Analysis of Epigenetic Gestational Age Acceleration Relative to Chronological Age

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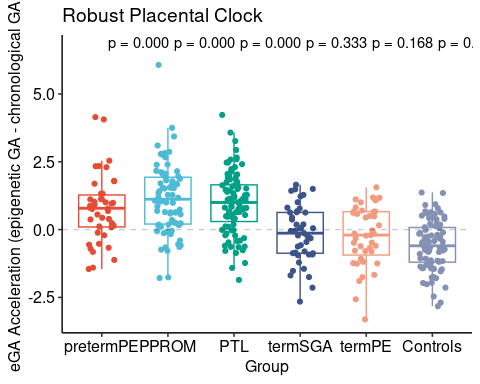
### Calculate,compare, and plot epigenetic gestational age acceleration

analyze\_eGA\_acceleration <- function(data, ega\_column, chronological\_column, groups, title=NULL) {  
 data <- data |>   
 mutate(eGA\_acceleration = !!sym(ega\_column) - !!sym(chronological\_column)) |>   
 mutate(Group = factor(Group2, levels = unique(groups)))  
  
 # Performing one-sided t-tests to determine if eGA is significantly different from chronological age  
 test\_results <- data |>   
 group\_by(Group) |>   
 summarise(t\_value = t.test(eGA\_acceleration, mu = 0, alternative = "two.sided")$statistic,  
 p\_value = t.test(eGA\_acceleration, mu = 0, alternative = "two.sided")$p.value,  
 mean\_eGA\_acceleration = mean(eGA\_acceleration, na.rm = TRUE),  
 sd\_eGA\_acceleration = sd(eGA\_acceleration, na.rm = TRUE),  
 n = n())   
  
 # Plotting  
 max\_y <- max(data$eGA\_acceleration, na.rm = TRUE)  
 p\_value\_annotation <- mutate(test\_results, y.position = max\_y \* 1.1)  
 colors <- brewer.pal(n = length(unique(data$Group)), name = "Set2")  
 grayscale\_colors <- gray.colors(n = length(unique(data$Group)))  
 nature\_palette <- c("#E64B35", # Reddish  
 "#4DBBD5", # Bluish  
 "#00A087", # Teal  
 "#3C5488", # Dark Blue  
 "#F39B7F", # Peach  
 "#8491B4", # Light Blue  
 "#91D1C2", # Light Teal  
 "#DC0000", # Bright Red  
 "#7E6148", # Brown  
 "#B09C85") # Light Brown  
  
 box\_plot <- ggboxplot(data, x = "Group", y = "eGA\_acceleration",  
 color = "Group", palette = nature\_palette, add = "jitter",  
 ylab = "eGA Acceleration (epigenetic GA - chronological GA)",   
 xlab = "Group") +  
 labs(title = title) +  
 theme\_pubr() +  
 theme(legend.position = "none") # Remove legend for cleaner plot  
  
 # Adding p-value annotations manually  
 box\_plot<- box\_plot + geom\_text(data = test\_results,   
 aes(x = Group, y = max\_y \* 1.1,   
 label = sprintf("p = %.3f", p\_value)),  
 hjust = -0.1, vjust = 0) +  
 geom\_hline(yintercept = 0,linetype=2,alpha=0.2)  
  
 return(box\_plot)  
}

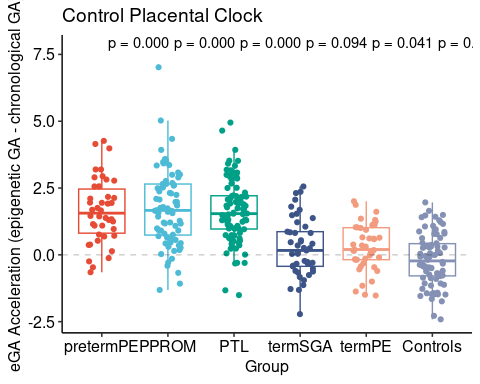
groups <- c("pretermPE","PPROM","PTL","termSGA","termPE","Controls")

## Compare eGA acceleration Using different clocks

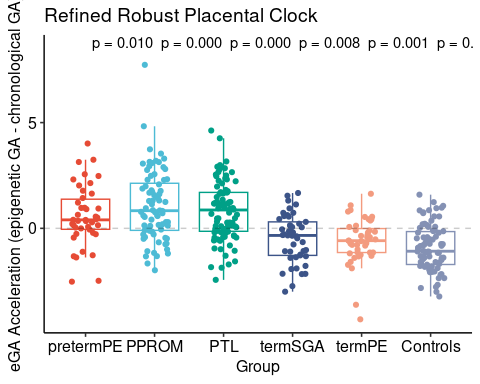
rpc\_results <- analyze\_eGA\_acceleration(ano, "ga\_rpc", "Del\_GA\_Calc",  
 groups=groups,  
 title="Robust Placental Clock")  
rpc\_results



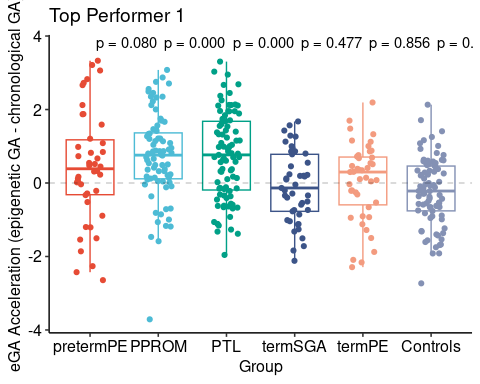
cpc\_results <- analyze\_eGA\_acceleration(ano, "ga\_cpc", "Del\_GA\_Calc",  
 groups=groups,  
 title="Control Placental Clock")  
cpc\_results



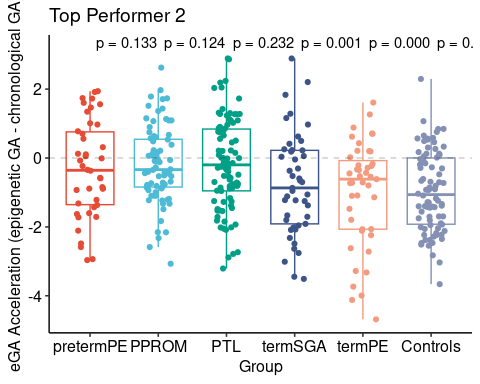
rrpc\_results <- analyze\_eGA\_acceleration(ano, "ga\_rrpc", "Del\_GA\_Calc",  
 groups=groups,  
 title="Refined Robust Placental Clock")  
rrpc\_results



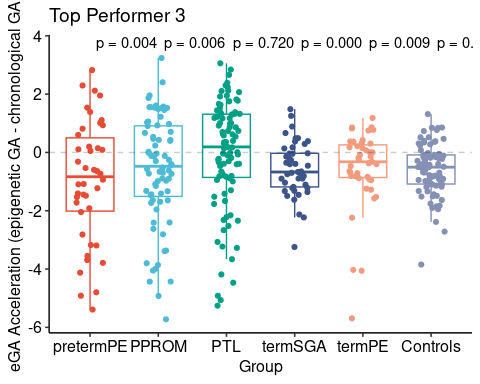
top\_teams <- test\_ranking |>   
 group\_by(submitterid) |>   
 slice\_min(Test\_rmse, n = 1, with\_ties = FALSE) |>   
 ungroup() |>   
 slice\_min(Test\_rmse, n = 3, with\_ties = FALSE) |>   
 mutate(stamp = paste("ga", submitterid, evaluationid, sep = "\_")) |>   
 pull(stamp)  
  
top\_team\_results\_1 <- analyze\_eGA\_acceleration(ano, top\_teams[1],"Del\_GA\_Calc",  
 groups=groups,  
 title="Top Performer 1")  
top\_team\_results\_1



top\_team\_results\_2 <- analyze\_eGA\_acceleration(ano, top\_teams[2],"Del\_GA\_Calc",  
 groups=groups,  
 title="Top Performer 2")  
top\_team\_results\_2



top\_team\_results\_3 <- analyze\_eGA\_acceleration(ano, top\_teams[3],"Del\_GA\_Calc",  
 groups=groups,  
 title="Top Performer 3")  
top\_team\_results\_3



woc\_results <- analyze\_eGA\_acceleration(ano, "ga\_woc","Del\_GA\_Calc",  
 groups=groups,  
 title="Top Performer")  
woc\_results

