

Blood Biochemical

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```
library(tidyverse)

## — Attaching packages — tidyverse 1.2.1 —

## ✔ ggplot2 3.1.0      ✔ purrr 0.3.2
## ✔ tibble 2.0.1       ✔ dplyr 0.8.0.1
## ✔ tidyr 0.8.3        ✔ stringr 1.3.1
## ✔ readr 1.3.1       ✔ forcats 0.4.0

## Warning: package 'tibble' was built under R version 3.5.2

## Warning: package 'tidyr' was built under R version 3.5.2

## Warning: package 'dplyr' was built under R version 3.5.2

## Warning: package 'forcats' was built under R version 3.5.2

## — Conflicts — tidyverse_conflicts() —
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag() masks stats::lag()

Full_Blood = read_tsv("marwa_Blood.tsv")

## Parsed with column specification:
## cols(
##   Variable = col_character(),
##   Group = col_character(),
##   Value = col_double()
## )

glimpse(Full_Blood)

## Observations: 197
## Variables: 3
## $ Variable <chr> "ALK", "ALK", "ALK", "ALK", "ALK", "ALK", "ALK", "ALK", ...
## $ Group <chr> "AD_Non_DM_High", "AD_Non_DM_High", "AD_Non_DM_High", "AD_Non_DM_High", "AD_Non_DM_High", "AD_Non_DM_High", "AD_Non_DM_High", "AD_Non_DM_High", ...
## $ Value <dbl> 325, 378, 390, 265, 271, 158, 214, 300, 174, 332, 181, ...

ggplot(Full_Blood) +
  geom_boxplot(aes(x = Group, y = Value, fill = Group)) +
  facet_wrap(~ Variable, scales = "free_y") +
  theme_light(base_size = 12) +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(angle = 70, hjust = 1))
```

