115e-10
## 2    control - HCV_Schisto 8.852180 8.582593e-19 2.574778e-18
```

```
## 3 HCV only - HCV_Schisto 3.838970 1.235516e-04 1.235516e-04
```

```
ggplot(IFN, aes(x= Patient.Group, y= TP..g.dL.)) +  
geom_boxplot(fill = "grey40", color = "black") +  
scale_x_discrete() + labs(x = "groups", y = "Alb...g.dL.")
```



```
conf9<-diff(tapply(IFN$Alb...g.dL., IFN$Patient.Group, mean))  
quantile(conf9, prob = 0.025)
```

```
##      2.5%  
## -1.898607
```

```
quantile(conf9, prob = 0.975)
```

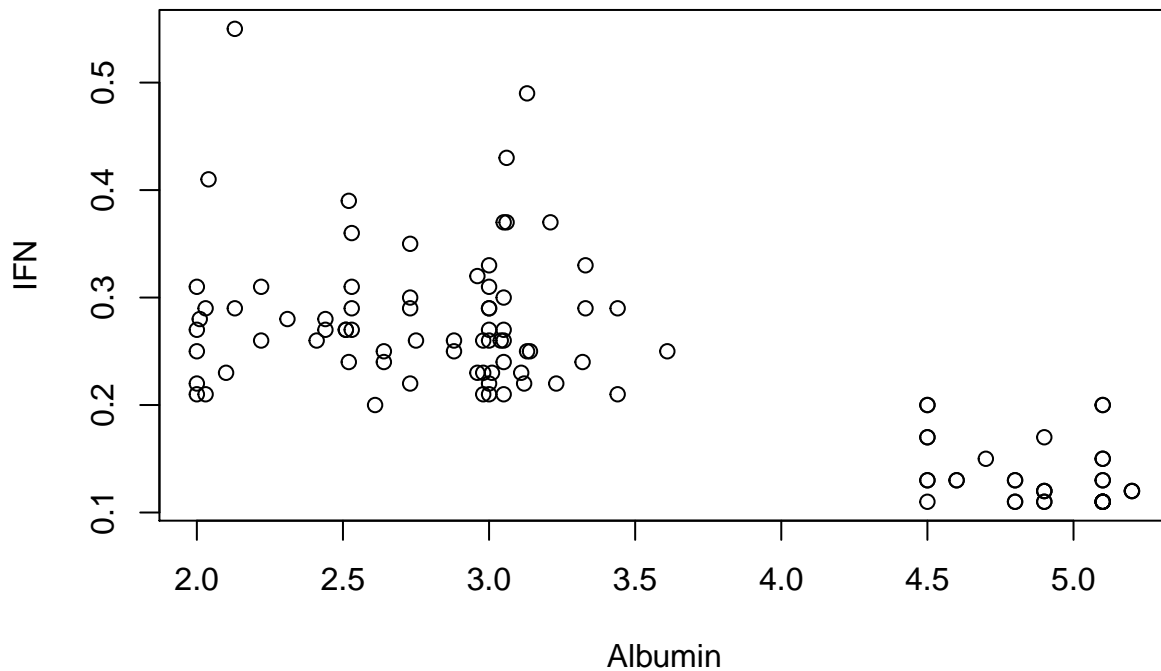
```
##      97.5%  
## -0.6904836
```

- p-value of all groups is less than 0.05 so reject null hypothesis
- Confidence interval shows that there is a difference in means of Albumin between groups
- There is a significant difference in Albumin between groups

```
cor(IFN$Alb...g.dL., IFN$IFN....IU.mL., method = "spearman")
```

```
## [1] -0.6837915
```

```
plot(IFN$Alb...g.dL., IFN$IFN...IU.ml., xlab = "Albumin", ylab = "IFN")
```



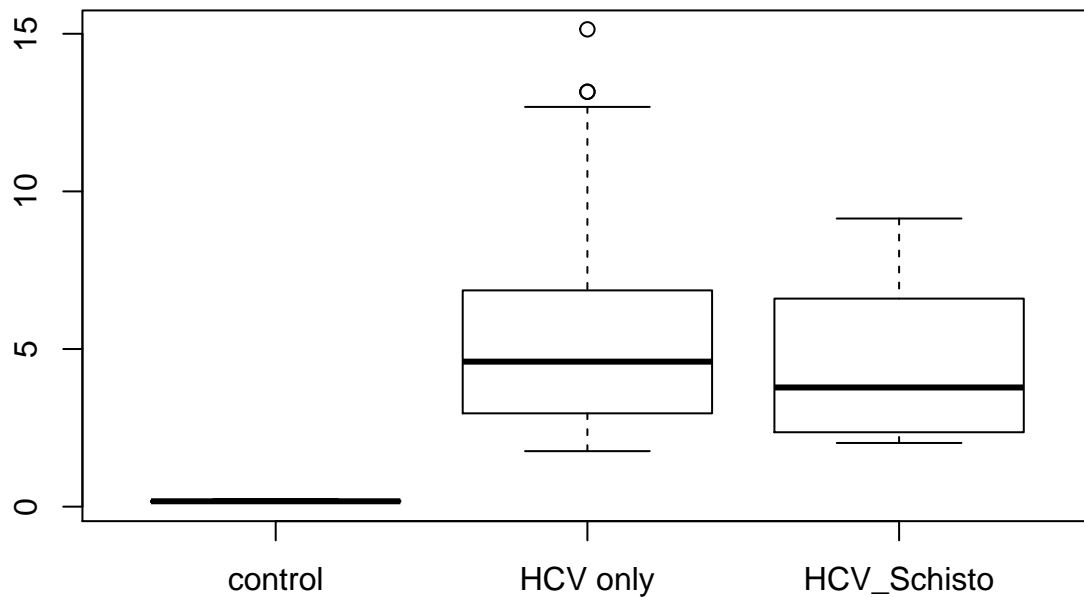
- There is a negative moderate linear relationship between PEG-IFN and Albumin.

Total bilirubin

```
options(tinytex.verbose = TRUE)
table13<-as.data.frame(IFN%>%summary_factorlist("TB...mg.dL.", "Patient.Group", p = F, add_dependent_la

## Warning in summary_factorlist(., "TB...mg.dL.", "Patient.Group", p = F, :
## Dependent is not a factor and will be treated as a continuous variable
table13

##   Dependent: TB...mg.dL.          Mean (sd)
## 1      Patient.Group      control 0.2 (0.0)
## 2                      HCV only 5.5 (3.4)
## 3                      HCV_Schisto 4.5 (2.3)
boxplot(TB...mg.dL.~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$TB...mg.dL.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$TB...mg.dL.
## W = 0.8667, p-value = 2.297e-08
# p-value is less than 0.05 so reject null hypothesis
# TB is not normally distributed
```

```
options(tinytex.verbose = TRUE)
kruskal.test(TB...mg.dL.~Patient.Group, data = IFN)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  TB...mg.dL. by Patient.Group
## Kruskal-Wallis chi-squared = 70.515, df = 2, p-value = 4.875e-16
```

```
dunnTest(TB...mg.dL.~Patient.Group, data = IFN)
```

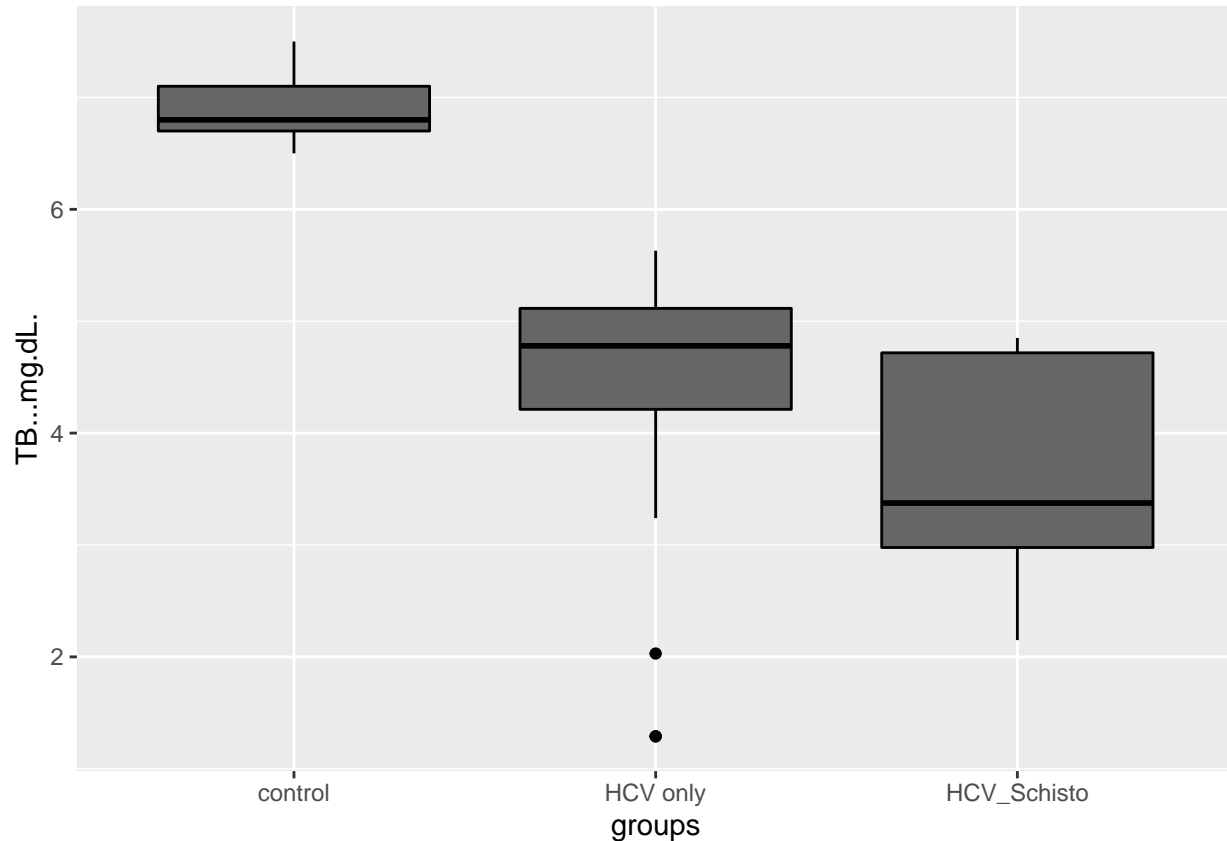
```
## Dunn (1964) Kruskal-Wallis multiple comparison
```

```
## p-values adjusted with the Holm method.
```

	Comparison	Z	P.unadj	P.adj
## 1	control - HCV only	-8.0645315	7.351725e-16	2.205517e-15
## 2	control - HCV_Schisto	-5.9003697	3.626879e-09	7.253759e-09

```
## 3 HCV only - HCV_Schisto 0.6722164 5.014459e-01 5.014459e-01
```

```
ggplot(IFN, aes(x= Patient.Group, y= TP..g.dL.)) +  
geom_boxplot(fill = "grey40", color = "black") +  
scale_x_discrete() + labs(x = "groups", y = "TB...mg.dL.")
```



```
conf10<-diff(tapply(IFN$TB...mg.dL.,IFN$Patient.Group,mean))  
quantile(conf10,prob = 0.025)
```

```
##      2.5%
```

```
## -0.8608782
```

```
quantile(conf10,prob = 0.975)
```

```
##      97.5%
```

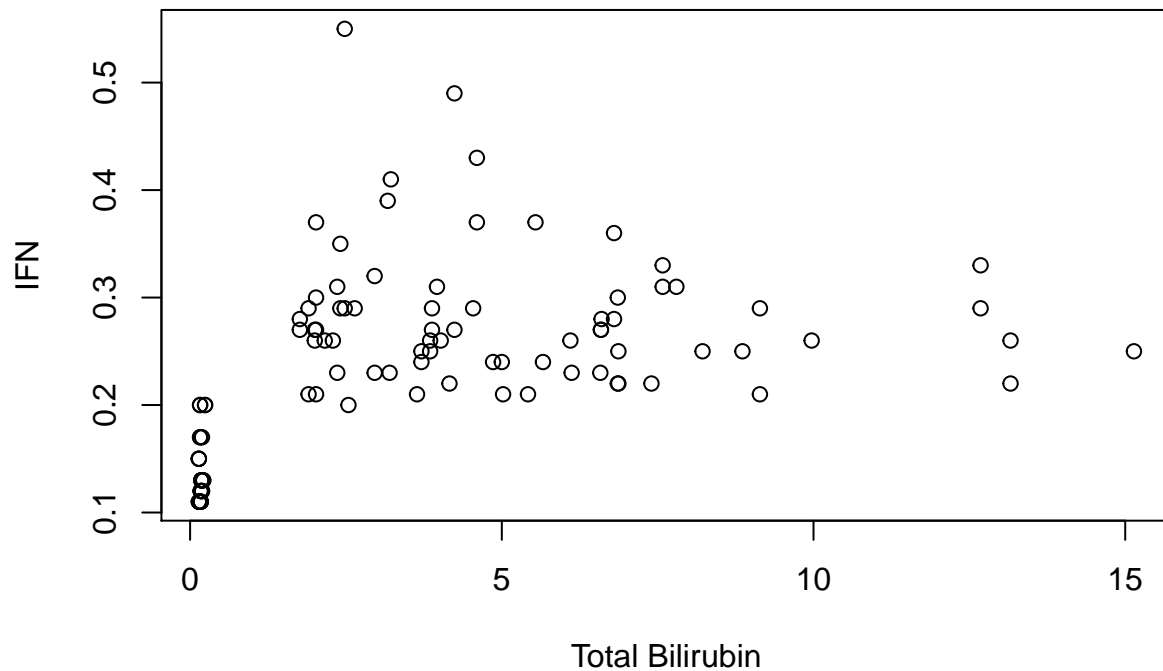
```
## 5.168476
```

- p-value of control-HCV and control-HCV_Schisto is less than 0.05 so reject null hypothesis
- p-value of HCV only-HCV_Schisto is more than 0.05 so fail to reject null hypothesis
- There is a highly significant difference between control-HCV and control-HCV_Schisto but no significant difference between HCV only-HCV_Schisto in TB
- Confidence interval shows that there is no a difference in means of TB between groups
- We conclude that Schistosoma infection don't significantly affect on TB level in patients with HCV

```
cor(IFN$TB...mg.dL., IFN$IFN....IU.mL., method = "spearman")
```

```
## [1] 0.6429762
```

```
plot(IFN$TB...mg.dL., IFN$IFN...IU.ml., xlab = "Total Bilirubin", ylab = "IFN")
```



- There is a positive moderate linear relationship between PEG-IFN and TB.

Direct bilirubin

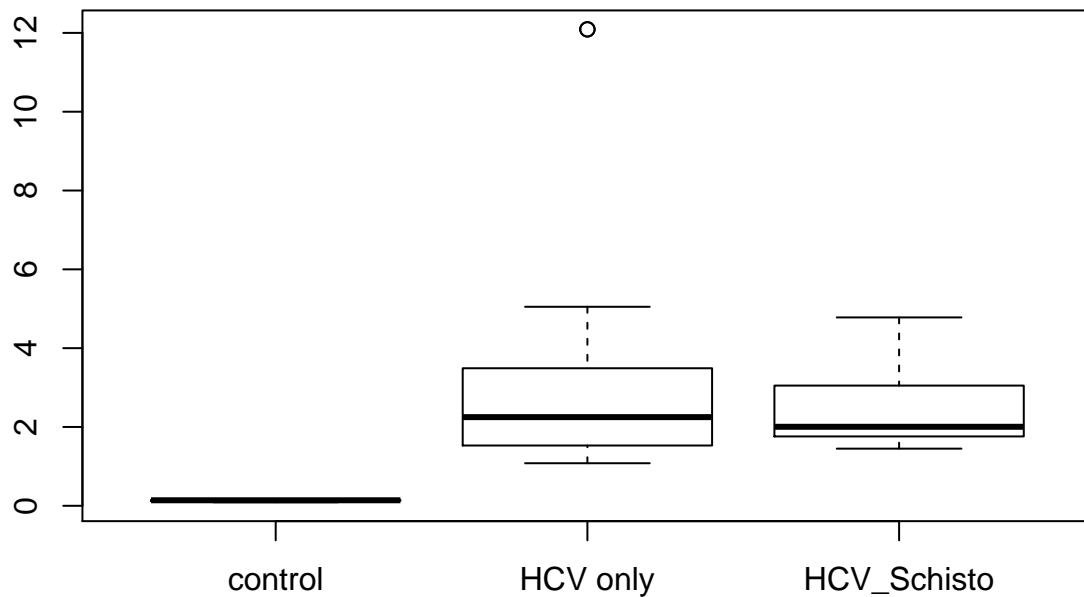
```
options(tinytex.verbose = TRUE)
table14<-as.data.frame(IFN%>%summary_factorlist("DB...mg.dL.", "Patient.Group", p = F, add_dependent_la
```

```
## Warning in summary_factorlist(., "DB...mg.dL.", "Patient.Group", p = F, :
## Dependent is not a factor and will be treated as a continuous variable
```

```
table14
```

```
##   Dependent: DB...mg.dL.           Mean (sd)
## 1      Patient.Group      control 0.1 (0.0)
## 2                      HCV only 2.8 (2.2)
## 3                      HCV_Schisto 2.4 (0.9)
```

```
boxplot(DB...mg.dL. ~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$DB...mg.dL.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$DB...mg.dL.
## W = 0.73797, p-value = 1.572e-12
# • p-value is less than 0.05 so reject null hypothesis
# • DB is not normally distributed
```

```
options(tinytex.verbose = TRUE)
kruskal.test(DB...mg.dL.~Patient.Group, data = IFN)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  DB...mg.dL. by Patient.Group
## Kruskal-Wallis chi-squared = 70.2, df = 2, p-value = 5.704e-16
```

```
dunnTest(DB...mg.dL.~Patient.Group, data = IFN)
```

```
## Dunn (1964) Kruskal-Wallis multiple comparison
```

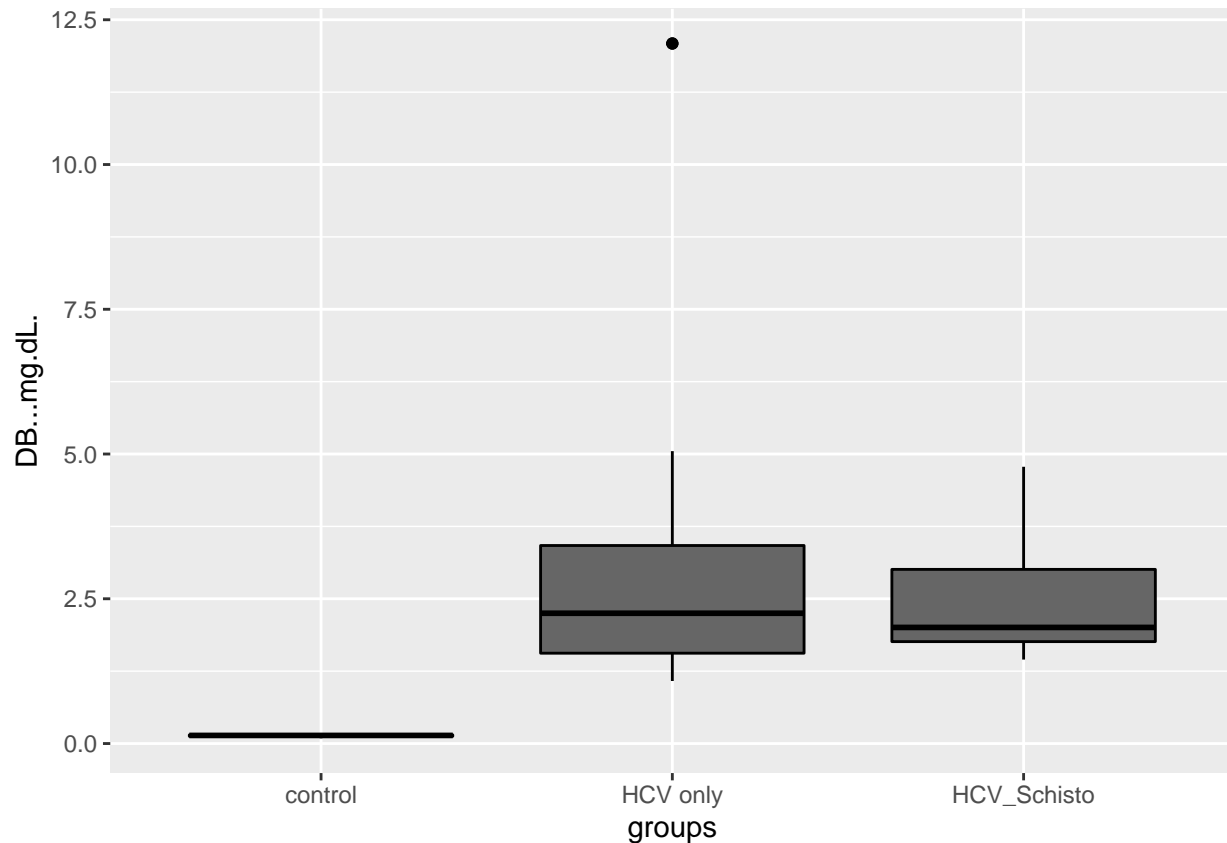
```
##  p-values adjusted with the Holm method.
```

```
##           Comparison      Z      P.unadj      P.adj
## 1    control - HCV only -7.84252368 4.415804e-15 1.324741e-14
## 2    control - HCV_Schisto -6.32934924 2.461973e-10 4.923946e-10
```



```
## 3 HCV only - HCV_Schisto 0.02476834 9.802397e-01 9.802397e-01
```

```
ggplot(IFN, aes(x= Patient.Group, y= DB...mg.dL.)) +  
geom_boxplot(fill = "grey40", color = "black") +  
scale_x_discrete() + labs(x = "groups", y = "DB...mg.dL.")
```



```
conf11<-diff(tapply(IFN$DB...mg.dL.,IFN$Patient.Group,mean))  
quantile(conf11,prob = 0.025)
```

```
##      2.5%  
## -0.3397562
```

```
quantile(conf11,prob = 0.975)
```

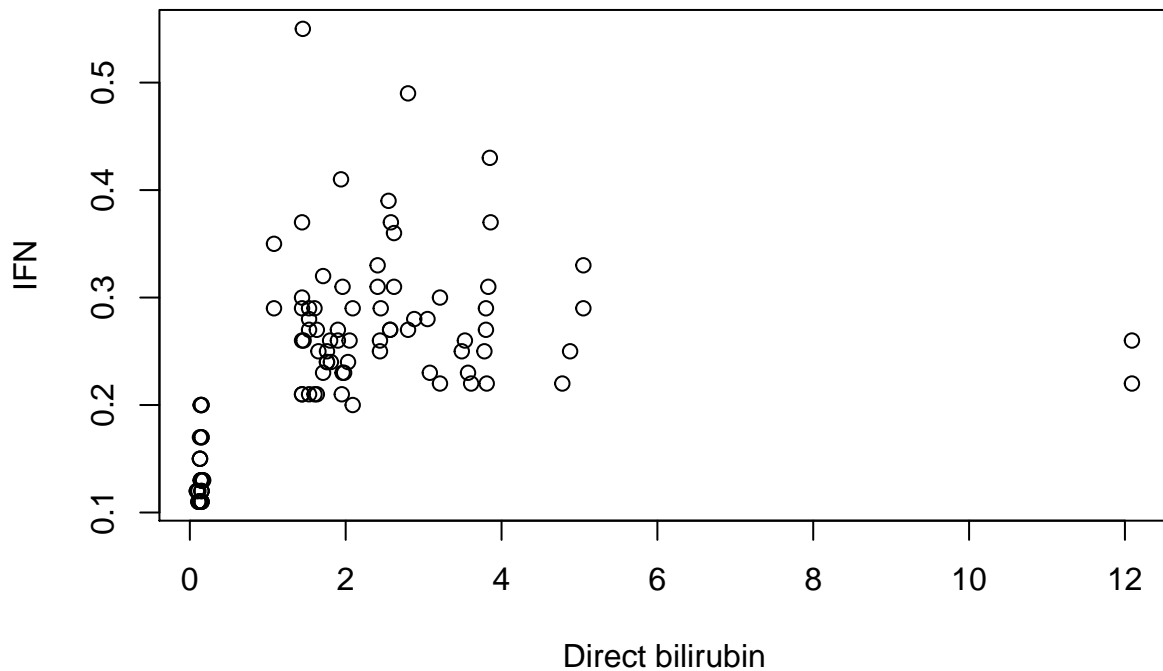
```
##      97.5%  
## 2.630743
```

- p-value of control-HCV and control-HCV_Schisto is less than 0.05 so reject null hypothesis
- p-value of HCV only-HCV_Schisto is more than 0.05 so fail to reject null hypothesis
- There is a highly significant difference between control-HCV and control-HCV_Schisto but no significant difference between HCV only-HCV_Schisto in DB -Confidence interval shows that there is no a difference in means of DB between groups
- We conclude that Schistosoma infection don't significantly affect on DB level in patients with HCV

```
cor(IFN$DB...mg.dL., IFN$IFN....IU.mL., method = "spearman")
```

```
## [1] 0.6841401
```

```
plot(IFN$DB...mg.dL., IFN$IFN...IU.ml., xlab = "Direct bilirubin", ylab = "IFN")
```



- There is a positive moderate linear relationship between PEG-IFN and DB.

HCV-RNA

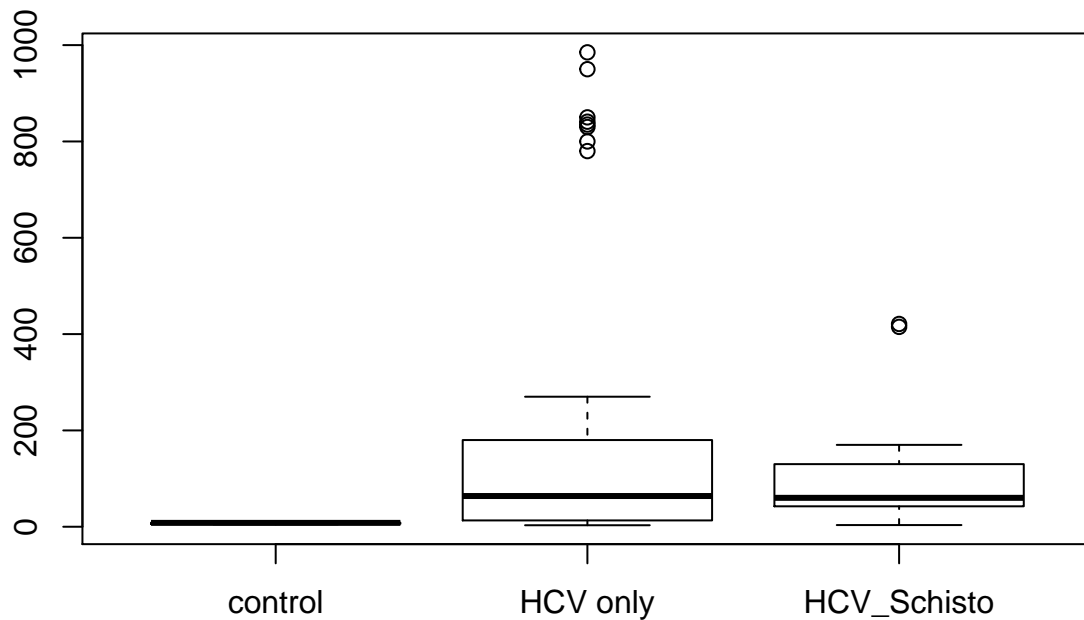
```
options(tinytex.verbose = TRUE)
table15<-as.data.frame(IFN%>%summary_factorlist("HCV.PCR..cpm.", "Patient.Group", p = F, add_dependent_
```

```
## Warning in summary_factorlist(., "HCV.PCR..cpm.", "Patient.Group", p = F, :
## Dependent is not a factor and will be treated as a continuous variable
```

```
table15
```

```
##   Dependent: HCV.PCR..cpm.      Mean (sd)
## 1      Patient.Group      control    7.3 (1.6)
## 2                      HCV only 190.7 (303.2)
## 3                      HCV_Schisto 103.9 (113.0)
```

```
boxplot(HCV.PCR..cpm. ~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$HCV.PCR..cpm.)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$HCV.PCR..cpm.
## W = 0.51257, p-value < 2.2e-16
• p-value is less than 0.05 so reject null hypothesis
• HCV.PCR..cpm. is not normally distributed
```

```
options(tinytex.verbose = TRUE)
kruskal.test(HCV.PCR..cpm.~Patient.Group, data = IFN)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  HCV.PCR..cpm. by Patient.Group
## Kruskal-Wallis chi-squared = 33.168, df = 2, p-value = 6.276e-08
```

```
dunnTest(HCV.PCR..cpm.~Patient.Group, data = IFN)
```

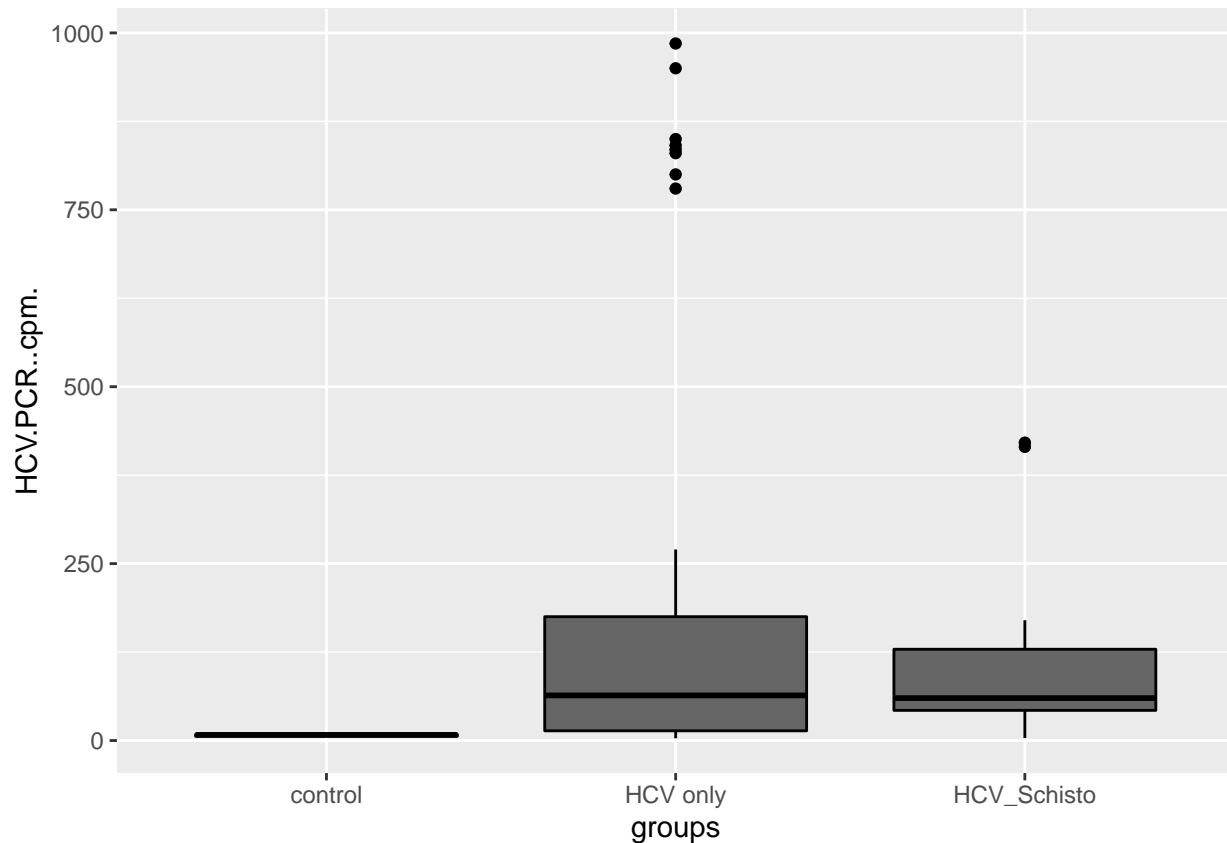
```
## Dunn (1964) Kruskal-Wallis multiple comparison
```

```
##  p-values adjusted with the Holm method.
```

```
##           Comparison      Z      P.unadj      P.adj
## 1    control - HCV only -5.1411393 2.730775e-07 8.192325e-07
## 2    control - HCV_Schisto -4.7315994 2.227576e-06 4.455153e-06
```

```
## 3 HCV only - HCV_Schisto -0.6031412 5.464148e-01 5.464148e-01
```

```
ggplot(IFN, aes(x= Patient.Group, y= HCV.PCR..cpm.)) +  
geom_boxplot(fill = "grey40", color = "black") +  
scale_x_discrete() + labs(x = "groups", y = "HCV.PCR..cpm.")
```



```
conf12<-diff(tapply(IFN$HCV.PCR..cpm.,IFN$Patient.Group,mean))  
quantile(conf12,prob = 0.025)
```

```
##      2.5%
```

```
## -80.02116
```

```
quantile(conf12,prob = 0.975)
```

```
##      97.5%
```

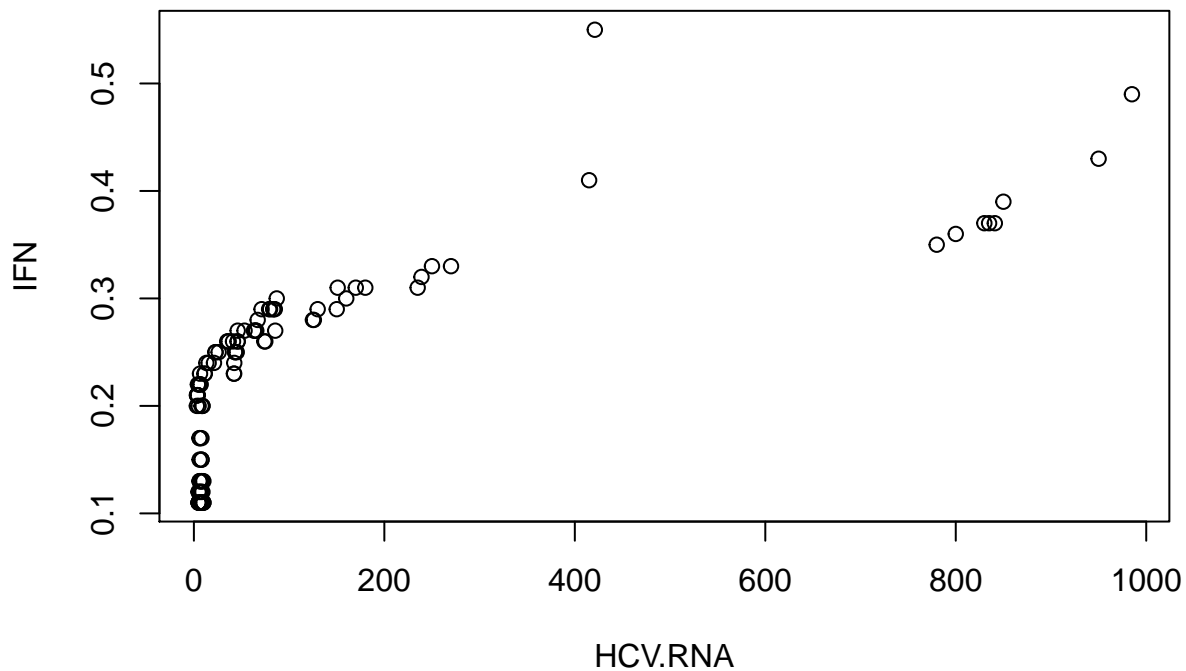
```
## 176.6786
```

- p-value of control-HCV and control-HCV_Schisto is less than 0.05 so reject null hypothesis
- p-value of HCV only-HCV_Schisto is more than 0.05 so fail to reject null hypothesis
- There is a highly significant difference between control-HCV and control-HCV_Schisto but no significant difference between HCV only-HCV_Schisto in HCV.PCR..cpm.
- Confidence interval shows that there is no a difference in means of HCV-RNA between groups
- We conclude that Schistosoma infection don't signifacantly affect on HCV-RNA level in patients with HCV

```
cor(IFN$HCV.PCR..cpm., IFN$IFN....IU.ml., method = "spearman")
```

```
## [1] 0.8702374
```

```
plot(IFN$HCV.PCR..cpm., IFN$IFN....IU.ml., xlab = "HCV.RNA", ylab = "IFN")
```



- There is a positive strong linear relationship between PEG-IFN and HCV.RNA.

antischist.ab.titer

```
options(tinytex.verbose = TRUE)
```

```
table16<-as.data.frame(IFN%>%summary_factorlist("antischist.ab.titer", "Patient.Group", p = F, add_deper
```

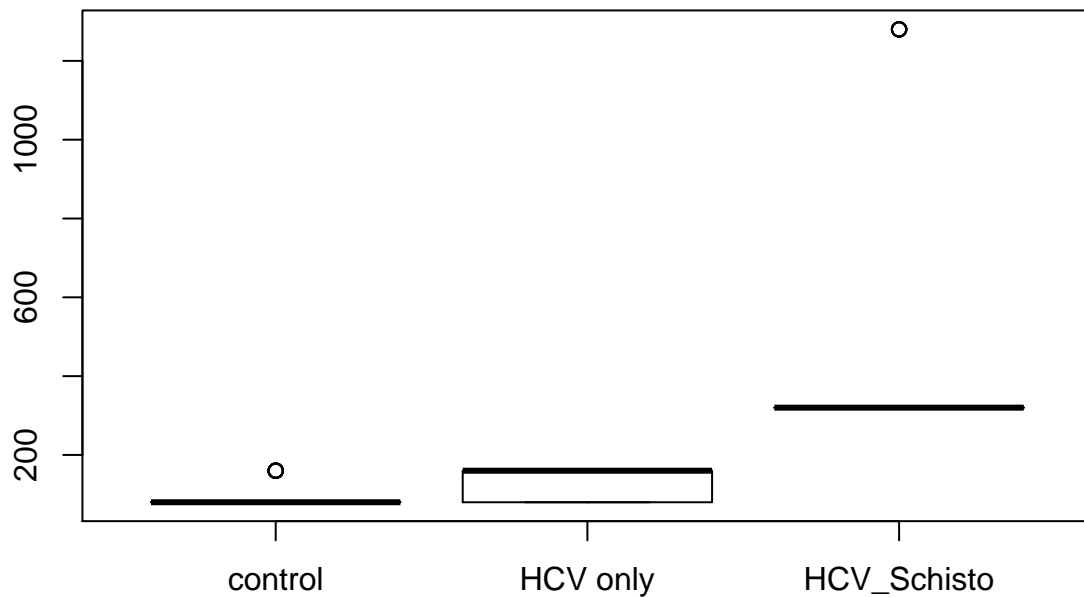
```
## Warning in summary_factorlist(., "antischist.ab.titer", "Patient.Group", :
```

```
## Dependent is not a factor and will be treated as a continuous variable
```

```
table16
```

```
##   Dependent: antischist.ab.titer      Mean (sd)
## 1      Patient.Group      control  98.3 (34.1)
## 2                      HCV only  123.2 (40.3)
## 3                      HCV_Schisto 538.2 (411.8)
```

```
boxplot(antischist.ab.titer~ Patient.Group, data= IFN)
```



```
shapiro.test(IFN$antischist.ab.titer)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  IFN$antischist.ab.titer
## W = 0.45849, p-value < 2.2e-16
• p-value is less than 0.05 so reject null hypothesis
• antischist.ab.titer is not normally distributed
```

```
options(tinytex.verbose = TRUE)
```

```
kruskal.test(antischist.ab.titer~Patient.Group, data = IFN)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  antischist.ab.titer by Patient.Group
## Kruskal-Wallis chi-squared = 64.836, df = 2, p-value = 8.336e-15
```

```
dunnTest(antischist.ab.titer~Patient.Group, data = IFN)
```

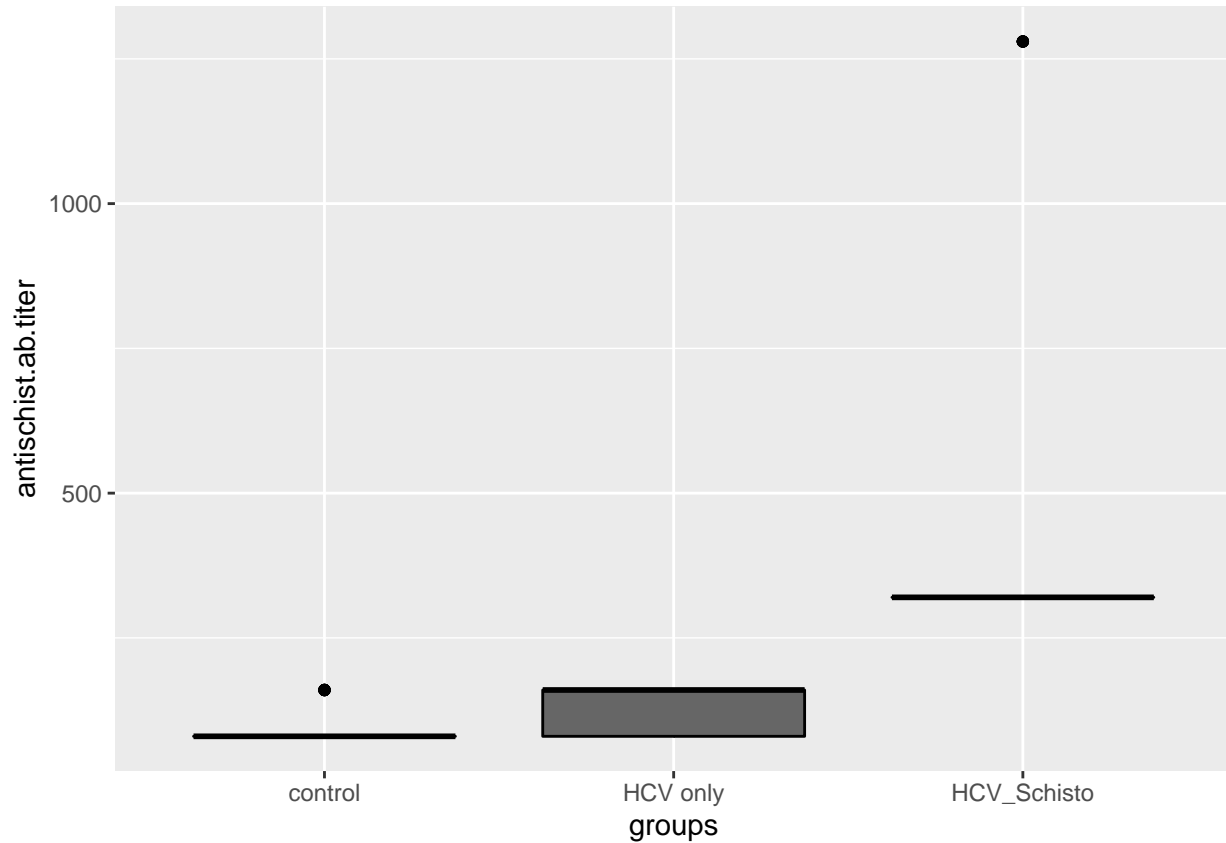
```
## Dunn (1964) Kruskal-Wallis multiple comparison
```

```
##  p-values adjusted with the Holm method.
```

```
##           Comparison      Z      P.unadj      P.adj
## 1    control - HCV only -2.088170 3.678253e-02 3.678253e-02
## 2    control - HCV_Schisto -7.832061 4.799380e-15 1.439814e-14
```

```
## 3 HCV only - HCV_Schisto -6.530288 6.564331e-11 1.312866e-10
```

```
ggplot(IFN, aes(x= Patient.Group, y= antischist.ab.titer)) +  
geom_boxplot(fill = "grey40", color = "black") +  
scale_x_discrete() + labs(x = "groups", y = "antischist.ab.titer")
```



```
conf13<-diff(tapply(IFN$antischist.ab.titer,IFN$Patient.Group,mean))  
quantile(conf13,prob = 0.025)
```

```
##      2.5%
```

```
## 34.66597
```

```
quantile(conf13,prob = 0.975)
```

```
##      97.5%
```

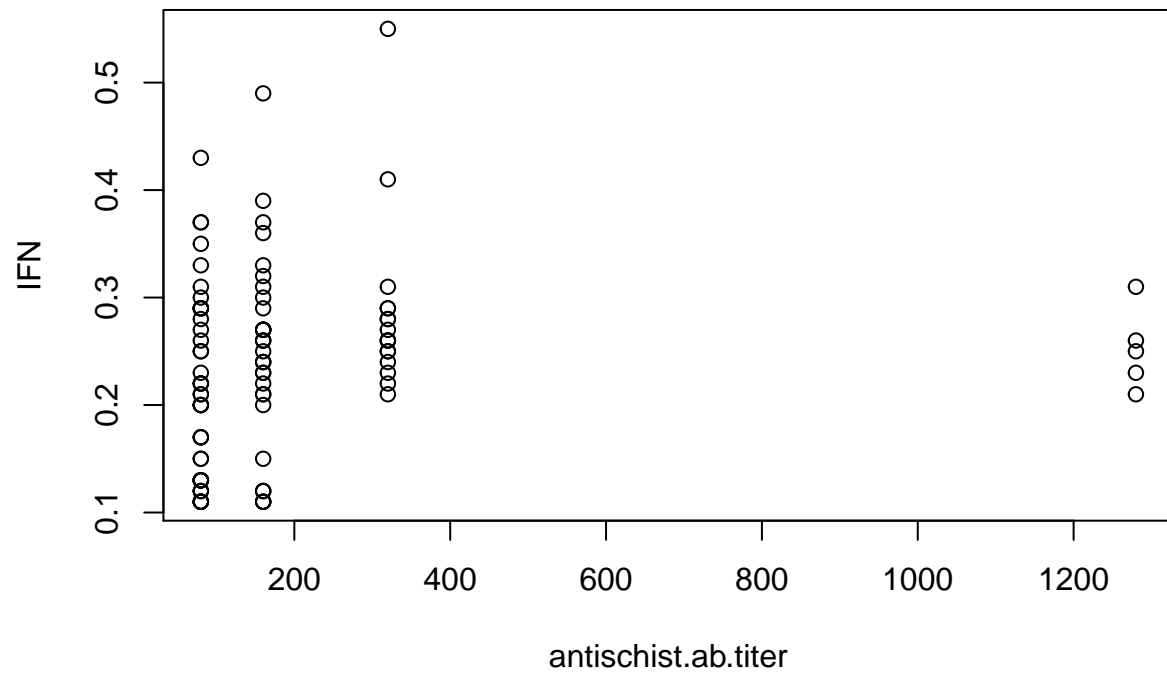
```
## 405.2301
```

- p-value of all groups is less than 0.05 so reject null hypothesis
- Confidence interval shows that there is a difference in means of antischist.ab.titer between groups
- There is a significant difference in antischist.ab.titer between groups

```
cor(IFN$antischist.ab.titer, IFN$IFN....IU.ml., method = "spearman")
```

```
## [1] 0.3001547
```

```
plot(IFN$antischist.ab.titer, IFN$IFN....IU.ml., xlab = "antischist.ab.titer", ylab = "IFN")
```



- There is a positive weak linear relation between PEG-IFN and antischist.ab.titer.