

Analyse statistique des données de qPCR du projet ATB biofilm

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Fonctions

Fonction pour importer les données et ajouter les colonnes “ID”, “[ADN]ng/μL” et “Dilution”.

Fonction de remplacement des données.

```
tri_qPCR = function(tab,Y.intercept,slope,gammeNTC=FALSE,LOQ,moyLOQ,target=FALSE,range=FALSE,ref){  
  #paramètre target pour sélectionner un gène en particulier pour la suite  
  if (target!=FALSE){  
    tab=subset(tab, Target==target)  
  }  
  
  #On calcule la moyenne et le range des Tm STD  
  m.Tm.STD=mean(as.numeric(tab$`Melt Temperature`[which(tab$ID=="STD" & tab$`Melt Temperature`!="None")])  
  #on attribue la même valeur au m.Tm.STD min et max pour  
  m.Tm.STD.min=m.Tm.STD  
  m.Tm.STD.max=m.Tm.STD
```

```

#si on choisit l'option range
if (range==TRUE){
  r.Tm.STD=range(as.numeric(tab$`Melt Temperature`[which(tab$ID=="STD" & tab$`Melt Temperature`!="None")]))
  m.Tm.STD.min=r.Tm.STD[1]
  m.Tm.STD.max=r.Tm.STD[2]
}

#On calcule le range des Cq STD
r.Cq.STD=range(as.numeric(tab$Cq[which(tab$ID=="STD" & tab$Cq!="None")]))

#Si on a des Tm différents des Tm Ok
tab$Cq_modif=tab$Cq #création d'une colonne pour les Cq modifiés (copie de la colonne Cq)
tab$Cq_modif[which(tab$Content!="NTC" & tab$`Melt Temperature`!="None" & (tab$`Melt Temperature`<=m.Tm.STD.min-1 | tab$`Melt Temperature`>=m.Tm.STD.max+1))]=40

#si on a des None pour les Tm
tab$Cq_modif[which(tab$`Melt Temperature`=="None")]=40

tab$Tm_QC="PASS" #création d'une colonne indiquant si le Cq de la ligne (l'échantillon) a été modifié
tab$Tm_QC[which(tab$Content!="NTC" & (tab$`Melt Temperature`<=m.Tm.STD.min-1 | tab$`Melt Temperature`>=m.Tm.STD.max+1))]=FALSE

#Si on a des NTC avec des Cq (pas NA), et des pics au même endroit que les Tm STD => on crée une liste
if (gammeNTC=="NTC"){
  li=which(tab$Content=="NTC" & is.na(tab$Cq)==FALSE & tab$`Melt Temperature`>=m.Tm.STD.min-1 & tab$`Melt Temperature`<=m.Tm.STD.max+1)
  tab$Tm_QC[li]=FALSE
  if (length(li)!=0){ #si cette liste existe bien (non vide)
    p.Cq.NTC=mean(as.numeric(tab$Cq[li]))
    r.Cq.NTC=range(as.numeric(tab$Cq[li]))
    #On visualise le range et la moyenne des Cq NTC
    print(p.Cq.NTC)
    print(r.Cq.NTC)
    #Pour les échantillons avec Tm +/- moy des Tm STD (Tm OK)
    ech=which(tab$`Melt Temperature`>=m.Tm.STD.min-1 & tab$`Melt Temperature`<=m.Tm.STD.max+1)
    #Si Cq(ech) >= LOQ (Cqmean NTC - 1)
    ech2=which(tab$Cq[ech]>=(p.Cq.NTC-1))
    if (length(ech2)!=0){ #si on vérifie bien cette condition
      tab$Tm_QC[ech]=FALSE
      #Si CqmeanNTC < 35
      if (p.Cq.NTC<35){
        tab$Cq_modif[ech]=p.Cq.NTC
      }
      #Si CqmeanNTC > 35
      else{
        tab$Cq_modif[ech]=35-2
      }
    }
  }
}

if (gammeNTC=="gamme"){
  #parametre gamme => oui => Cq le moins concentré range max +2 pour non quanti

```

```

    ech.out = which(tab$Cq > max(tab$Cq[which(tab$ID=="STD")))) #si Cq > à Cq le moins concentré
    tab$Cq_modif[ech.out]=moyLOQ+2
    tab$Tm_QC[ech.out]=FALSE
  }

#On calcule SQ avec les nouveaux Cq
# tab$SQ_final=10^((as.numeric(tab$Cq_modif)-Y.intercept)/slope)
tab$SQ_final=10^((as.numeric(tab$Cq_modif)-tab$"Y-Intercept")/tab$Slope)
#on garde la valeur de départ pour les STD
tab$SQ_final[which(tab$ID=="STD")]=tab$`Starting Quantity (SQ)`[which(tab$ID=="STD")]

#on rajoute col SQ/dil
tab$SQ_dil=tab$SQ_final #on copie la colonne SQ_final pour la modifier par rapport aux dilution des é
dil_ech=which(tab$Dilution!="NA" & tab$Dilution!="ND" & tab$Dilution!="24.02.20") #on sélectionne les
tab$SQ_dil[dil_ech]=tab$SQ_final[dil_ech]*as.numeric(tab$Dilution[dil_ech])

tab$rapport=tab$SQ_dil/ref #ou SQ_final

#on rajoute une colonne pour les log des rapports
tab$log_rapport=log(tab$rapport,10) #attention bien mettre la base 10 (sinon base exp(1))

tab$absolu=tab$SQ_dil*42
tab$absolu[which(tab$ID=="55")]=tab$SQ_dil[which(tab$ID=="55")]*325
tab$absolu[which(tab$ID=="54" | tab$ID=="56" | tab$ID=="57" | tab$ID=="58" | tab$ID=="119" | tab$ID=="120")]

tab$log_absolu=log(tab$absolu,10)

return(tab)
}

```

Test sur les données

Tri des données de qPCR

Plots

Graphique des Cq en fonction des Tm pour chaque gène qnr, permettant de vérifier les résultats obtenus avec la fonction de tri des données de qPCR.

Analyse statistique

Normalité des rapports SQgene/SQref (dilués)

Rapport SQgene/SQref

Vérification, pour chaque gène qnr, de la normalité des rapports SQ(gène)/SQ(ref) avec le test de Shapiro. Visualisation graphique de la répartition des données.

Log des rapports SQgene/SQref

Fusion des tableaux qPCR et metadata (pour avoir les facteurs dans le même tableau)

Modèle pour les campagnes AB

Analyse de la significativité des facteurs bioréacteur, matériel, inoculum, campagne et jour sur le rapport $SQ(\text{gène})/SQ(\text{ref})$.

Il y a 32 échantillons pour la campagnes A et B, mais que 2 échantillons à comparer entre 2 conditions (que Inoculum sans prendre en compte les autres facteurs par exemple)

Pb avec modele AB qui n'affiche pas I ???????????

La normalité n'étant pas toujours respectée, une transformation des rapports en log est nécessaire :

Modèle pour les campagnes EF

Analyse de la significativité des facteurs dosage (forte concentration ou faible concentration) et traitement en FQ sur le rapport $SQ(\text{gène})/SQ(\text{ref})$.

La normalité n'étant pas toujours respectée, une transformation des rapports en log est nécessaire :

Comparaison des moyennes au témoin

Campagnes AB

Campagnes EF

Comparaison au témoin (None) en fonction du type d'ATB (FQ1, FQ2 ou FQ1+FQ2) :

Comparaison au témoin (None) en fonction du dosage (High ou Low) :

Fonction finale résultats

```
results_log = function(tab,metadata,testNormalite=FALSE,extendedResults=FALSE){

  for (i in 1:20){
    metadata$ID_ech[i]=str_sub(row.names(metadata)[i],11,end=-19)
  }
  for (i in 21:58){
    metadata$ID_ech[i]=str_sub(row.names(metadata)[i],18,end=-19)
  }

  tab_lm = merge(tab,metadata, by.x = "ID",by.y = "ID_ech", all.x=TRUE)

  #séparation du tableau complet en sous tableaux pour les camapagnes AB et EF (on enlève les échantill
  tab_lm_AB = subset(tab_lm, Content=="Unkn" & (Campain=="A" | Campain=="B"))
  tab_lm_EF = subset(tab_lm, Content=="Unkn" & (Campain=="E" | Campain=="F"))
  nrow(tab_lm_AB)
  nrow(tab_lm_EF)

  cat("\n")
  cat(paste("\t\t","*****","Campagnes A et B","*****",sep=""),'\n\n')
  cat('\n')
  cat(paste("\t","*****","Facteurs significatifs","*****",sep=""),'\n\n')
```

```

B=as.factor(tab_lm_AB$Bioreacteur)
M=as.factor(tab_lm_AB$Material)
I=as.factor(tab_lm_AB$Inoculum)
C=as.factor(tab_lm_AB$Campain)
Jour=as.factor(tab_lm_AB$Day)
AB.log= tab_lm_AB$log_absolu
if (testNormalite==TRUE){
  p1=ggplot(tab_lm_AB, aes(x=ID,y=log_absolu,label=ID)) + geom_point(size=0.5) + geom_text(size=2.5)
}

shapiro.test(AB.log) #p-value = 0.07119 (qnrA); 9.862e-08 (qnrB); 0.0009526 (qnrS); 0.07227 (qnrC); 0
#AB=μAB+B+M+I+M*I+C+J+I*J+J*M+J*M*I+e
model.AB.log=lm(AB.log~1+B+M+I+M:I+C+Jour+I:Jour+Jour:M)
if (extendedResults==TRUE){
  par(mfrow=c(2,2)) ; plot(model.AB.log) ; par(mfrow=c(1,1))
}
#pour Anova : Normalité des résidus ou Normalité de chacun des groupes
if (testNormalite==TRUE){
  print(shapiro.test(model.AB.log$residuals))
}
#p-value = 0.7034
if (extendedResults==TRUE){
  print("####ANOVA")
  print(anova(model.AB.log))
}
cat('\n\n')
print("####Summary model")
print(summary(model.AB.log))
cat('\n\n')
if (extendedResults==TRUE){
  print("####Tukey")
  print(TukeyHSD(aov(AB.log~1+B+M+I+M:I+C+Jour+I:Jour+Jour:M), ordered=TRUE))
}

cat("\n\n")
cat(paste("\t", "*****", "Comparaison au témoin", "*****", sep=""), '\n\n')
cat('\n\n')

tab_lm_AB_dunnett = subset(tab_lm, Content=="Unkn" & Campain!="E" & Campain!="F") #on prend tous les
# tab_lm_AB_dunnett$Inoculum[which(tab_lm_AB_dunnett$Material==0 | tab_lm_AB_dunnett$ID==55)]= "envt"
tab_lm_AB_dunnett$Inoculum[which(tab_lm_AB_dunnett$ID==0)]= "WW_envt"
tab_lm_AB_dunnett$Inoculum[which(tab_lm_AB_dunnett$ID==55)]= "BF_envt"

if (extendedResults==TRUE){
  model.AB.dunnett <- aov(log_absolu~Inoculum, data = tab_lm_AB_dunnett)
  shapiro.test(model.AB.dunnett$residuals) #si non normalité des résidus on fait Dunn test ?
  print(summary(model.AB.dunnett))
  print(kruskal.test(log_absolu~Inoculum, data = tab_lm_AB_dunnett))
}
print(ggplot(tab_lm_AB_dunnett, aes(x=Inoculum, y=log_absolu,color=Inoculum)) +
  geom_boxplot(outlier.colour="black", outlier.shape=16,outlier.size=2, notch=FALSE) +
  scale_color_manual(values=c("#196f3d", "#1abc9c", "#56B4E9", "#2471a3")) +
  geom_dotplot(binaxis='y', stackdir='center',

```

```

        position=position_dodge(1)))

#Dunn test non paramétrique
print(dunnTest(log_absolu ~ Inoculum,
              data=tab_lm_AB_dunnett,
              method="bonferroni"))

cat("\n\n\n")
cat(paste("\t\t", "*****", "Campagnes E et F", "*****", sep=""), '\n\n')

cat(paste("\t", "*****", "Facteurs significatifs", "*****", sep=""), '\n\n')
# cat('\n')

D=as.factor(tab_lm_EF$Dosage) #Dosage confondu avec la campagne
FQ1=as.factor(tab_lm_EF$FQ1) #présence absence
FQ2=as.factor(tab_lm_EF$FQ2) #présence absence
#J=as.factor(tab_lm_EF$Day) #J14 pour tous les échantillons donc on peut supprimer ce facteur
EF.log=tab_lm_EF$log_absolu
if (testNormalite==TRUE){
  p1=ggplot(tab_lm_EF, aes(x=ID,y=log_absolu,label=ID)) + geom_point(size=0.5) + geom_text(size=2.5)
}
shapiro.test(EF.log)
#EF= $\mu_{EF} + D + FQ1 + FQ2 + FQ1 * FQ2 + J + J * FQ1 + J * FQ2 + J * FQ1 * FQ2 + e$  #D*FQ1+D*FQ2+D*FQ1*FQ2 => effet dosage sur traite
model.EF.log=lm(EF.log~1+FQ1+FQ2+FQ1:FQ2)
if (extendedResults==TRUE){
  par(mfrow=c(2,2)) ; plot(model.EF.log) ; par(mfrow=c(1,1))
}
if (testNormalite==TRUE){
  print(shapiro.test(model.EF.log$residuals))
}
if (extendedResults==TRUE){
  print("####ANOVA")
  print(anova(model.EF.log))
}
cat('\n\n')
print("####Summary model")# on regarde la significativité des prédicteurs pour savoir lesquels garder
print(summary(model.EF.log)) #si significatif => montre différences significatives entre les moyennes
cat('\n')
if (extendedResults==TRUE){
  print("####Tukey")
  print(TukeyHSD(aov(EF.log~1+FQ1+FQ2+FQ1:FQ2), ordered=TRUE))
}

cat("\n")
cat(paste("\t", "*****", "Comparaison au témoin", "*****", sep=""), '\n\n')
cat('\n')

cat("\n")
cat(paste("***", "ATB_type", "***", sep=""), '\n\n')
cat('\n')

tab_lm_EF_Dunnett=tab_lm_EF

```

```

tab_lm_EF_Dunnett$ATB_type[which(tab_lm_EF_Dunnett$ATB_type=="None")]
tab_lm_EF_Dunnett$ATB_type <- relevel(factor(tab_lm_EF_Dunnett$ATB_type), ref="None")

if (extendedResults==TRUE){
  model.EF.ATB_type <- aov(log_absolu~ATB_type, data = tab_lm_EF_Dunnett)
  shapiro.test(model.EF.ATB_type$residuals)
  summary(model.EF.ATB_type)
}
#boxplot(log_absolu~ATB_type, data = tab_lm_EF_Dunnett)
print(ggplot(tab_lm_EF_Dunnett, aes(x=ATB_type, y=log_absolu,color=ATB_type)) +
  geom_boxplot(outlier.colour="black", outlier.shape=16,outlier.size=2, notch=FALSE) +
  scale_color_manual(values=c("#c0392b", "#E69F00", "#56B4E9", "#999999")) +
  geom_dotplot(binaxis='y', stackdir='center',
    position=position_dodge(1)))

print(DunnettTest(x=tab_lm_EF_Dunnett$log_absolu, g=tab_lm_EF_Dunnett$ATB_type))

cat('\n')
cat("\n")
cat(paste("***", "Dosage", "***", sep=""), '\n\n')
cat('\n')

tab_lm_EF_Dunnett=tab_lm_EF
tab_lm_EF_Dunnett$ATB_type[which(tab_lm_EF_Dunnett$ATB_type=="None")]="None"
tab_lm_EF_Dunnett$Dosage[which(tab_lm_EF_Dunnett$ATB_type=="None")]="None"
tab_lm_EF_Dunnett$Dosage <- relevel(factor(tab_lm_EF_Dunnett$Dosage), ref="None")

if (extendedResults==TRUE){
  model.EF.Dosage <- aov(log_absolu~Dosage, data = tab_lm_EF_Dunnett)
  shapiro.test(model.EF.Dosage$residuals)
  print(summary(model.EF.Dosage))
}
#boxplot(log_absolu~Dosage, data = tab_lm_EF_Dunnett)
print(ggplot(tab_lm_EF_Dunnett, aes(x=Dosage, y=log_absolu,color=Dosage)) + geom_boxplot(outlier.colour="black",
  position=position_dodge(1)))

library(DescTools)
print(DunnettTest(x=tab_lm_EF_Dunnett$log_absolu, g=tab_lm_EF_Dunnett$Dosage))
}

```

Résultats

16S

```
results_log(PCR_18_16S_tri,metadata)
```

```

##
##      *****Campagnes A et B*****
##

```

```

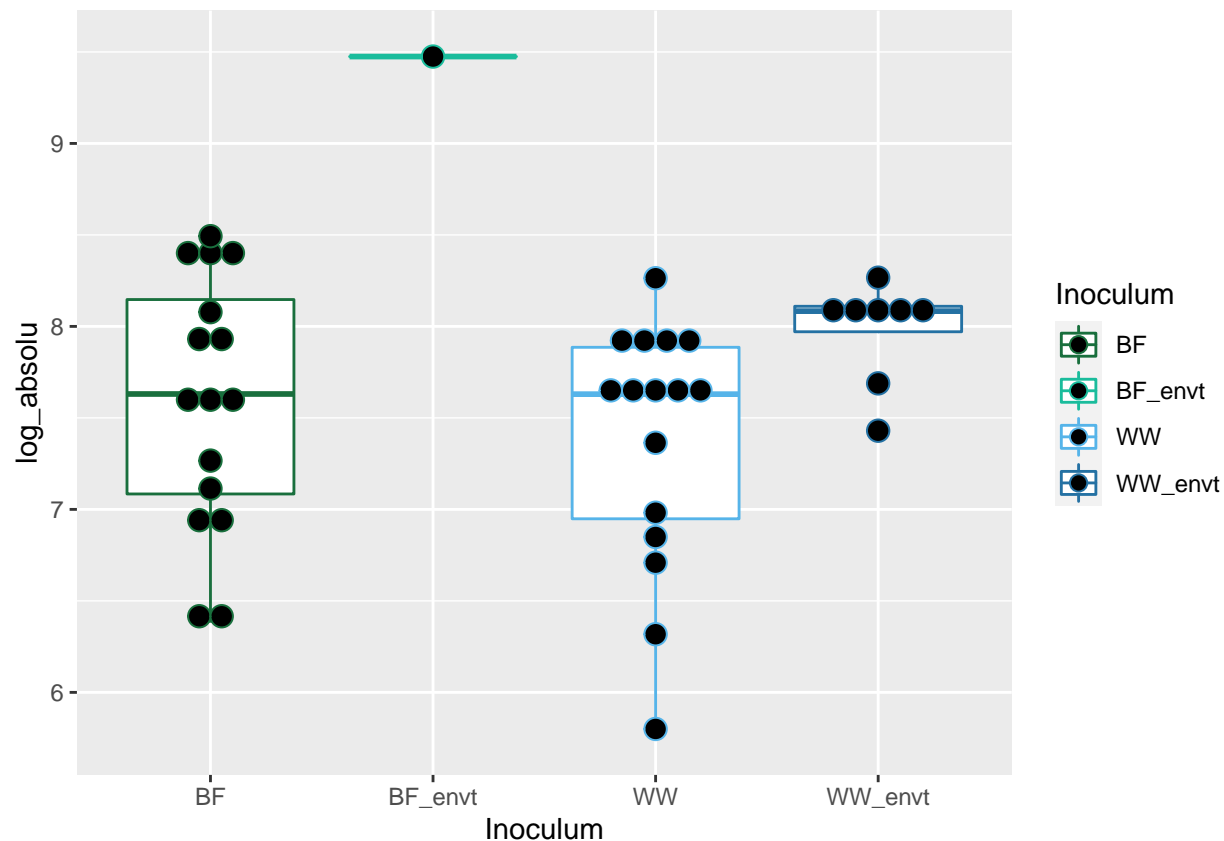
##
## *****Facteurs significatifs*****
##
##
##
## [1] "####Summary model"
##
## Call:
## lm(formula = AB.log ~ 1 + B + M + I + M:I + C + Jour + I:Jour +
##     Jour:M)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.7764 -0.3034  0.1192  0.2858  0.7868
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  7.05152    0.27280  25.849 < 2e-16 ***
## BB2          0.27813    0.24400   1.140  0.26660
## BB3          0.78822    0.34506   2.284  0.03237 *
## BB4          0.62917    0.34506   1.823  0.08187 .
## MP          -1.01175    0.29883  -3.386  0.00266 **
## IWW           NA         NA       NA      NA
## CB           0.24853    0.17253   1.440  0.16381
## JourJ14       0.48245    0.29883   1.614  0.12069
## MP:IWW        0.53670    0.34506   1.555  0.13413
## IWW:JourJ14   0.18581    0.34506   0.538  0.59566
## MP:JourJ14   -0.09607    0.34506  -0.278  0.78331
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.488 on 22 degrees of freedom
## Multiple R-squared:  0.6359, Adjusted R-squared:  0.487
## F-statistic:  4.27 on 9 and 22 DF,  p-value: 0.002614
##
##
##
## *****Comparaison au témoin*****

## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Dunn (1964) Kruskal-Wallis multiple comparison

## p-values adjusted with the Bonferroni method.

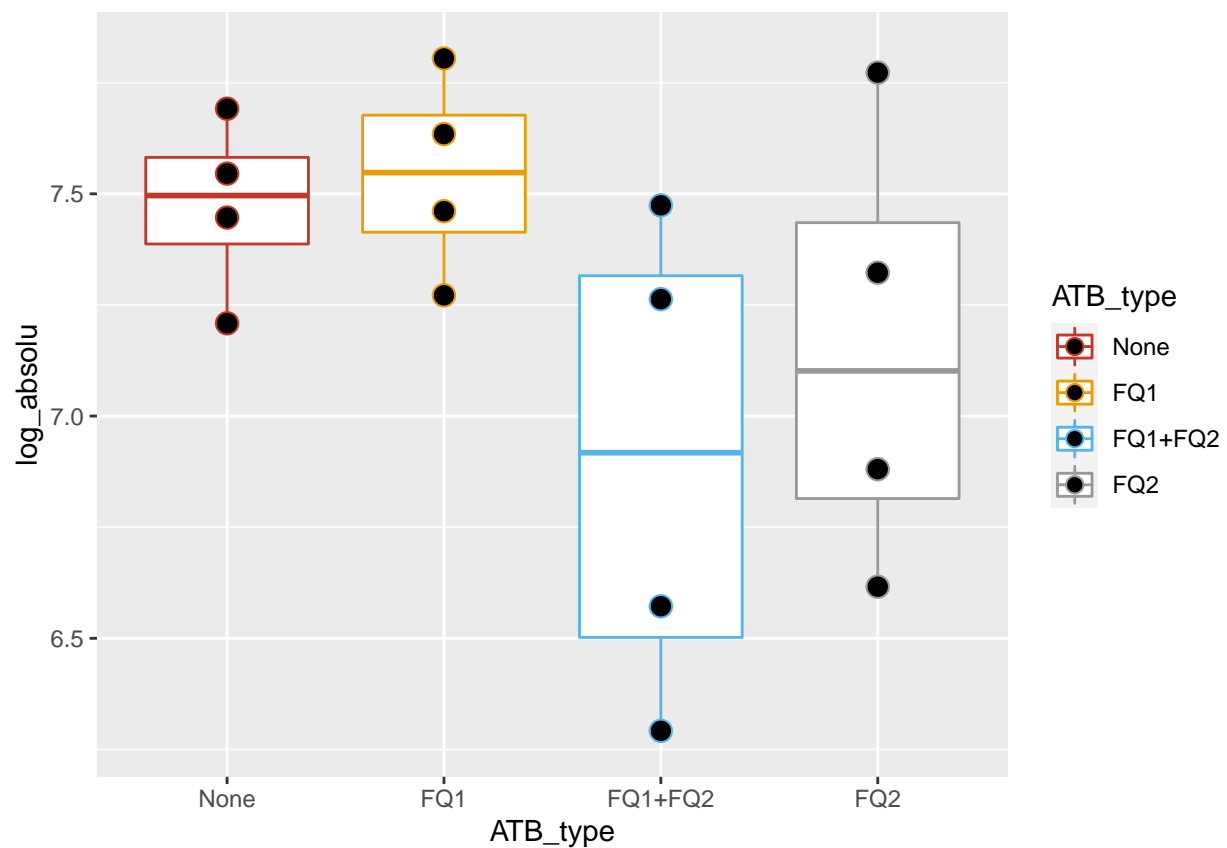
```

```
##      Comparison      Z    P.unadj    P.adj
## 1    BF - BF_envt -1.6551500 0.09789408 0.5873645
## 2      BF - WW    0.9887212 0.32279955 1.0000000
## 3    BF_envt - WW    1.9942786 0.04612162 0.2767297
## 4    BF - WW_envt -1.5543297 0.12010580 0.7206348
## 5 BF_envt - WW_envt 0.9739642 0.33007431 1.0000000
## 6    WW - WW_envt -2.3616172 0.01819542 0.1091725
##
##
##      *****Campagnes E et F*****
##
##      *****Facteurs significatifs*****
##
##
## [1] "####Summary model"
##
## Call:
## lm(formula = EF.log ~ 1 + FQ1 + FQ2 + FQ1:FQ2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.60840 -0.26846  0.02301  0.22924  0.62477
##
## Coefficients:
```

```
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  7.47312    0.20386  36.658 1.09e-13 ***
## FQ11         0.06981    0.28830   0.242   0.813
## FQ21        -0.32513    0.28830  -1.128   0.281
## FQ11:FQ21   -0.31753    0.40772  -0.779   0.451
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4077 on 12 degrees of freedom
## Multiple R-squared:  0.3489, Adjusted R-squared:  0.1862
## F-statistic: 2.144 on 3 and 12 DF,  p-value: 0.1479
##
##
## *****Comparaison au témoin*****
##
##
##
## ***ATB_type***
```

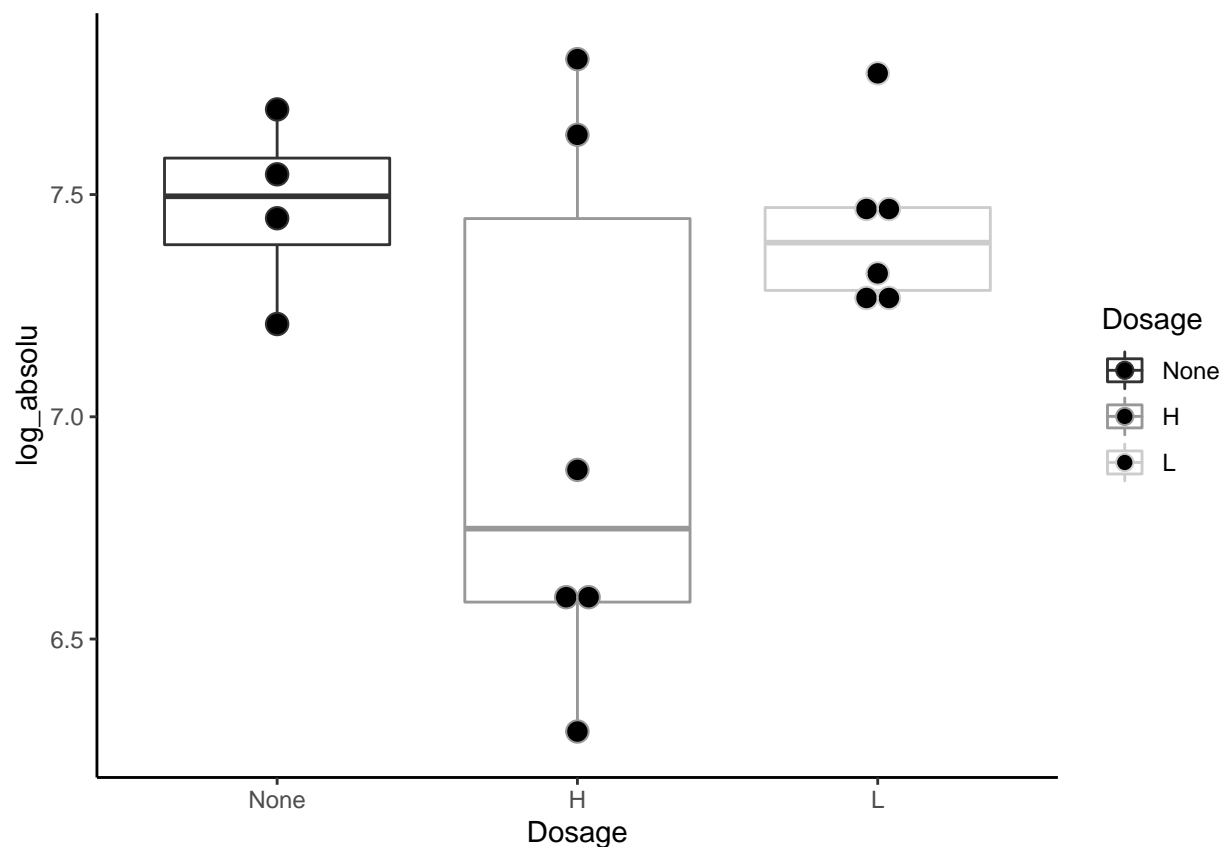
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```



```
##
## Dunnett's test for comparing several treatments with a control :
## 95% family-wise confidence level
```

```
##
## $None
##           diff      lwr.ci    upr.ci    pval
## FQ1-None      0.0698115 -0.7037962 0.8434192 0.9897
## FQ1+FQ2-None -0.5728418 -1.3464496 0.2007659 0.1645
## FQ2-None      -0.3251255 -1.0987332 0.4484823 0.5557
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## ***Dosage***
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```



```
##
## Dunnett's test for comparing several treatments with a control :
## 95% family-wise confidence level
##
## $None
##           diff      lwr.ci    upr.ci    pval
## H-None -0.5064965 -1.1592162 0.1462233 0.1320
## L-None -0.0456074 -0.6983272 0.6071124 0.9769
##
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

qnrA

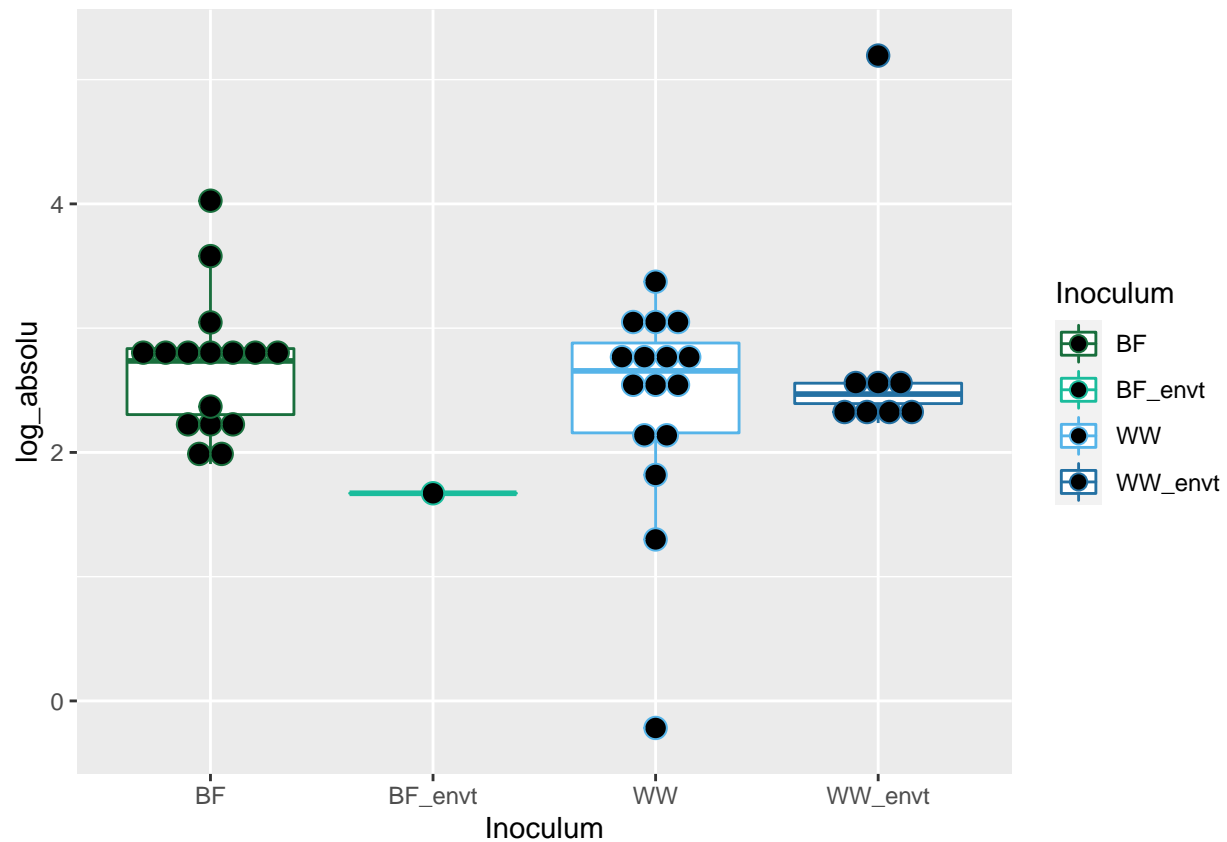
```
results_log(PCR_19_qnrA_tri,metadata)
```

```
##
## *****Campagnes A et B*****
##
## *****Facteurs significatifs*****
##
##
## [1] "####Summary model"
##
## Call:
## lm(formula = AB.log ~ 1 + B + M + I + M:I + C + Jour + I:Jour +
##     Jour:M)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.2572 -0.2533  0.0658  0.3784  0.7784
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.039563   0.397187   5.135 3.8e-05 ***
## BB2          0.190967   0.355255   0.538  0.596
## BB3          0.692576   0.502406   1.379  0.182
## BB4          0.616956   0.502406   1.228  0.232
## MP          -0.479349   0.435096  -1.102  0.282
## IWW          NA         NA         NA     NA
## CB           0.062779   0.251203   0.250  0.805
## JourJ14      0.701274   0.435096   1.612  0.121
## MP:IWW       0.512697   0.502406   1.020  0.319
## IWW:JourJ14  0.005192   0.502406   0.010  0.992
## MP:JourJ14  -0.540746   0.502406  -1.076  0.293
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7105 on 22 degrees of freedom
## Multiple R-squared:  0.3305, Adjusted R-squared:  0.05665
## F-statistic: 1.207 on 9 and 22 DF,  p-value: 0.3397
##
##
##
## *****Comparaison au témoin*****

## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

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

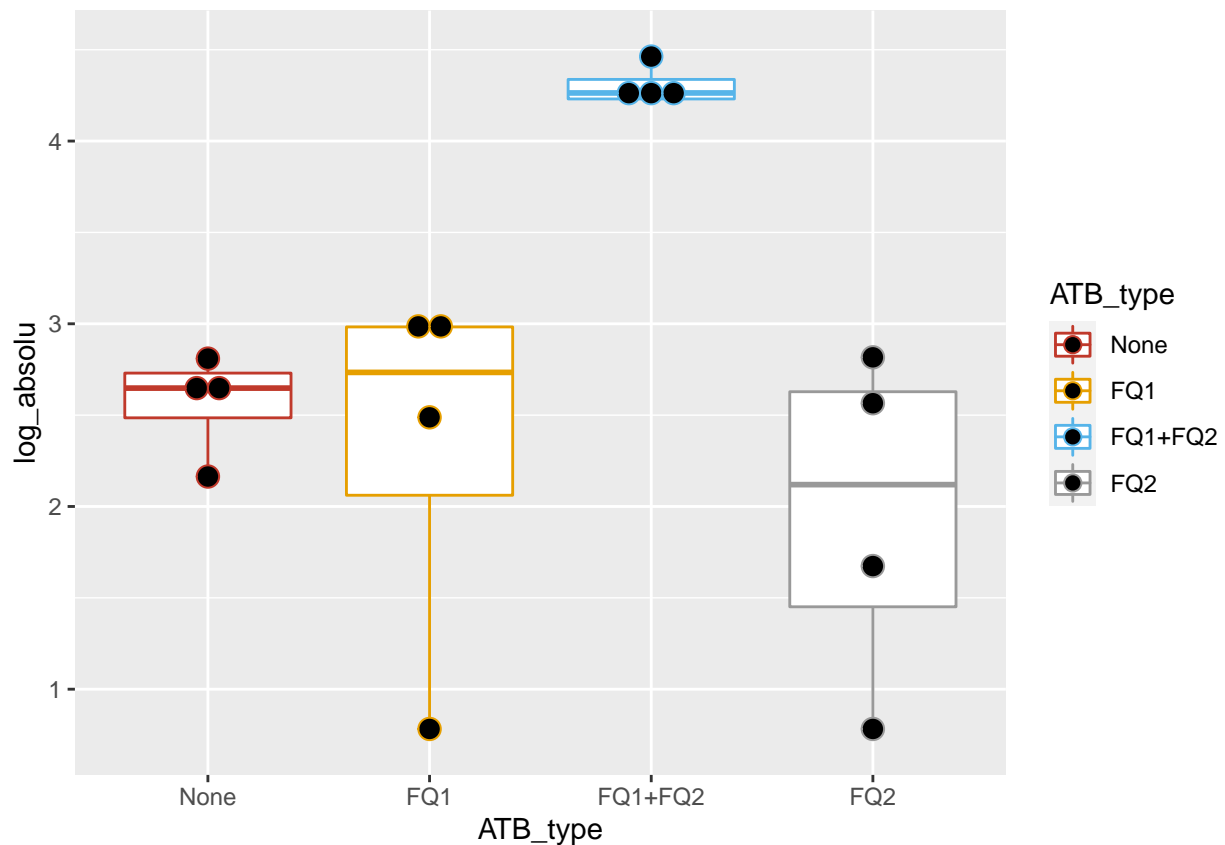
```
## p-values adjusted with the Bonferroni method.
```



```
## Comparison      Z    P.unadj    P.adj
## 1 BF - BF_envt  1.6146570 0.1063850 0.6383100
## 2 BF - WW      0.4279540 0.6686846 1.0000000
## 3 BF_envt - WW -1.4678700 0.1421395 0.8528372
## 4 BF - WW_envt  0.7349931 0.4623437 1.0000000
## 5 BF_envt - WW_envt -1.2691049 0.2044037 1.0000000
## 6 WW - WW_envt  0.3855702 0.6998150 1.0000000
##
##
## *****Campagnes E et F*****
##
## *****Facteurs significatifs*****
##
##
## [1] "####Summary model"
##
## Call:
## lm(formula = EF.log ~ 1 + FQ1 + FQ2 + FQ1:FQ2)
##
```

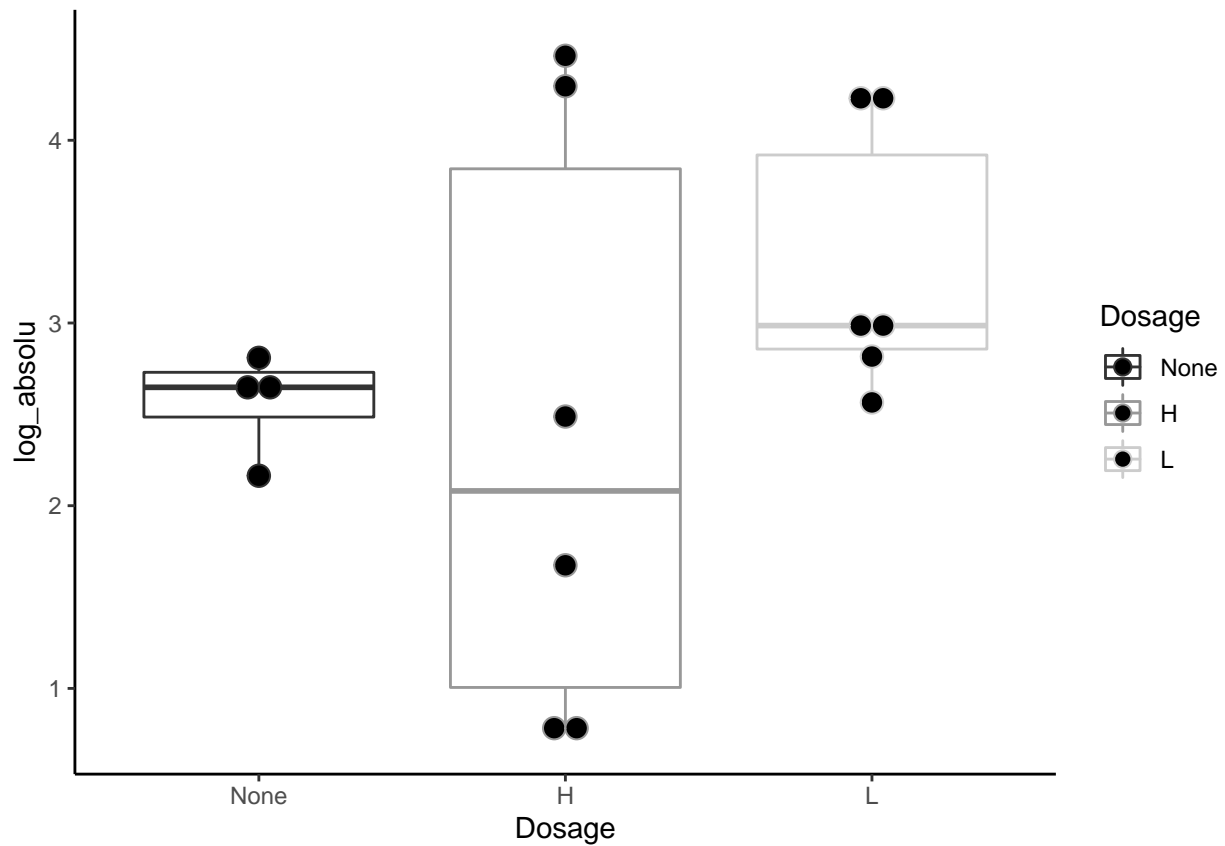
```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.52812 -0.12811  0.08067  0.33296  0.85690
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.5673     0.3572   7.188 1.11e-05 ***
## FQ11          -0.2568     0.5051  -0.508  0.62039
## FQ21          -0.6078     0.5051  -1.203  0.25205
## FQ11:FQ21      2.6019     0.7144   3.642  0.00337 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7144 on 12 degrees of freedom
## Multiple R-squared:  0.6807, Adjusted R-squared:  0.6008
## F-statistic: 8.526 on 3 and 12 DF,  p-value: 0.002649
##
##
## *****Comparaison au témoin*****
##
##
## ***ATB_type***

## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```



```
##
## Dunnett's test for comparing several treatments with a control :
## 95% family-wise confidence level
##
## $None
##          diff      lwr.ci      upr.ci    pval
## FQ1-None    -0.256813 -1.6122644  1.0986384  0.9200
## FQ1+FQ2-None 1.737285  0.3818336  3.0927363  0.0127 *
## FQ2-None    -0.607840 -1.9632914  0.7476114  0.5087
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## ***Dosage***
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```



```
##
## Dunnett's test for comparing several treatments with a control :
## 95% family-wise confidence level
##
## $None
##          diff      lwr.ci      upr.ci    pval
```

```
## H-None -0.1531450 -1.944592 1.638302 0.9657
## L-None 0.7348997 -1.056547 2.526347 0.4994
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

qnrB

```
results_log(PCR_20_qnrB_tri,metadata)
```

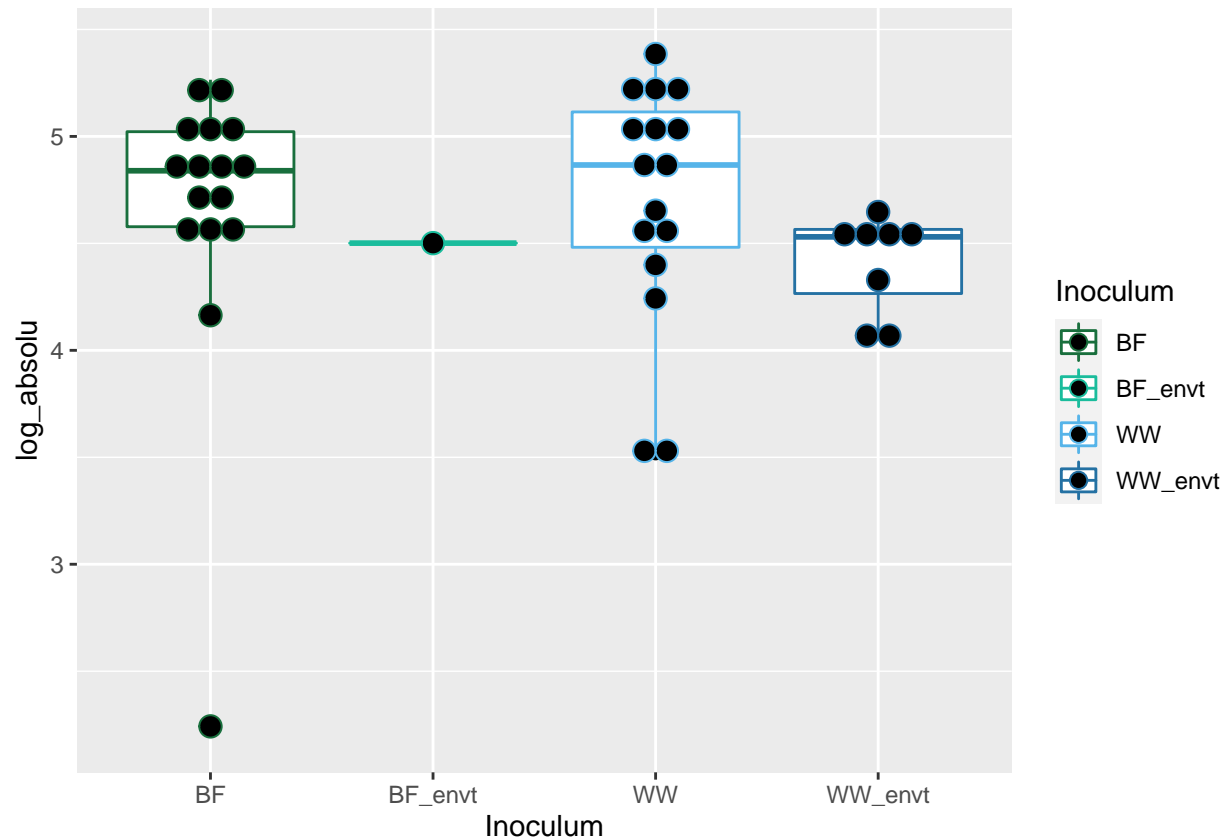
```
##
##      *****Campagnes A et B*****
##
##
## *****Facteurs significatifs*****
##
##
##
## [1] "####Summary model"
##
## Call:
## lm(formula = AB.log ~ 1 + B + M + I + M:I + C + Jour + I:Jour +
##      Jour:M)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.81037 -0.39666  0.09122  0.35401  0.94131
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.00518    0.35752  11.203 1.47e-10 ***
## BB2          0.34503    0.31978   1.079  0.292
## BB3          0.04736    0.45224   0.105  0.918
## BB4          0.22121    0.45224   0.489  0.630
## MP           0.35772    0.39165   0.913  0.371
## IWW          NA         NA        NA     NA
## CB           0.36715    0.22612   1.624  0.119
## JourJ14      0.55625    0.39165   1.420  0.170
## MP:IWW      -0.01390    0.45224  -0.031  0.976
## IWW:JourJ14  0.04219    0.45224   0.093  0.927
## MP:JourJ14  -0.48367    0.45224  -1.069  0.296
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6396 on 22 degrees of freedom
## Multiple R-squared:  0.2602, Adjusted R-squared:  -0.04247
## F-statistic: 0.8597 on 9 and 22 DF,  p-value: 0.5729
##
##
##
## *****Comparaison au témoin*****
```



```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

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

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



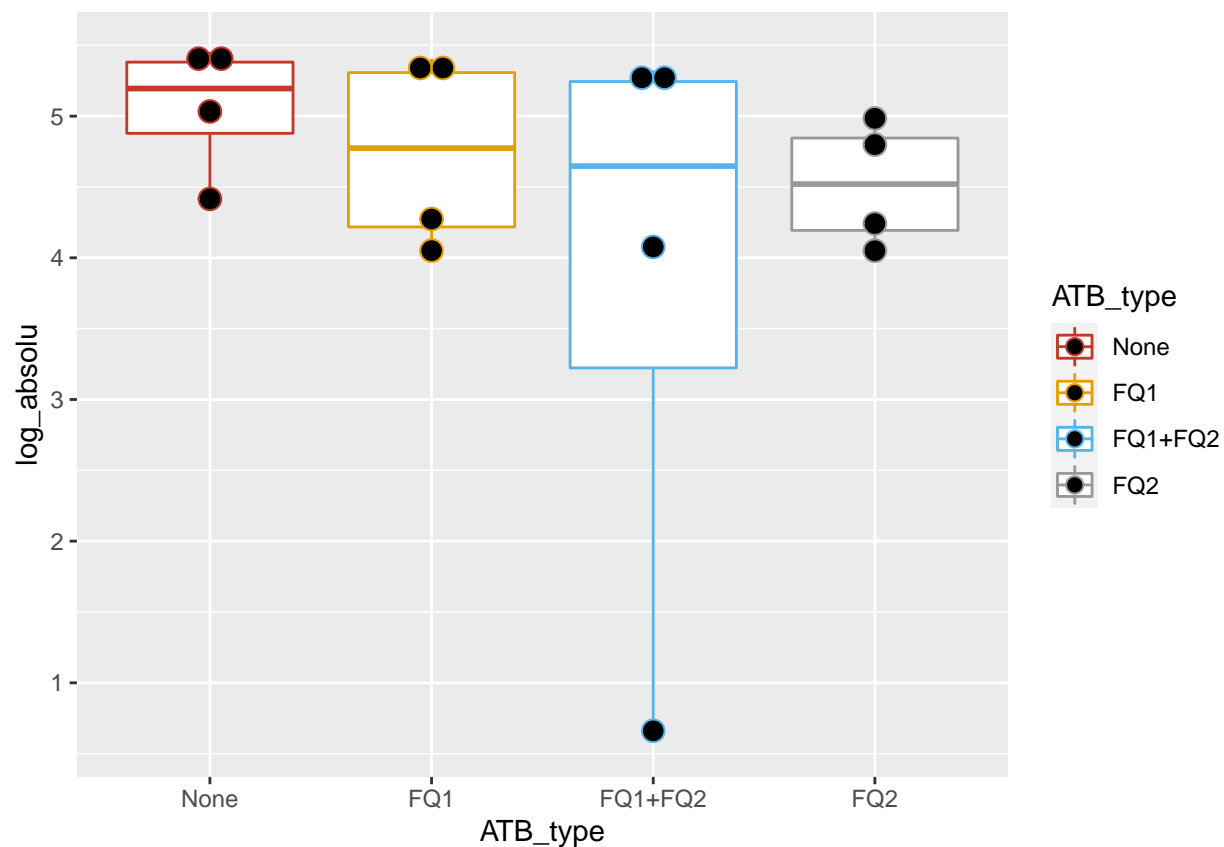
```
##      Comparison      Z  P.unadj  P.adj
## 1    BF - BF_envt  1.1034333 0.2698390 1.0000000
## 2      BF - WW    0.0000000 1.0000000 1.0000000
## 3  BF_envt - WW  -1.1034333 0.2698390 1.0000000
## 4    BF - WW_envt  2.2652247 0.0234989 0.1409934
## 5 BF_envt - WW_envt -0.1475703 0.8826819 1.0000000
## 6    WW - WW_envt  2.2652247 0.0234989 0.1409934
##
##
##      *****Campagnes E et F*****
##
##      *****Facteurs significatifs*****
##
##
## [1] "####Summary model"
##
## Call:
```

```

## lm(formula = EF.log ~ 1 + FQ1 + FQ2 + FQ1:FQ2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.1588 -0.4709  0.2686  0.4802  1.5040
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.0650     0.5939   8.528 1.94e-06 ***
## FQ11          -0.3140     0.8399  -0.374   0.715
## FQ21          -0.5463     0.8399  -0.650   0.528
## FQ11:FQ21     -0.3849     1.1879  -0.324   0.751
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.188 on 12 degrees of freedom
## Multiple R-squared:  0.1655, Adjusted R-squared:  -0.04318
## F-statistic: 0.793 on 3 and 12 DF,  p-value: 0.5209
##
##
##
## *****Comparaison au témoin*****
##
##
##
## ***ATB_type***

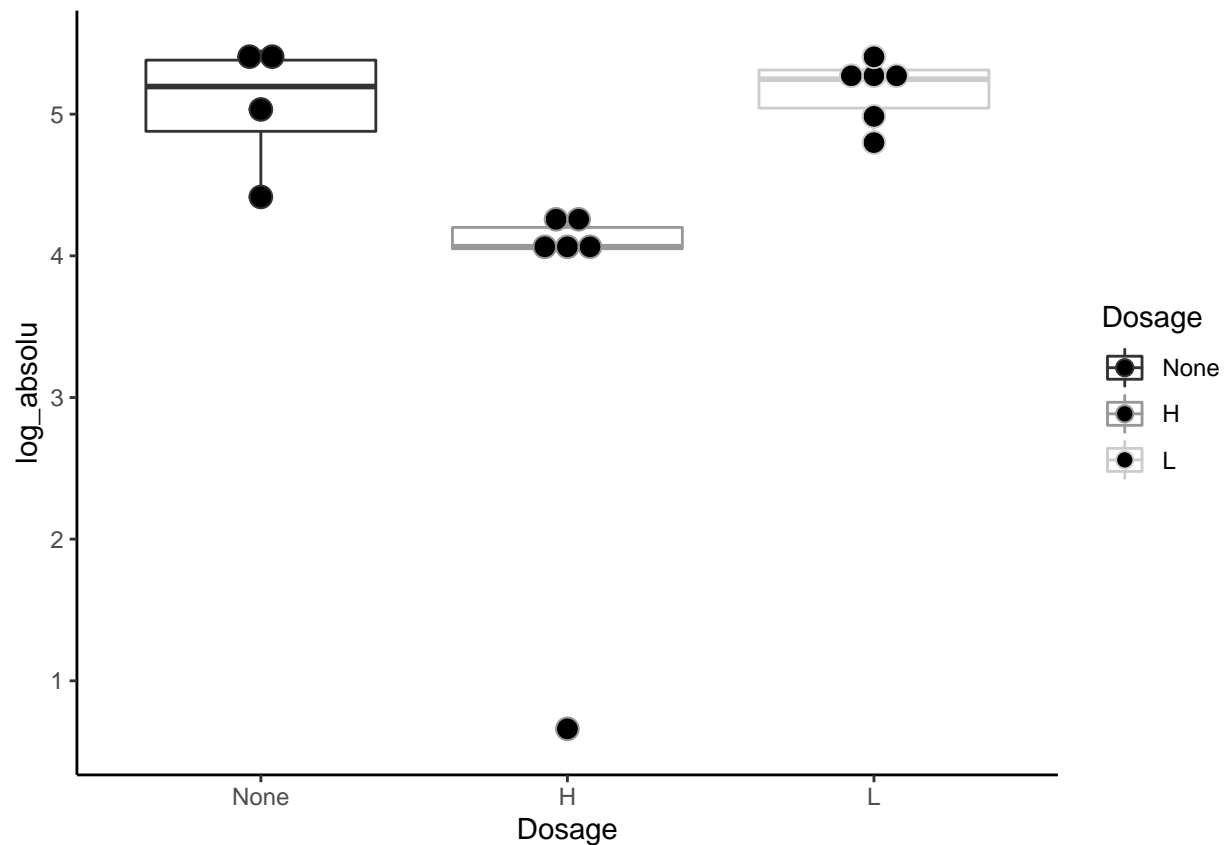
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

```



```
##
##   Dunnett's test for comparing several treatments with a control :
##     95% family-wise confidence level
##
## $None
##           diff      lwr.ci   upr.ci    pval
## FQ1-None     -0.3139703 -2.567822  1.939881  0.9649
## FQ1+FQ2-None -1.2451423 -3.498994  1.008709  0.3539
## FQ2-None     -0.5462763 -2.800128  1.707575  0.8531
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## ***Dosage***

## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```



```
##
## Dunnett's test for comparing several treatments with a control :
## 95% family-wise confidence level
##
## $None
##      diff      lwr.ci      upr.ci    pval
## H-None -1.5060242 -2.969521 -0.04252703 0.0438 *
## L-None  0.1024316 -1.361066  1.56592881 0.9768
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

qnrS

```
results_log(PCR_21_qnrS_tri,metadata)
```

```
##
## *****Campagnes A et B*****
##
##
## *****Facteurs significatifs*****
##
##
```

```

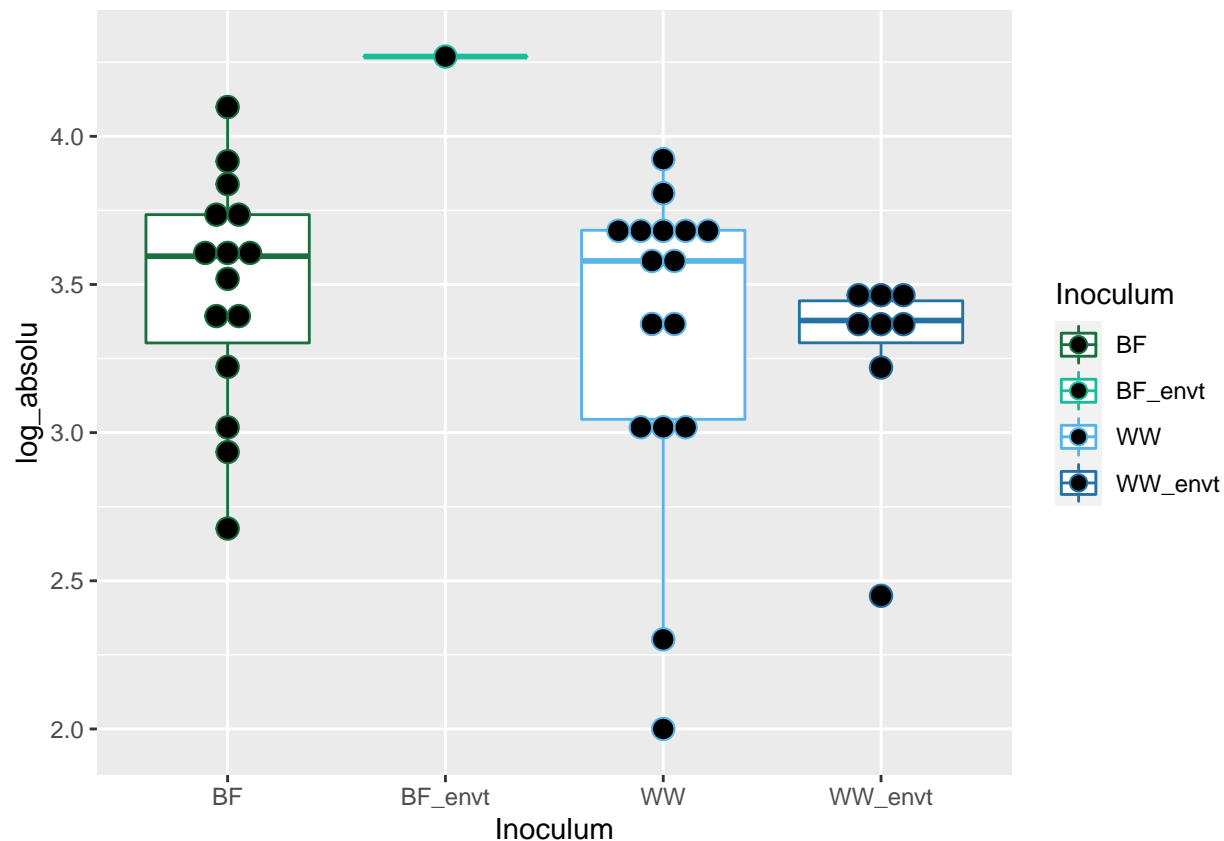
##
## [1] "####Summary model"
##
## Call:
## lm(formula = AB.log ~ 1 + B + M + I + M:I + C + Jour + I:Jour +
##      Jour:M)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.82963 -0.25259  0.04557  0.25497  0.68883
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.82961    0.23270  12.160  5.7e-11 ***
## BB2          0.40464    0.20627   1.962  0.0632 .
## BB3          0.75771    0.29827   2.540  0.0190 *
## BB4          0.53311    0.29171   1.828  0.0819 .
## MP          -0.39951    0.25454  -1.570  0.1315
## IWW          NA         NA      NA      NA
## CB           0.37086    0.14913   2.487  0.0214 *
## JourJ14      0.27619    0.26930   1.026  0.3168
## MP:IWW       0.42812    0.29827   1.435  0.1659
## IWW:JourJ14  0.06677    0.29827   0.224  0.8250
## MP:JourJ14  -0.26209    0.29827  -0.879  0.3895
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4125 on 21 degrees of freedom
## Multiple R-squared:  0.4703, Adjusted R-squared:  0.2433
## F-statistic: 2.072 on 9 and 21 DF,  p-value: 0.08129
##
##
##
## *****Comparaison au témoin*****

## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Dunn (1964) Kruskal-Wallis multiple comparison

##  p-values adjusted with the Bonferroni method.

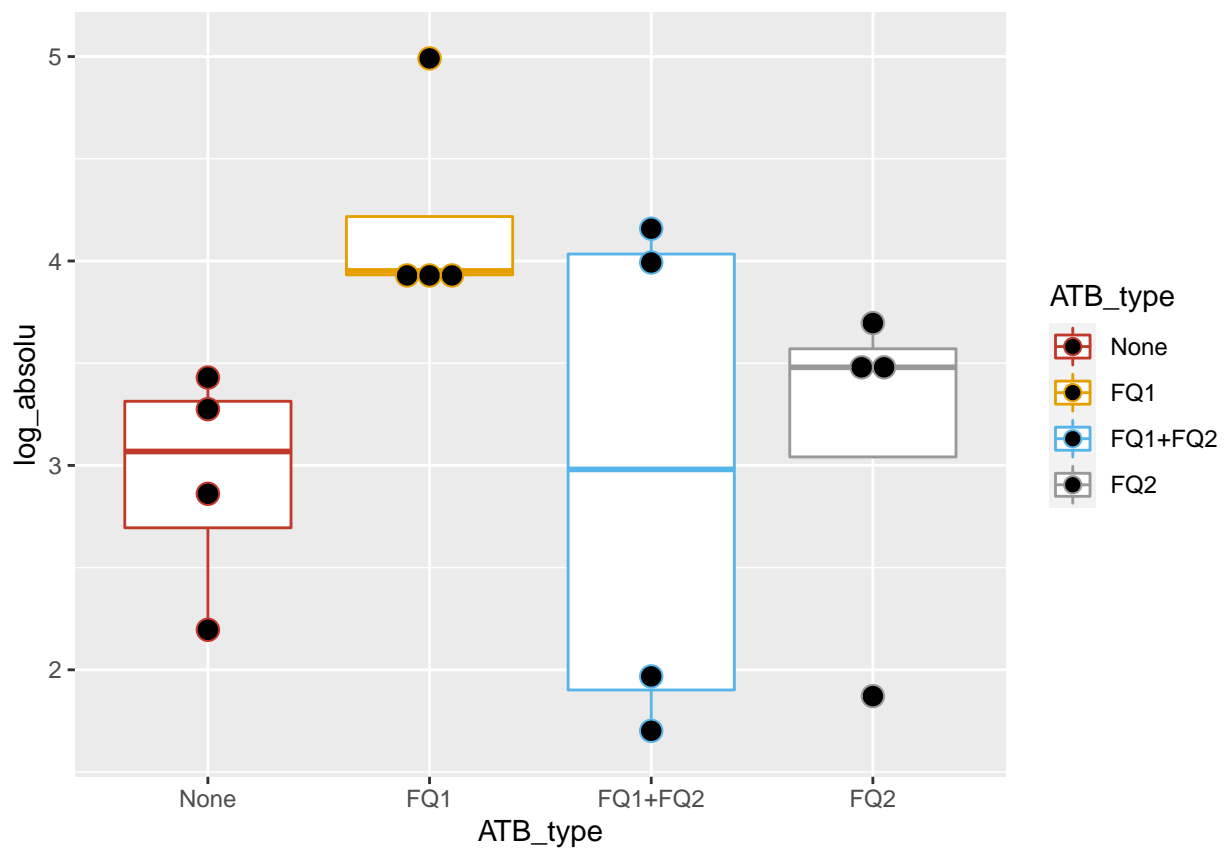
```



```
##      Comparison      Z    P.unadj    P.adj
## 1    BF - BF_envt -1.4632177 0.14340781 0.8604469
## 2      BF - WW    0.4214744 0.67340873 1.0000000
## 3    BF_envt - WW  1.6130381 0.10673622 0.6404173
## 4    BF - WW_envt  1.5305306 0.12588545 0.7553127
## 5 BF_envt - WW_envt 2.0565185 0.03973257 0.2383954
## 6    WW - WW_envt  1.1976221 0.23106415 1.0000000
##
##
##      *****Campagnes E et F*****
##
##      *****Facteurs significatifs*****
##
##
## [1] "####Summary model"
##
## Call:
## lm(formula = EF.log ~ 1 + FQ1 + FQ2 + FQ1:FQ2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.2606 -0.4106  0.1101  0.5081  1.2029
##
## Coefficients:
```

```
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.9404     0.4324   6.800  1.9e-05 ***
## FQ11          1.2578     0.6116   2.057   0.0621 .
## FQ21          0.1915     0.6116   0.313   0.7596
## FQ11:FQ21     -1.4347     0.8649  -1.659   0.1230
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8649 on 12 degrees of freedom
## Multiple R-squared:  0.3255, Adjusted R-squared:  0.1569
## F-statistic: 1.931 on 3 and 12 DF,  p-value: 0.1785
##
##
## *****Comparaison au témoin*****
##
##
## ***ATB_type***
```

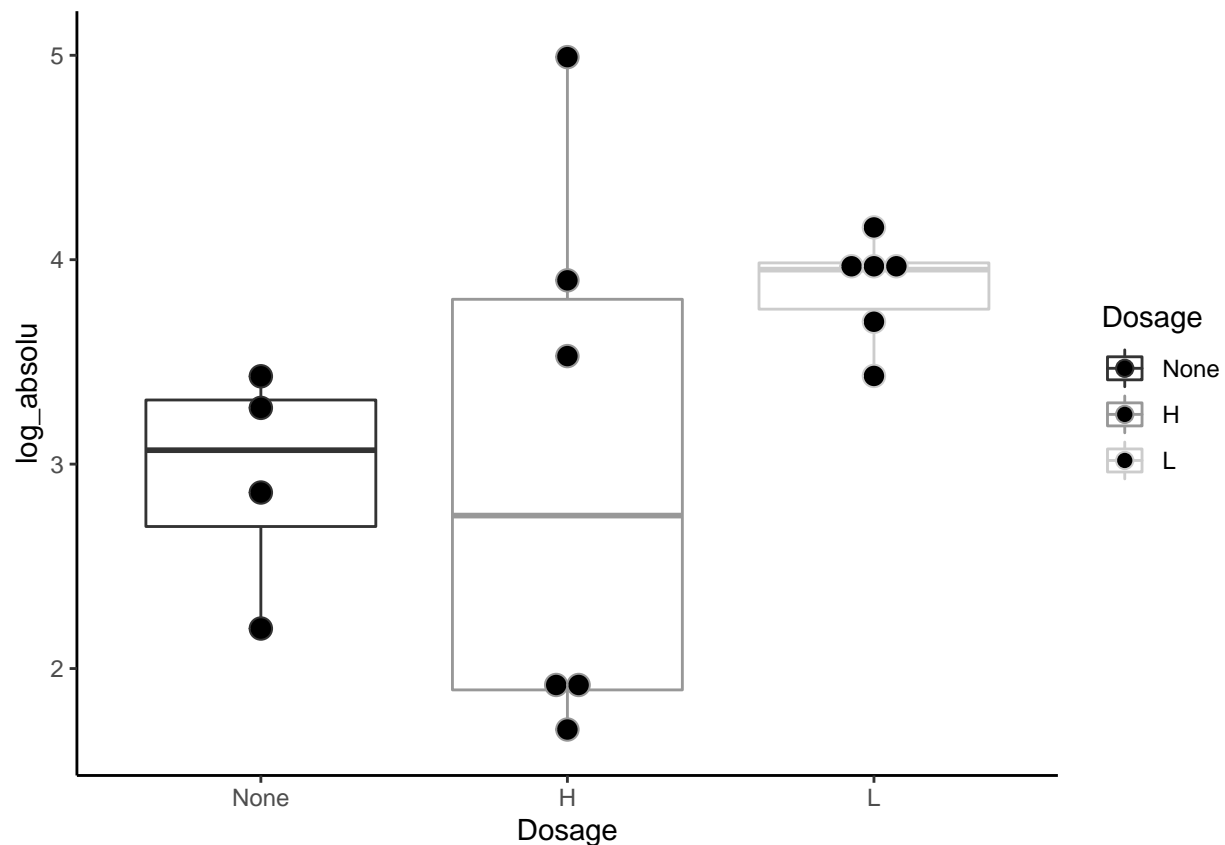
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```



```
##
## Dunnett's test for comparing several treatments with a control :
## 95% family-wise confidence level
```

```
##
## $None
##           diff      lwr.ci   upr.ci   pval
## FQ1-None    1.25776401 -0.3832793 2.898807 0.1472
## FQ1+FQ2-None 0.01458289 -1.6264604 1.655626 1.0000
## FQ2-None     0.19148238 -1.4495609 1.832526 0.9786
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## ***Dosage***
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```



```
##
## Dunnett's test for comparing several treatments with a control :
## 95% family-wise confidence level
##
## $None
##           diff      lwr.ci   upr.ci   pval
## H-None 0.05279651 -1.3617055 1.467298 0.9933
## L-None 0.92308968 -0.4914123 2.337592 0.2162
##
```



```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

qnrD

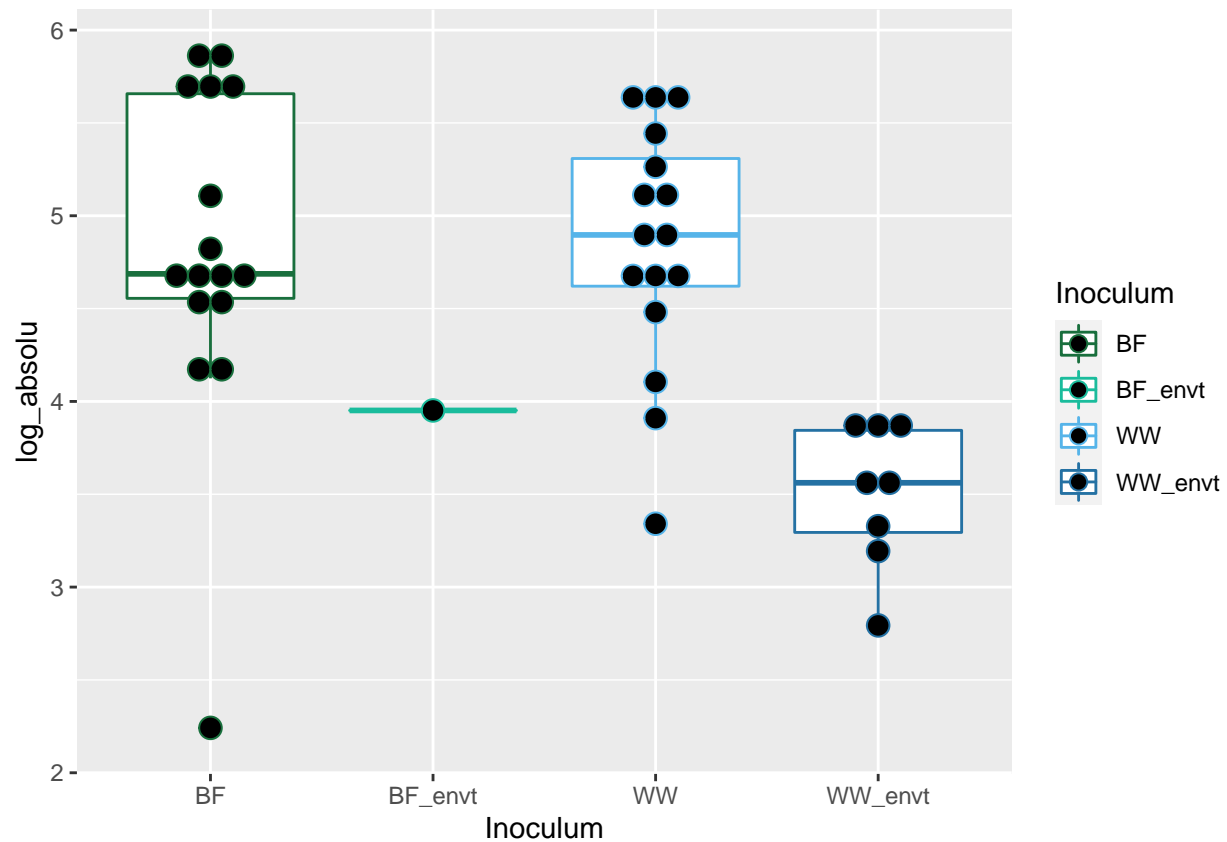
```
results_log(PCR_22_qnrD_tri,metadata)
```

```
##
##      *****Campagnes A et B*****
##
##
##      *****Facteurs significatifs*****
##
##
## [1] "####Summary model"
##
## Call:
## lm(formula = AB.log ~ 1 + B + M + I + M:I + C + Jour + I:Jour +
##      Jour:M)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.4031 -0.4033  0.1171  0.5446  1.0557
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.83402     0.47353  10.209 8.28e-10 ***
## BB2           0.31998     0.42353   0.756  0.458
## BB3          -0.12657     0.59897  -0.211  0.835
## BB4           0.42462     0.59897   0.709  0.486
## MP           -0.41122     0.51872  -0.793  0.436
## IWW           NA          NA       NA      NA
## CB            0.05204     0.29948   0.174  0.864
## JourJ14       -0.11468     0.51872  -0.221  0.827
## MP:IWW        -0.14802     0.59897  -0.247  0.807
## IWW:JourJ14   0.18305     0.59897   0.306  0.763
## MP:JourJ14    0.27379     0.59897   0.457  0.652
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8471 on 22 degrees of freedom
## Multiple R-squared:  0.1592, Adjusted R-squared:  -0.1848
## F-statistic: 0.4627 on 9 and 22 DF,  p-value: 0.8839
##
##
##
##      *****Comparaison au témoin*****

## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

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

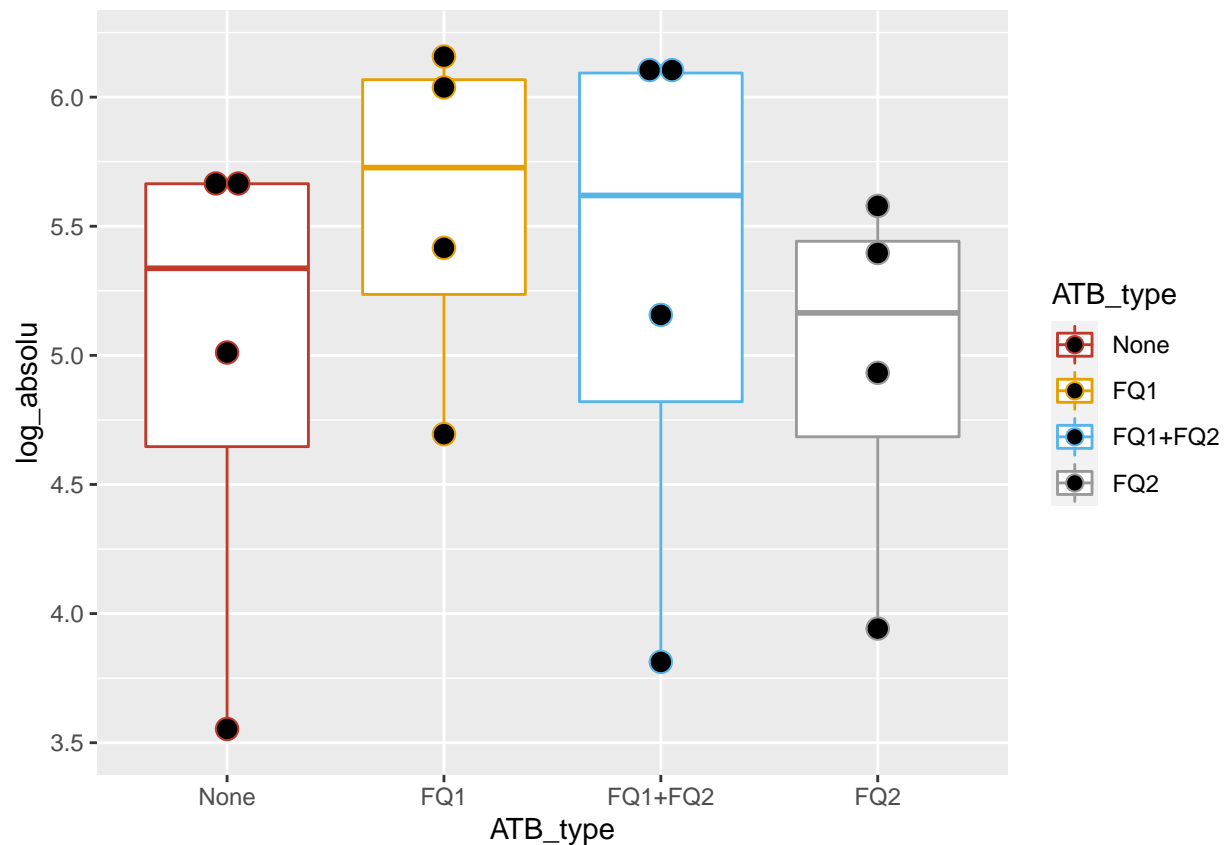
```
## p-values adjusted with the Bonferroni method.
```



```
## Comparison      Z      P.unadj      P.adj
## 1 BF - BF_envt  1.05281711 0.2924248237 1.0000000000
## 2 BF - WW      0.02951407 0.9764546001 1.0000000000
## 3 BF_envt - WW -1.04269386 0.2970901007 1.0000000000
## 4 BF - WW_envt  3.59062206 0.0003298897 0.001979338
## 5 BF_envt - WW_envt 0.44271100 0.6579747835 1.0000000000
## 6 WW - WW_envt  3.56652393 0.0003617478 0.002170487
##
##
## *****Campagnes E et F*****
##
## *****Facteurs significatifs*****
##
##
## [1] "####Summary model"
##
## Call:
## lm(formula = EF.log ~ 1 + FQ1 + FQ2 + FQ1:FQ2)
##
```

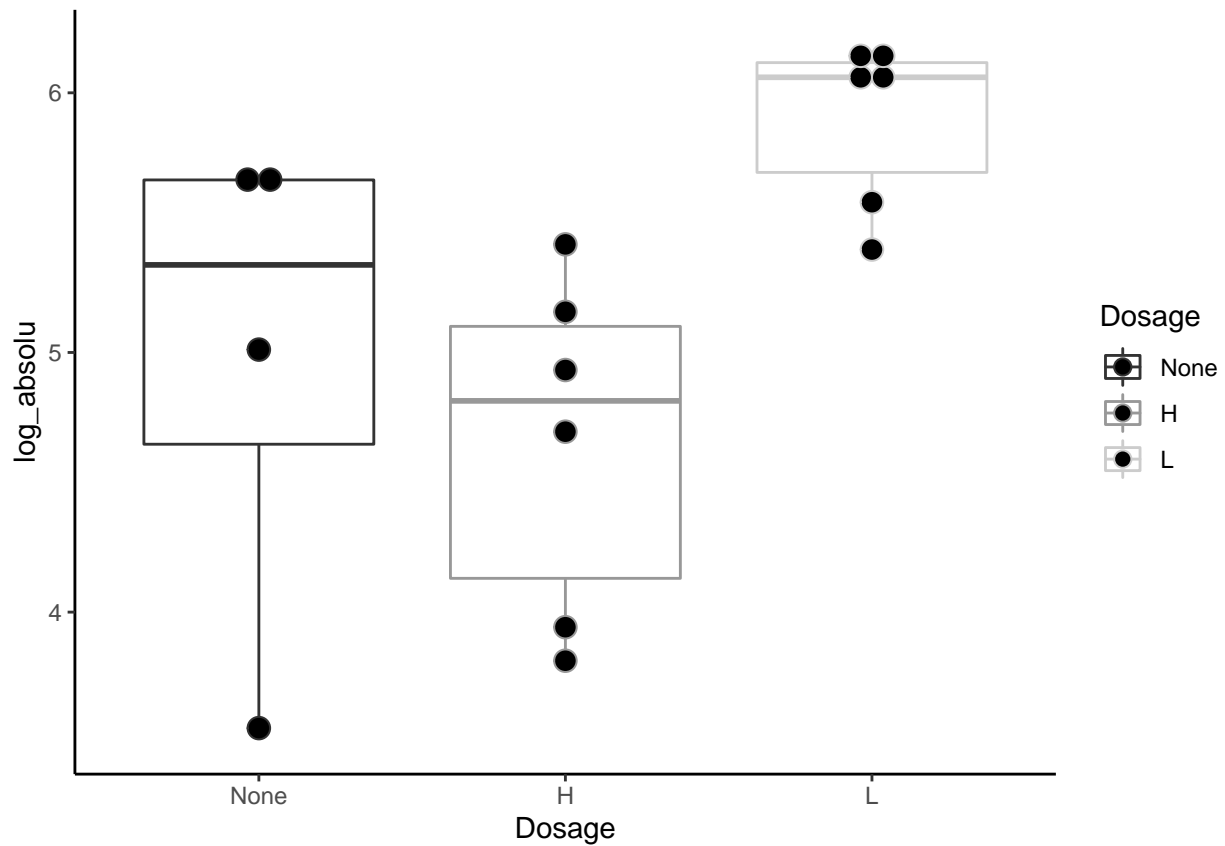
```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4819 -0.3406  0.2356  0.6347  0.8329
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.97387    0.44414  11.199 1.04e-07 ***
## FQ11         0.60261    0.62811   0.959   0.356
## FQ21        -0.01156    0.62811  -0.018   0.986
## FQ11:FQ21    -0.27018    0.88828  -0.304   0.766
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8883 on 12 degrees of freedom
## Multiple R-squared:  0.09839,    Adjusted R-squared:  -0.127
## F-statistic: 0.4365 on 3 and 12 DF,  p-value: 0.7309
##
##
## *****Comparaison au témoin*****
##
##
## ***ATB_type***

## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```



```
##
## Dunnett's test for comparing several treatments with a control :
## 95% family-wise confidence level
##
## $None
##          diff      lwr.ci    upr.ci    pval
## FQ1-None    0.60260560 -1.082822  2.288034  0.6642
## FQ1+FQ2-None 0.32086805 -1.364560  2.006296  0.9192
## FQ2-None    -0.01155901 -1.696987  1.673869  1.0000
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## ***Dosage***
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```



```
##
## Dunnett's test for comparing several treatments with a control :
## 95% family-wise confidence level
##
## $None
##          diff      lwr.ci    upr.ci    pval
```

```
## H-None -0.3147451 -1.3594619 0.7299718 0.6718
## L-None 0.9226882 -0.1220287 1.9674050 0.0837 .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```