

R Notebook

```
library(dplyr)
```

```
##
## Attachement du package : 'dplyr'
## Les objets suivants sont masqués depuis 'package:stats':
##
##     filter, lag
## Les objets suivants sont masqués depuis 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(ggplot2)
```

```
Data_seahorse <- read.table("../..//Manip lignee IDH/Seahorse_24_05.csv", sep = "\t", header = T)
Data_seahorse$OCR_ECAR <- Data_seahorse$BASAL_OCR / Data_seahorse$ECAR
Data_seahorse$OCR_ECAR_Ext <- Data_seahorse$BASAL_OCR_Ext / Data_seahorse$ECAR_Ext
Data_seahorse$Beta_oxy <- ((Data_seahorse$BASAL_OCR - Data_seahorse$BASAL_OCR_Ext) / Data_seahorse$BASAL_OCR) * 100
Data_seahorse$Glyco <- (Data_seahorse$BASAL_OCR_Ext / Data_seahorse$BASAL_OCR) * 100
Data_seahorse$pheno <- paste(Data_seahorse$Cell_line, Data_seahorse$IDH_statut, Data_seahorse$Replicat_tech)

Data_seahorse_pulled <- lapply(unique(Data_seahorse$pheno), function(Pheno){
  tmp <- dplyr::filter(Data_seahorse, pheno == Pheno)
  colMeans(tmp[,5:20]) %>% as.data.frame() %>% t() %>% as.data.frame()
}) %>% data.table::rbindlist()
rownames(Data_seahorse_pulled) <- unique(Data_seahorse$pheno)
Sub_pheno <- Data_seahorse[Data_seahorse$Replicat_tech == 1, 1:4]
Data_seahorse_pulled <- cbind(Sub_pheno, Data_seahorse_pulled)
Data_seahorse_pulled$Beta_oxy <- ((Data_seahorse_pulled$BASAL_OCR - Data_seahorse_pulled$BASAL_OCR_Ext) / Data_seahorse_pulled$BASAL_OCR) * 100
Data_seahorse_pulled$No_B_oxy <- (Data_seahorse_pulled$BASAL_OCR_Ext / Data_seahorse_pulled$BASAL_OCR) * 100
```

BASAL OCR

```
Basal_OCR <- ggplot(Data_seahorse_pulled, aes(x = Cell_line, y = BASAL_OCR, fill = factor(IDH_statut, levels = c("WT", "IDH1", "IDH2")),
  geom_boxplot(position = position_dodge(width = 0.7), width = 0.5) +
  geom_point(aes(x = Cell_line,
    color = factor(IDH_statut, levels = c("WT", "IDH1", "IDH2")),
    color = "#000000",
    shape = factor(Replicat_bio, levels = c(1, 2, 3))),
    position = position_dodge(width = 0.7)) +
  labs(fill = c("IDH"), shape = c("Replicat"), color = c("IDH")) +
  scale_fill_manual(values = c("#44BB44", "#4444BB", "#BB4444")) +
  ggtitle("Basal OCR") +
  scale_color_manual(values = c("#44BB44", "#4444BB", "#BB4444"))
```

```
## Warning: Duplicated aesthetics after name standardisation: colour
```

```
Basal_OCR
```

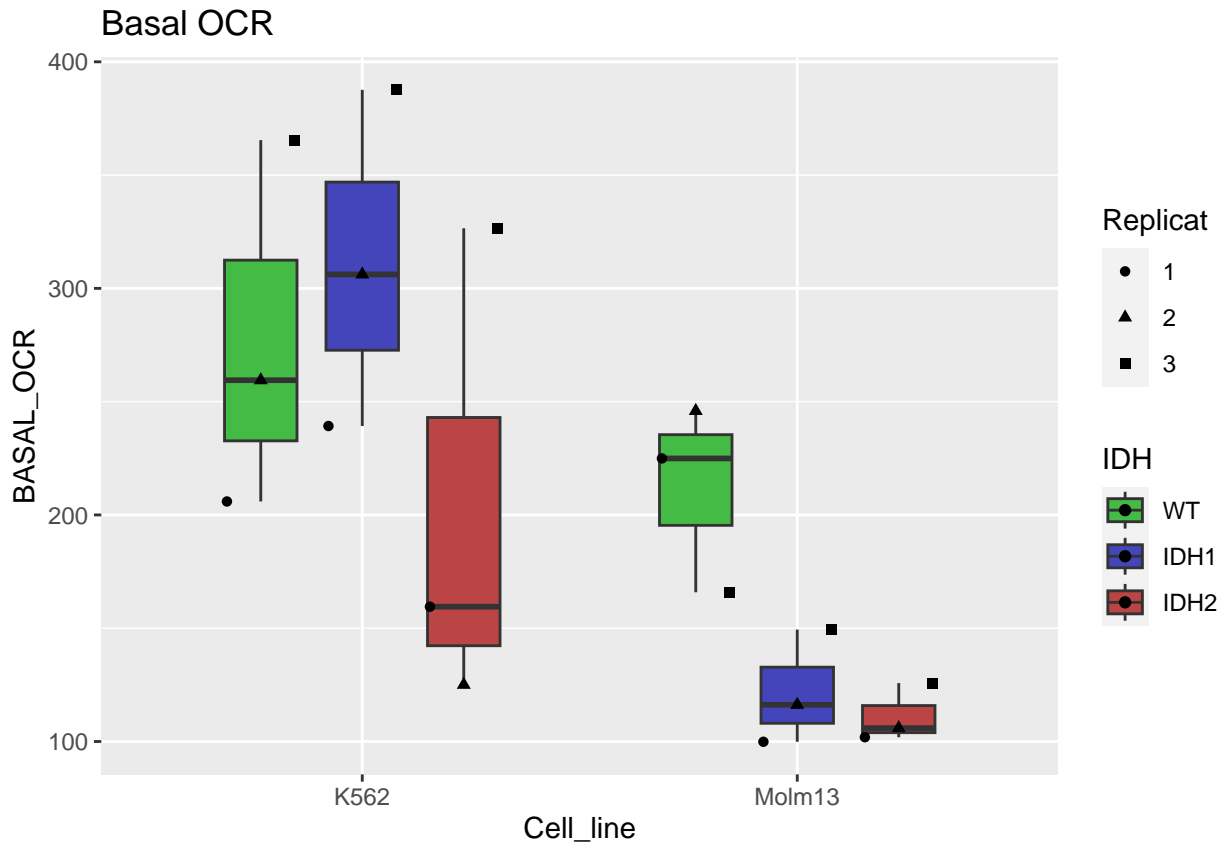
```
## Warning: Duplicated aesthetics after name standardisation: colour
```

```
## New names:
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## New names:
```

```
## * `colour` -> `colour...2`
```

```
## * `colour` -> `colour...3`
```



```
Basal OCR + Ext
```

```
Basal_OCR_Ext <- dplyr::filter(Data_seahorse_pulled, Replicat_bio != 3) %>% ggplot(aes(x = Cell_line, y = Basal_OCR_Ext)) +
  geom_boxplot(position = position_dodge(width = 0.7), width = 0.5) +
  geom_point(aes(x = Cell_line, y = Basal_OCR_Ext,
    color = factor(IDH_statut, levels = c("WT", "IDH1", "IDH2")),
    color = "#000000",
    shape=factor(Replicat_bio, levels = c(1, 2))),
    position = position_dodge(width = 0.7)) +
  labs(fill = c("IDH"), shape = c("Replicat"), color = c("IDH")) +
  scale_fill_manual(values = c("#44BB44", "#4444BB", "#BB4444")) +
  ggtitle("Basal OCR + Ext")
```

```
## Warning: Duplicated aesthetics after name standardisation: colour
```

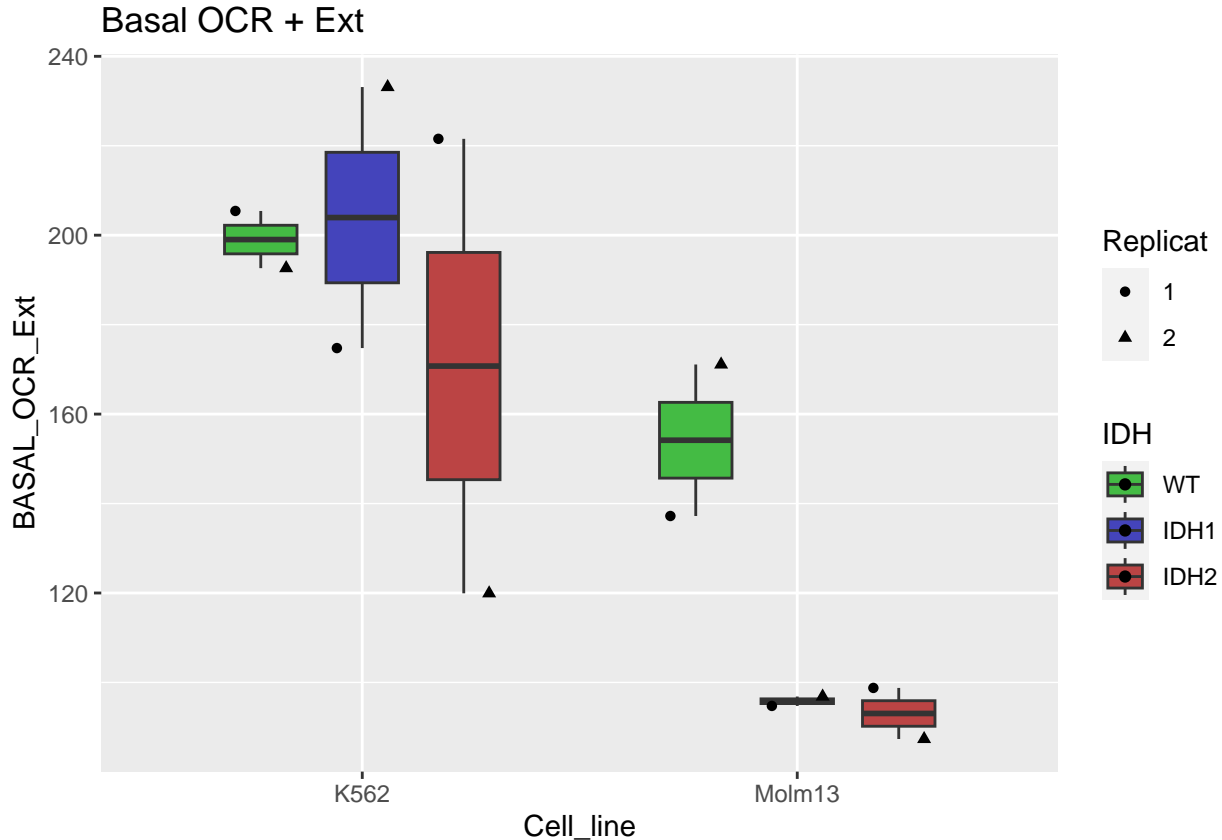
```
Basal_OCR_Ext
```

```
## Warning: Duplicated aesthetics after name standardisation: colour
```

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## New names:
```

```
## New names:
```

```
## * `colour` -> `colour...2`
## * `colour` -> `colour...3`
```



OCR / ECAR

```
OCR_ECAR_plot <- ggplot(Data_seahorse_pulled, aes(x = Cell_line, y = OCR_ECAR, fill = factor(IDH_statut
  geom_boxplot(position = position_dodge(width = 0.7), width = 0.5) +
  geom_point(aes(x = Cell_line,
    color = factor(IDH_statut, levels = c("WT", "IDH1", "IDH2")),
    color = "#000000",
    shape=factor(Replicat_bio, levels = c(1, 2, 3))),
    position = position_dodge(width = 0.7)) +
  labs(fill = c("IDH"), shape = c("Replicat"), color = c("IDH")) +
  scale_fill_manual(values = c("#44BB44", "#4444BB", "#BB4444")) +
  ggtitle("OCR/ECAR")
```

```
## Warning: Duplicated aesthetics after name standardisation: colour
```

```
OCR_ECAR_plot
```

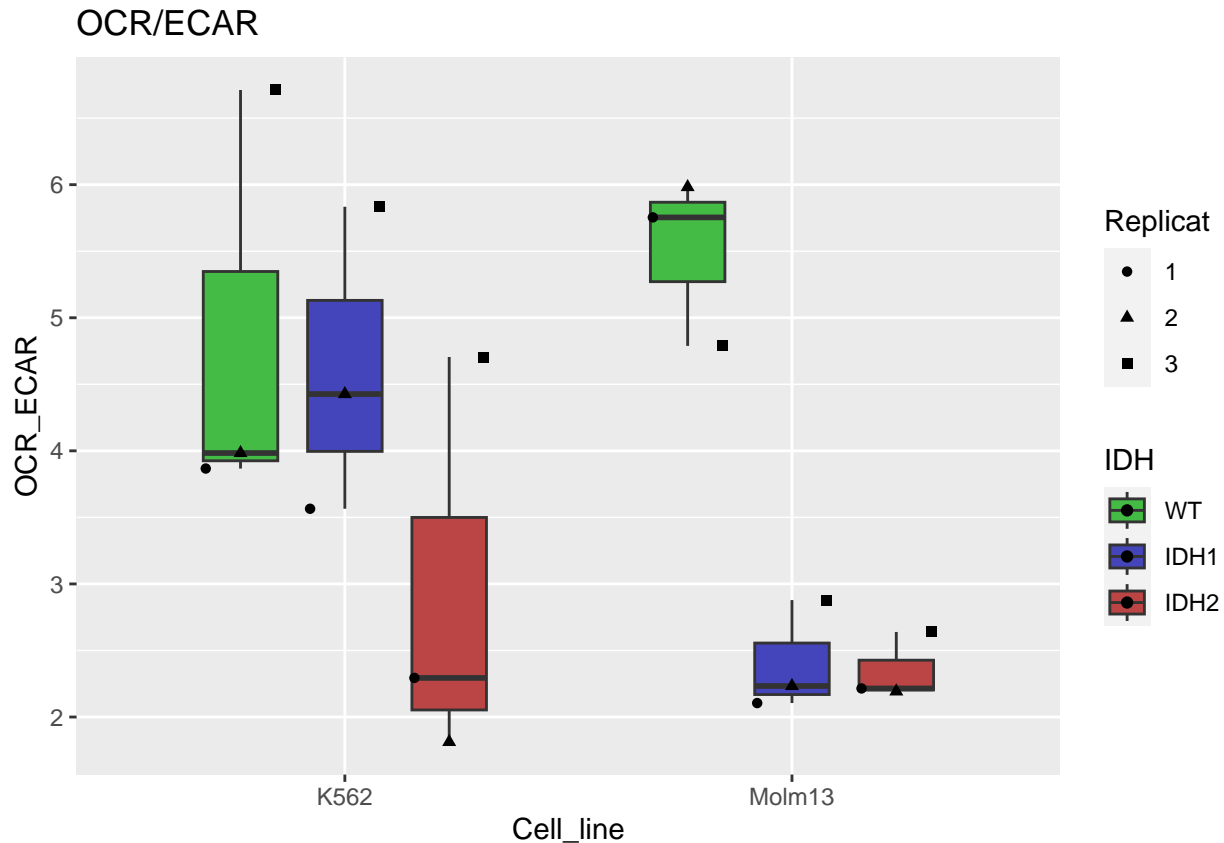
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## Warning: Duplicated aesthetics after name standardisation: colour
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## New names:
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## New names:
```

```
## * `colour` -> `colour...2`
```

```
## * `colour` -> `colour...3`
```



OCR / ECAR + Ext

```
OCR_ECER_Ext_plot <- dplyr::filter(Data_seahorse_pulled, Replicat_bio != 3) %>% ggplot(aes(x = Cell_line,
  geom_boxplot(position = position_dodge(width = 0.7), width = 0.5) +
  geom_point(aes(x = Cell_line,
    color = factor(IDH_statut, levels = c("WT", "IDH1", "IDH2")),
    color = "#000000",
    shape=factor(Replicat_bio, levels = c(1, 2))),
    position = position_dodge(width = 0.7)) +
  labs(fill = c("IDH"), shape = c("Replicat"), color = c("IDH")) +
  scale_fill_manual(values = c("#44BB44", "#4444BB", "#BB4444")) + ggtitle("OCR/ECAR + Ext")
```

```
## Warning: Duplicated aesthetics after name standardisation: colour
```

```
OCR_ECER_Ext_plot
```

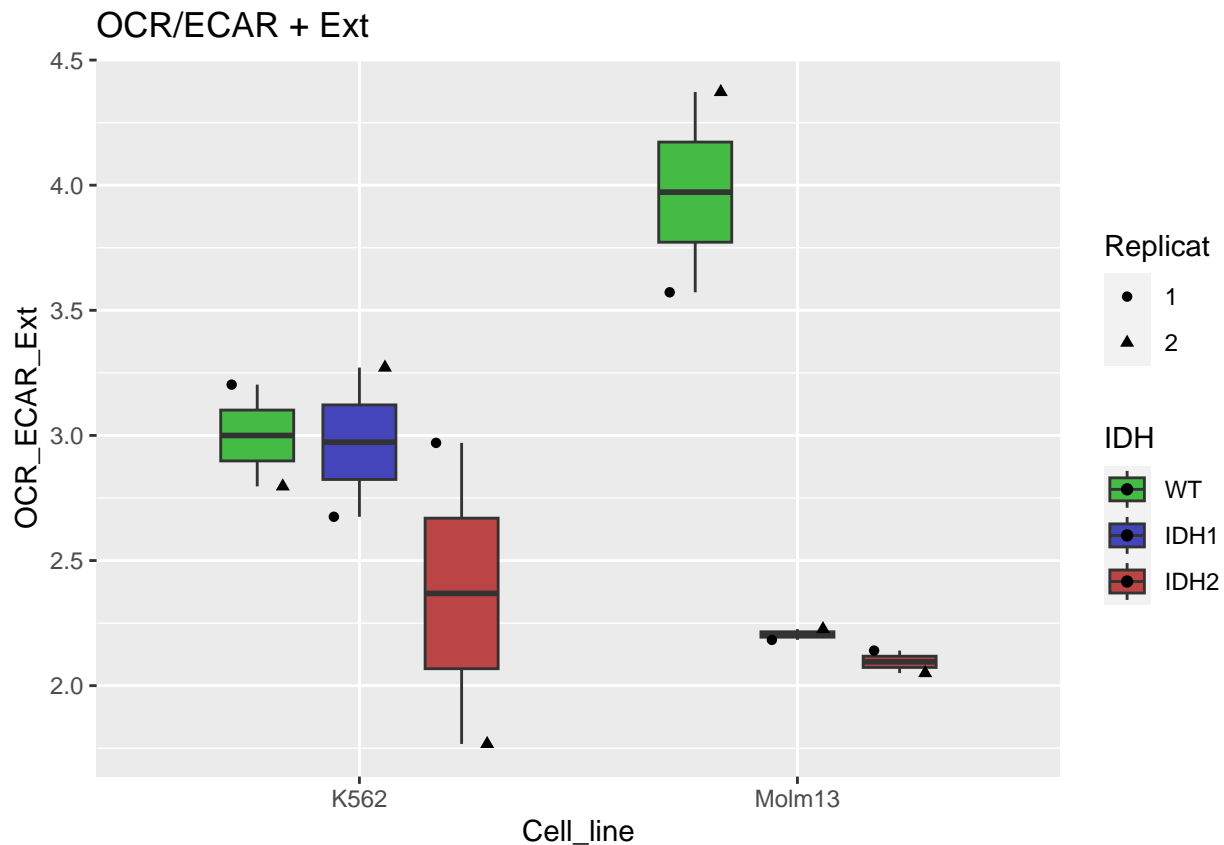
```
## Warning: Duplicated aesthetics after name standardisation: colour
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## New names:
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## New names:
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```
## * `colour` -> `colour...2`
```

```
## * `colour` -> `colour...3`
```



ECAR

```
ECAR_plot <- ggplot(Data_seahorse_pulled, aes(x = Cell_line, y = ECAR, fill = factor(IDH_statut, levels = c("WT", "IDH1", "IDH2")),
  geom_boxplot(position = position_dodge(width = 0.7), width = 0.5) +
  geom_point(aes(x = Cell_line,
    color = factor(IDH_statut, levels = c("WT", "IDH1", "IDH2")),
    color = "#000000",
    shape=factor(Replicat_bio, levels = c(1, 2, 3))),
    position = position_dodge(width = 0.7)) +
  labs(fill = c("IDH"), shape = c("Replicat"), color = c("IDH")) +
  scale_fill_manual(values = c("#44BB44", "#4444BB", "#BB4444")) + ggtitle("ECAR")
```

```
## Warning: Duplicated aesthetics after name standardisation: colour
```

```
ECAR_plot
```

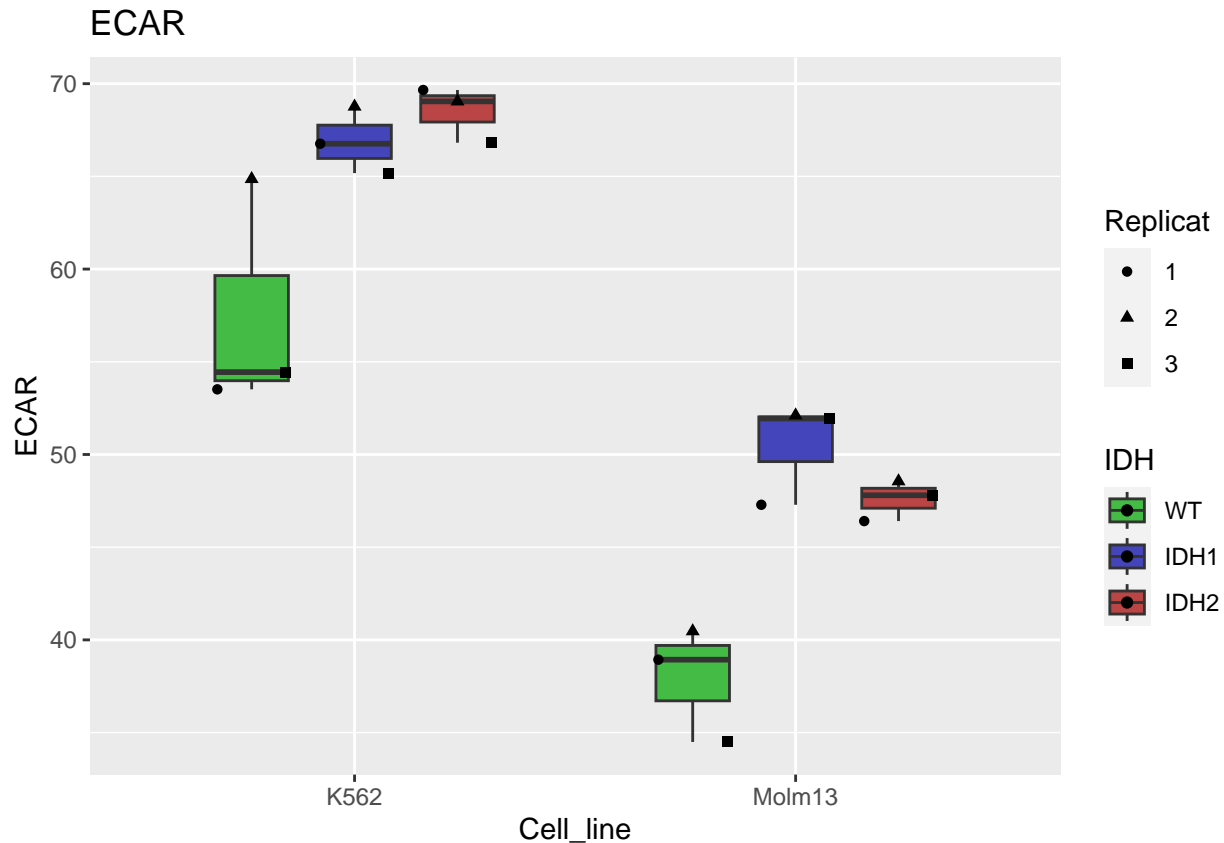
```
## Warning: Duplicated aesthetics after name standardisation: colour
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## New names:
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## New names:
```

```
## * `colour` -> `colour...2`
```

```
## * `colour` -> `colour...3`
```



ECAR + Ext

```
ECAR_Ext_plot <- dplyr::filter(Data_seahorse_pulled, Replicat_bio != 3) %>% ggplot(aes(x = Cell_line, y = ECAR)) +
  geom_boxplot(position = position_dodge(width = 0.7), width = 0.5) +
  geom_point(aes(x = Cell_line, y = ECAR, color = factor(IDH_statut, levels = c("WT", "IDH1", "IDH2")),
                 color = "#000000",
                 shape=factor(Replicat_bio, levels = c(1, 2))),
             position = position_dodge(width = 0.7)) +
  labs(fill = c("IDH"), shape = c("Replicat"), color = c("IDH")) +
  scale_fill_manual(values = c("#44BB44", "#4444BB", "#BB4444")) + ggtitle("ECAR + Ext")
```

```
## Warning: Duplicated aesthetics after name standardisation: colour
```

```
ECAR_Ext_plot
```

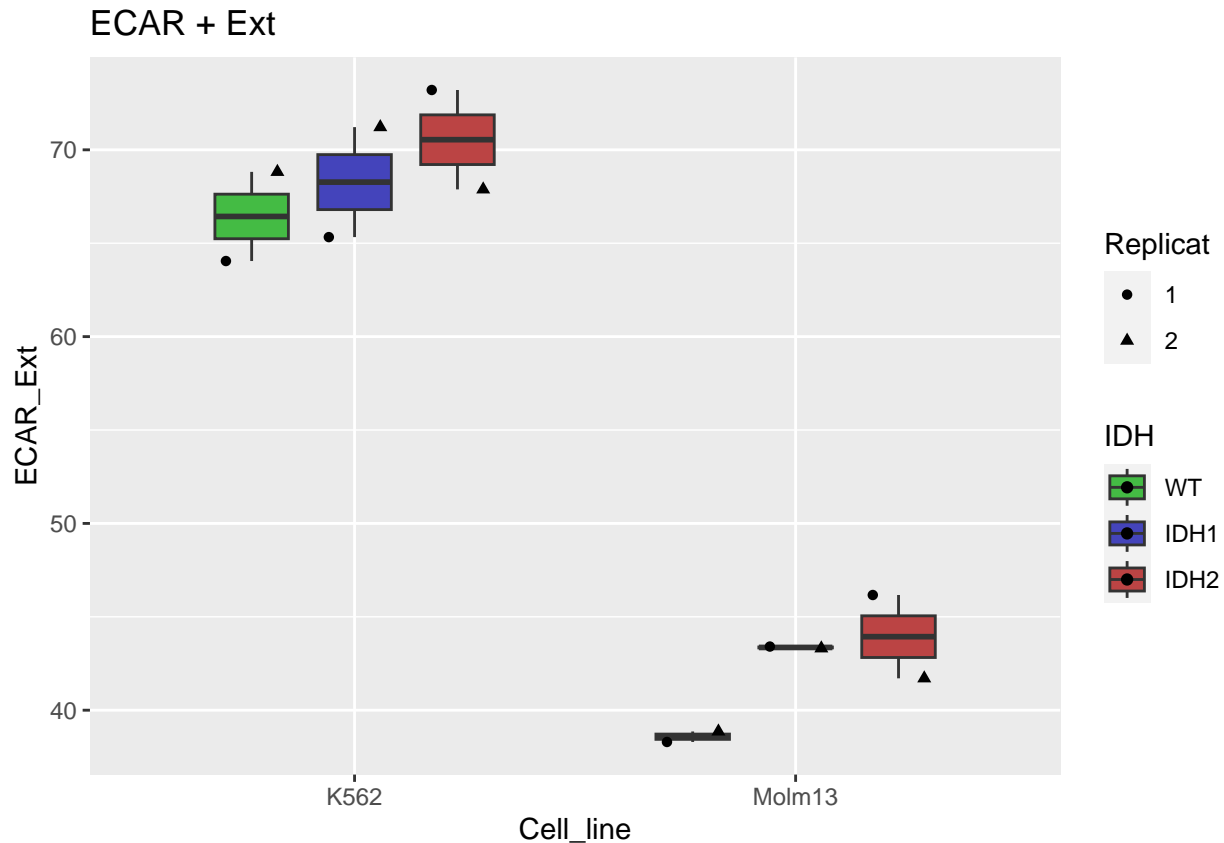
```
## Warning: Duplicated aesthetics after name standardisation: colour
```

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## New names:
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## New names:
```

```
## * `colour` -> `colour...2`
```

```
## * `colour` -> `colour...3`
```



Beta_Oxy

```
Beta_oxy_plot <- dplyr::filter(Data_seahorse_pulled, Replicat_bio != 3) %>% ggplot(aes(x = Cell_line, y
  geom_boxplot(position = position_dodge(width = 0.7), width = 0.5) +
  geom_point(aes(x = Cell_line,
    color = factor(IDH_statut, levels = c("WT", "IDH1", "IDH2")),
    color = "#000000",
    shape=factor(Replicat_bio, levels = c(1, 2))),
    position = position_dodge(width = 0.7)) +
  labs(fill = c("IDH"), shape = c("Replicat"), color = c("IDH")) +
  scale_fill_manual(values = c("#44BB44", "#4444BB", "#BB4444")) + ggtitle("% B-oxydation")
```

```
## Warning: Duplicated aesthetics after name standardisation: colour
```

```
Beta_oxy_plot
```

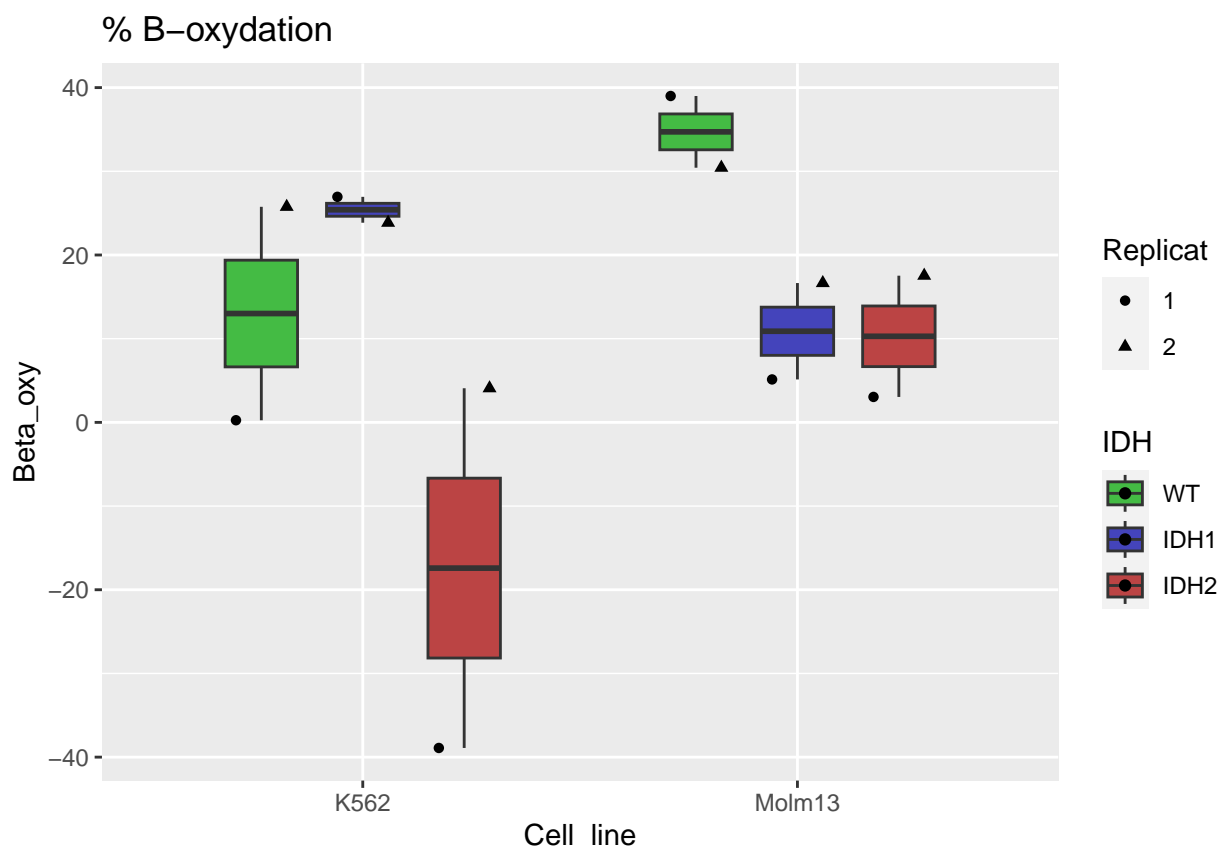
```
## Warning: Duplicated aesthetics after name standardisation: colour
```

```
## New names:
```

```
## New names:
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```
## * `colour` -> `colour...2`
```

```
## * `colour` -> `colour...3`
```



```
No_B_oxy_plot <- dplyr::filter(Data_seahorse_pulled, Replicat_bio != 3) %>% ggplot(aes(x = Cell_line, y = Beta_oxy)) +
  geom_boxplot(position = position_dodge(width = 0.7), width = 0.5) +
  geom_point(aes(x = Cell_line, y = Beta_oxy,
    color = factor(IDH_statut, levels = c("WT", "IDH1", "IDH2")),
    color = "#000000",
    shape = factor(Replicat_bio, levels = c(1, 2))),
    position = position_dodge(width = 0.7)) +
  labs(fill = c("IDH"), shape = c("Replicat"), color = c("IDH")) +
  scale_fill_manual(values = c("#44BB44", "#4444BB", "#BB4444")) + ggtitle("% - B Oxy")
```

```
## Warning: Duplicated aesthetics after name standardisation: colour
```

```
No_B_oxy_plot
```

```
## Warning: Duplicated aesthetics after name standardisation: colour
```

```
## New names:
```

```
## New names:
```

```
## * `colour` -> `colour...2`
```

```
## * `colour` -> `colour...3`
```