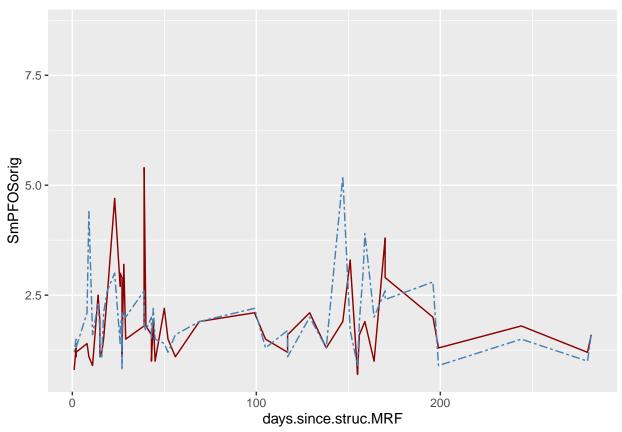
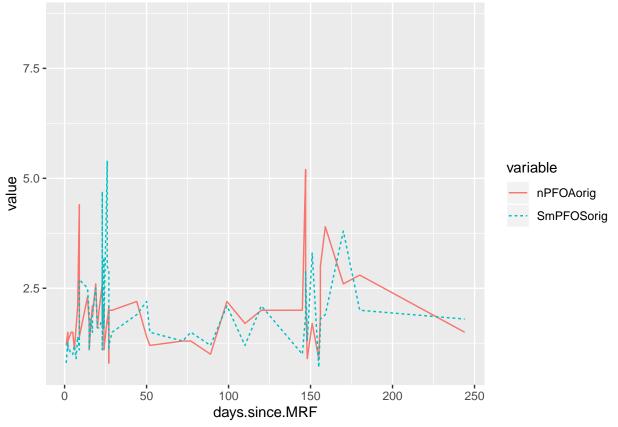
TFD longitudinal analyses

Amy Nematollahi and Julia Fisher 7/16/2020

Should I remove subject 2009 (missing fire info) from FireTuk?

For the densities, include a color grouping for time (1 or 2). For the scatterplots, include lines between data points from the same person (to get a better understanding of slope). This corresponds to a grouping for each participant ID. We could include an additional grouping for ethnicity by gender if we want or a facet for ethnicity by gender.





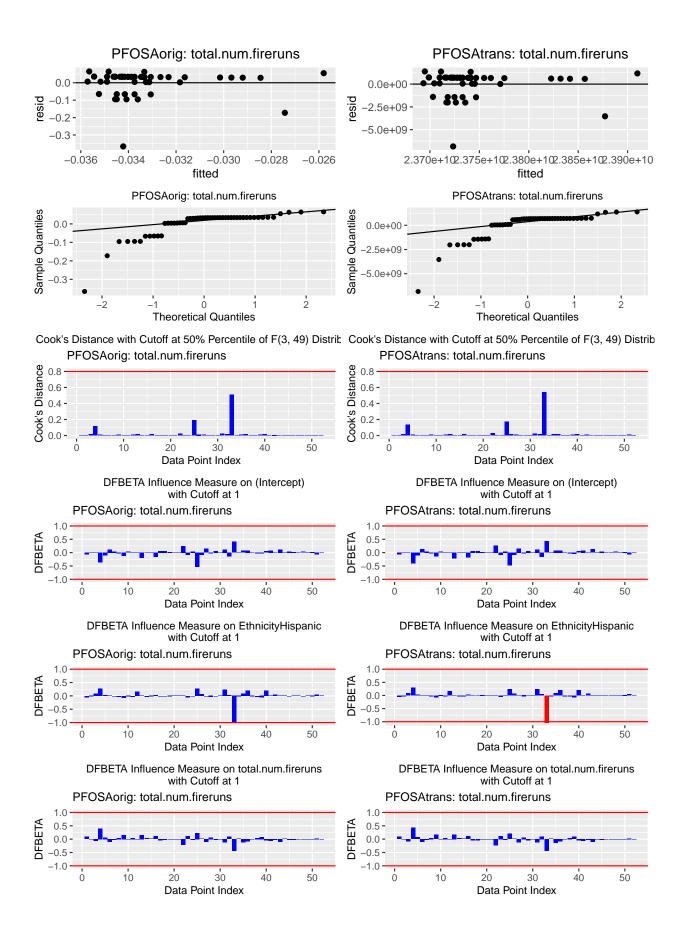
```
# For each PFAS create separate models for:
# total structural number fire runs
# total duration
# structural fire duration
# time (in years since baseline)
# time since most recent fire run
# time since MR structural fire
# total number of fireruns
#write a function for different variables
# 6/30: removed women from FireChange, removed interaction term ethn.gen and replaced with Ethnicity
#Had to change the structure of the code in the model statements a bit due to the following error:
#Error in parse(text = trans_model_statement) :
# <text>:1:67: unexpected '='
#1: model_trans <- lm(PFOSAtrans ~ Ethnicity + total.num.firerunsdata =</pre>
exp_fxn <- function(dta, orig_outcome, trans_outcome, exp_outcome) {</pre>
 orig_model_statement <- paste0("model_orig <- lm(", orig_outcome,</pre>
                                  " ~ ", exp_outcome, " + Ethnicity, data = dta)")
  eval(parse(text = orig_model_statement))
  trans_model_statement <- paste0("model_trans <- lm(", trans_outcome,</pre>
                                  " ~ ", exp_outcome, " + Ethnicity, data = dta)")
  eval(parse(text = trans_model_statement))
  out <- list(model_orig = model_orig,</pre>
              model_trans = model_trans)
}
```

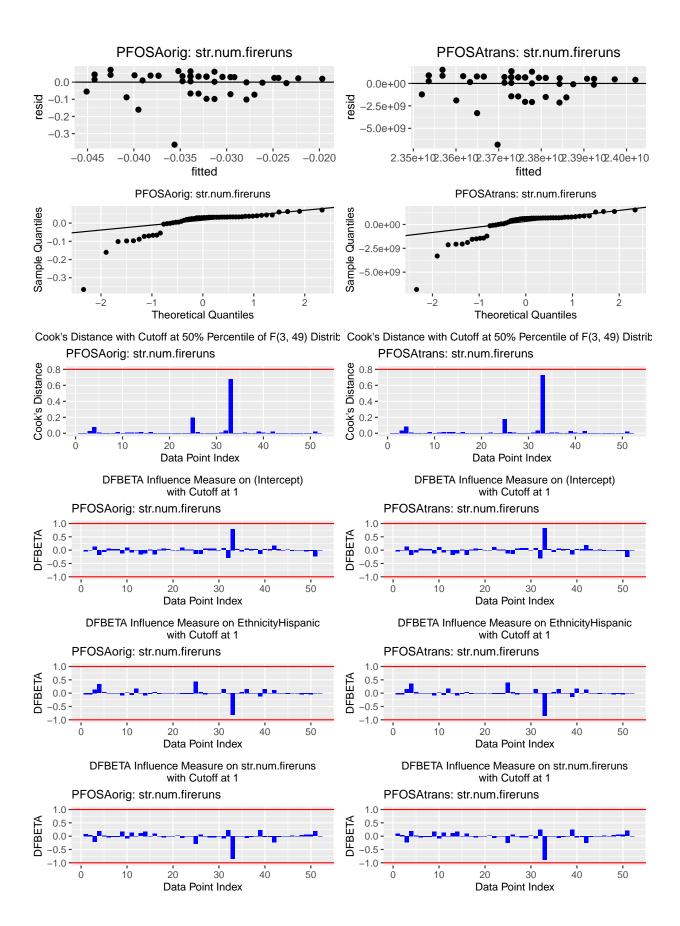
```
analytes <- c("PFOSA", "nPFOA", "nPFOS", "PFDEA", "PFHXS", "PFNA", "PFUA", "SbPFOA", "SmPFOS")
exposures <- c("total.num.fireruns", "str.num.fireruns", "total.duration.hrs", "str.duration.hrs",</pre>
                "days.since.MRF", "days.since.struc.MRF", "time.since.baseline")
model list <- list()</pre>
mean.change <- data.frame(Ethnicity = as.character(),</pre>
                           emmean = as.numeric(),
                           lower.CL = as.numeric(),
                           upper.CL = as.numeric(),
                           exposure = as.character(),
                           analyte = as.character(),
                           stringsAsFactors = FALSE)
for (analyte in analytes) {
  for (exposure in exposures) {
  orig_var <- paste0(analyte, "orig")</pre>
  trans_var <- paste0(analyte, "trans")</pre>
  out_info <- exp_fxn(FireChange, orig_var, trans_var, exposure)</pre>
  ggarrange(plot(resid(out_info$model_orig) ~ fitted(out_info$model_orig)) + abline(h = 0),
            plot(resid(out_info$model_trans) ~ fitted(out_info$model_trans)) + abline(h = 0),
            qqnorm(resid(out_info$model_orig)),
            qqnorm(resid(out_info$model_trans)),
            nrow = 2, ncol = 2)
  stargazer(out_info$model_trans)
}
for (analyte in analytes) {
  model_list[[analyte]] <- list()</pre>
  for (exposure in exposures) {
    orig_var <- paste0(analyte, "orig")</pre>
    trans_var <- paste0(analyte, "trans")</pre>
    out_info <- exp_fxn(FireChange2, orig_var, trans_var, exposure)</pre>
    model_list[[analyte]][[exposure]] <- out_info</pre>
    meanNH <- mean(FireChange2 %% filter(Ethnicity== 'Non-hispanic') %% .[, exposure], na.rm = TRUE)
    meanH <- mean(FireChange2 %>% filter(Ethnicity== 'Hispanic') %>% .[, exposure], na.rm = TRUE)
    NH.mean.change <- eval(parse(text = paste0("emmeans(model_list[[analyte]][[exposure]]$model_orig, '</pre>
      summary() %>%
      filter(Ethnicity == "Non-hispanic")
    H.mean.change <- eval(parse(text = paste0("emmeans(model_list[[analyte]][[exposure]]$model_orig, 'E</pre>
      summary() %>%
      filter(Ethnicity == "Hispanic")
    mean.change <- rbind(mean.change,</pre>
                          rbind(H.mean.change, NH.mean.change) %>%
                            mutate(exposure = exposure,
                                   analyte = analyte) %>%
                            dplyr::select(-SE, -df))
  }
  # print(ggarrange(plot(resid(out_info$model_orig) ~ fitted(out_info$model_orig)) + abline(h = 0),
              plot(resid(out_info$model_trans) ~ fitted(out_info$model_trans)) + abline(h = 0),
  #
              qqnorm(resid(out_info$model_orig)),
              qqnorm(resid(out_info$model_trans)),
```

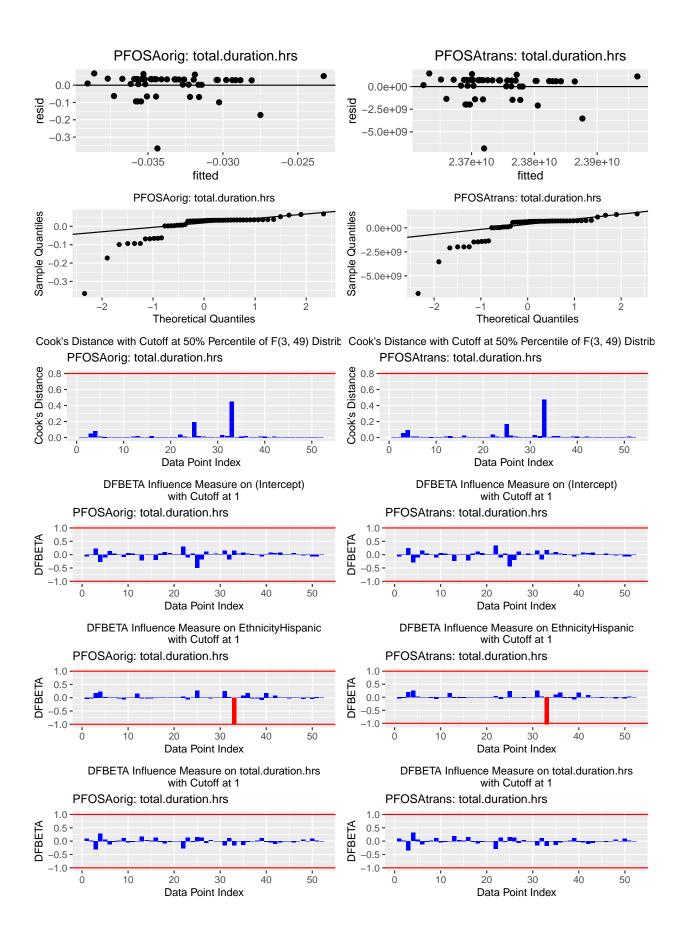
```
nrow = 2, ncol = 2))
  stargazer(model_list[[analyte]][[exposures[1]]]$model_orig,
            model_list[[analyte]][[exposures[2]]]$model_orig,
            model_list[[analyte]][[exposures[3]]]$model_orig,
            model_list[[analyte]][[exposures[4]]]$model_orig,
            title = "PFAS Change Score Model Results (No Transformation)",
            single.row = FALSE, header = FALSE,
            omit.stat = c("f", "ser"), report = "vctp*",
            intercept.bottom = FALSE, intercept.top = TRUE,
            digits = 3, font.size = "scriptsize")
  stargazer(model_list[[analyte]][[exposures[5]]]$model_orig,
            model_list[[analyte]][[exposures[6]]]$model_orig,
            model_list[[analyte]][[exposures[7]]]$model_orig,
            title = "PFAS Change Score Model Results (No Transformation)",
            single.row = FALSE, header = FALSE,
            omit.stat = c("f", "ser"), report = "vctp*",
            intercept.bottom = FALSE, intercept.top = TRUE,
            digits = 3, font.size = "scriptsize")
}
true.mean <- mean.change %>%
 filter(exposure == 'str.num.fireruns') %>%
  left_join(mean.frame, by = c("Ethnicity", "analyte")) # You should compare these to the scatterplots
knitr::opts_template$set("kill_prefix"=list(comment=NA, null_prefix=TRUE))
pfas.list <- c("PFOSAorig", "nPFOAorig", "nPFOSorig", "PFDEAorig", "PFHXSorig", "PFNAorig", "PFUAorig"
                "SbPFOAorig", "SmPFOSorig")
pfastrans.list <- c("PFOSAtrans", "nPFOAtrans", "nPFOStrans", "PFDEAtrans", "PFHXStrans",
              "PFNAtrans", "PFUAtrans", "SbPFOAtrans", "SmPFOStrans")
fire.list <- c("total.num.fireruns", "str.num.fireruns", "total.duration.hrs", "str.duration.hrs",
               "days.since.MRF", "days.since.struc.MRF", "time.since.baseline")
change_plot_fxn <- function(df, pfas, pfas.trans, fire.var) {</pre>
  pfas_orig <- paste0("pfasmdl <- lm(", pfas, " ~ ", fire.var, " + Ethnicity, data = df)")
  eval(parse(text = pfas_orig))
  pfas_trans <- paste0("transmdl <- lm(", pfas.trans, " ~ ", fire.var, " + Ethnicity, data = df)")
  eval(parse(text = pfas_trans))
  out <- list(pfasmdl = pfasmdl,
              transmdl = transmdl)
}
for (i in 1:length(pfas.list)) {
  pfas.name <- pfas.list[i]</pre>
  Tpfas.name <- pfastrans.list[i]</pre>
  for (fire.var in fire.list) {
   out_info <- change_plot_fxn(FireChange2, pfas.name, Tpfas.name, fire.var)</pre>
    #FItted vs. residuals
    orig.resid <- ggplot(data.frame(resid = resid(out info$pfasmdl),
                                   fitted = fitted(out_info$pfasmdl)),
                        aes(x = fitted, y = resid)) +
      geom_point(size = 2) +
```

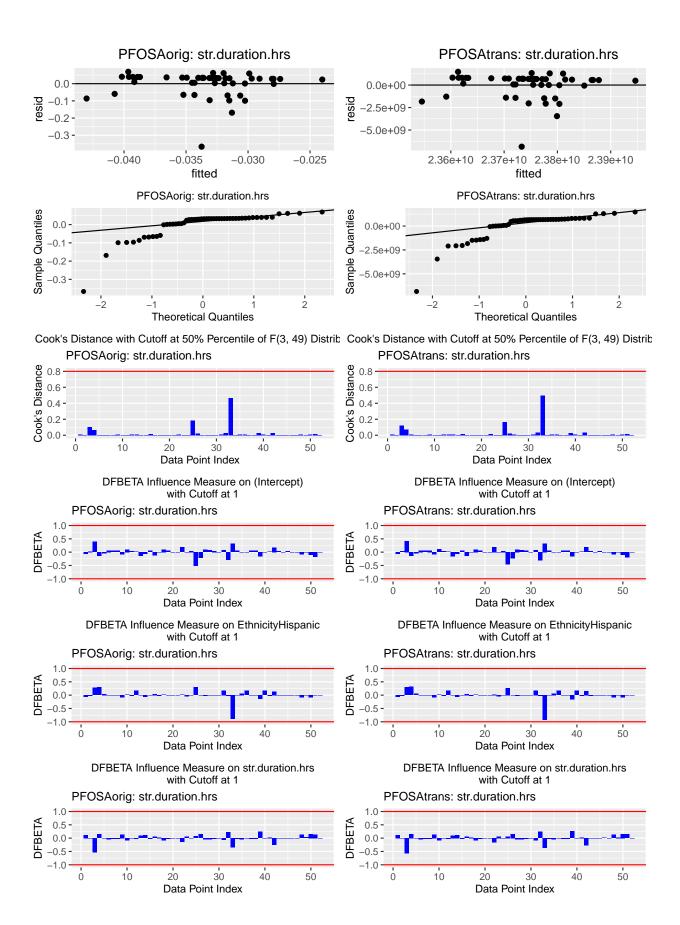
```
geom_hline(yintercept = 0) +
      theme(axis.text = element_text(size = 10),
            plot.title = element_text(hjust = 0.5)) +
      labs(title = paste0(out_info$pfasmdl$terms[[2]], ": ",
                          out_info$pfasmdl$terms[[3]][2]))
    trans.resid <- ggplot(data.frame(resid = resid(out_info$transmdl),</pre>
                                      fitted = fitted(out_info$transmdl)),
                          aes(x = fitted, y = resid)) +
      geom point(size = 2) +
      geom hline(yintercept = 0) +
      theme(axis.text = element_text(size = 10),
            plot.title = element_text(hjust = 0.5)) +
      labs(title = paste0(out_info$transmdl$terms[[2]], ": ",
                          out_info$pfasmdl$terms[[3]][2]))
   ys.orig <- quantile(qqnorm(resid(out_info$pfasmdl), plot.it = F)$y, probs = c(0.25, 0.75),
                        qtype = 7)
   xs.orig <- quantile(qqnorm(resid(out_info$pfasmdl), plot.it = F)$x, probs = c(0.25, 0.75),</pre>
                        qtype = 7)
   m.orig <- (ys.orig[2] - ys.orig[1])/(xs.orig[2] - xs.orig[1])</pre>
   b.orig <- ys.orig[2] - m.orig*xs.orig[2]</pre>
   ys.trans <- quantile(qqnorm(resid(out_info$transmdl), plot.it = F)$y,
                         probs = c(0.25, 0.75), qtype = 7)
    xs.trans <- quantile(qqnorm(resid(out info$transmdl), plot.it = F)$x, probs = c(0.25, 0.75),
                         qtype = 7)
   m.trans <- (ys.trans[2] - ys.trans[1])/(xs.trans[2] - xs.trans[1])</pre>
   b.trans <- ys.trans[2] - m.trans*xs.trans[2]</pre>
  assumptions.df <- data.frame(orig_qq_theor = qqnorm(resid(out_info$pfasmdl), plot.it = F)$x,
                               orig_qq_samp = qqnorm(resid(out_info$pfasmdl), plot.it = F)$y,
                                                               stringsAsFactors = F)
  assumptions.df.t <- data.frame(trans_qq_theor = qqnorm(resid(out_info$transmdl),
                                                          plot.it = F)x,
                               trans_qq_samp = qqnorm(resid(out_info$transmdl), plot.it = F)$y,
                                                               stringsAsFactors = F)
qq.plot.orig <- ggplot(assumptions.df, aes(x = orig_qq_theor, y = orig_qq_samp)) +
   geom_point() +
   geom_abline(intercept = b.orig, slope = m.orig) +
   labs(x = "Theoretical Quantiles",
         y = "Sample Quantiles",
         title = pasteO(out_info$pfasmdl$terms[[2]], ": ",
                          out_info$pfasmdl$terms[[3]][2])) +
   theme(plot.title = element_text(hjust = 0.5, size = 10),
          axis.title = element_text(size = 10))
qq.plot.trans <- ggplot(assumptions.df.t, aes(x = trans_qq_theor, y = trans_qq_samp)) +
   geom_point() +
    geom_abline(intercept = b.trans, slope = m.trans) +
   labs(x = "Theoretical Quantiles",
        y = "Sample Quantiles",
```

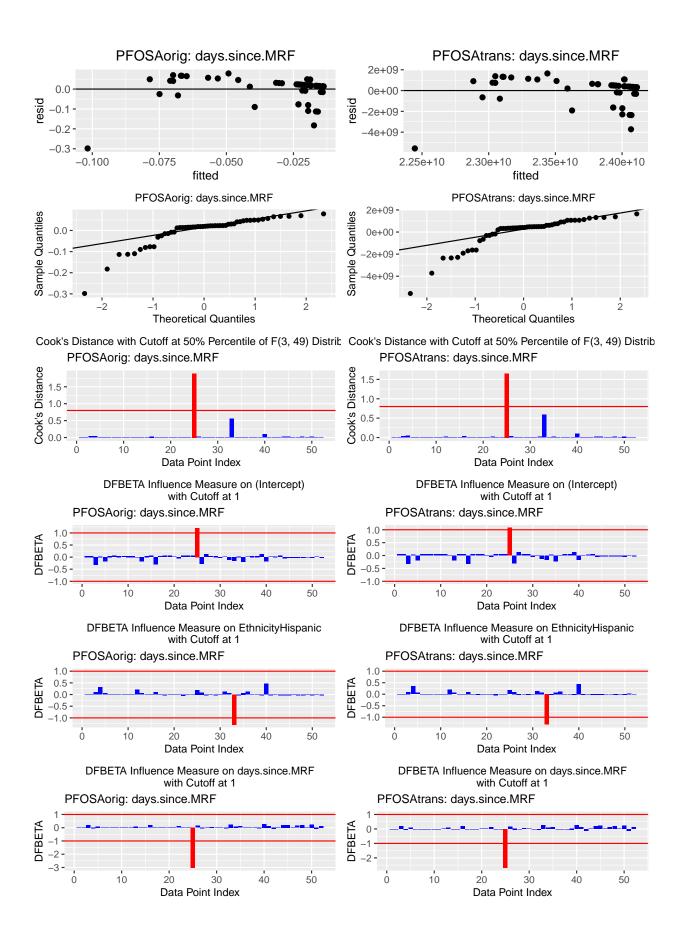
```
title = paste0(out_info$transmdl$terms[[2]], ": ",
                           out_info$transmdl$terms[[3]][2])) +
    theme(plot.title = element_text(hjust = 0.5, size = 10),
          axis.title = element_text(size = 10))
#Cooks distance plots
cd.plot.orig <- cooks_distance_plot(out_info$pfasmdl,</pre>
                                      paste0(out info$pfasmdl$terms[[2]], ": ",
                                             out_info$pfasmdl$terms[[3]][2]))
cd.plot.trans <- cooks_distance_plot(out_info$transmdl, paste0(out_info$transmdl$terms[[2]], ": ",</pre>
                                                                 out_info$transmdl$terms[[3]][2]))
#DFBETA plots
fbeta1 <- fbetas_plot(out_info$pfasmdl, paste0(out_info$pfasmdl$terms[[2]], ": ",</pre>
                                                       out_info$pfasmdl$terms[[3]][2]))
fbeta2 <- fbetas_plot(out_info$transmdl, paste0(out_info$transmdl$terms[[2]], ": ",</pre>
                                                        out_info$transmdl$terms[[3]][2]))
beta.fire <- list(fbeta1[[2]][1]$plot, fbeta2[[2]][1]$plot)</pre>
plotlist.a <- list(orig.resid, trans.resid, qq.plot.orig, qq.plot.trans,</pre>
                    cd.plot.orig$plot, cd.plot.trans$plot,
                    fbeta1$`(Intercept)`$plot, fbeta2$`(Intercept)`$plot,
                    fbeta1$EthnicityHispanic$plot, fbeta2$EthnicityHispanic$plot,
                    fbeta1[[2]][1]$plot, fbeta2[[2]][1]$plot)
print(ggarrange(plotlist = plotlist.a, nrow = 6, ncol = 2))
 }
```

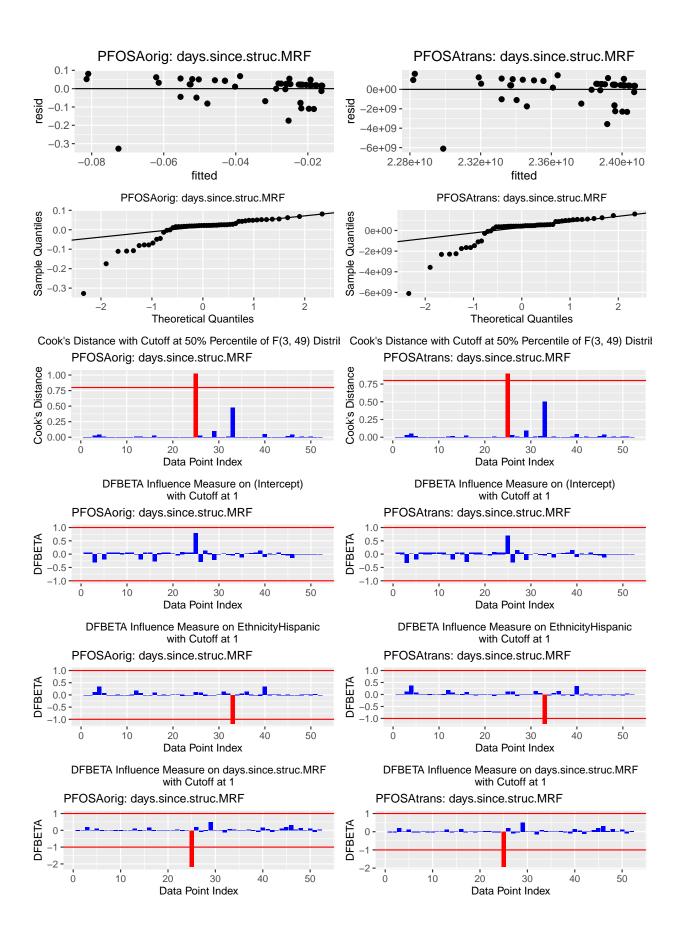


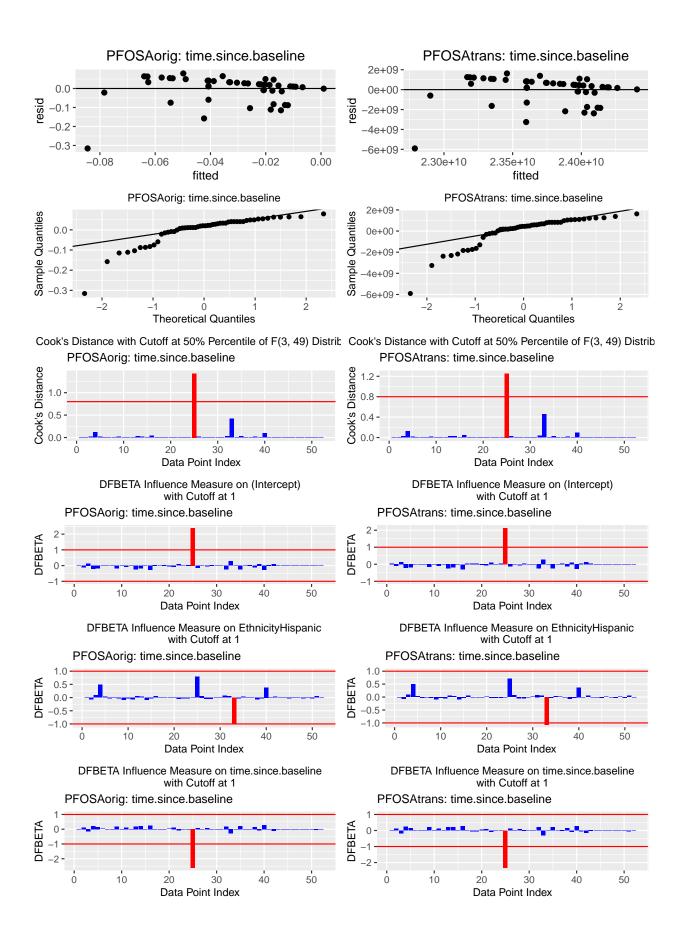


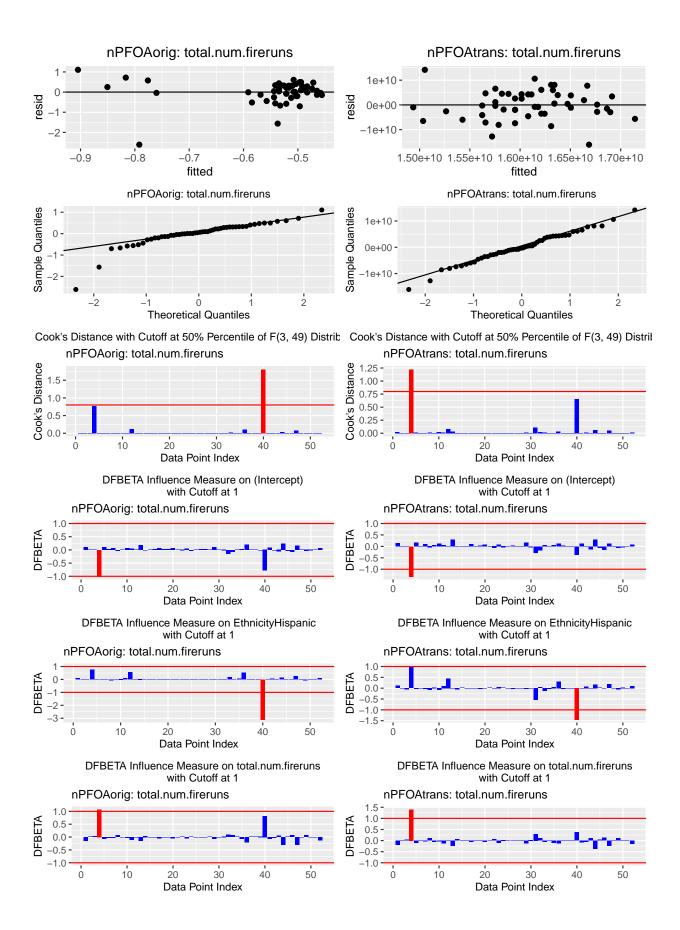


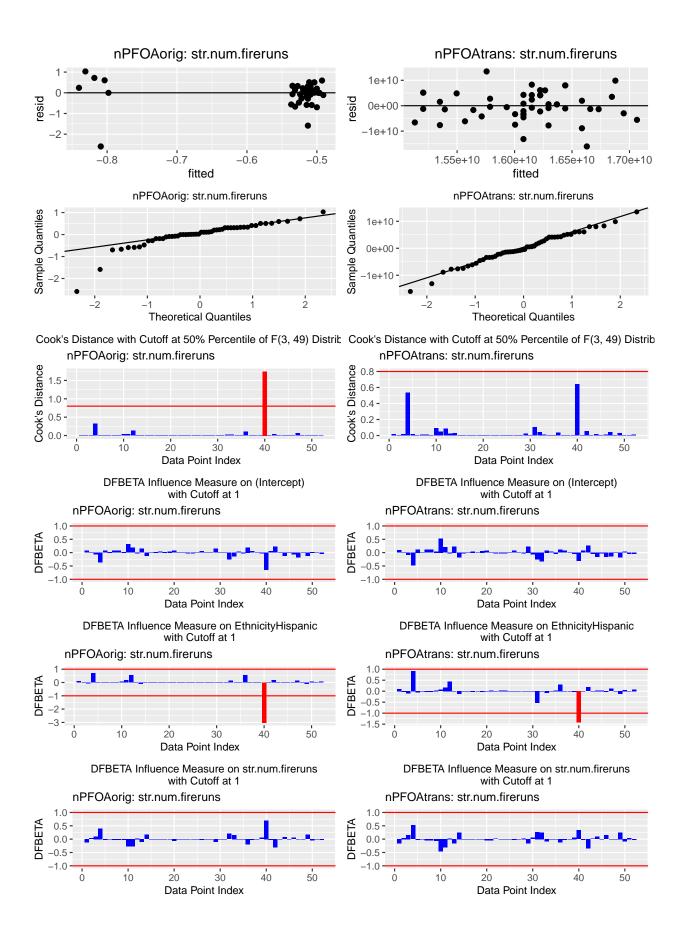


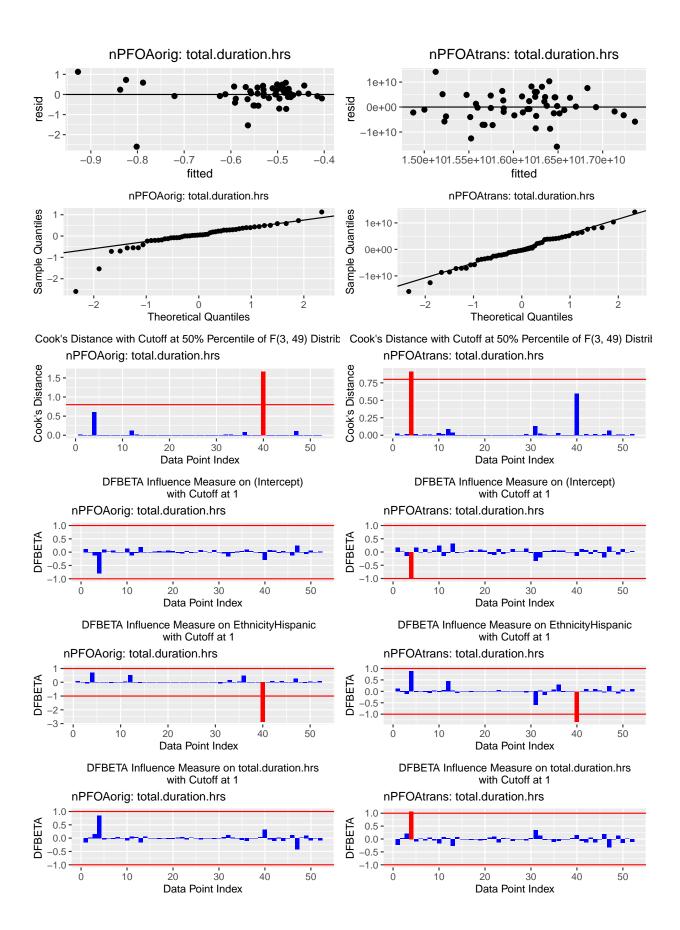


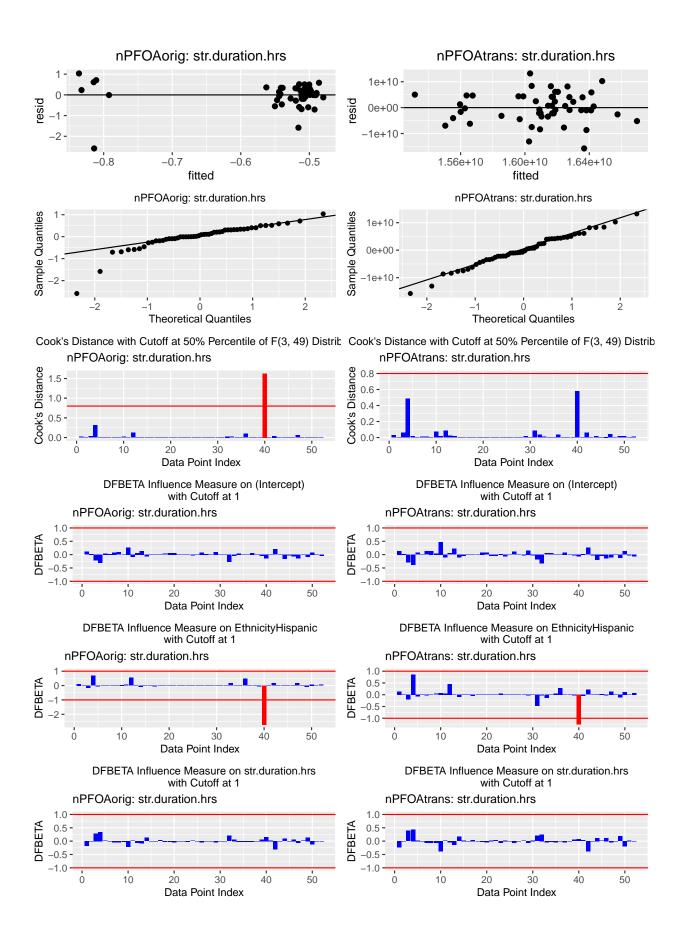


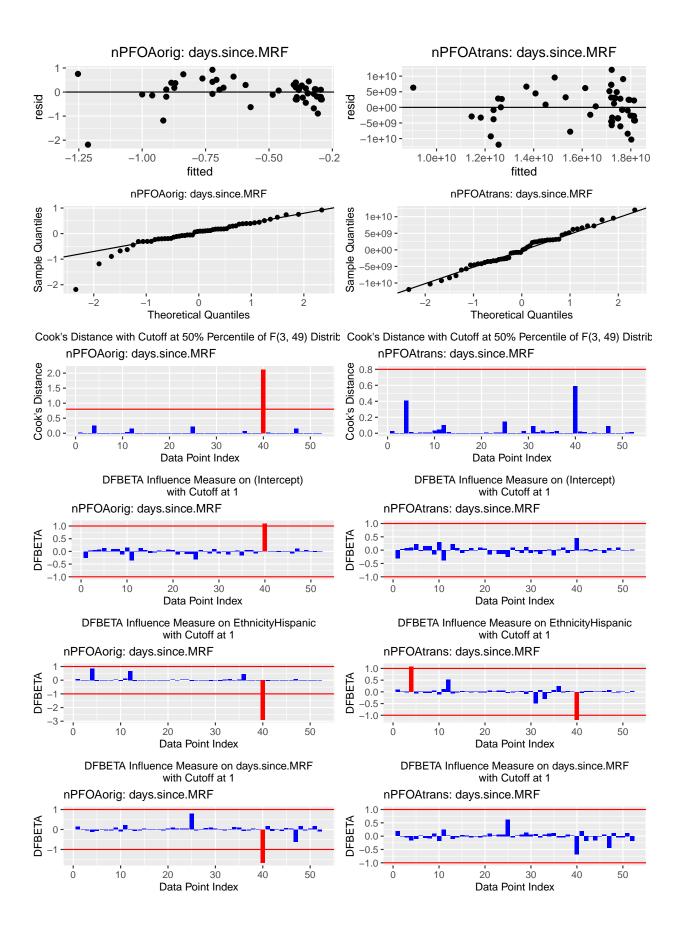


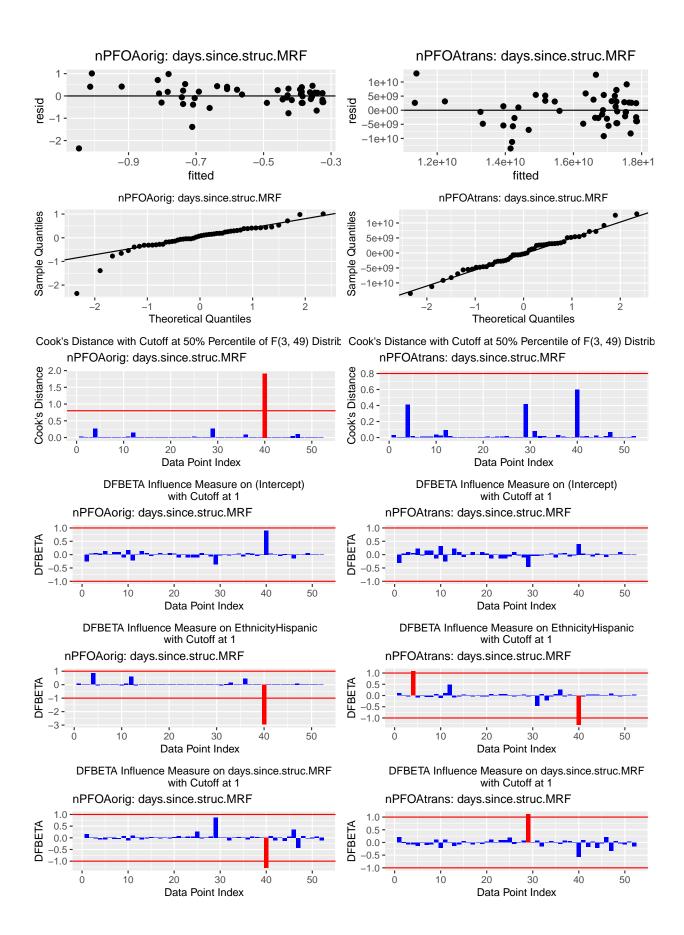


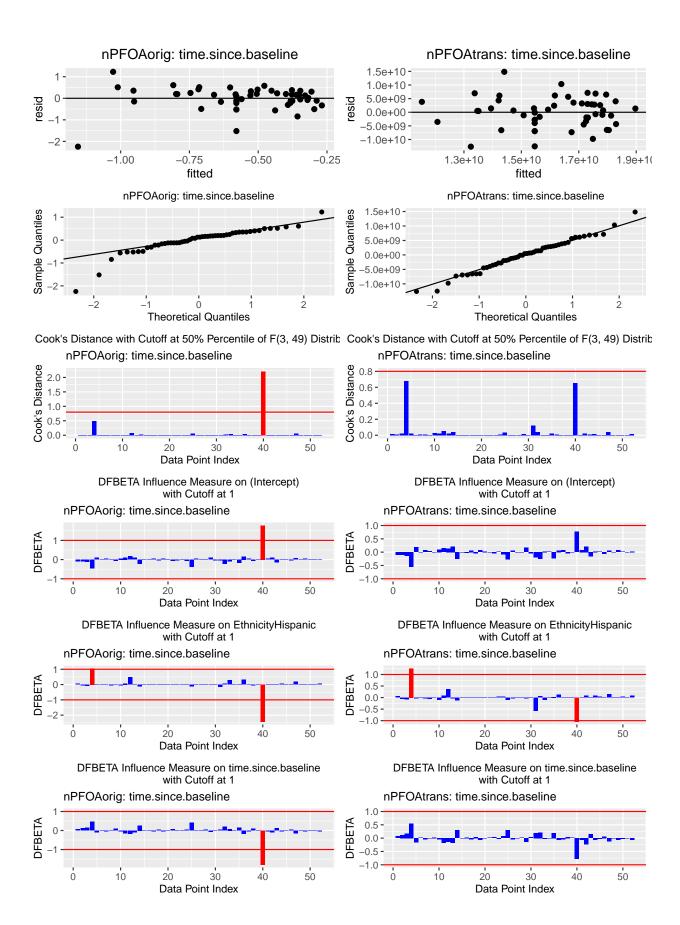


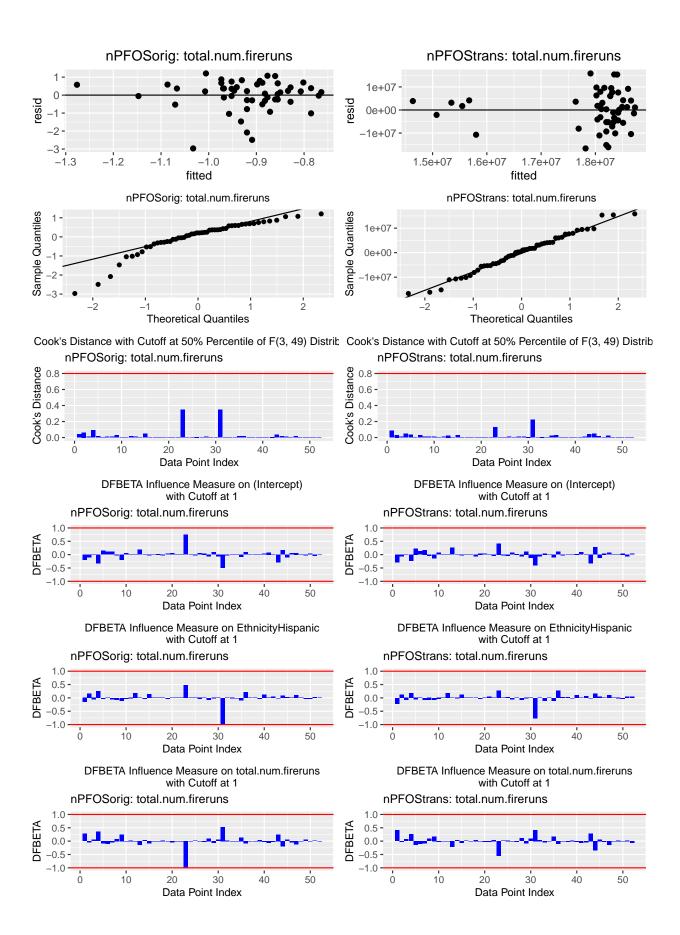


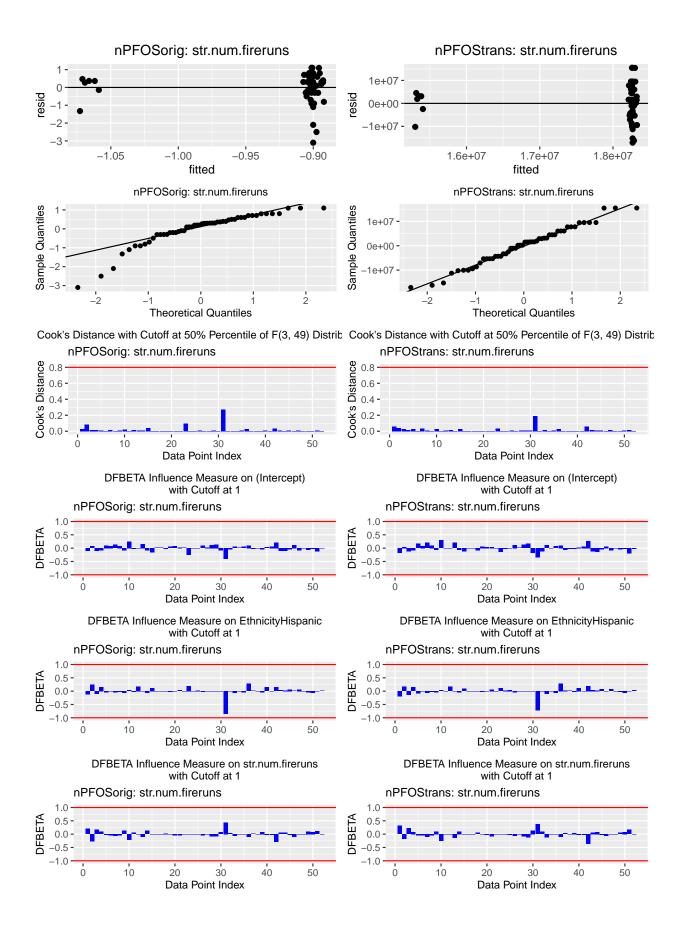


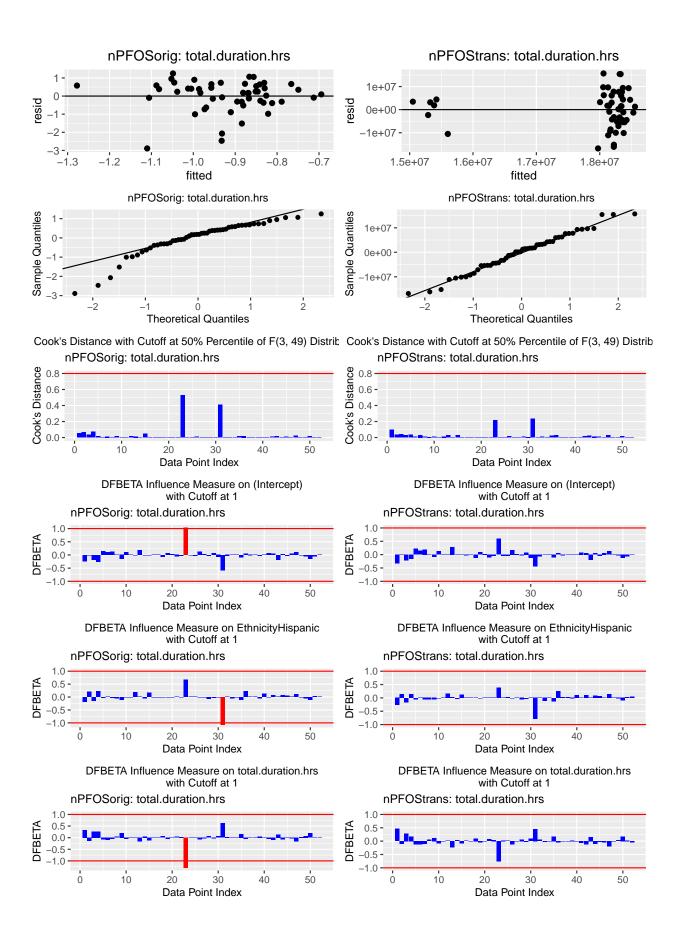


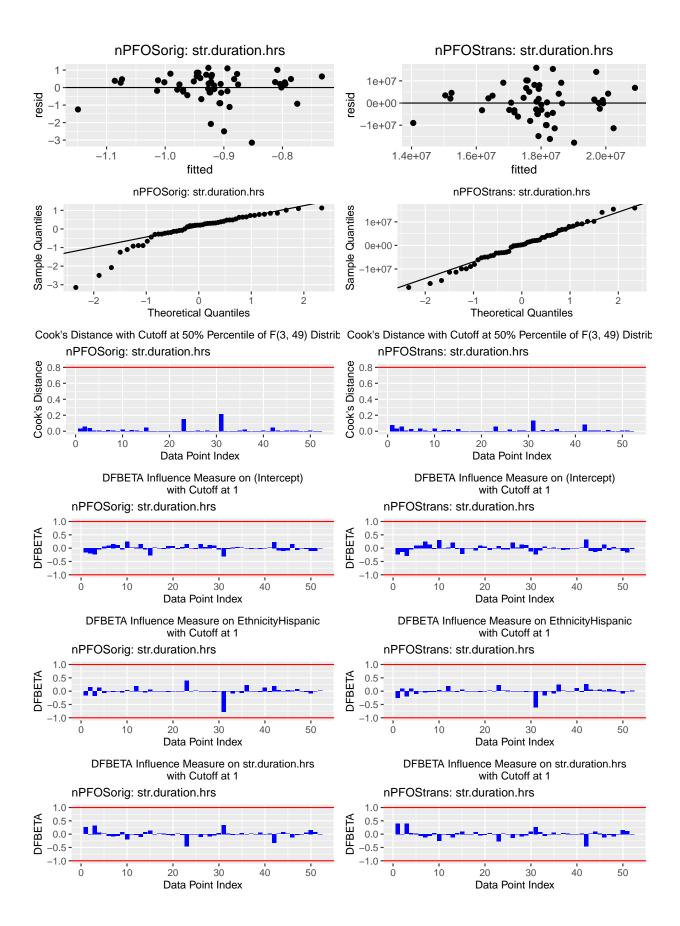


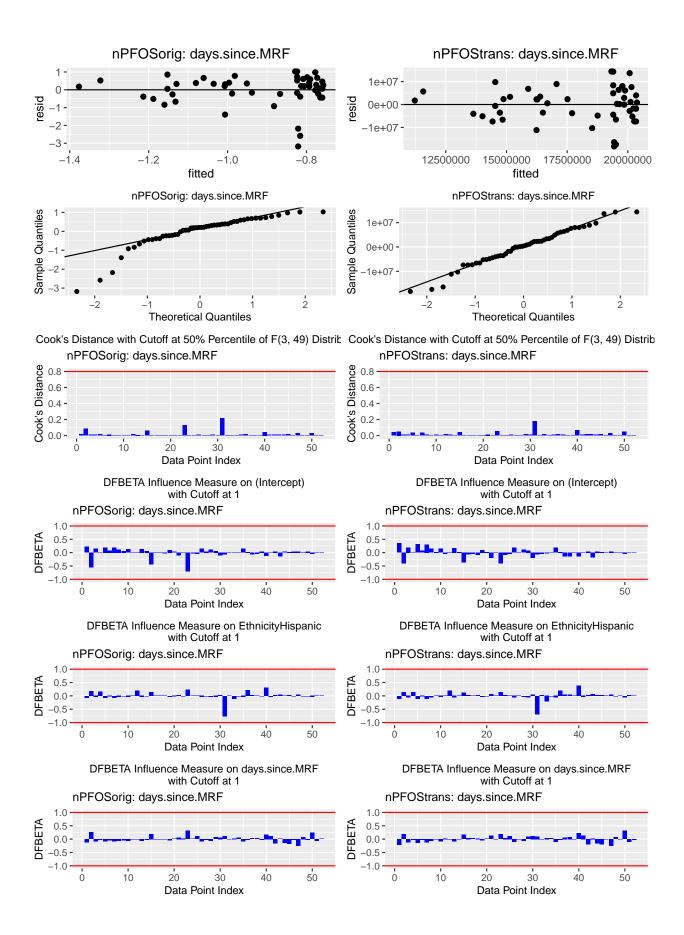


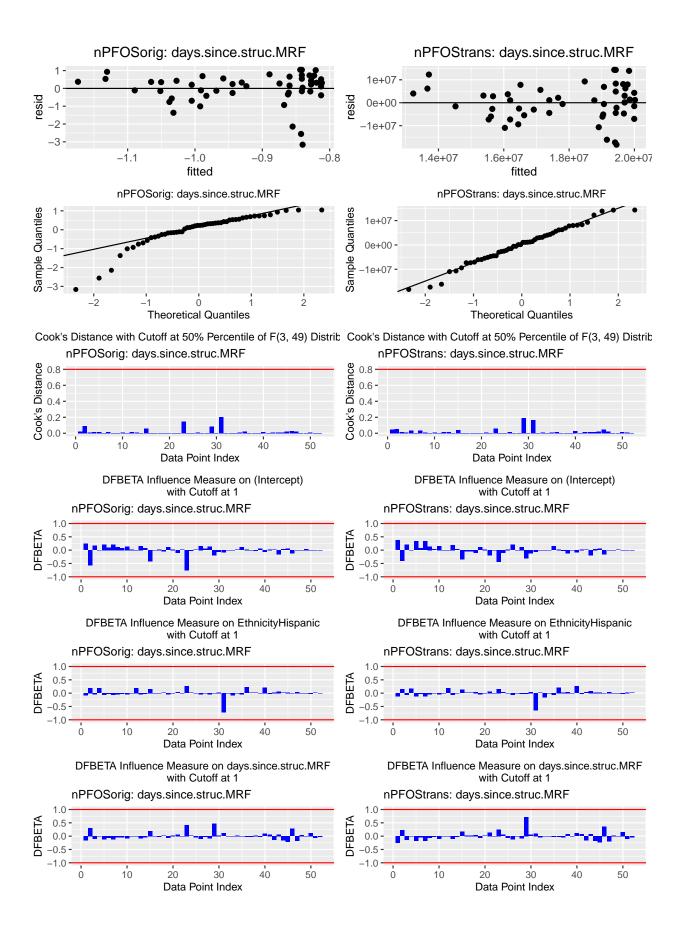


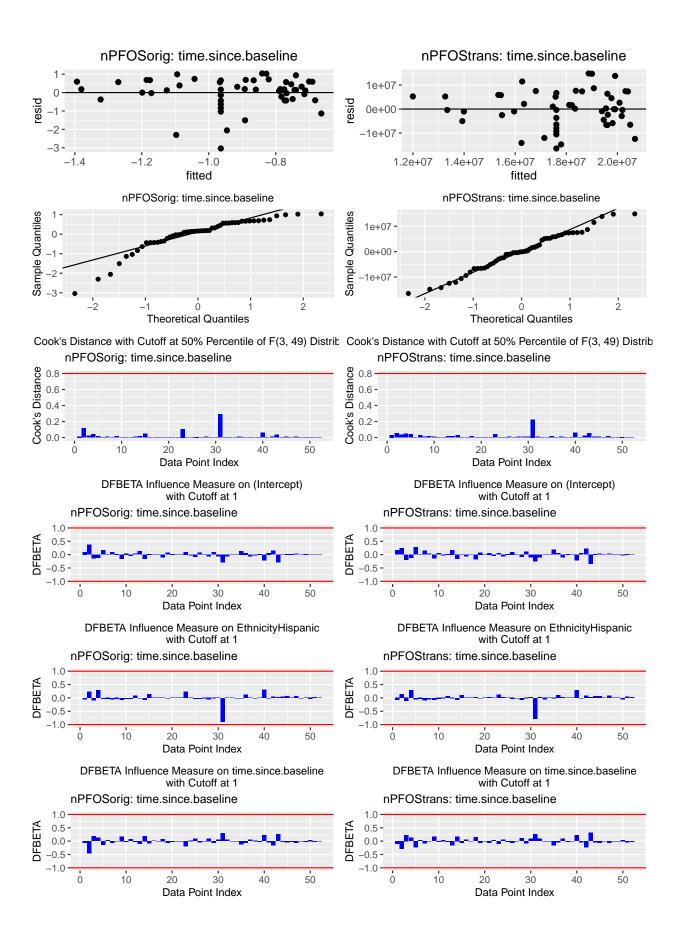


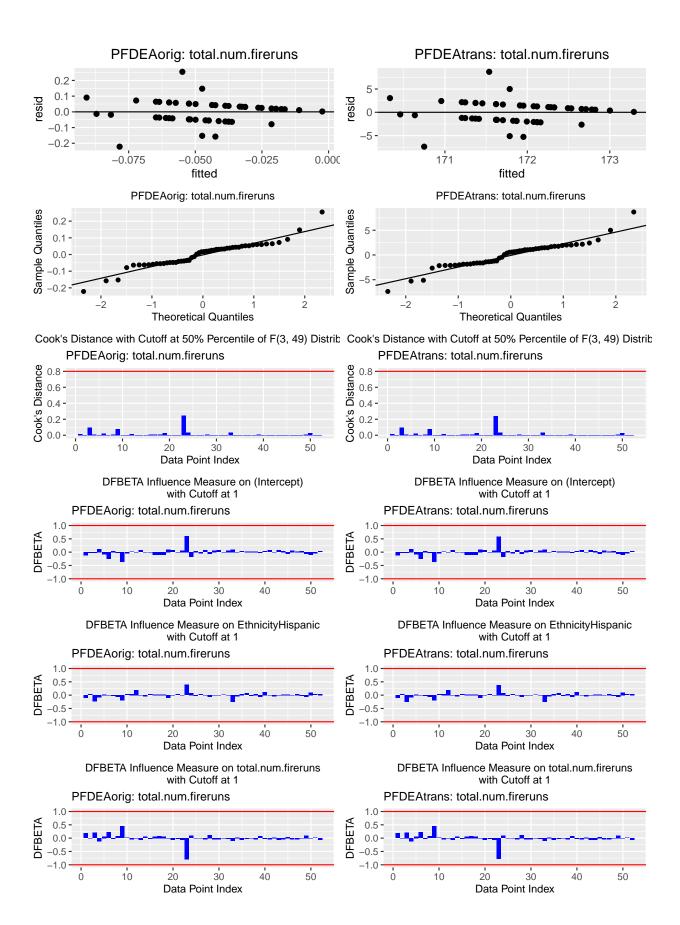


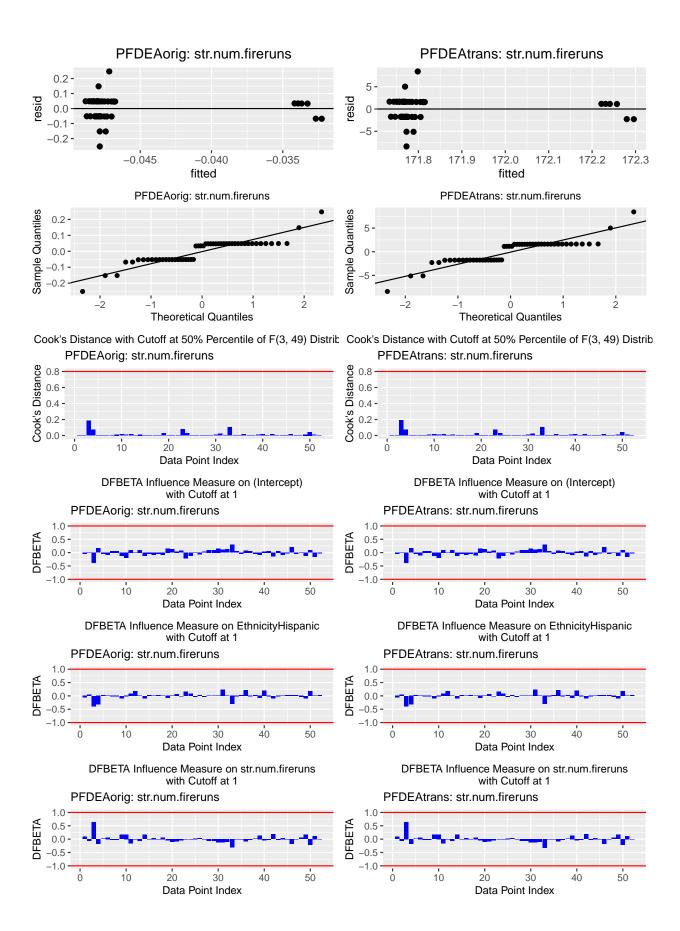


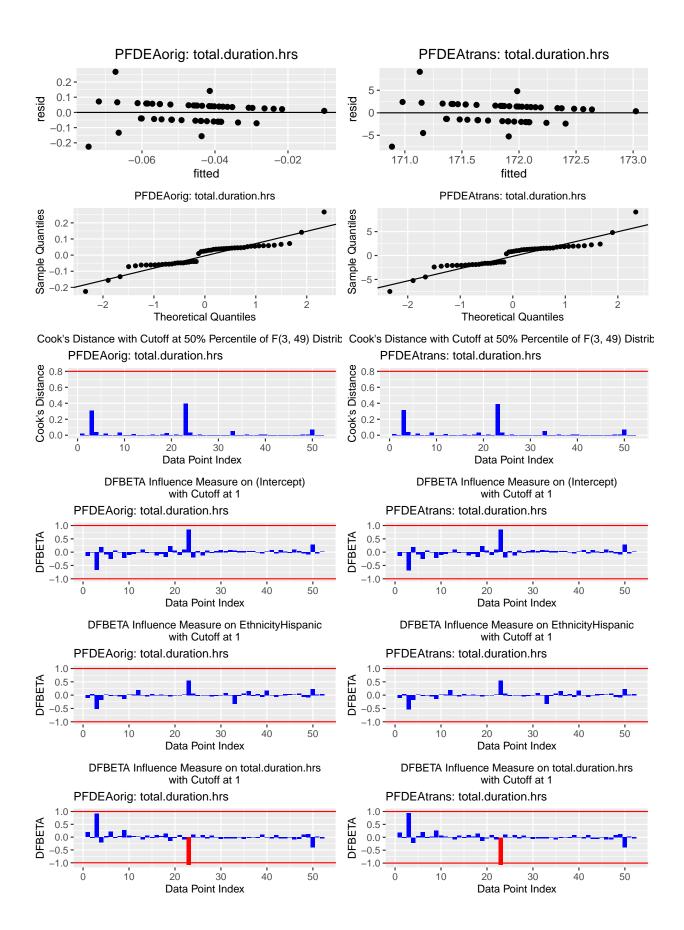


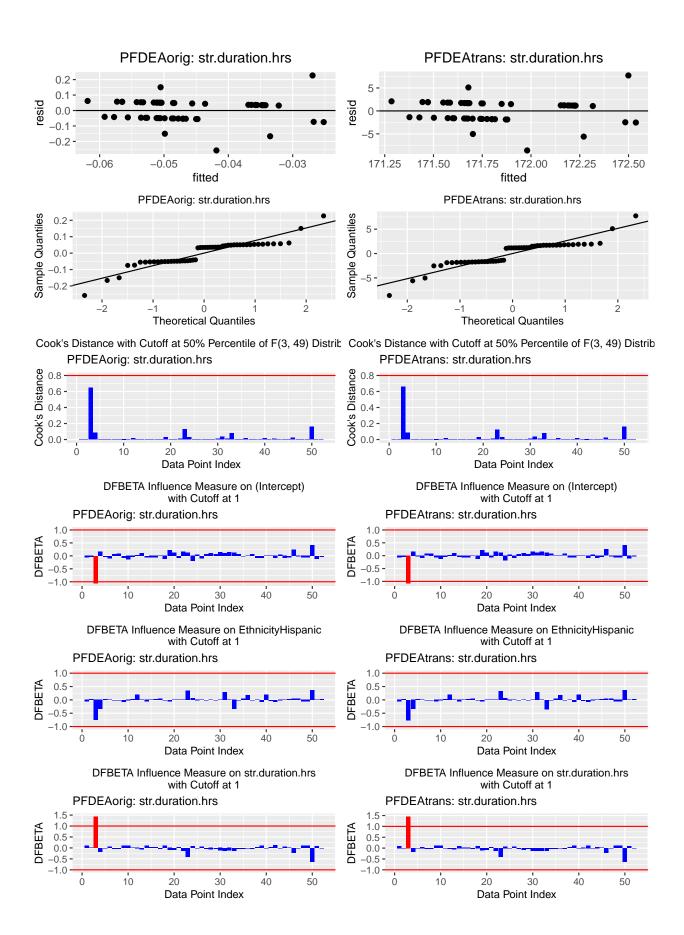


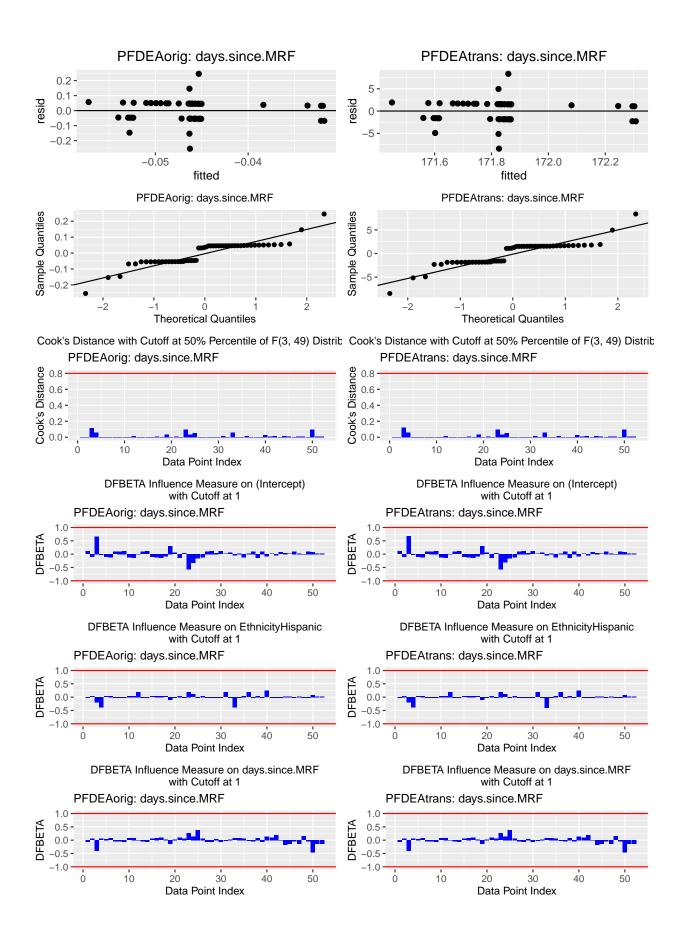


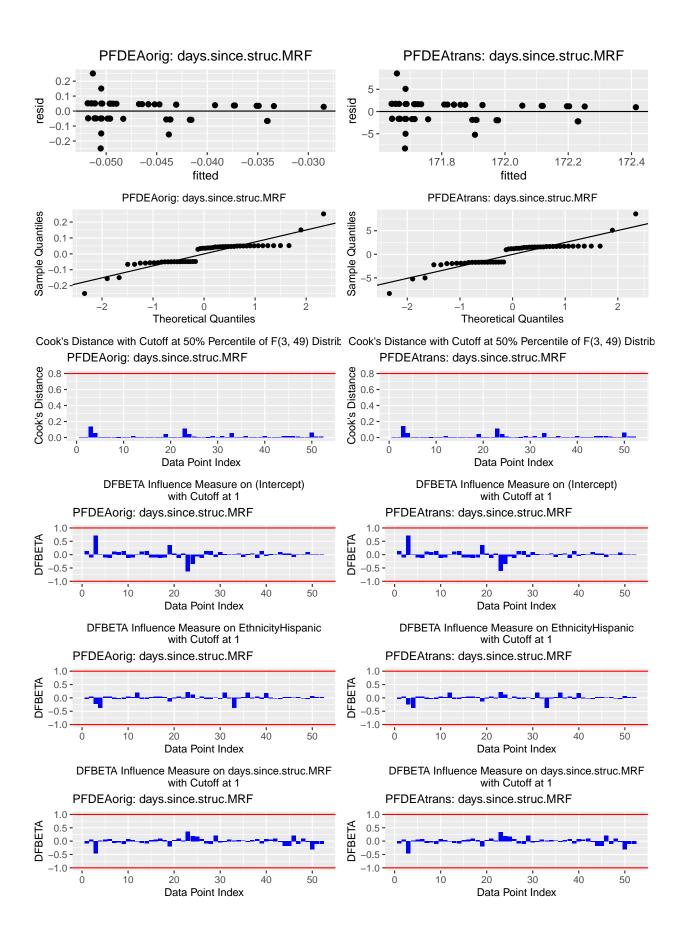


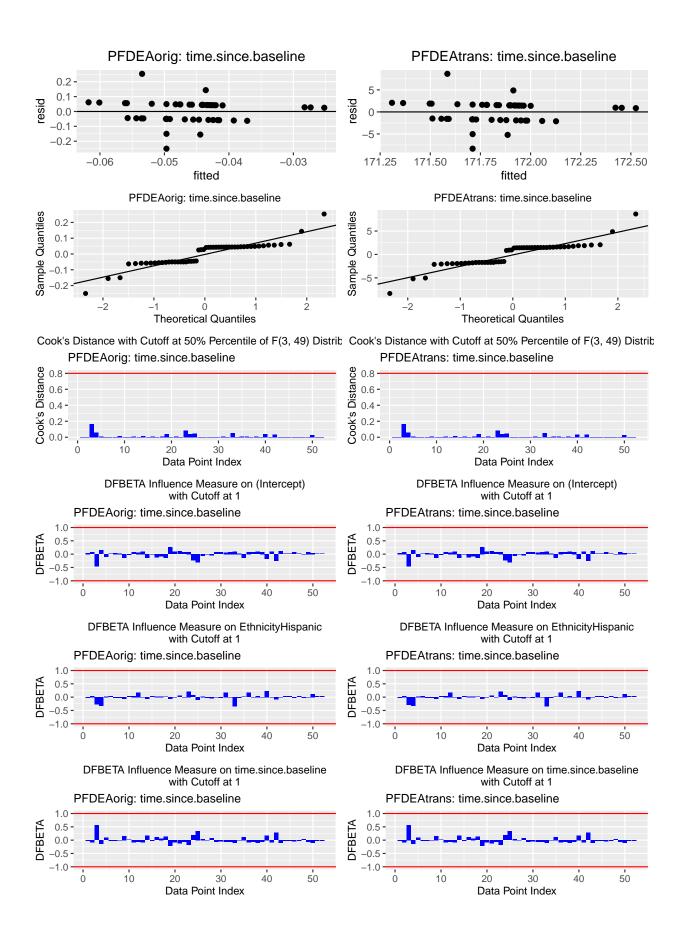


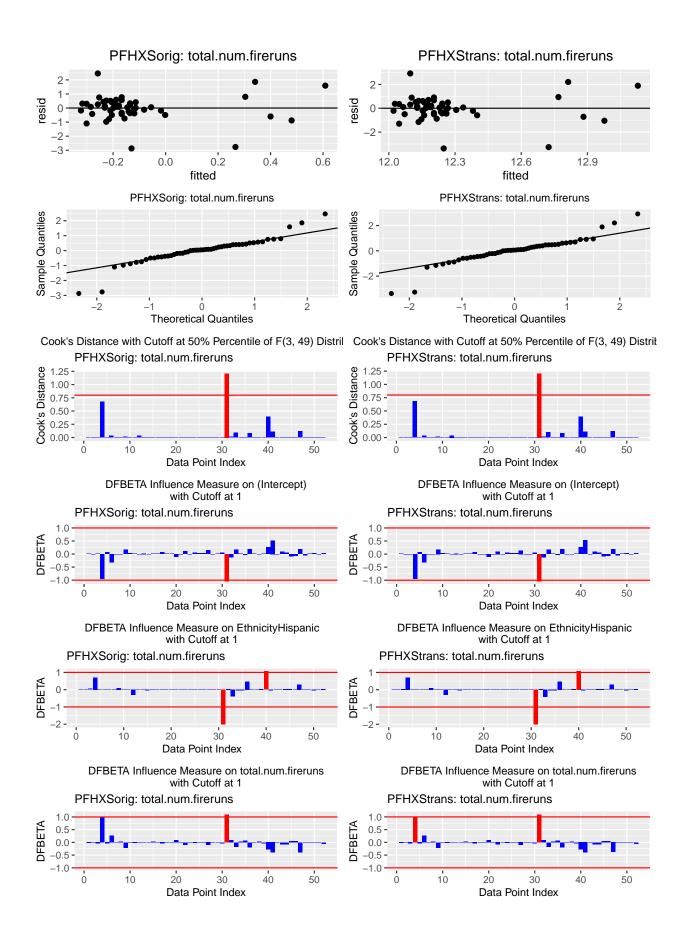


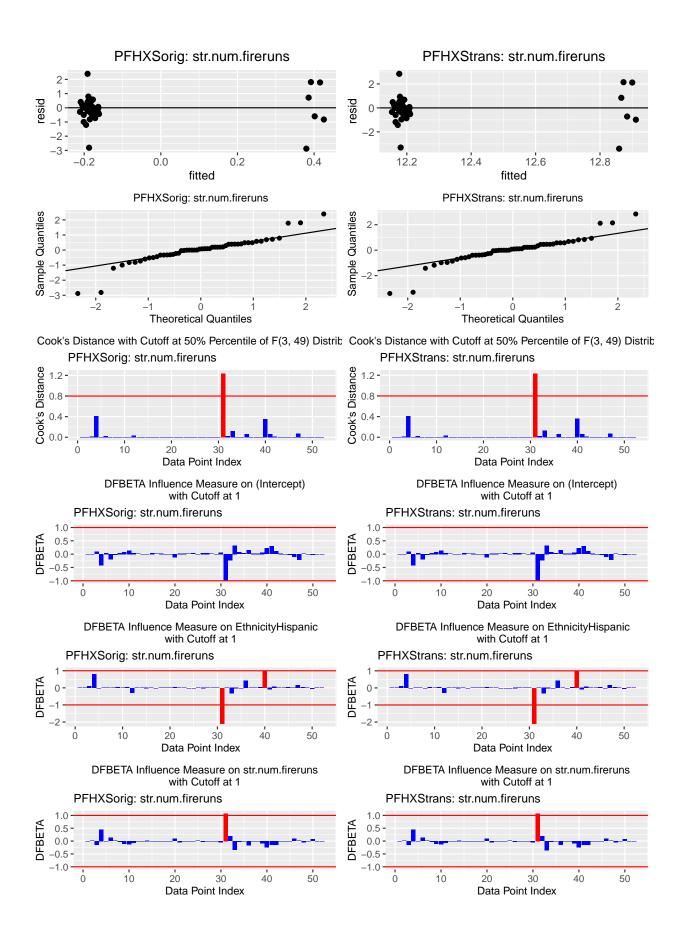


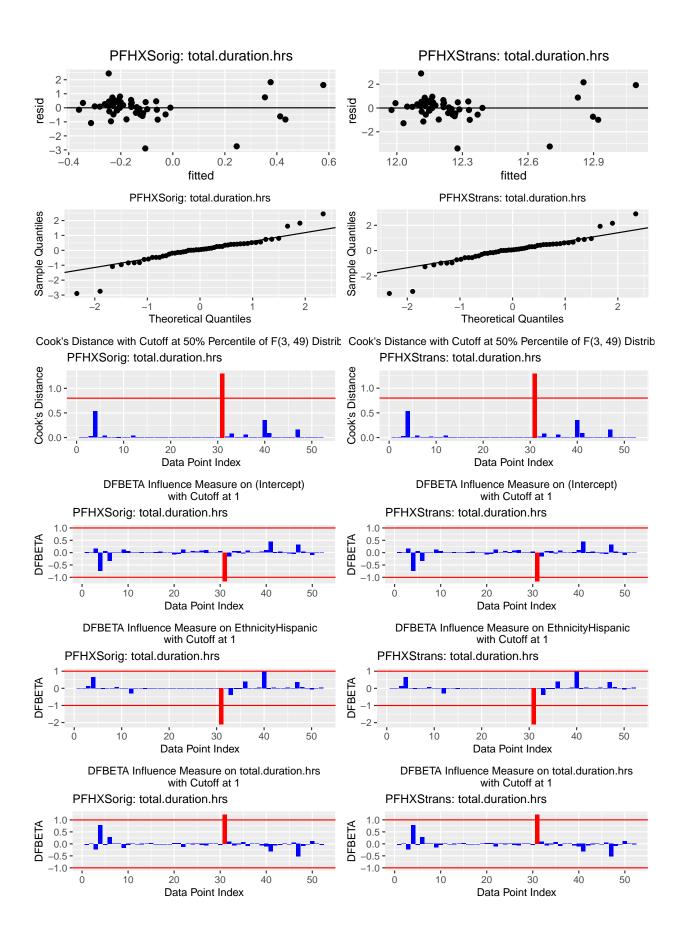


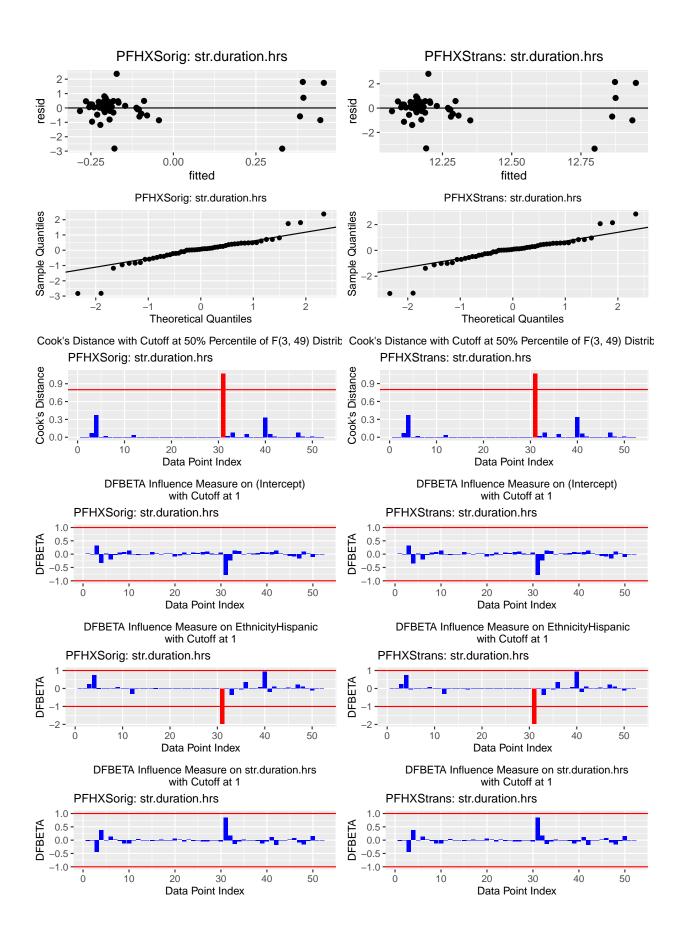


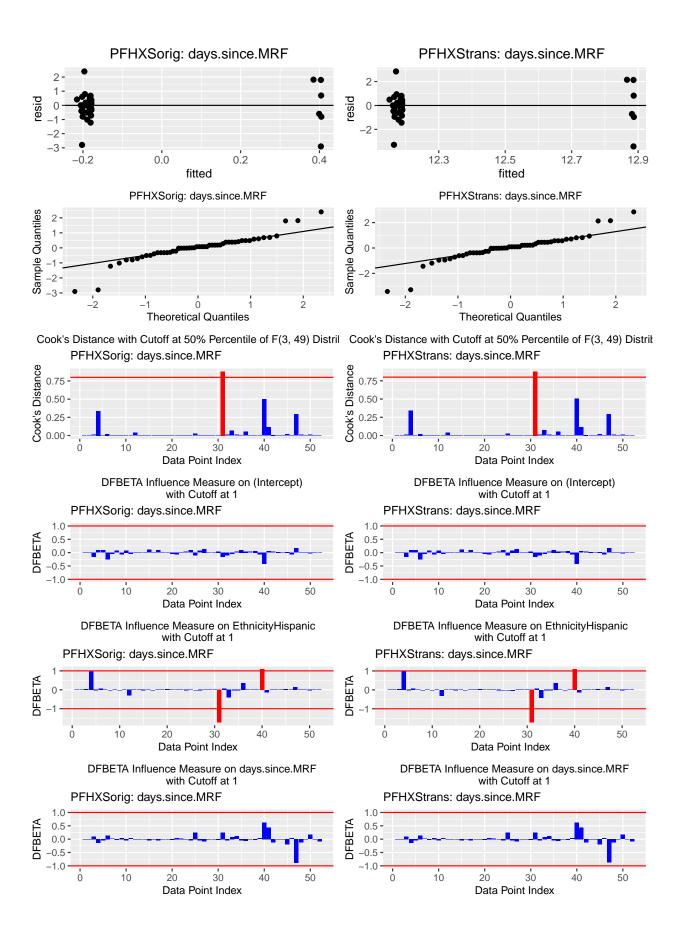


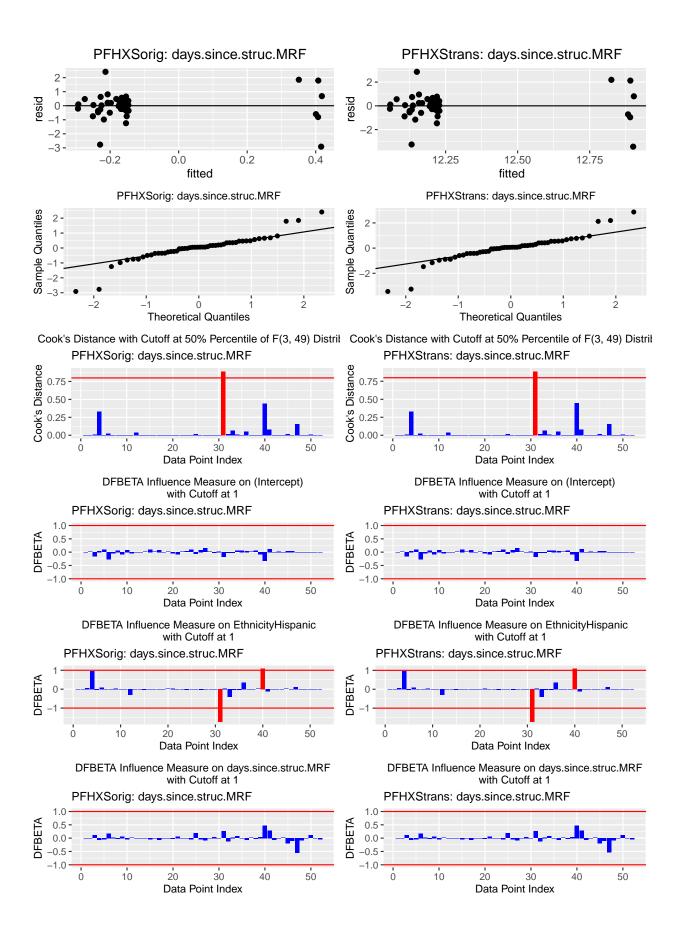


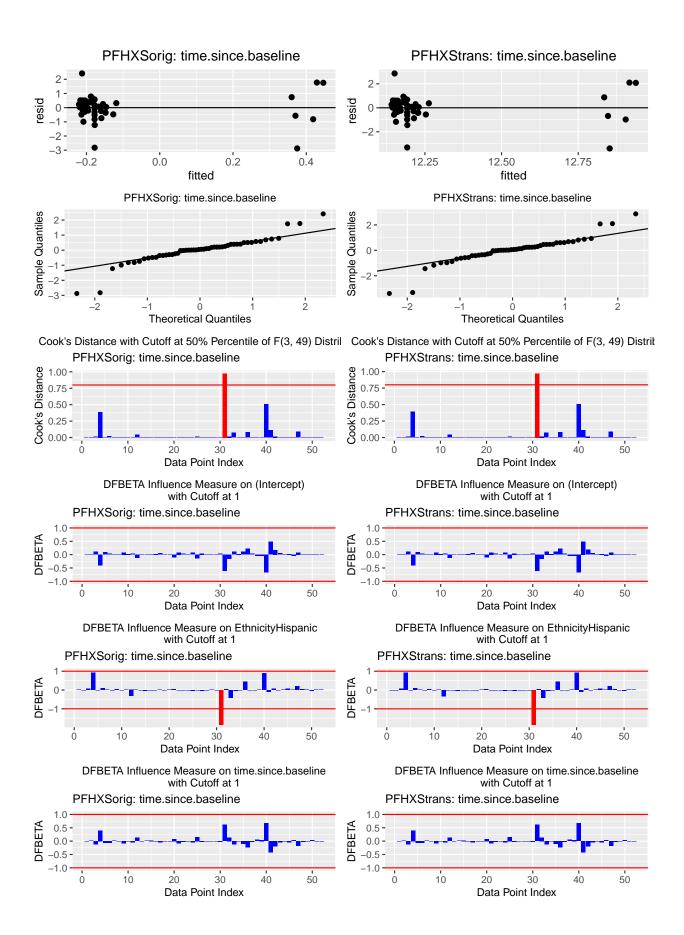


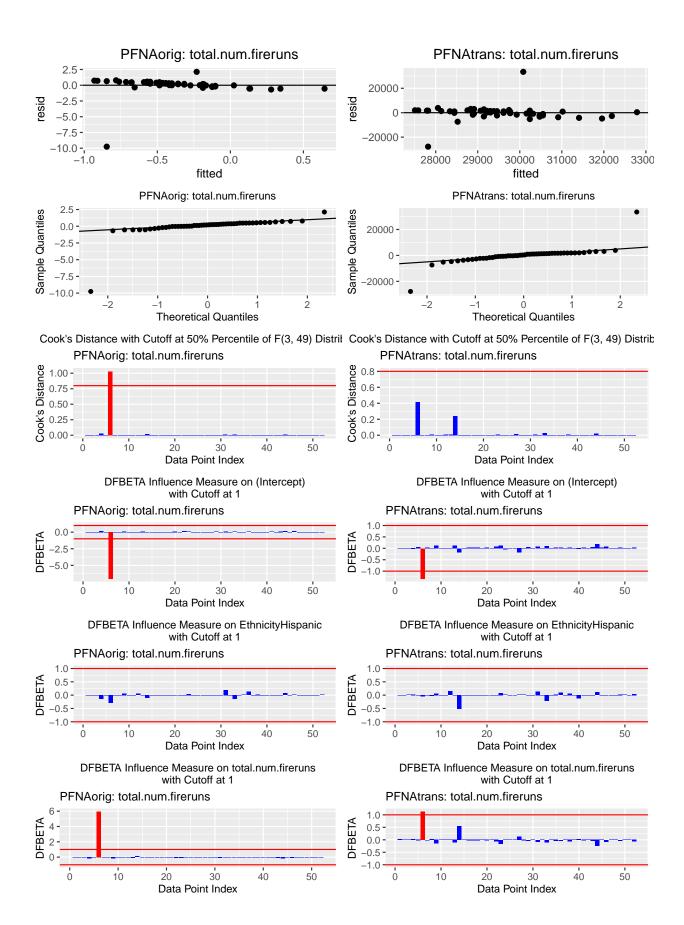


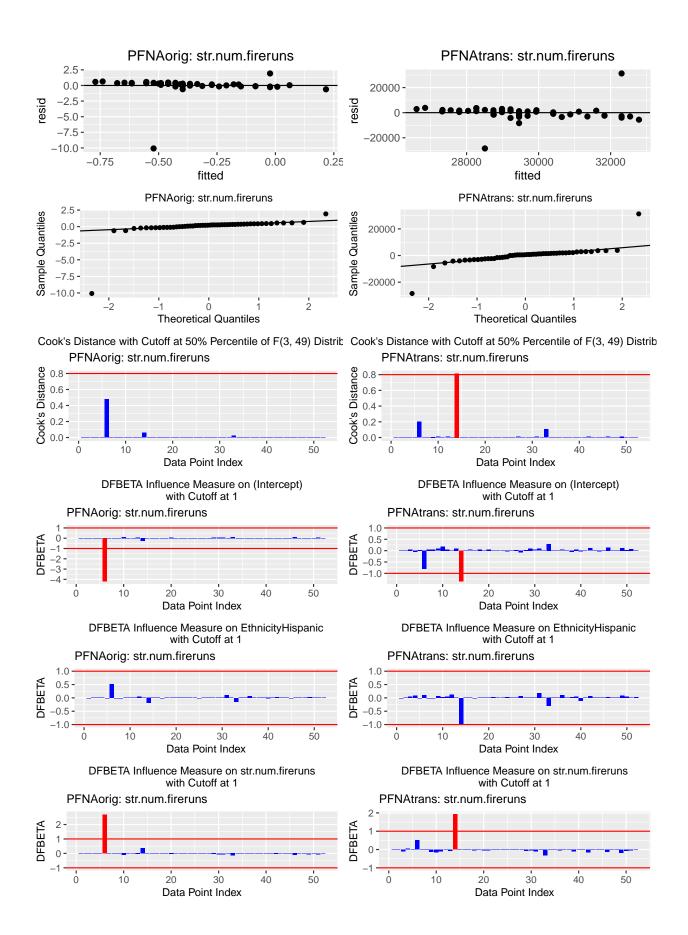


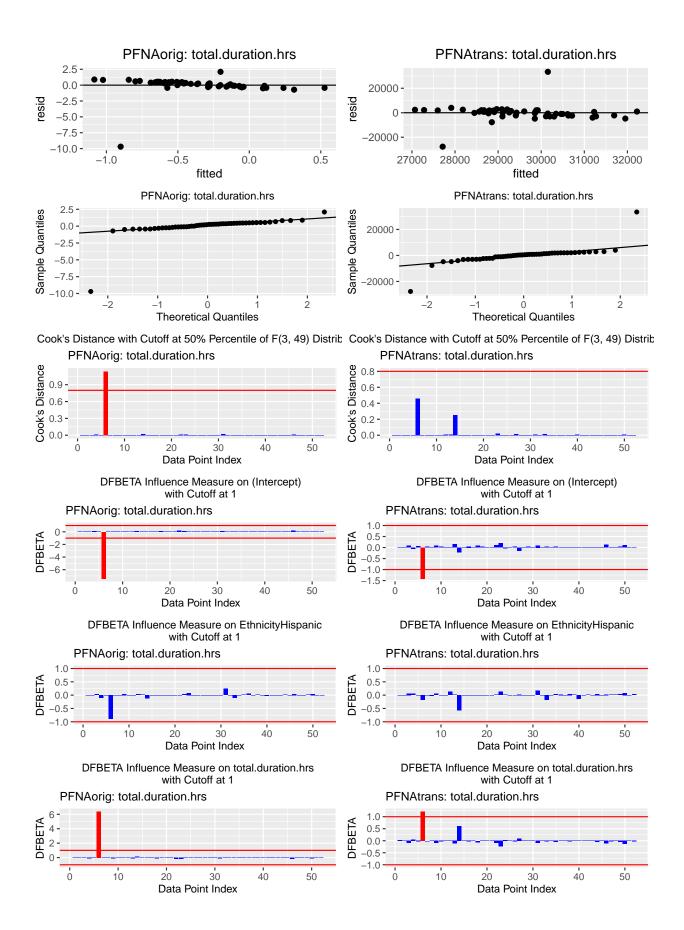


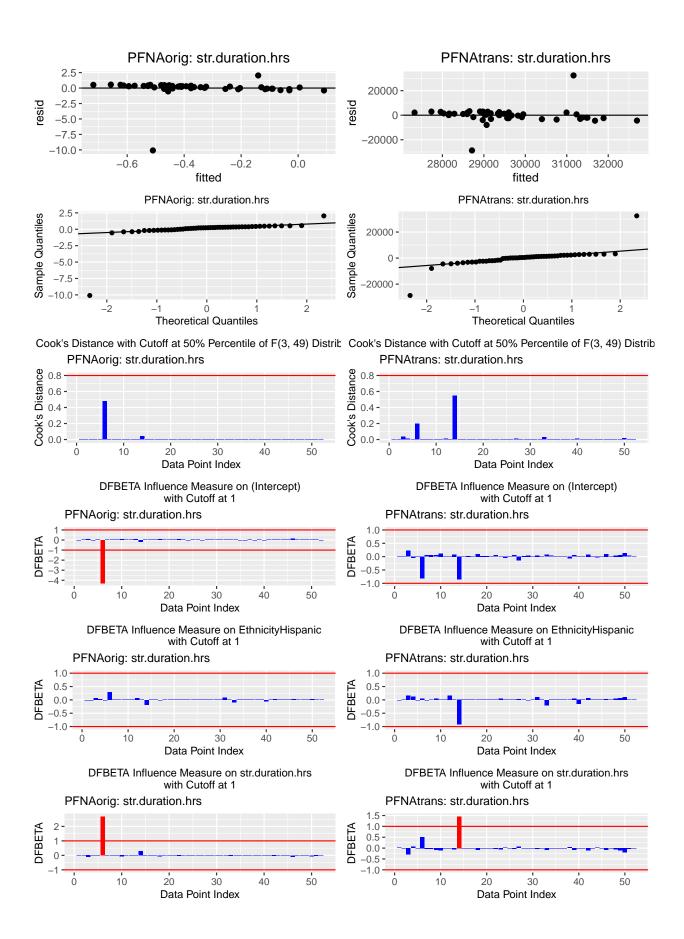


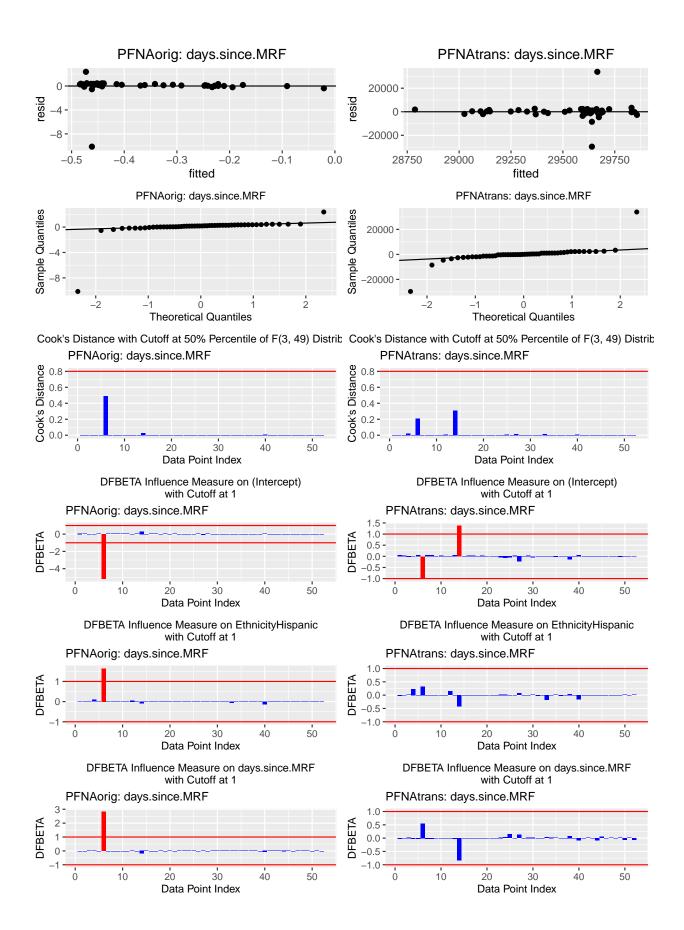


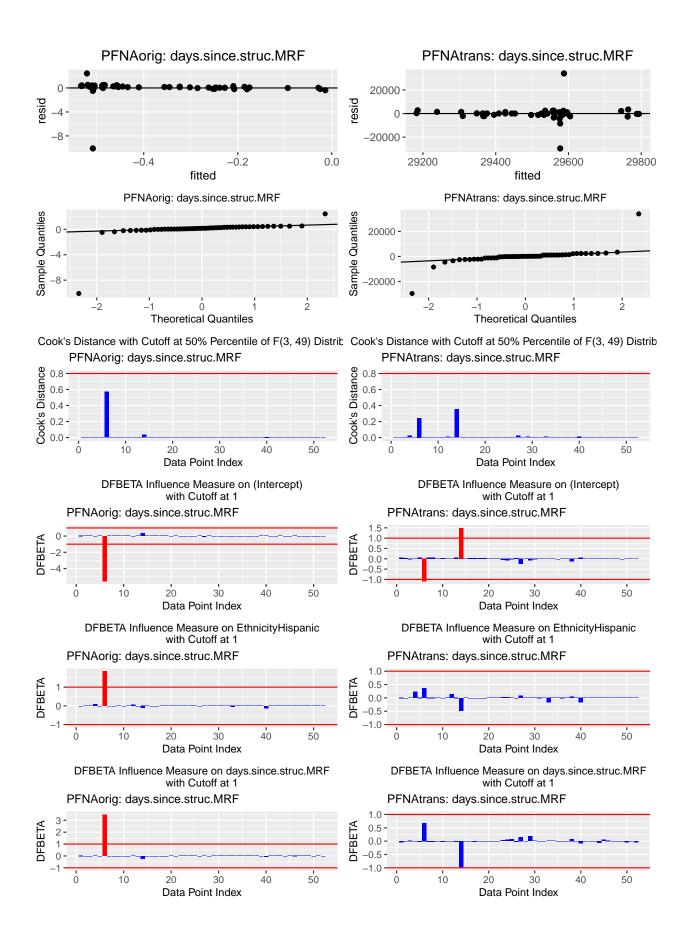


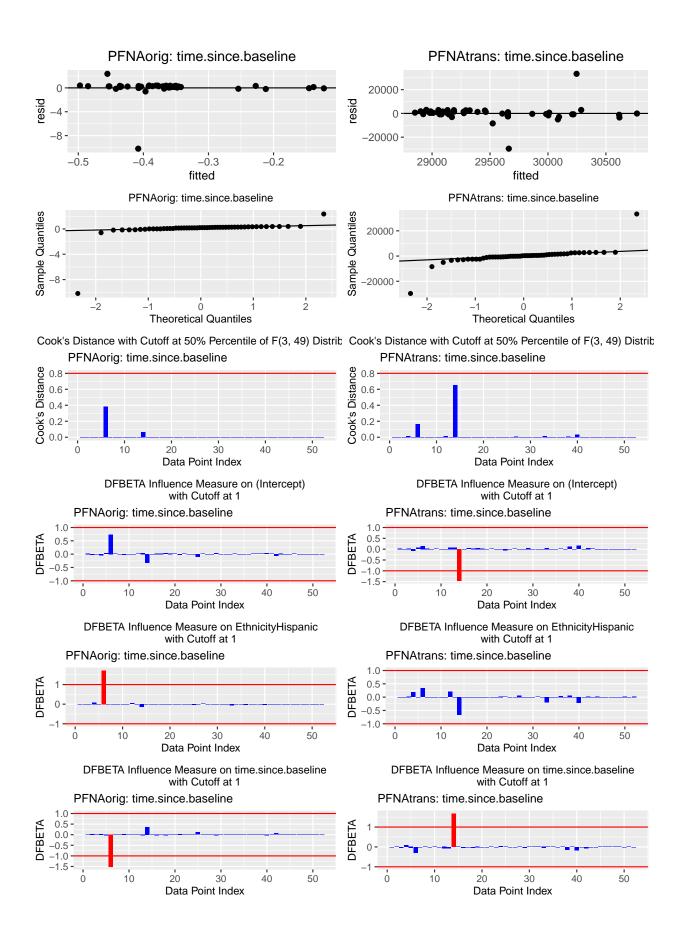


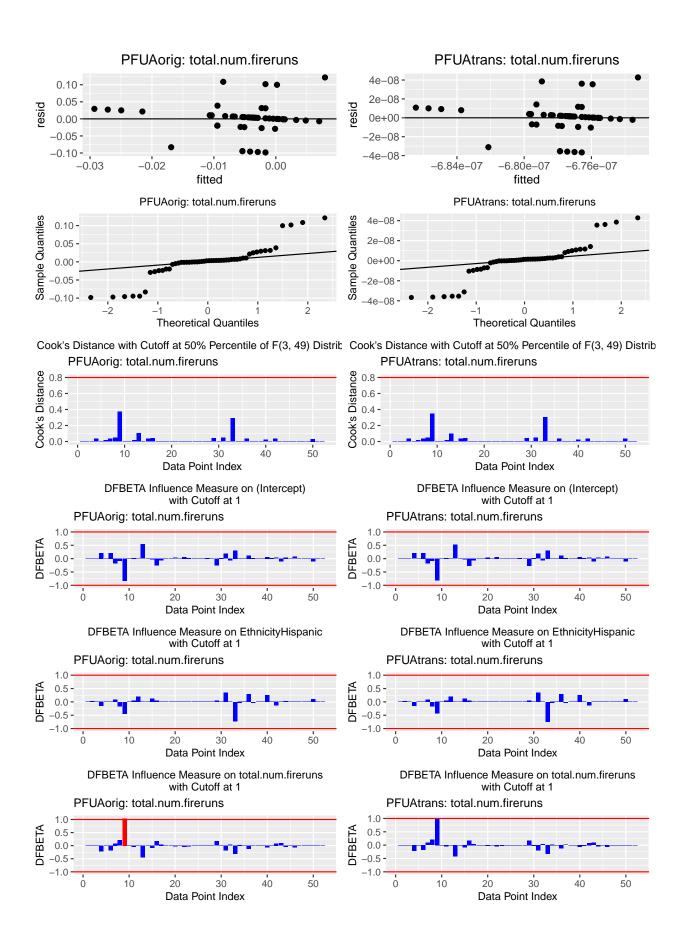


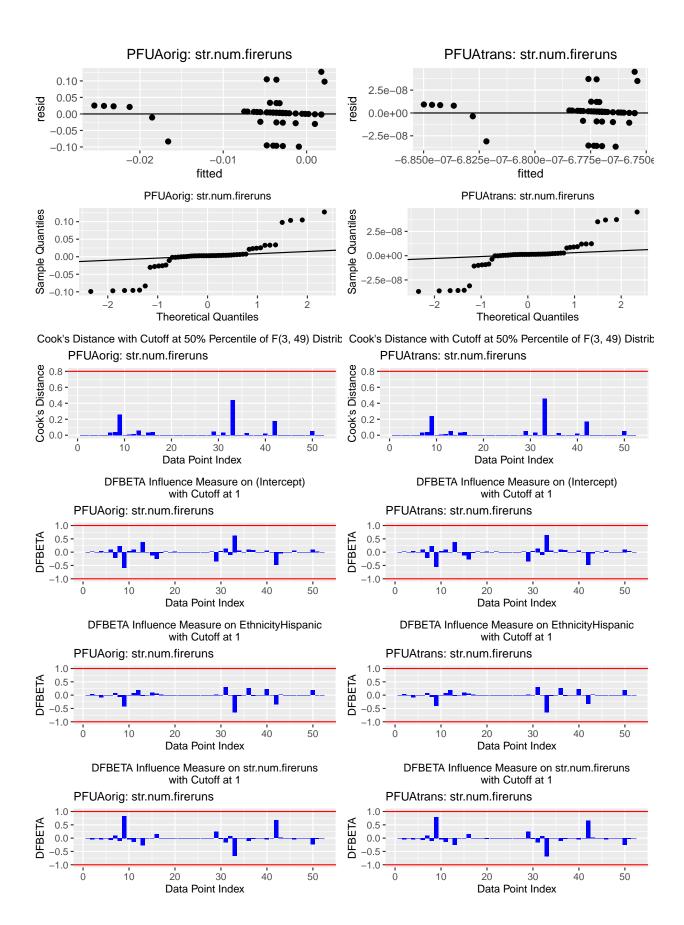


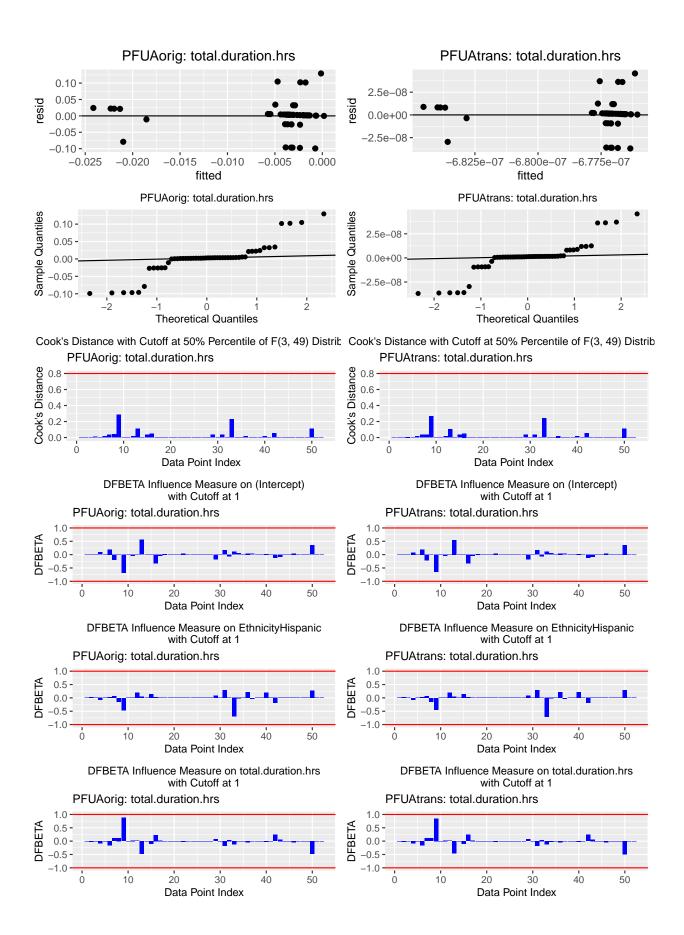


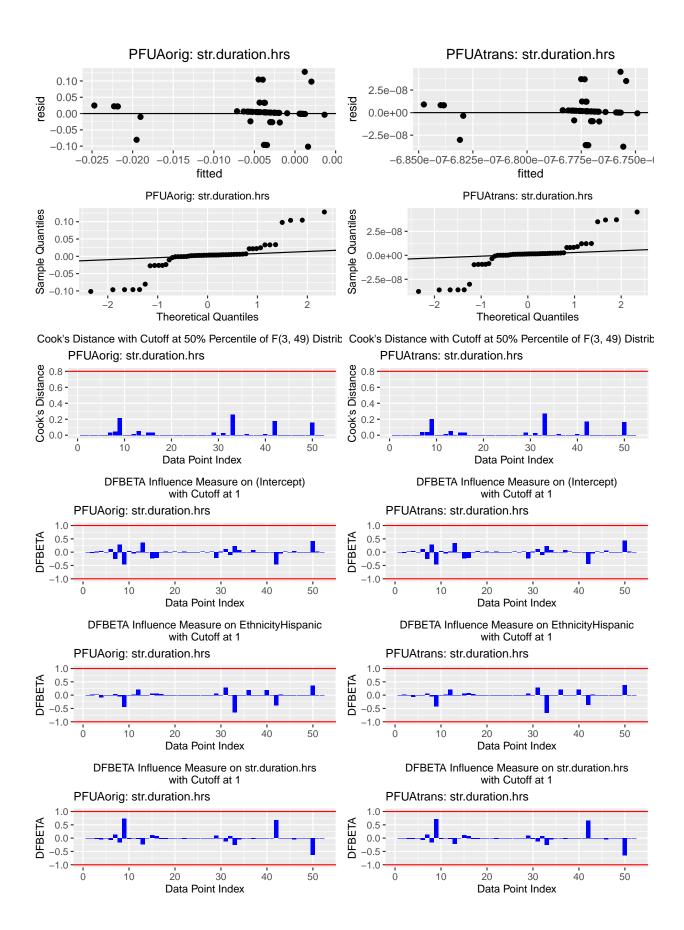


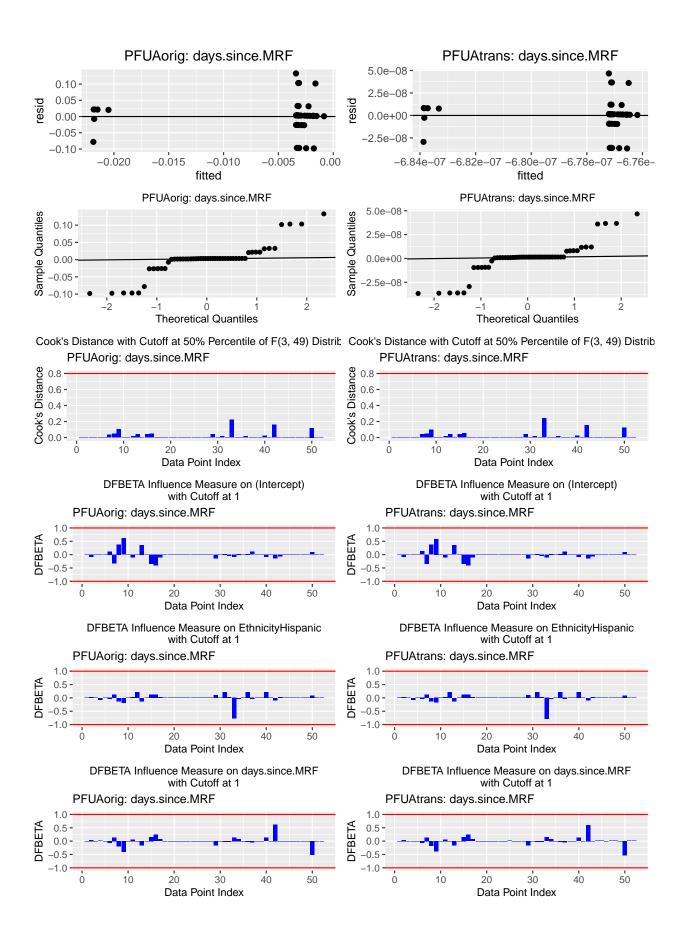


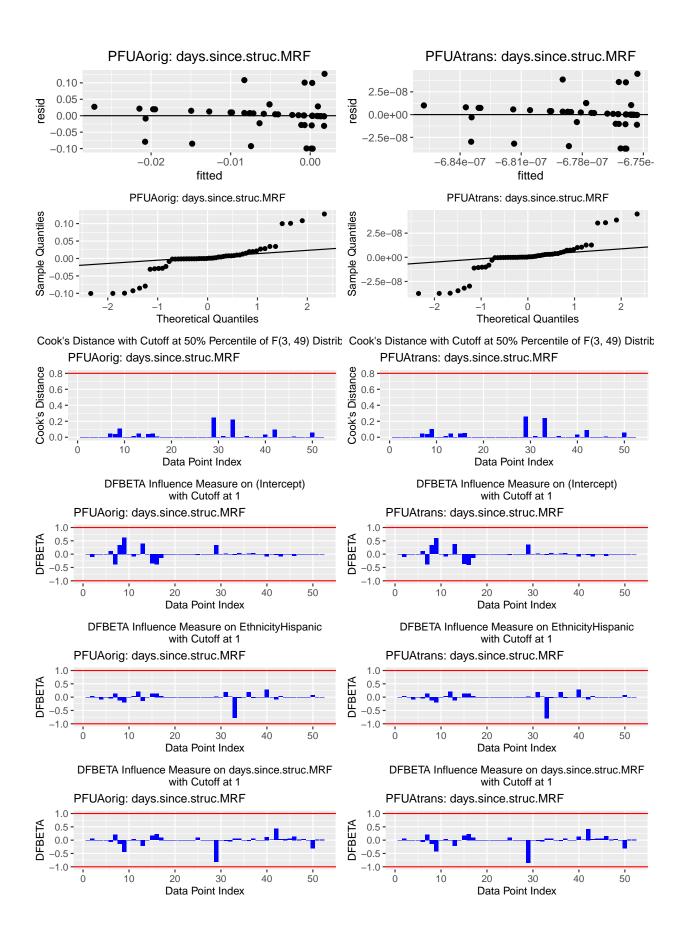


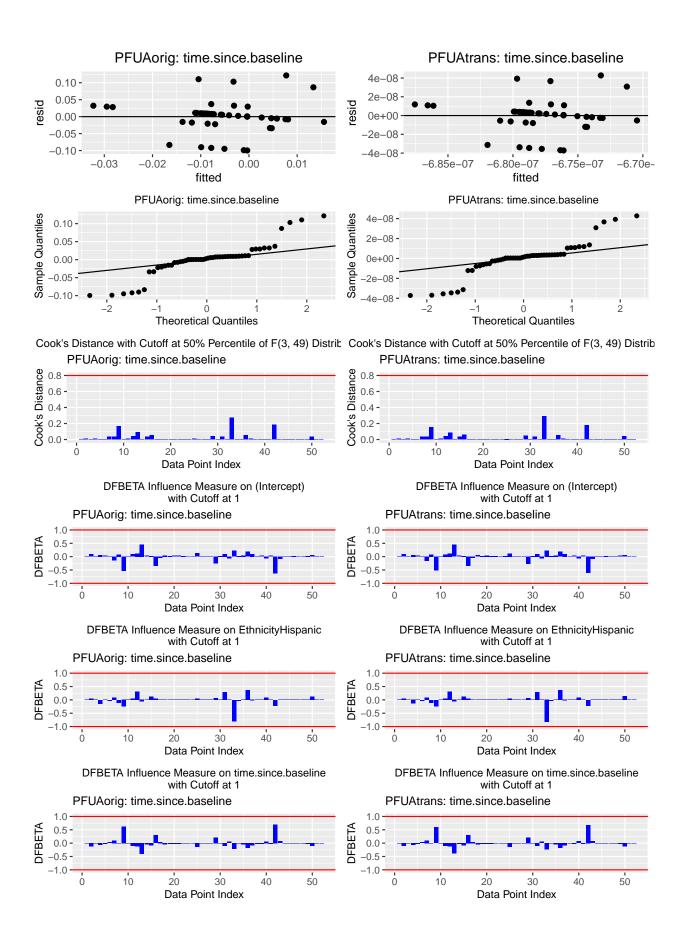


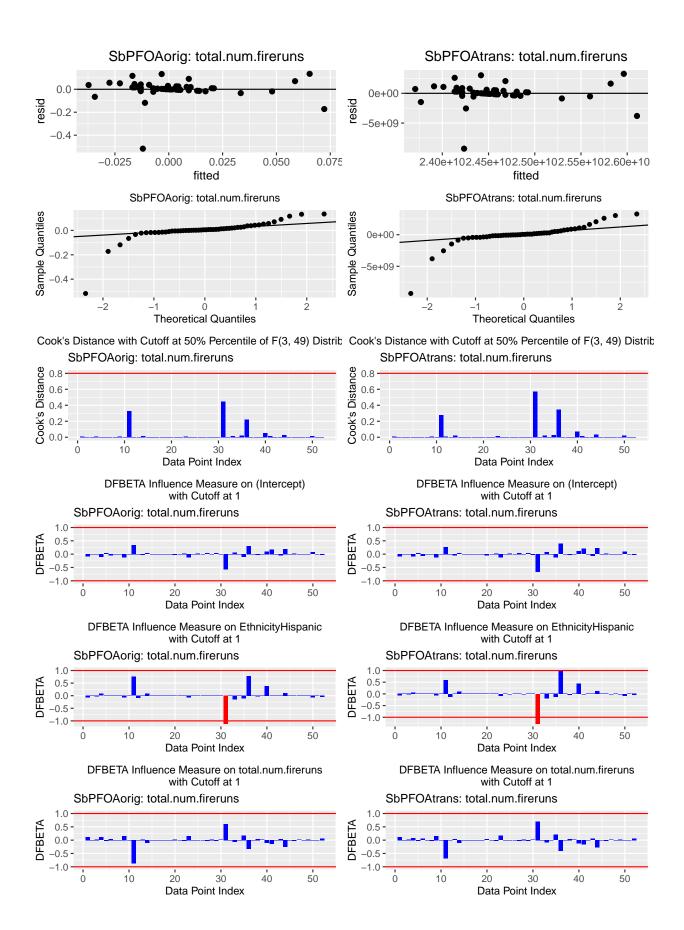


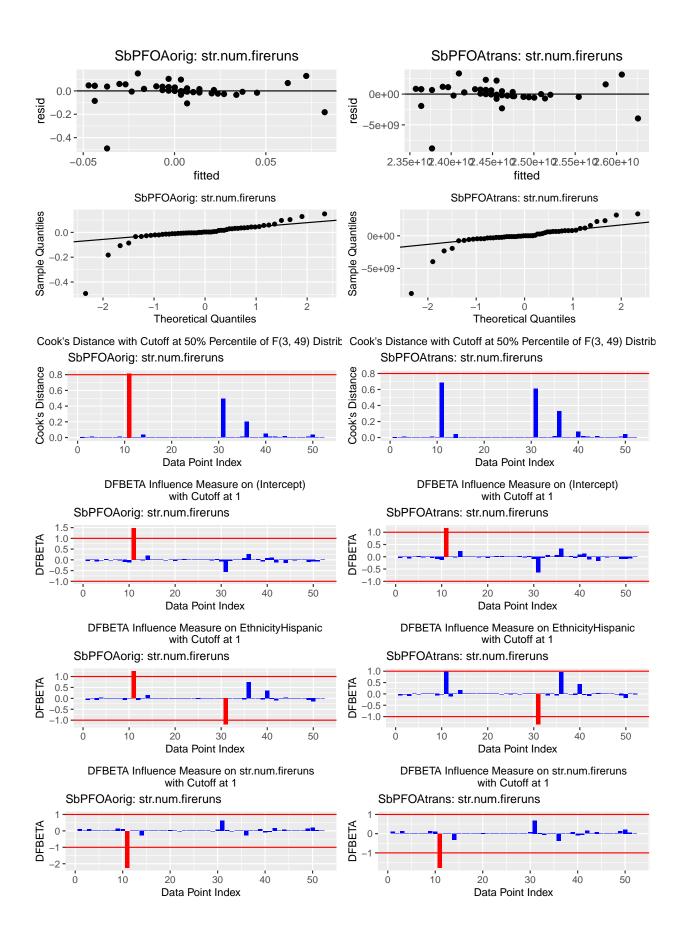


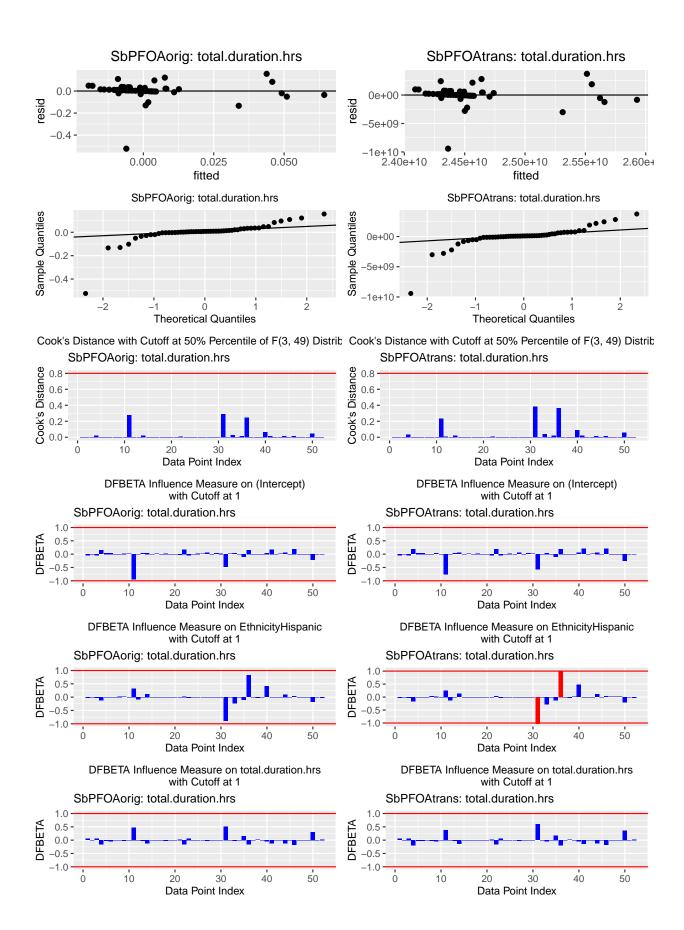


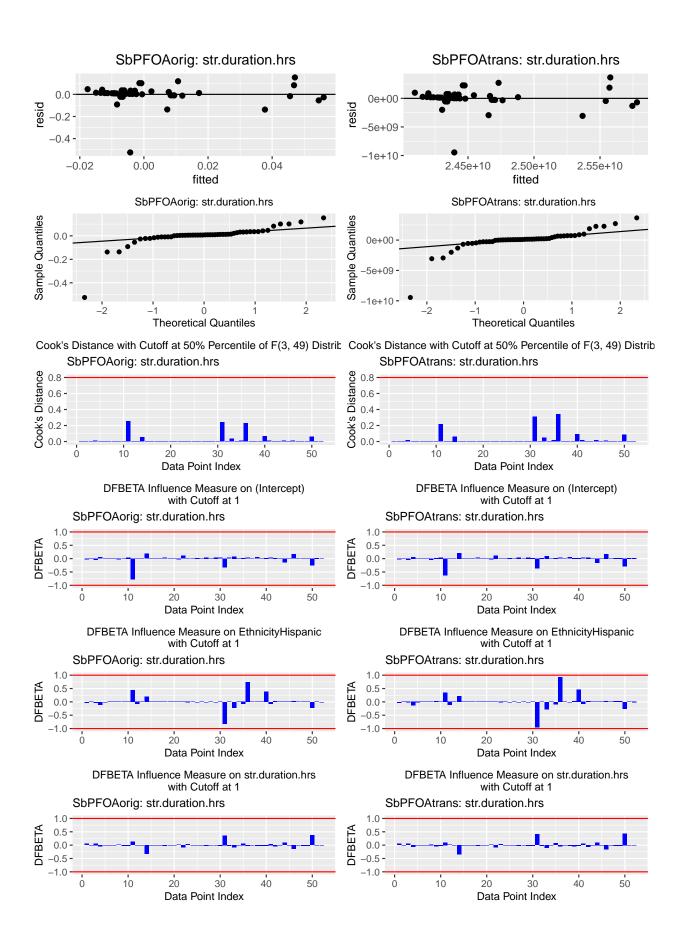


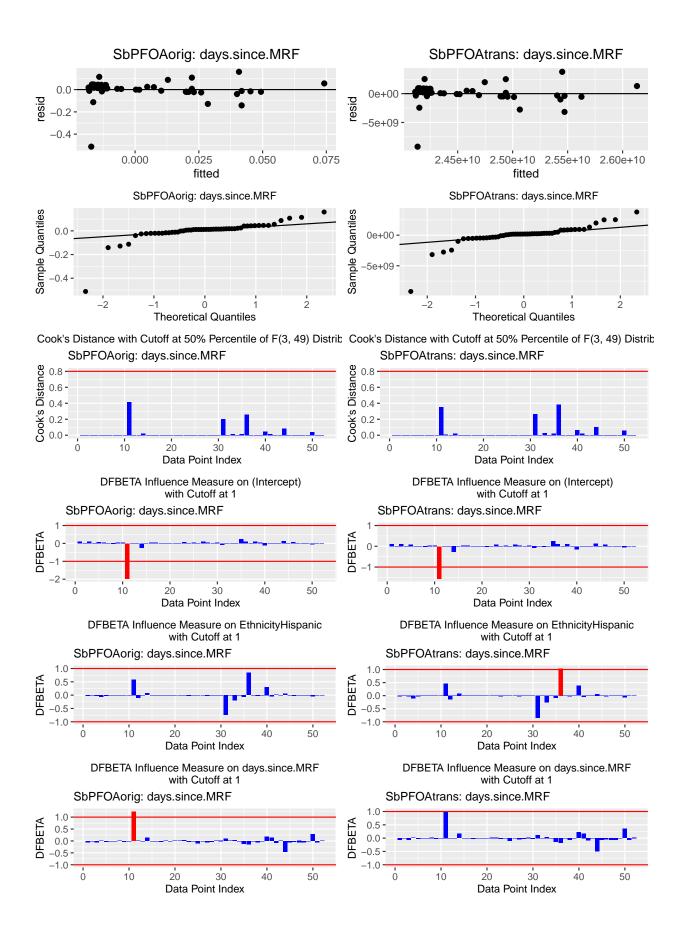


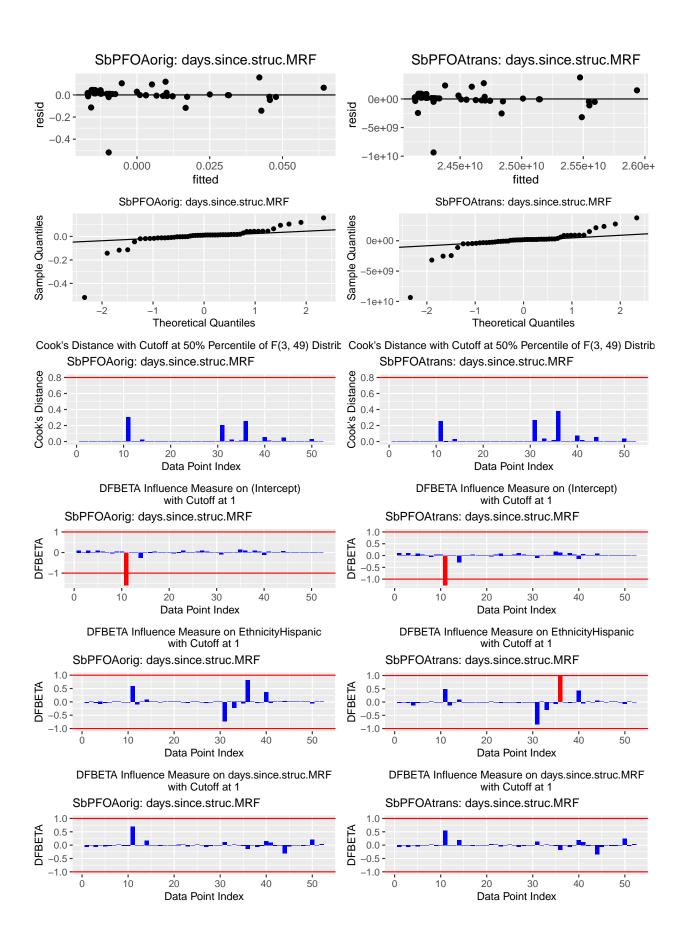


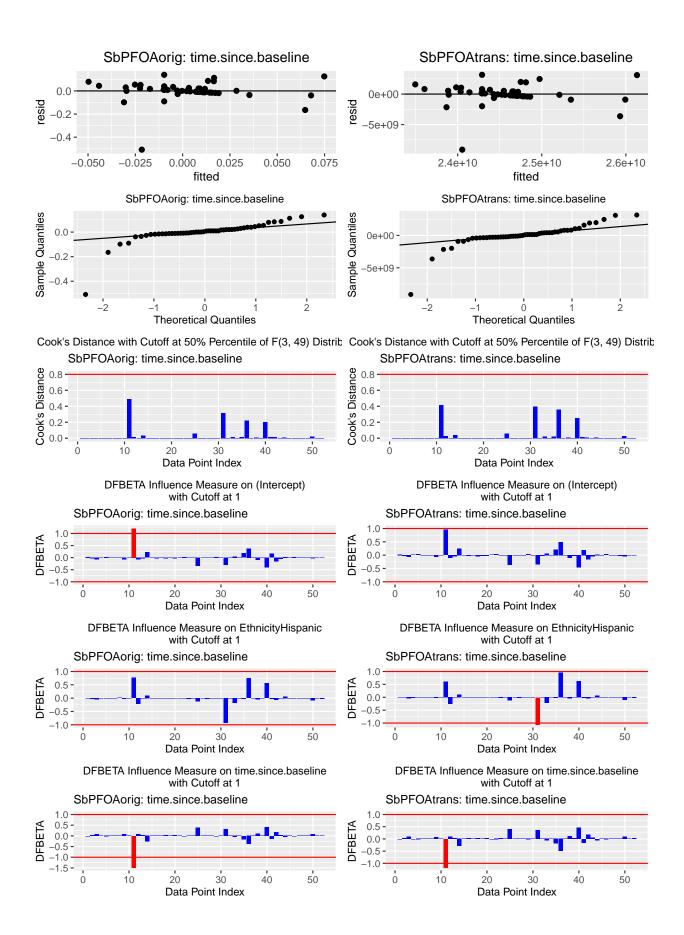


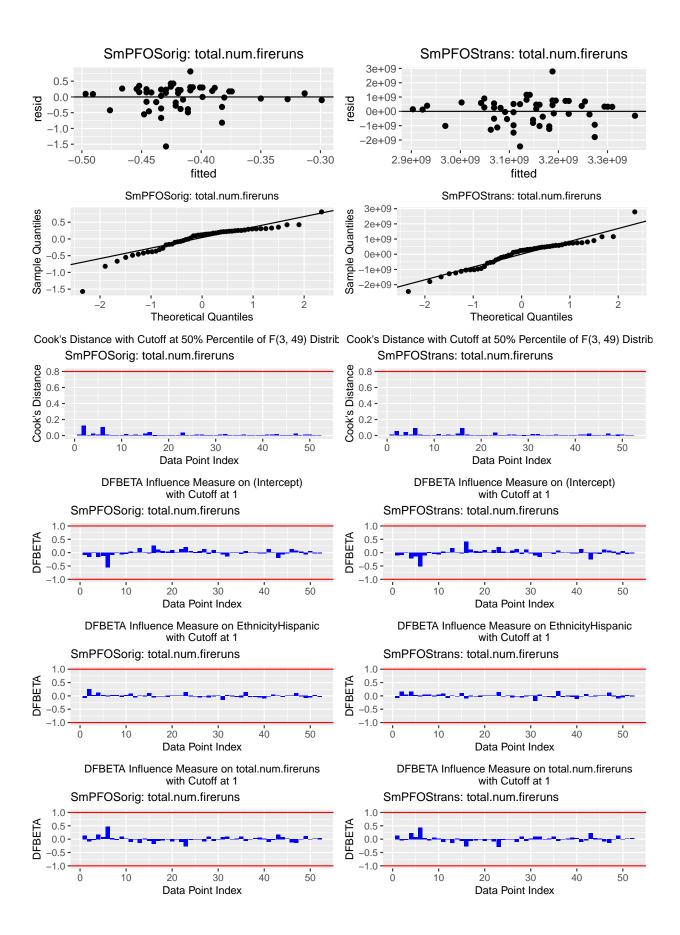


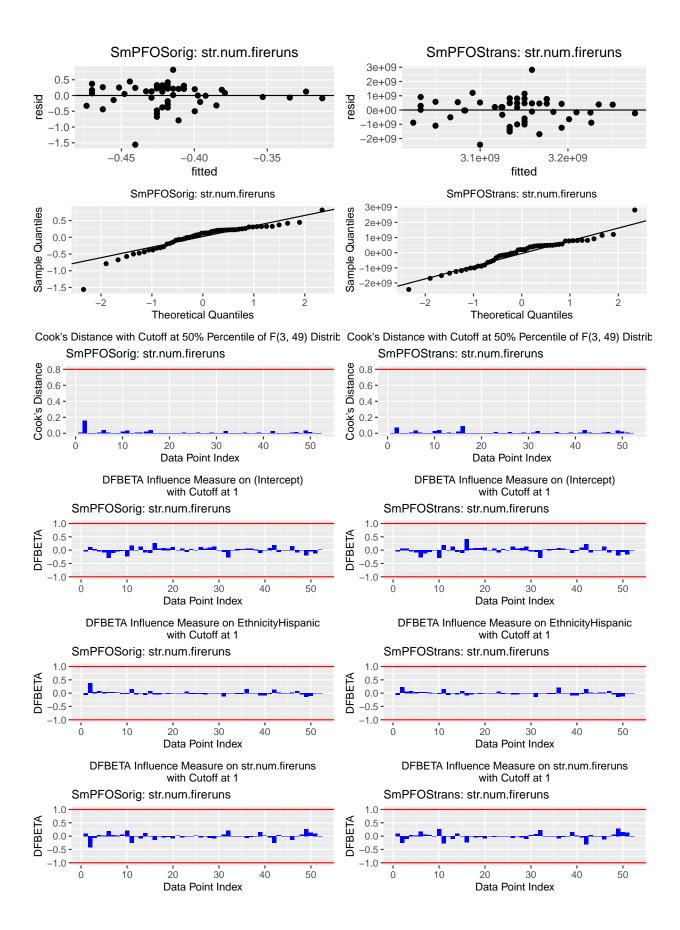


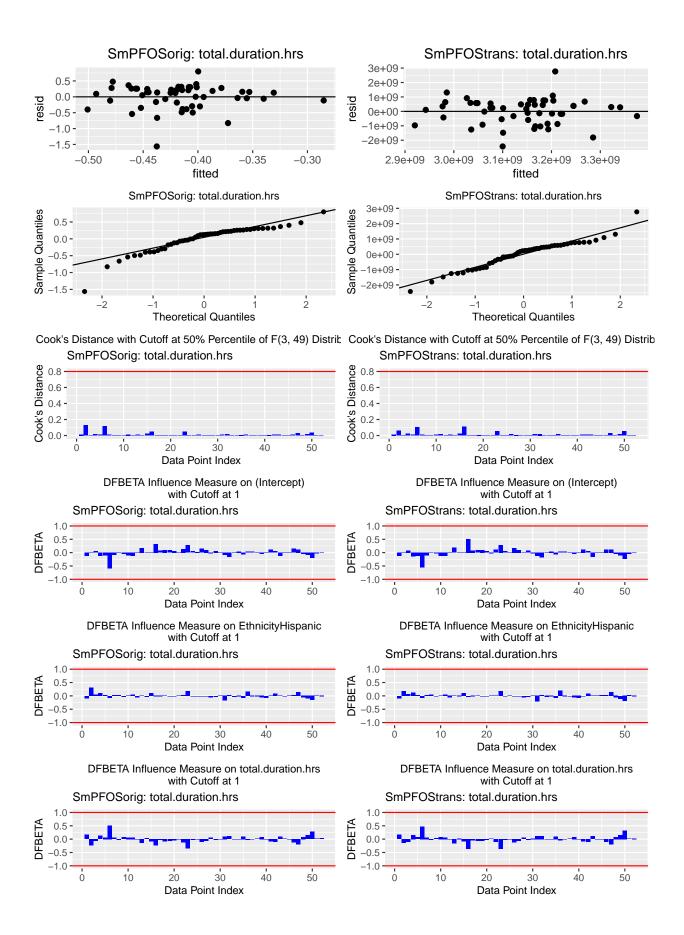


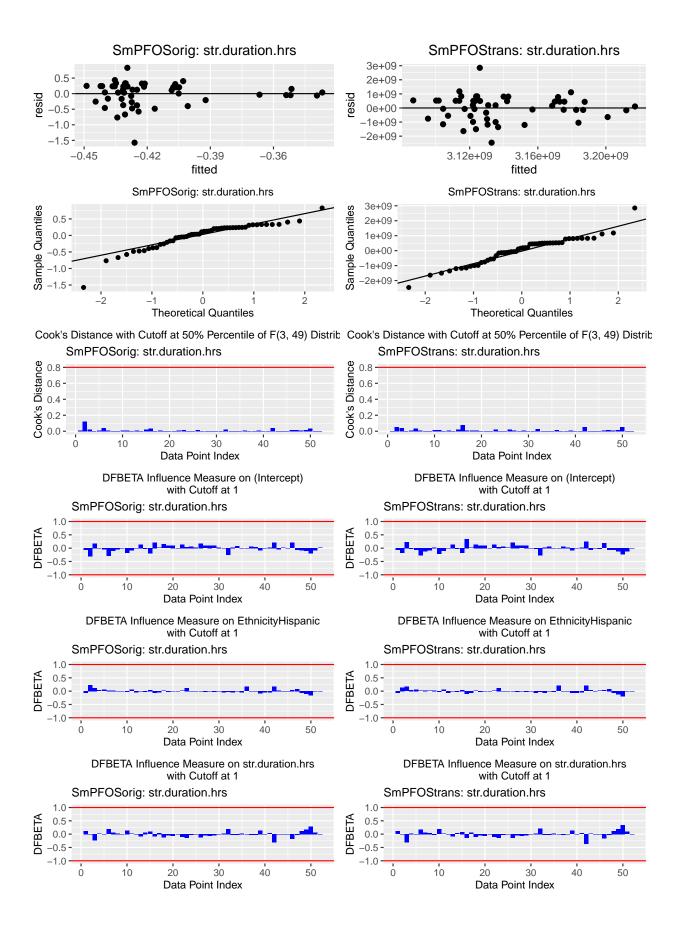


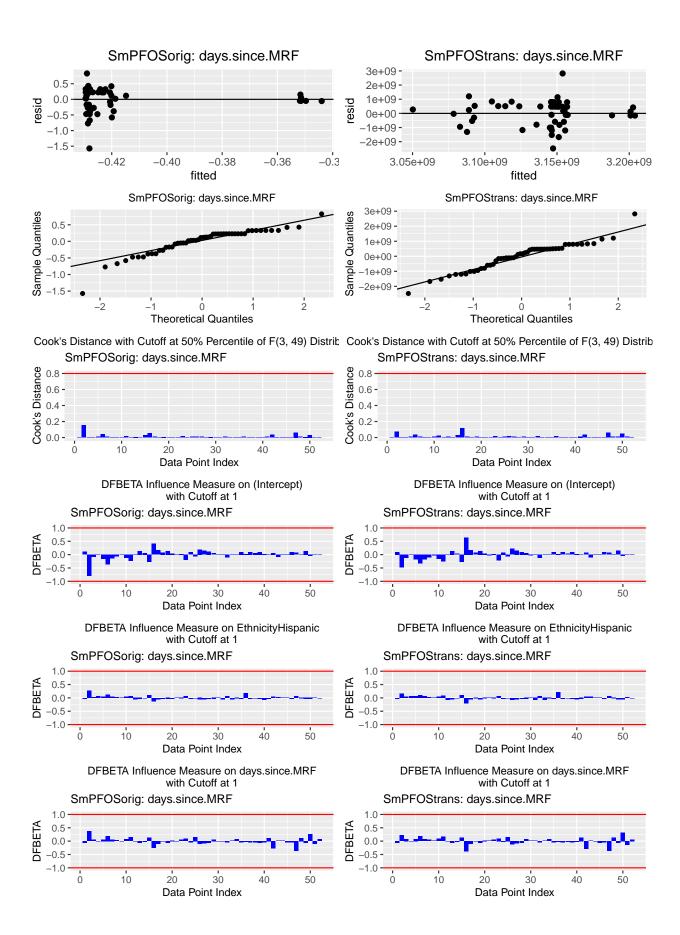


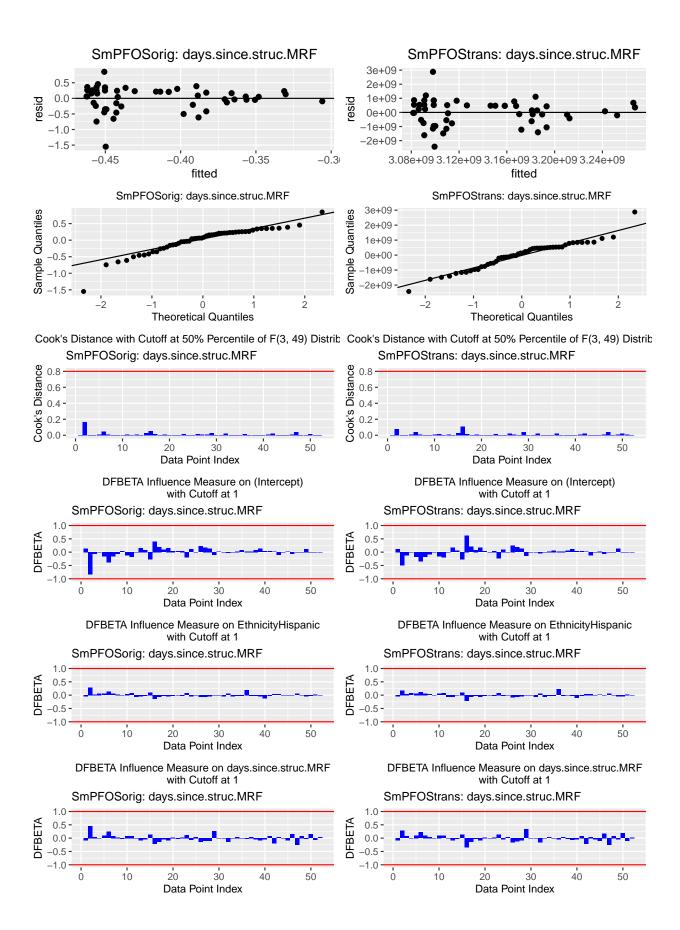


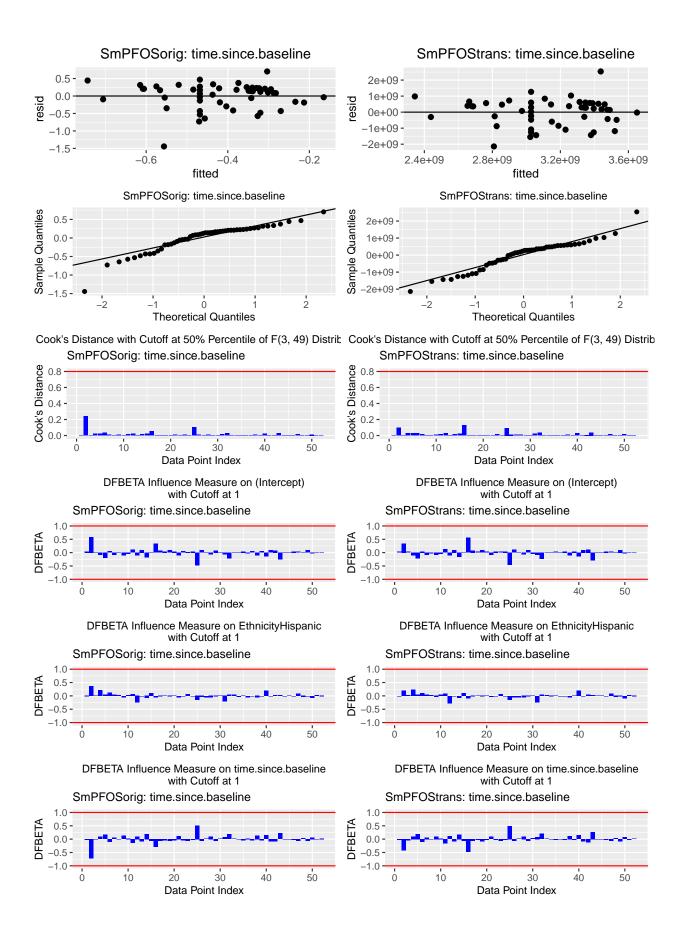












add CD plots and DFBETA plots to forloop above to keep all relevant mdls together interpret results Write function for sensitivity analyses

```
for (i in 1:length(pfas.list)) {
  pfas.name <- pfas.list[i]</pre>
  Tpfas.name <- pfastrans.list[i]</pre>
  for (fire.var in fire.list) {
    out_info <- change_plot_fxn(FireChange2, pfas.name, Tpfas.name, fire.var)</pre>
    #Cooks distance plots
    CDplots <- sapply(list(out_info$pfasmdl, out_info$transmdl), cooks_distance_plot)
    print(ggarrange(plotlist = CDplots) +
     labs(title = paste0(out_info$transmdl$terms[[2]], ": ",
                           out_info$pfasmdl$terms[[3]][2]))
  }
}
for (i in 1:length(pfas.list)) {
  pfas.name <- pfas.list[i]</pre>
  Tpfas.name <- pfastrans.list[i]</pre>
  for (fire.var in fire.list) {
    out_info <- change_plot_fxn(FireChange2, pfas.name, Tpfas.name, fire.var)</pre>
   #DFBETA plots
            fbeta1 <- fbetas_plot(out_info$pfasmdl, paste0(out_info$pfasmdl$terms[[2]], ": ",</pre>
                                              out_info$pfasmdl$terms[[3]][2]))
            fbeta2 <- fbetas_plot(out_info$transmdl, paste0(out_info$transmdl$terms[[2]], ": ",
                                              out_info$transmdl$terms[[3]][2]))
            FBplots <- list(fbeta1$`(Intercept)`$plot, fbeta1$total.num.fireruns$plot,
                  fbeta1$EthnicityHispanic$plot, fbeta2$`(Intercept)`$plot,
                  fbeta2$total.num.fireruns$plot, fbeta2$EthnicityHispanic$plot)
            print(ggarrange(plotlist = FBplots))
       }
     }
```

For every change score models, get more diagnostic information (cooks distance, and dfbetas) for both original and transformed models: https://cran.r-project.org/web/packages/olsrr/vignettes/influence_measures.html

options: get rid of a point or two, or transform. would probably prefer to transform because we can leave the point in the model. Use ggarrange to condense the output a little

- Look through residuals.
- Get rid of age and bmi from change scores.
- Add in baseline pfas to each model as follow-up as sensitivity
- add each age & bmi as sensitivity
- Take women out. Done. still need to ask Dean about this.
- We have a month.
- I should look through Amy's incumbent vs. new recruit info.
- Make sure longitudinal models are done
- need to do dichotomous models
- Think about how to control for multiple comparisons