

## regression\_plot

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library(ggplot2)
library(ggpmisc)

## For news about 'ggpmisc', please, see https://www.r4photobiology.info/
## For on-line documentation see https://docs.r4photobiology.info/ggpmisc/
master <- read.csv("v2_v1_pss10_ssGSEA.csv", row.names=1)

genes <- as.vector(unlist(colnames(master)))

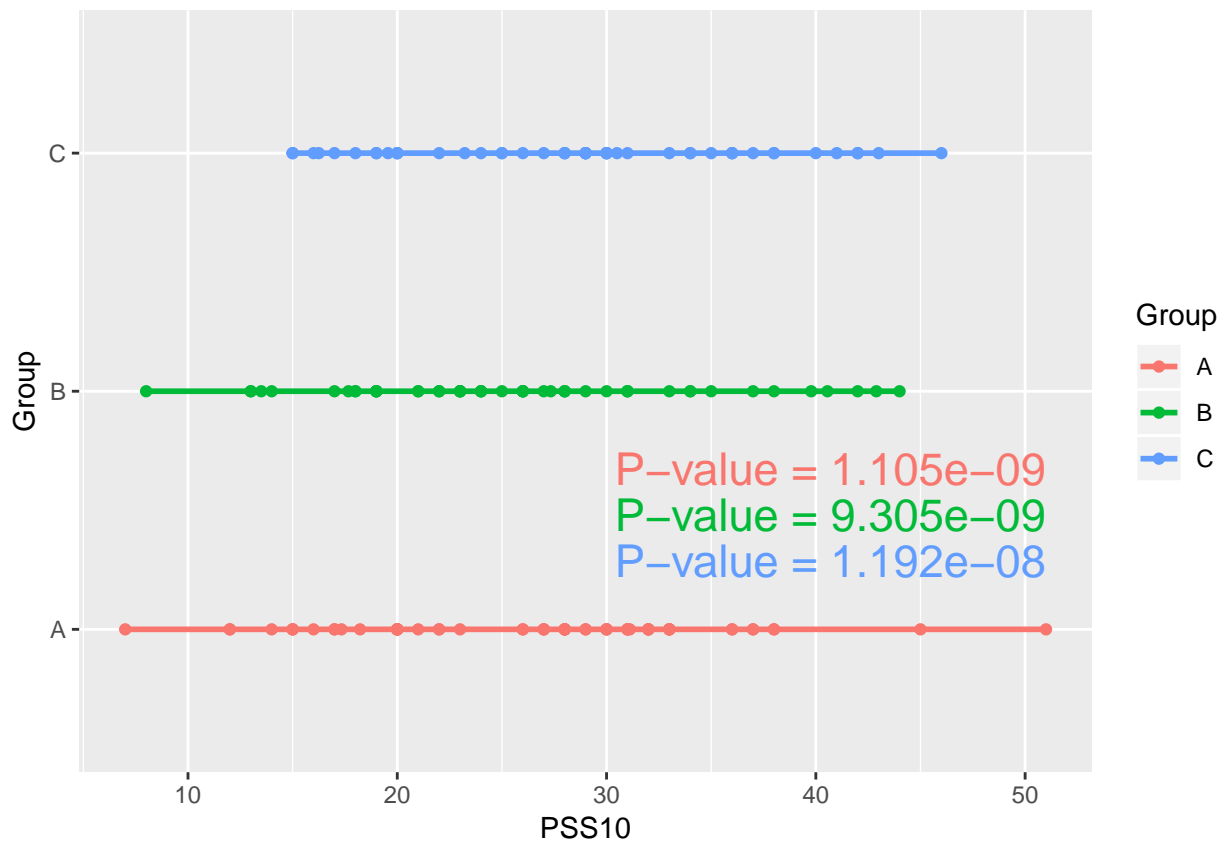
formula <- y ~ x

for(i in genes){
  print(ggplot(master, aes_string(x= "PSS10", y=i, color = "Group")) + geom_point(alpha = 1) +
    geom_smooth(method = "lm", formula = formula, se = F) + xlab("PSS10") +
    stat_fit_glance(method = 'lm', method.args = list(formula = formula), geom = 'text',
    aes(label = paste("P-value = ", signif(..p.value.., digits = 4), sep = "")),
    label.x.npc = 'right', label.y.npc = 0.35, size = 6))
}

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