

Code_PartB — Combined Document

CoVPN 3008 (Ubuntu Study) — Analysis Code and Figures

Compiled from recovered archive contents

Part 1 — Analysis Scripts

5 R files

CoxRegression/cox_final_primary.R

```
#####
# This file documents code that conducts a calendar-time-based Cox regression
# analysis for CoVPN 3008 Ubuntu Study (M18 Final Analysis).
#####
# Input: adtte_shuffled.sas7bdat
# Output: primary_comparison_results.csv
#####
# Load packages
library(dplyr)
library(survival)
library(splines)
library(haven)
library(lubridate)
#####
# Set the directory and load the dataset
dt = read_sas('adtte.sas7bdat')
dt1 = read.csv('ADTTE.csv')
dt_adsl = read_sas('adsl.sas7bdat')

dt_rscov = dt_adsl %>%
  dplyr::select(SUBJID, RSCOV2M6)

dt = merge(dt, dt_rscov, by = 'SUBJID')
#####
# Primary analysis I
# Analysis cohort: RM6FL == 'Y'

# ADJ
dt1_adj = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'AJ14M18') %>% # n = 3988 = 2014 Bi + 1974 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
         tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
         eventInd = 1 - CNSR,
         A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m1_adj = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
               TBM6FL + RSCOV2M6 + strata(s),
               data = dt1_adj)

# CDC
dt1_cdc = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'CD14M18') %>% # n = 3988 = 2014 Bi + 1974 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
         tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
         eventInd = 1 - CNSR,
         A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m1_cdc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
               TBM6FL + RSCOV2M6 + strata(s),
               data = dt1_cdc)
```

CoxRegression/cox_final_primary.R (cont.)

```
dt1_cdc_hybrid = dt1_cdc %>%
  filter(SCOV2M6 == 'Hybrid immunity')

m1_cdc_hybrid = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  TBM6FL + RSCOV2M6 + strata(s),
  data = dt1_cdc_hybrid)

dt1_cdc_vac = dt1_cdc %>%
  filter(SCOV2M6 == 'Vaccine immunity')

m1_cdc_vac = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  strata(s),
  data = dt1_cdc_vac)

# CDC
dt1_cdc_hybrid_vs_vaccine = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'CD14M18') %>% # n = 3988 = 2014 Bi + 1974 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  filter(TRT03A == 'Monovalent (mRNA 1273)') %>%
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
    tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
    eventInd = 1 - CNSR,
    A_dich = ifelse(SCOV2M6 == 'Hybrid immunity', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  TBM6FL + RSCOV2M6 + strata(s),
  data = dt1_cdc_hybrid_vs_vaccine)

dt1_cdc_hybrid_vs_vaccine = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'CD14M18') %>% # n = 3988 = 2014 Bi + 1974 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  #filter(TRT03A == 'Bivalent (mRNA 1273.222)') %>%
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
    tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
    eventInd = 1 - CNSR,
    A_dich = ifelse(RSCOV2M6 == 'Positive', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  TBM6FL + strata(s),
  data = dt1_cdc_hybrid_vs_vaccine)

dt1_cdc_hybrid_vs_vaccine = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'CD14M18') %>% # n = 3988 = 2014 Bi + 1974 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  filter(TRT03A == 'Bivalent (mRNA 1273.222)') %>%
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
    tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
    eventInd = 1 - CNSR,
    A_dich = ifelse(SCOV2M6 == 'Hybrid immunity', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
```

CoxRegression/cox_final_primary.R (cont.)

```
TBM6FL + RSCOV2M6 + strata(s),
data = dt1_cdc_hybrid_vs_vaccine)

#####
# Primary analysis II
# A subset of RM6 who were PP in both parts
# Analysis cohort: RM6FL == 'Y' & PPROTFL == 'Y'

# ADJ
dt2_adj = dt %>%
  filter(RM6FL == 'Y' & PPROTFL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'AJ14M18') %>% # n = 3963 = 2002 Bi + 1961 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
         tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
         eventInd = 1 - CNSR,
         A_dich = ifelse(TR03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m2_adj = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
              TBM6FL + RSCOV2M6 + strata(s),
              data = dt2_adj)

# CDC
dt2_cdc = dt %>%
  filter(RM6FL == 'Y' & PPROTFL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'CD14M18') %>% # n = 3963 = 2002 Bi + 1961 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
         tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
         eventInd = 1 - CNSR,
         A_dich = ifelse(TR03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m2_cdc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
              TBM6FL + RSCOV2M6 + strata(s),
              data = dt2_cdc)

dt2_cdc_hybrid = dt2_cdc %>%
  filter(SCOV2M6 == 'Hybrid immunity')

m2_cdc_hybrid = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
                    TBM6FL + RSCOV2M6 + strata(s),
                    data = dt2_cdc_hybrid)

dt2_cdc_vac = dt2_cdc %>%
  filter(SCOV2M6 == 'Vaccine immunity')

m2_cdc_vac = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
                  strata(s),
                  data = dt2_cdc_vac)

#####
# Collect all primary comparison results and output
print_p_val <- function(p_val) ifelse(p_val < 0.001, '< .001',
                                     round(p_val, 3))

print_res <- function(md)
  return(c(round(summary(md)$conf.int['A_dich', c('exp(coef)', 'lower .95', 'upper .95')], 2),
          print_p_val(summary(md)$coefficients['A_dich', 5])))
```

CoxRegression/cox_final_primary.R (cont.)

```
res_primary_comparison = rbind(
  print_res(m1_adj), # Primary I, AJ14M18
  print_res(m1_cdc), # Primary I, CD14M18
  print_res(m1_cdc_hybrid),
  print_res(m1_cdc_vac),
  print_res(m2_adj), # Primary II, AJ14M18
  print_res(m2_cdc), # Primary II, CD14M18
  print_res(m2_cdc_hybrid),
  print_res(m2_cdc_vac))

rownames(res_primary_comparison) = c('Primary I, AJ14M18',
                                     'Primary I, CD14M18',
                                     'Primary I, CD14M18, Hybrid',
                                     'Primary I, CD14M18, Vaccine',
                                     'Primary II, AJ14M18',
                                     'Primary II, CD14M18',
                                     'Primary II, CD14M18, Hybrid',
                                     'Primary II, CD14M18, Vaccine')

colnames(res_primary_comparison) = c('HR', 'Low', 'High', 'P-value')

# Write to dir: results/primary_comparison_results.csv
write.csv(res_primary_comparison, './results/primary_comparison_results.csv')
```

CoxRegression/cox_final_primary_anyinf.R

```
#####
# This file documents code that conducts a calendar-time-based Cox regression
# analysis for CoVPN 3008 Ubuntu Study (M18 Final Analysis).
#####
# Input: adtte_shuffled.sas7bdat
# Output: anyinf_results.csv
#####
# Load packages
library(dplyr)
library(survival)
library(splines)
library(haven)
library(lubridate)
#####
# Set the directory and load the dataset
dt = read.csv('ADTTE.csv')
dt_adsl = read_sas('adsl.sas7bdat')

dt_rscov = dt_adsl %>%
  dplyr::select(SUBJID, RSCOV2M6)

dt = merge(dt, dt_rscov, by = 'SUBJID')
#####
# Primary analysis I
# Analysis cohort: RM6FL == 'Y'

# ANYINF
dt1_subc = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'ANYINF') %>% # n = 3988 = 2014 Bi + 1974 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(TR03SDT = as.Date(TR03SDT),
         STARTDT = as.Date(STARTDT),
         ADT = as.Date(ADT)) %>%
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT, time_origin, units = 'days')),
         tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
         eventInd = 1 - CNSR,
         A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m1_subc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
               TBM6FL + RSCOV2M6 + strata(s),
               data = dt1_subc)

dt1_subc_hybrid = dt1_subc %>%
  filter(SCOV2M6 == 'Hybrid immunity')

m1_subc_hybrid = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
                      TBM6FL + RSCOV2M6 + strata(s),
                      data = dt1_subc_hybrid)

dt1_subc_vac = dt1_subc %>%
  filter(SCOV2M6 == 'Vaccine immunity')

m1_subc_vac = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
                    strata(s),
                    data = dt1_subc_vac)

#PLWoH
dt1_subc_PLWoH = dt1_subc %>%
```

CoxRegression/cox_final_primary_anyinf.R (cont.)

```
filter(AGRP1N == 3 | AGRP1N == 4)

m1_subc_PLWoH = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX + RSCOV2M6 +
  strata(s),
  data = dt1_subc_PLWoH)

#PLWH
dt1_subc_PLWH = dt1_subc %>%
  filter(AGRP1N == 1 | AGRP1N == 2)

m1_subc_PLWH = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  TBM6FL + RSCOV2M6 + CD4B2GR1 + HIVDETL2 + strata(s),
  data = dt1_subc_PLWH)

#####
# Primary analysis II
# A subset of RM6 who were PP in both parts
# Analysis cohort: RM6FL == 'Y' & PPROTFL == 'Y'

# CDC
dt2_subc = dt %>%
  filter(RM6FL == 'Y' & PPROTFL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'ANYINF') %>% # n = 3988 = 2014 Bi + 1974 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(TR03SDT = as.Date(TR03SDT),
    STARTDT = as.Date(STARTDT),
    ADT = as.Date(ADT)) %>%
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT, time_origin, units = 'days')),
    tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
    eventInd = 1 - CNSR,
    A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m2_subc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  TBM6FL + RSCOV2M6 + strata(s),
  data = dt2_subc)

dt2_subc_hybrid = dt2_subc %>%
  filter(SCOV2M6 == 'Hybrid immunity')

m2_subc_hybrid = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  TBM6FL + RSCOV2M6 + strata(s),
  data = dt2_subc_hybrid)

dt2_subc_vac = dt2_subc %>%
  filter(SCOV2M6 == 'Vaccine immunity')

m2_subc_vac = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  strata(s),
  data = dt2_subc_vac)

#PLWoH
dt2_subc_PLWoH = dt2_subc %>%
  filter(AGRP1N == 3 | AGRP1N == 4)

m2_subc_PLWoH = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX + RSCOV2M6 +
  strata(s),
  data = dt2_subc_PLWoH)

#PLWH
dt2_subc_PLWH = dt2_subc %>%
```

CoxRegression/cox_final_primary_anyinf.R (cont.)

```
filter(AGRP1N == 1 | AGRP1N == 2)

m2_subc_PLWH = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
                    TBM6FL + RSCOV2M6 + CD4B2GR1 + HIVDETBL2 +strata(s),
                    data = dt2_subc_PLWH)

#####
# Collect all primary comparison results and output
print_p_val <- function(p_val) ifelse(p_val < 0.001, '< .001',
                                     round(p_val, 3))

print_res <- function(md)
  return(c(round(summary(md)$conf.int['A_dich', c('exp(coef)', 'lower .95', 'upper .95')], 2),
          print_p_val(summary(md)$coefficients['A_dich', 5])))

res_primary_comparison = rbind(
  print_res(m1_subc), # ANYINF FM6
  print_res(m1_subc_hybrid),
  print_res(m1_subc_vac),
  print_res(m1_subc_PLWoH),
  print_res(m1_subc_PLWH),
  print_res(m2_subc), # ANYINF PP
  print_res(m2_subc_hybrid),
  print_res(m2_subc_vac),
  print_res(m2_subc_PLWoH),
  print_res(m2_subc_PLWH))

rownames(res_primary_comparison) = c('FM6, ANYINF',
                                     'FM6, ANYINF, Hybrid',
                                     'FM6, ANYINF, Vaccine',
                                     'FM6, ANYINF, PLWoH',
                                     'FM6, ANYINF, PLWH',
                                     'PP, ANYINF',
                                     'PP, ANYINF, Hybrid',
                                     'PP, ANYINF, Vaccine',
                                     'PP, ANYINF, PLWoH',
                                     'PP, ANYINF, PLWH')

colnames(res_primary_comparison) = c('HR', 'Low', 'High', 'P-value')

# Write to dir: results/primary_comparison_results.csv
write.csv(res_primary_comparison, './results/anyinf_results.csv')
```

CoxRegression/cox_final_primary_subc.R

```
#####
# This file documents code that conducts a calendar-time-based Cox regression
# analysis for CoVPN 3008 Ubuntu Study (M18 Final Analysis).
#####
# Input: adtte_shuffled.sas7bdat
# Output: asymp_results.csv
#####
# Load packages
library(dplyr)
library(survival)
library(splines)
library(haven)
library(lubridate)
#####
# Set the directory and load the dataset
dt = read.csv('ADTTE.csv')
dt_adsl = read_sas('adsl.sas7bdat')

dt_rscov = dt_adsl %>%
  dplyr::select(SUBJID, RSCOV2M6)

dt = merge(dt, dt_rscov, by = 'SUBJID')
#####
# Primary analysis I
# Analysis cohort: RM6FL == 'Y'

# Subclinical
dt1_subc = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'SUBCINF') %>% # n = 3988 = 2014 Bi + 1974 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(TR03SDT = as.Date(TR03SDT),
         STARTDT = as.Date(STARTDT),
         ADT = as.Date(ADT)) %>%
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT, time_origin, units = 'days')),
         tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
         eventInd = 1 - CNSR,
         A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m1_subc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
               TBM6FL + RSCOV2M6 + strata(s),
               data = dt1_subc)

dt1_subc_hybrid = dt1_subc %>%
  filter(SCOV2M6 == 'Hybrid immunity')

m1_subc_hybrid = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
                      TBM6FL + RSCOV2M6 + strata(s),
                      data = dt1_subc_hybrid)

dt1_subc_vac = dt1_subc %>%
  filter(SCOV2M6 == 'Vaccine immunity')

m1_subc_vac = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
                    strata(s),
                    data = dt1_subc_vac)

#PLWoH
dt1_subc_PLWoH = dt1_subc %>%
```

CoxRegression/cox_final_primary_subc.R (cont.)

```
filter(AGRP1N == 3 | AGRP1N == 4)

m1_subc_PLWoH = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX + RSCOV2M6 +
  strata(s),
  data = dt1_subc_PLWoH)

#PLWH
dt1_subc_PLWH = dt1_subc %>%
  filter(AGRP1N == 1 | AGRP1N == 2)

m1_subc_PLWH = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  TBM6FL + RSCOV2M6 + CD4B2GR1 + HIVDETL2 + strata(s),
  data = dt1_subc_PLWH)

#####
# Primary analysis II
# A subset of RM6 who were PP in both parts
# Analysis cohort: RM6FL == 'Y' & PPROTFL == 'Y'

# CDC
dt2_subc = dt %>%
  filter(RM6FL == 'Y' & PPROTFL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'SUBCINF') %>% # n = 3988 = 2014 Bi + 1974 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(TR03SDT = as.Date(TR03SDT),
    STARTDT = as.Date(STARTDT),
    ADT = as.Date(ADT)) %>%
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT, time_origin, units = 'days')),
    tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
    eventInd = 1 - CNSR,
    A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m2_subc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  TBM6FL + RSCOV2M6 + strata(s),
  data = dt2_subc)

dt2_subc_hybrid = dt2_subc %>%
  filter(SCOV2M6 == 'Hybrid immunity')

m2_subc_hybrid = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  TBM6FL + RSCOV2M6 + strata(s),
  data = dt2_subc_hybrid)

dt2_subc_vac = dt2_subc %>%
  filter(SCOV2M6 == 'Vaccine immunity')

m2_subc_vac = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  strata(s),
  data = dt2_subc_vac)

#PLWoH
dt2_subc_PLWoH = dt2_subc %>%
  filter(AGRP1N == 3 | AGRP1N == 4)

m2_subc_PLWoH = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX + RSCOV2M6 +
  strata(s),
  data = dt2_subc_PLWoH)

#PLWH
dt2_subc_PLWH = dt2_subc %>%
```

CoxRegression/cox_final_primary_subc.R (cont.)

```
filter(AGRP1N == 1 | AGRP1N == 2)

m2_subc_PLWH = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
                    TBM6FL + RSCOV2M6 + CD4B2GR1 + HIVDETBL2 +strata(s),
                    data = dt2_subc_PLWH)

#####
# Collect all primary comparison results and output
print_p_val <- function(p_val) ifelse(p_val < 0.001, '< .001',
                                       round(p_val, 3))

print_res <- function(md)
  return(c(round(summary(md)$conf.int['A_dich', c('exp(coef)', 'lower .95', 'upper .95')], 2),
          print_p_val(summary(md)$coefficients['A_dich', 5])))

res_primary_comparison = rbind(
  print_res(m1_subc), # Subclinical FM6
  print_res(m1_subc_hybrid),
  print_res(m1_subc_vac),
  print_res(m1_subc_PLWoH),
  print_res(m1_subc_PLWH),
  print_res(m2_subc), # Subclinical PP
  print_res(m2_subc_hybrid),
  print_res(m2_subc_vac),
  print_res(m2_subc_PLWoH),
  print_res(m2_subc_PLWH))

rownames(res_primary_comparison) = c('FM6, Subclinical',
                                     'FM6, Subclinical, Hybrid',
                                     'FM6, Subclinical, Vaccine',
                                     'FM6, Subclinical, PLWoH',
                                     'FM6, Subclinical, PLWH',
                                     'PP, Subclinical',
                                     'PP, Subclinical, Hybrid',
                                     'PP, Subclinical, Vaccine',
                                     'PP, Subclinical, PLWoH',
                                     'PP, Subclinical, PLWH')

colnames(res_primary_comparison) = c('HR', 'Low', 'High', 'P-value')

# Write to dir: results/primary_comparison_results.csv
write.csv(res_primary_comparison, './results/asypm_results.csv')
```

CoxRegression/cox_final_secondary.R

```
#####
# This file documents code that conducts a calendar-time-based Cox regression
# analysis for CoVPN 3008 Ubuntu Study (M18 Final Analysis).
# The analysis in this file considers the following secondary analyses:
# 1. Comparing CDC and COVE endpoints (AJ1M18/CD1M18) among monovalent and bivalent ppts in RM6
# 3. Comparing CDC and COVE endpoints (AJ14M18/CD14M18) among monovalent and
#    bivalent ppts in PLWH/PLWoH ppts in RM6
# 4. Comparing CDC and COVE endpoints (AJ1M18/CD1M18) among monovalent and
#    bivalent ppts in PLWH/PLWoH ppts in RM6
# 5. Comparing CDC and COVE endpoints (AJ14M18/CD14M18) among monovalent and
#    bivalent ppts in PLWH/PLWoH ppts in FPP

# Note:
# A total of 3 severe endpoints so secondary analysis 2 is canceled
# Fewer than 10 ADJ endpoints so only focus on CDC endpoints
#####
# Input: adtte_shuffled.sas7bdat
# Output: secondary_comparison_results.csv
#####
# Load packages
library(dplyr)
library(survival)
library(splines)
library(haven)
library(lubridate)
#####
# Set the directory and load the dataset
dt = read_sas('adtte.sas7bdat')
dt_adsl = read_sas('adsl.sas7bdat')

dt_rscov = dt_adsl %>%
  dplyr::select(SUBJID, RSCOV2M6)

dt = merge(dt, dt_rscov, by = 'SUBJID')
#####
# Secondary analysis I
# Analysis cohort: RM6FL == 'Y'
# Counting from M6 vaccination

# CDC
dt1_cdc = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(PARAMCD == 'CD1M18') %>% # n = 3988 = 2014 Bi + 1974 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT, time_origin, units = 'days')),
         tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
         eventInd = 1 - CNSR,
         A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m1_cdc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
               TBM6FL + RSCOV2M6 + strata(s),
               data = dt1_cdc)

#####
# Secondary analysis III
# Analysis cohort: RM6FL == 'Y'
# PLWH

# CDC
dt3_PLWH_cdc = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(AGRP1N == 1 | AGRP1N == 2) %>%
```

CoxRegression/cox_final_secondary.R (cont.)

```
filter(PARAMCD == 'CD14M18') %>% # n = 3963 = 2002 Bi + 1961 Mono
filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
mutate(time_origin = min(TR03SDT)) %>%
mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
       tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
       eventInd = 1 - CNSR,
       A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
filter(tstop > tstart) %>%
mutate(s = paste0(AGRP1N, "_", REGION))

m3_PLWH_cdc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
                  TBM6FL + RSCOV2M6 + CD4B2GR1 + HIVDETL2 +strata(s),
                  data = dt3_PLWH_cdc)

# PLWoH
# CDC
dt3_PLWoH_cdc = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(AGRP1N == 3 | AGRP1N == 4) %>%
  filter(PARAMCD == 'CD14M18') %>% # n = 3963 = 2002 Bi + 1961 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
         tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
         eventInd = 1 - CNSR,
         A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m3_PLWoH_cdc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX + RSCOV2M6 +
                  strata(s), # no event in TBM6FL == 1 group
                  data = dt3_PLWoH_cdc)

#####
# Secondary analysis IV
# Analysis cohort: RM6FL == 'Y'
# Counting from M6
# PLWH
# CDC
dt4_PLWH_cdc = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(AGRP1N == 1 | AGRP1N == 2) %>%
  filter(PARAMCD == 'CD1M18') %>% # n = 3963 = 2002 Bi + 1961 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT, time_origin, units = 'days')),
         tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
         eventInd = 1 - CNSR,
         A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m4_PLWH_cdc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
                  TBM6FL + RSCOV2M6 + CD4B2GR1 + HIVDETL2 +strata(s),
                  data = dt4_PLWH_cdc)

# PLWoH
# CDC
dt4_PLWoH_cdc = dt %>%
  filter(RM6FL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(AGRP1N == 3 | AGRP1N == 4) %>%
  filter(PARAMCD == 'CD1M18') %>% # n = 3963 = 2002 Bi + 1961 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT, time_origin, units = 'days')),
```

CoxRegression/cox_final_secondary.R (cont.)

```
tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
eventInd = 1 - CNSR,
A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
filter(tstop > tstart) %>%
mutate(s = paste0(AGRP1N, "_", REGION))

m4_PLWoH_cdc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX + RSCOV2M6 +
  strata(s),
  data = dt4_PLWoH_cdc)

#####
# Secondary analysis V
# Analysis cohort: RM6FL == 'Y' & PPROTFL == 'Y'

# PLWH
# CDC
dt5_PLWH_cdc = dt %>%
  filter(RM6FL == 'Y' & PPROTFL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(AGRP1N == 1 | AGRP1N == 2) %>%
  filter(PARAMCD == 'CD14M18') %>% # n = 3963 = 2002 Bi + 1961 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
    tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
    eventInd = 1 - CNSR,
    A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m5_PLWH_cdc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX +
  TBM6FL + RSCOV2M6 + CD4B2GR1 + HIVDETL2 + strata(s),
  data = dt5_PLWH_cdc)

# PLWoH
# CDC
dt5_PLWoH_cdc = dt %>%
  filter(RM6FL == 'Y' & PPROTFL == 'Y') %>%
  filter(!is.na(AGRP1N)) %>%
  filter(AGRP1N == 3 | AGRP1N == 4) %>%
  filter(PARAMCD == 'CD14M18') %>% # n = 3963 = 2002 Bi + 1961 Mono
  filter(!is.na(TR03SDT)) %>% # A person needs to receive a M6 booster shot
  mutate(time_origin = min(TR03SDT)) %>%
  mutate(tstart = as.numeric(difftime(STARTDT + days(14), time_origin, units = 'days')),
    tstop = as.numeric(difftime(ADT, time_origin, units = 'days')),
    eventInd = 1 - CNSR,
    A_dich = ifelse(TRT03A == 'Bivalent (mRNA 1273.222)', 1, 0)) %>% # A = 1 if bivalent
  filter(tstop > tstart) %>%
  mutate(s = paste0(AGRP1N, "_", REGION))

m5_PLWoH_cdc = coxph(Surv(tstart, tstop, eventInd) ~ A_dich + SEX + RSCOV2M6 +
  strata(s), # no event in TBM6FL == 1 group
  data = dt5_PLWoH_cdc)

#####
# Collect all primary comparison results and output
print_p_val <- function(p_val) ifelse(p_val < 0.001, '< .001',
  round(p_val, 3))

print_res <- function(md)
  return(c(round(summary(md)$conf.int['A_dich', c('exp(coef)', 'lower .95', 'upper .95')], 2),
    print_p_val(summary(md)$coefficients['A_dich', 5])))

res_secondary_comparison = rbind(
  print_res(m1_cdc), # Secondary I, CD1M18, RM6
  print_res(m3_PLWH_cdc), # Secondary III, CD14M18, PLWH, RM6
  print_res(m3_PLWoH_cdc), # Secondary III, CD14M18, PLWoH, RM6
  print_res(m4_PLWH_cdc), # Secondary IV, CD1M18, PLWH, RM6
```

CoxRegression/cox_final_secondary.R (cont.)

```
print_res(m4_PLWoH_cdc), # Secondary IV, CD1M18, PLWoH, RM6
print_res(m5_PLWH_cdc), # Secondary V, CD14M18, PLWH, FPP
print_res(m5_PLWoH_cdc) # Secondary V, CD14M18, PLWoH, FPP
)

rownames(res_secondary_comparison) = c('Secondary I',
                                       'Secondary III, PLWH',
                                       'Secondary III, PLWoH',
                                       'Secondary IV, PLWH',
                                       'Secondary IV, PLWoH',
                                       'Secondary V, PLWH',
                                       'Secondary V, PLWoH')

colnames(res_secondary_comparison) = c('HR', 'Low', 'High', 'P-value')

# Write to dir: results/primary_comparison_results.csv
write.csv(res_secondary_comparison, './results/secondary_comparison_results.csv')
```

CumulativeIncidence/AddlDescriptives_PostM6.R

```
require(haven)
source("/Volumes/trials/covpn/p3008/analysis/manuscripts/postM6/CumulativeIncidence/CFSurv_PostM6.R")
source("/Volumes/trials/covpn/p3008/analysis/manuscripts/postM6/CumulativeIncidence/confbandhazplusindiv_
v2.R")

path.adtte <- "/Volumes/trials/covpn/p3008/analysis/adata/SCHARP ADaM/postM6/06FEB2024/adtte.sas7bdat"
path.ads1 <- "/Volumes/trials/covpn/p3008/analysis/adata/SCHARP ADaM/postM6/06FEB2024/ads1.sas7bdat"

dat.adrisk <- as.data.frame(read_sas(path.adtte))
dat.adtte <- as.data.frame(read_sas(path.ads1))

## Target population: Participants randomized to monovalent or bivalent under Protocol Version 6 (RM6)
## Endpoint: COVE-/CDC-based COVID-19 endpoints counted 14 days after M6 vaccination (Note -- too few COV
E cases)
## Time frame: 13 days post M6 vaccination to M12/M18 visit

sub.dat.adrisk <- subset(dat.adrisk,
                        PARAMCD == "CD14M12" &
                        RM6FL == "Y")
sub.ids <- sub.dat.adrisk$SUBJID
sub.dat.adtte <- dat.adtte[dat.adtte$SUBJID %in% sub.ids,]

sub.dat.adrisk <- sub.dat.adrisk[order(sub.dat.adrisk$SUBJID),]
sub.dat.adtte <- sub.dat.adtte[order(sub.dat.adtte$SUBJID),]

A <- ifelse(sub.dat.adrisk$TRT03A == "Bivalent (mRNA 1273.222)", 1, 0)
time <- sub.dat.adrisk$AVAL
event <- 1 - sub.dat.adrisk$CNSR # need
W <- cbind(ifelse(sub.dat.adrisk$SGRPN == 1, 1, 0),
           ifelse(sub.dat.adrisk$SGRPN == 2, 1, 0),
           ifelse(sub.dat.adrisk$SGRPN == 3, 1, 0),
           ifelse(sub.dat.adrisk$SGRPN == 4, 1, 0),
           ifelse(sub.dat.adtte$RSCOV2M6 == "Positive", 1, 0))

t0 <- max(time[event == 1])

text.add <- "HR = 1.00 (95% CI: [0.69, 1.45])"
fit.rm6.cdc14m12 <- CumulativeIncidenceFit(event = event, time = time, A = A, W = W,
                                           t0 = t0, fit.times = seq(1, t0, 1), np = FALSE,
                                           randomized = TRUE)
out.rm6.cdc14m12 <- CumulativeIncidenceSummary(time = time, event = event, W = W,
                                              A = A, t0 = t0, fit = fit.rm6.cdc14m12, comp = " ",
                                              t.start = 30, label = "COVID-19 incidence over study time"
,
                                              path.suffix = "MB_BB_RM6_CDC14M12_Primary_Max_t0",
                                              tx0.label = "Monovalent M6 booster",
                                              tx1.label = "Bivalent M6 booster",
                                              tx0.label2 = "Monovalent",
                                              tx1.label2 = "Bivalent",
                                              time.axis.label = "Time (Days, starting 13 days after M6 b
ooster)",
                                              y.axis.bound.risk = .08,
                                              override.t0 = TRUE, text.add = text.add)

tmin <- 1 #min(time[event == 1])
tmax <- 165 #max(time[event == 1])
ngrid <- 100
band11 <- (tmax - tmin)/2
band2 <- band1 <- 0
biasadjust <- tails1 <- tailsu <- TRUE
Nv <- 0

hazFit <- Confbandhazplusindiv(time = time, delta = event, Rx = A + 1, N = 10000,
                              Ngraph=0, u1=tmin, u2=tmax,
                              t1 = tmin, t2 = tmax, band11, ngrid, band1, band2,
                              bandpool = 0, numband = 1, biasadjust, tails1, tailsu, Nv)
```

CumulativeIncidence/AddlDescriptives_PostM6.R (cont.)

```
#plot the hazard for the treatment group
Fit.0 <- hazFit[[2]]
timeGrid.0 <- Fit.0[,1]
haz.0 <- Fit.0[, 2]
ptLB.0 <- pmax(Fit.0[, 3], 0)
ptUB.0 <- Fit.0[, 4]
smLB.0 <- pmax(Fit.0[, 5], 0)
smUB.0 <- Fit.0[, 6]

Fit.1 <- hazFit[[3]]
timeGrid.1 <- Fit.1[,1]
haz.1 <- Fit.1[, 2]
ptLB.1 <- pmax(Fit.1[, 3], 0)
ptUB.1 <- Fit.1[, 4]
smLB.1 <- pmax(Fit.1[, 5], 0)
smUB.1 <- Fit.1[, 6]

path <- "/Volumes/trials/covpn/p3008/analysis/manuscripts/postM6/CumulativeIncidence/Figures/hazard_MB_BB
_RM6_CDC14M12.pdf"

pdf(file = path)
par(las=1, cex.axis=.8, cex.lab=1.35, tcl= -0.35, mar=c(8, 6.25, 6, 0.5),
    oma = c(2, 1, 1, 1), mgp = c(2.3, 0.5, 0))

plot(c(timeGrid.0, timeGrid.1), c(haz.0, haz.1),
     xlab="Time (Days, starting 13 days after M6 vaccination)",
     ylab="Hazard", type="n", bty="l",
     main="Hazard over study time",
     ylim = c(min(c(smLB.0, smLB.1)), max(c(smUB.0, smUB.1))))
lines(timeGrid.0, haz.0, lwd=3.5, col = "#F2502A")
# lines(timeGrid.0, ptLB.0, lty="dashed", lwd=3, col = "#F2502A")
# lines(timeGrid.0, ptUB.0, lty="dashed", lwd=3, col = "#F2502A")
lines(timeGrid.0, smLB.0, lty="dashed", lwd=3, col = "#F2502A")
lines(timeGrid.0, smUB.0, lty="dashed", lwd=3, col = "#F2502A")

lines(timeGrid.1, haz.1, lwd=3.5, col = "blue")
# lines(timeGrid.1, ptLB.1, lty="dashed", lwd=3, col = "blue")
# lines(timeGrid.1, ptUB.1, lty="dashed", lwd=3, col = "blue")
lines(timeGrid.1, smLB.1, lty="dashed", lwd=3, col = "blue")
lines(timeGrid.1, smUB.1, lty="dashed", lwd=3, col = "blue")

legend("topleft", legend=c("Monovalent", "Bivalent"), cex=1, lwd=3,
     lty=c(1, 1), bty="n", x.intersp=0.7,
     col = c("#F2502A", "blue"))

dev.off()

sum(1 - subset(dat.adrisk, PARAMCD == "CD14M12" & RM6FL == "Y")$CNSR)
sum(1 - subset(dat.adrisk, PARAMCD == "AJ14M12" & RM6FL == "Y")$CNSR)
sum(1 - subset(dat.adrisk, PARAMCD == "SAJ14M12" & RM6FL == "Y")$CNSR)

#####
path <- "/Volumes/trials/covpn/p3008/analysis/manuscripts/postM6/CumulativeIncidence/Figures/hazard_MB_BB
_RM6_CDC14M12_preDec15.pdf"

pdf(file = path)
par(las=1, cex.axis=.8, cex.lab=1.35, tcl= -0.35, mar=c(8, 6.25, 6, 0.5),
    oma = c(2, 1, 1, 1), mgp = c(2.3, 0.5, 0))

m6dt <- as.Date(sub.dat.adrisk$TR03SDT)
hazFit.preDec15 <- Confbandhazplusindiv(time = time[m6dt <= as.Date("2022-12-15")],
    delta = event[m6dt <= as.Date("2022-12-15")],
    Rx = A[m6dt <= as.Date("2022-12-15")] + 1, N = 10000,
    Ngraph=0, u1=tmin, u2=tmax,
    t1 = tmin, t2 = tmax, band11, ngrid, band1, band2,
    bandpool = 0, numband = 1, biasadjust, tails1, tailsu, Nv)
```

CumulativeIncidence/AddlDescriptives_PostM6.R (cont.)

```
#plot the hazard for the treatment group
Fit.0 <- hazFit.preDec15[[2]]
timeGrid.0 <- Fit.0[,1]
haz.0 <- Fit.0[, 2]
ptLB.0 <- pmax(Fit.0[, 3], 0)
ptUB.0 <- Fit.0[, 4]
smLB.0 <- pmax(Fit.0[, 5], 0)
smUB.0 <- Fit.0[, 6]

Fit.1 <- hazFit.preDec15[[3]]
timeGrid.1 <- Fit.1[,1]
haz.1 <- Fit.1[, 2]
ptLB.1 <- pmax(Fit.1[, 3], 0)
ptUB.1 <- Fit.1[, 4]
smLB.1 <- pmax(Fit.1[, 5], 0)
smUB.1 <- Fit.1[, 6]

# pdf(file = path)
par(las=1, cex.axis=.8, cex.lab=1.35, tcl= -0.35, mar=c(8, 6.25, 6, 0.5),
    oma = c(2, 1, 1, 1), mgp = c(2.3, 0.5, 0))

plot(c(timeGrid.0, timeGrid.1), c(haz.0, haz.1),
     xlab="Time (Days, starting 13 days after M6 vaccination)",
     ylab="Hazard", type="n", bty="l",
     main ="Hazard over study time (M6 boost before Dec-15-2022)",
     ylim = c(0, .002), xlim = c(0, tmax))
lines(timeGrid.0, haz.0, lwd=3.5, col = "#F2502A")
# lines(timeGrid.0, ptLB.0, lty="dashed", lwd=3, col = "#F2502A")
# lines(timeGrid.0, ptUB.0, lty="dashed", lwd=3, col = "#F2502A")
lines(timeGrid.0, smLB.0, lty="dashed", lwd=3, col = "#F2502A")
lines(timeGrid.0, smUB.0, lty="dashed", lwd=3, col = "#F2502A")

lines(timeGrid.1, haz.1, lwd=3.5, col = "blue")
# lines(timeGrid.1, ptLB.1, lty="dashed", lwd=3, col = "blue")
# lines(timeGrid.1, ptUB.1, lty="dashed", lwd=3, col = "blue")
lines(timeGrid.1, smLB.1, lty="dashed", lwd=3, col = "blue")
lines(timeGrid.1, smUB.1, lty="dashed", lwd=3, col = "blue")

legend("topleft", legend=c("Monovalent","Bivalent"), cex=1, lwd=3,
      lty=c(1, 1), bty="n", x.intersp=0.7,
      col = c("#F2502A", "blue"))

dev.off()

path <- "/Volumes/trials/covpn/p3008/analysis/manuscripts/postM6/CumulativeIncidence/Figures/hazard_MB_BB
_RM6_CDC14M12_postDec15.pdf"

pdf(file = path)
par(las=1, cex.axis=.8, cex.lab=1.35, tcl= -0.35, mar=c(8, 6.25, 6, 0.5),
    oma = c(2, 1, 1, 1), mgp = c(2.3, 0.5, 0))

hazFit.postDec15 <- Confbandhazplusindiv(time = time[m6dt > as.Date("2022-12-15")],
    delta = event[m6dt > as.Date("2022-12-15")],
    Rx = A[m6dt > as.Date("2022-12-15")] + 1, N = 10000,
    Ngraph=0, u1=tmin, u2=tmax,
    t1 = tmin, t2 = tmax, band11, ngrid, band1, band2,
    bandpool = 0, numband = 1, biasadjust, tails1, tailsu, Nv)

#plot the hazard for the treatment group
Fit.0 <- hazFit.postDec15[[2]]
timeGrid.0 <- Fit.0[,1]
haz.0 <- Fit.0[, 2]
ptLB.0 <- pmax(Fit.0[, 3], 0)
ptUB.0 <- Fit.0[, 4]
smLB.0 <- pmax(Fit.0[, 5], 0)
smUB.0 <- Fit.0[, 6]
```

CumulativeIncidence/AddlDescriptives_PostM6.R (cont.)

```
Fit.1 <- hazFit.postDec15[[3]]
timeGrid.1 <- Fit.1[,1]
haz.1 <- Fit.1[, 2]
ptLB.1 <- pmax(Fit.1[, 3], 0)
ptUB.1 <- Fit.1[, 4]
smLB.1 <- pmax(Fit.1[, 5], 0)
smUB.1 <- Fit.1[, 6]

# pdf(file = path)
par(las=1, cex.axis=.8, cex.lab=1.35, tcl= -0.35, mar=c(8, 6.25, 6, 0.5),
    oma = c(2, 1, 1, 1), mgp = c(2.3, 0.5, 0))

plot(c(timeGrid.0, timeGrid.1), c(haz.0, haz.1),
     xlab="Time (Days, starting 13 days after M6 vaccination)",
     ylab="Hazard", type="n", bty="l",
     main ="Hazard over study time (M6 boost after Dec-15-2022)",
     ylim = c(0, .002), xlim = c(0, tmax))
lines(timeGrid.0, haz.0, lwd=3.5, col = "#F2502A")
# lines(timeGrid.0, ptLB.0, lty="dashed", lwd=3, col = "#F2502A")
# lines(timeGrid.0, ptUB.0, lty="dashed", lwd=3, col = "#F2502A")
lines(timeGrid.0, smLB.0, lty="dashed", lwd=3, col = "#F2502A")
lines(timeGrid.0, smUB.0, lty="dashed", lwd=3, col = "#F2502A")

lines(timeGrid.1, haz.1, lwd=3.5, col = "blue")
# lines(timeGrid.1, ptLB.1, lty="dashed", lwd=3, col = "blue")
# lines(timeGrid.1, ptUB.1, lty="dashed", lwd=3, col = "blue")
lines(timeGrid.1, smLB.1, lty="dashed", lwd=3, col = "blue")
lines(timeGrid.1, smUB.1, lty="dashed", lwd=3, col = "blue")

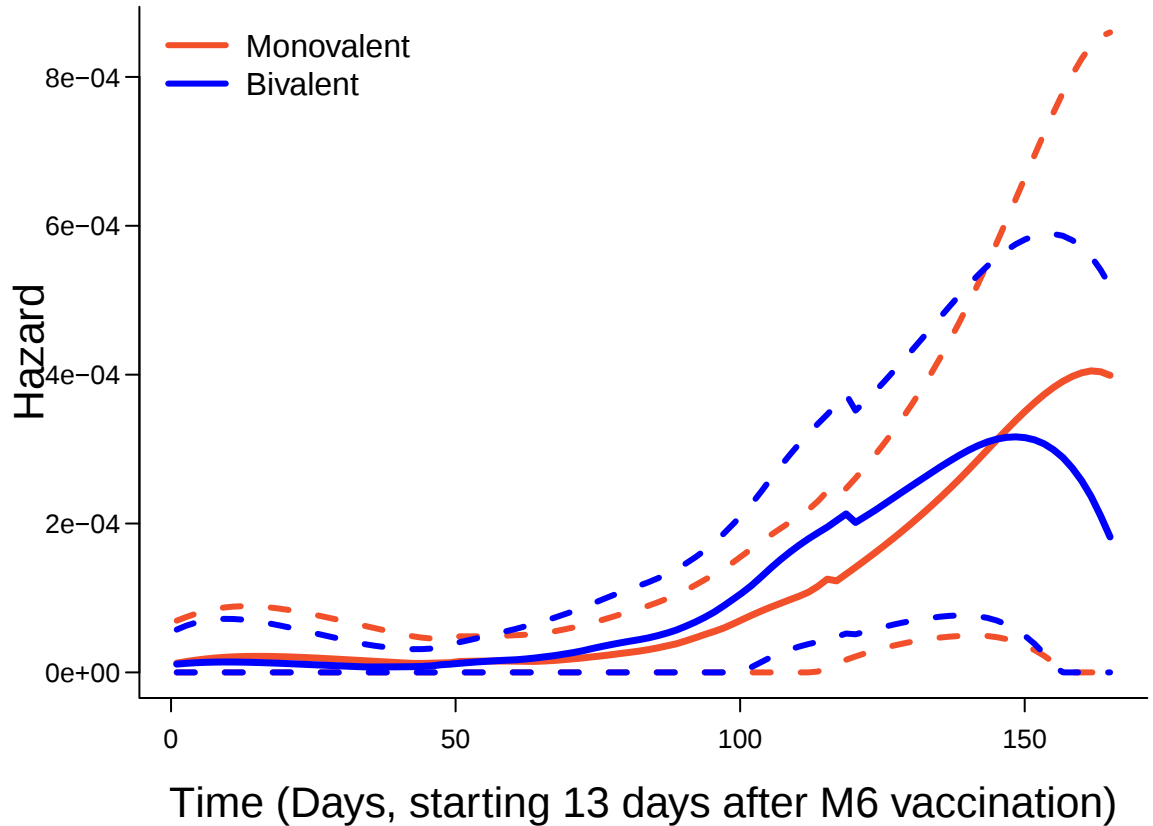
legend("topleft", legend=c("Monovalent","Bivalent"), cex=1, lwd=3,
      lty=c(1, 1), bty="n", x.intersp=0.7,
      col = c("#F2502A", "blue"))

dev.off()
```

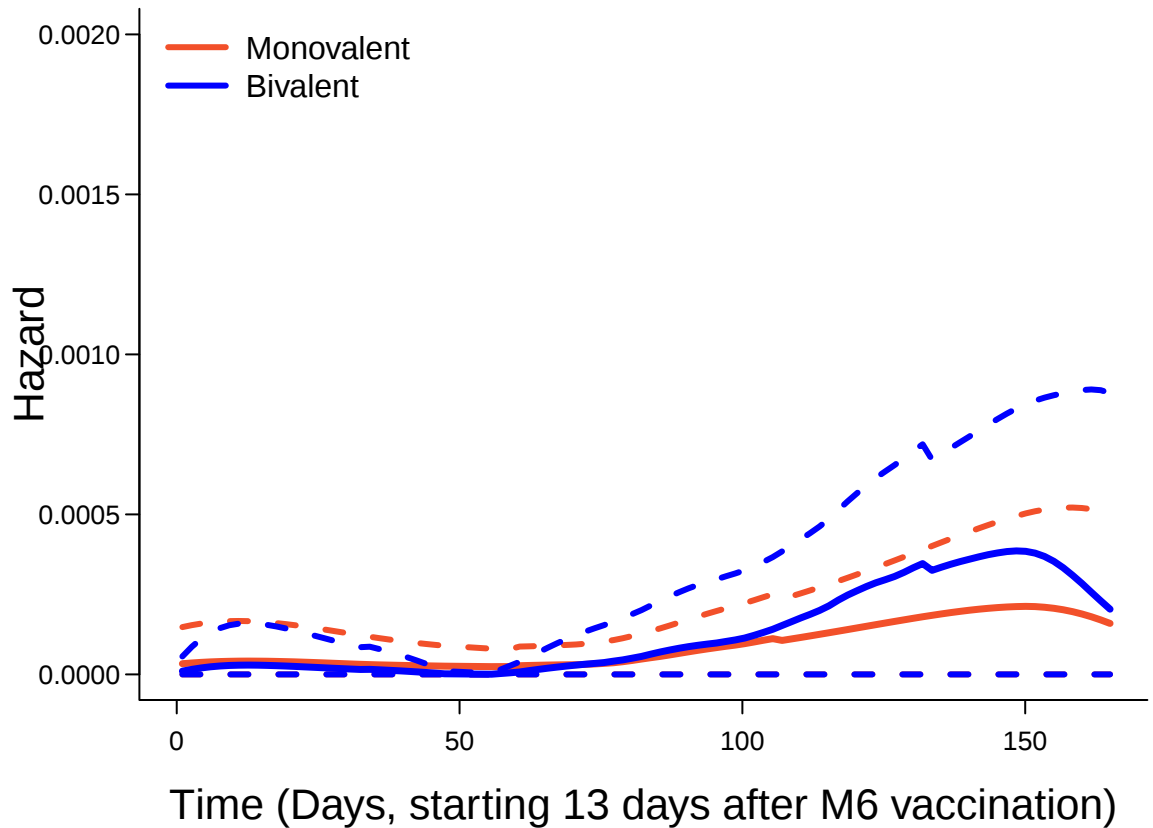
Part 2 — Figures

87 figures — Figures/

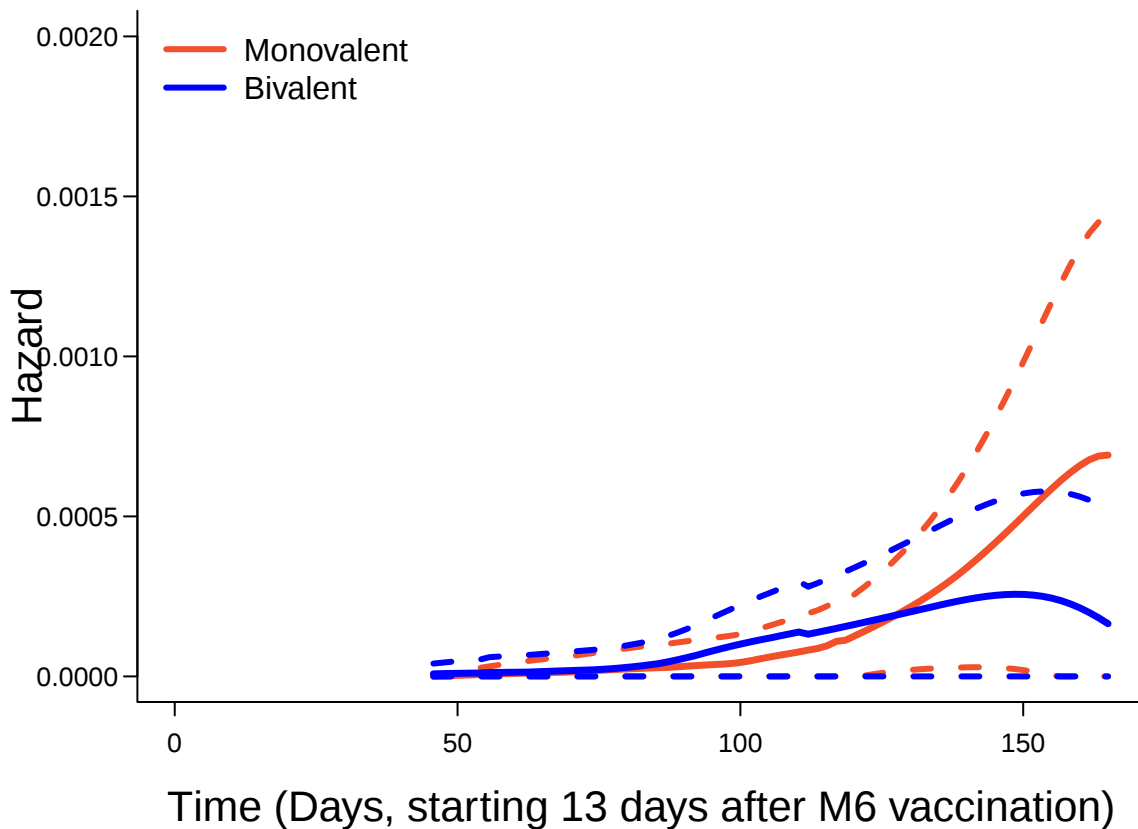
Hazard over study time



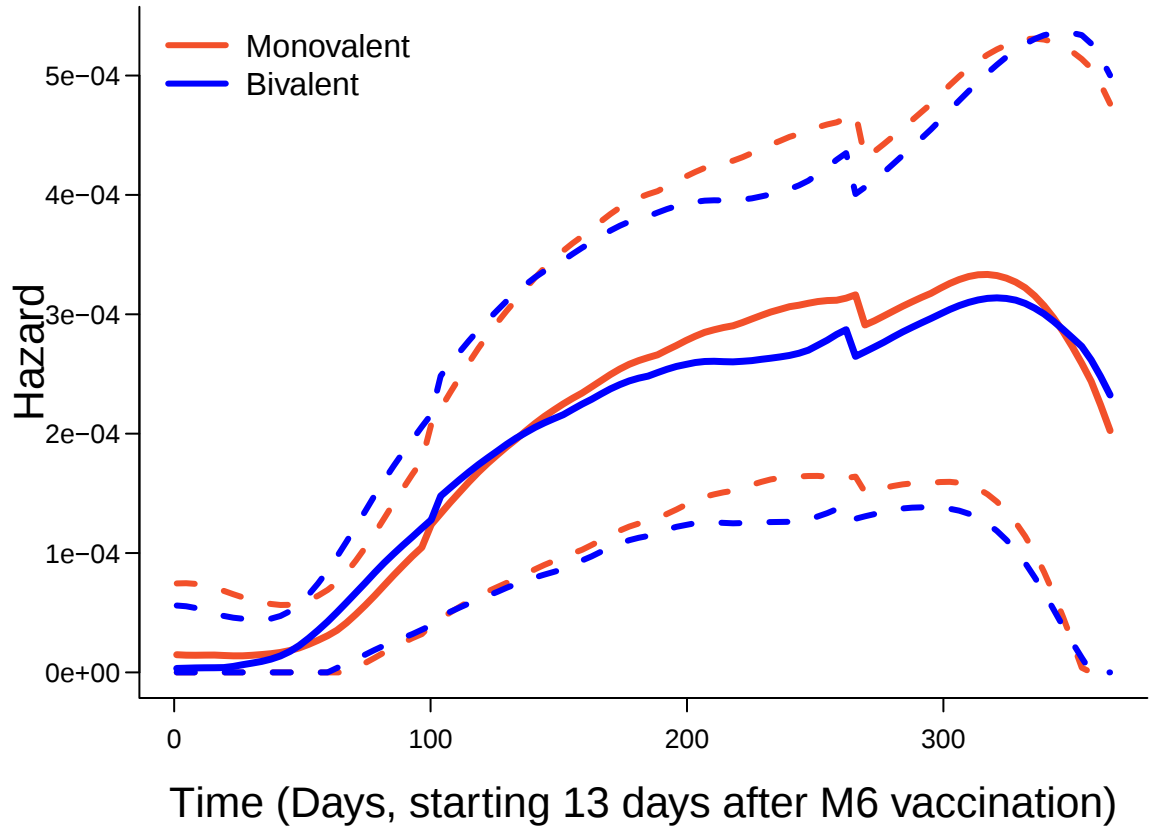
Hazard over study time (M6 boost after Dec-15-2022)



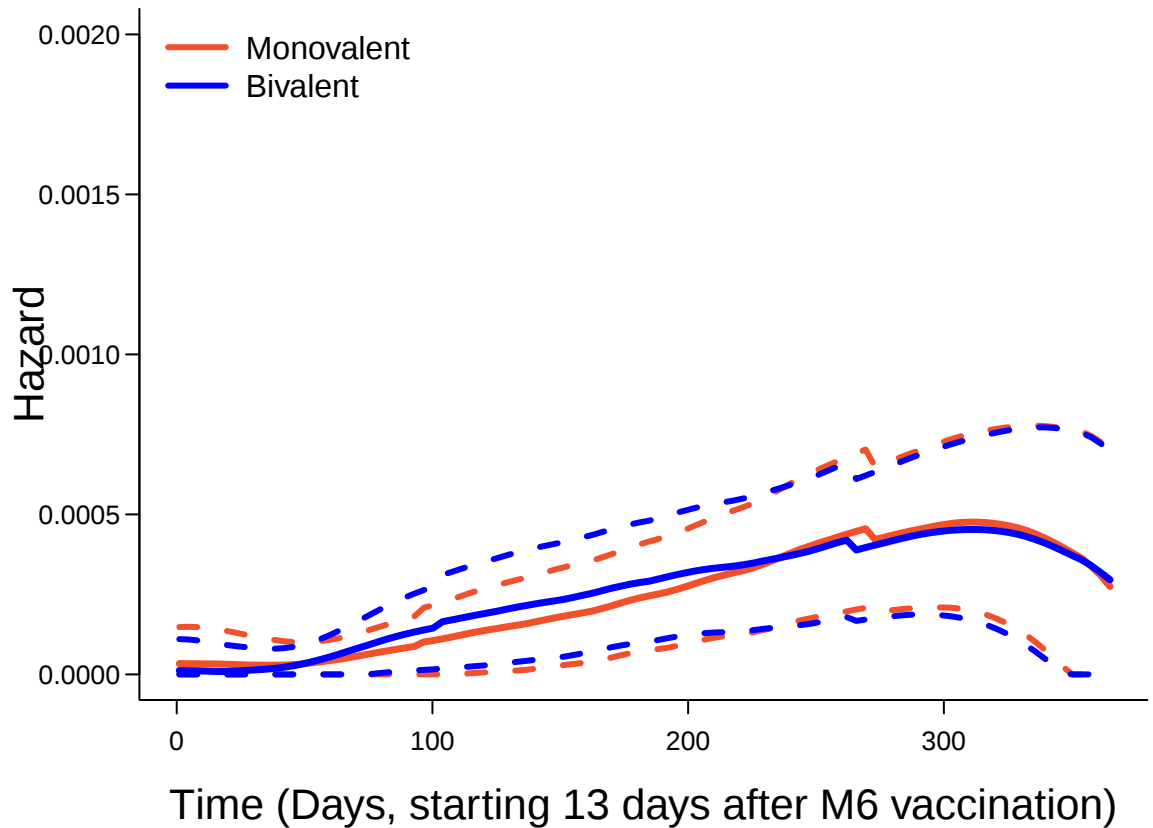
Hazard over study time (M6 boost before Dec-15-2022)



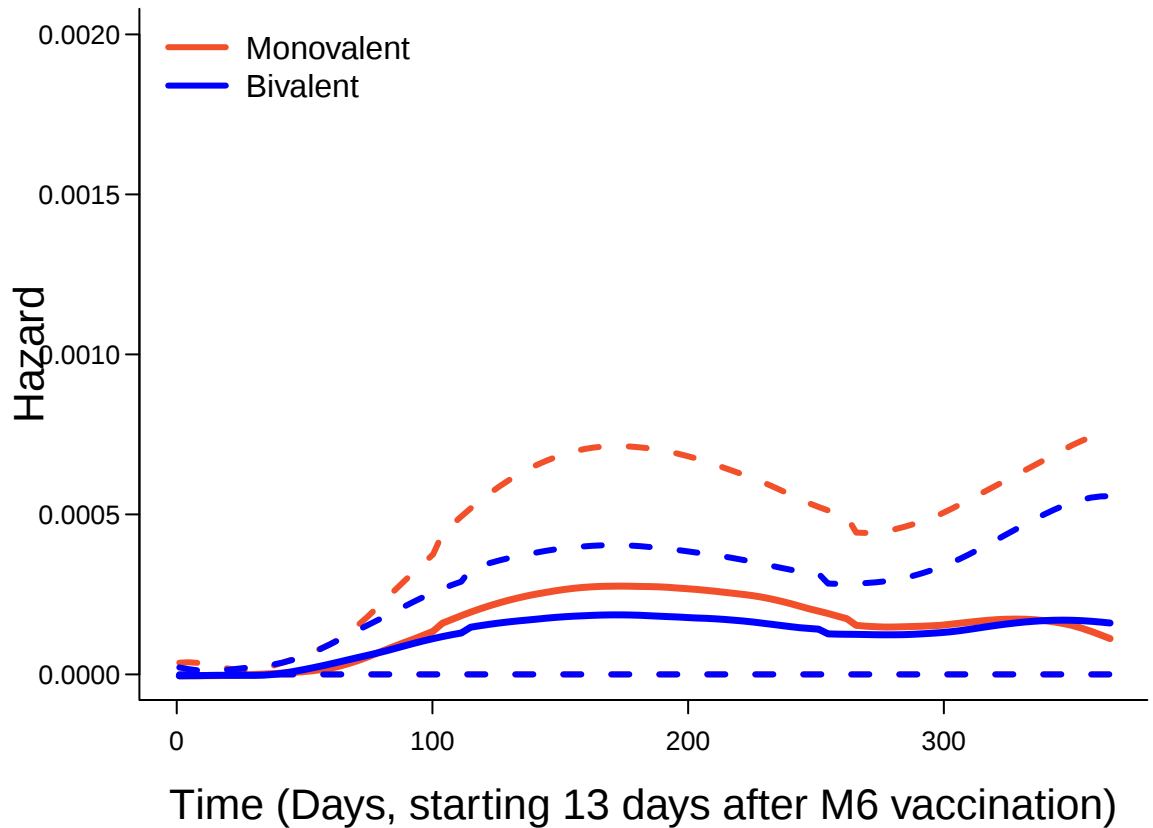
Hazard over study time



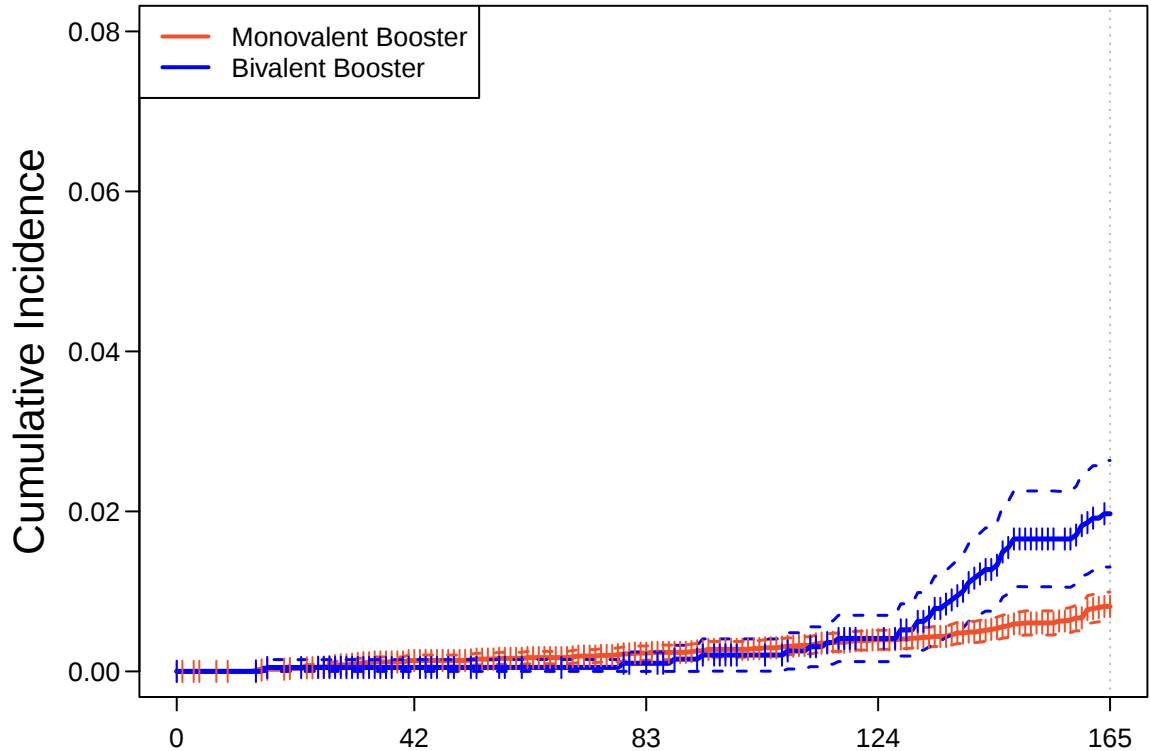
Hazard over study time (M6 boost after Dec-15-2022)



Hazard over study time (M6 boost before Dec-15-2022)



MBoost vs BBoost, FPP, CDC14M12, Primary



Time (Days, starting 13 days after M6 vaccination)

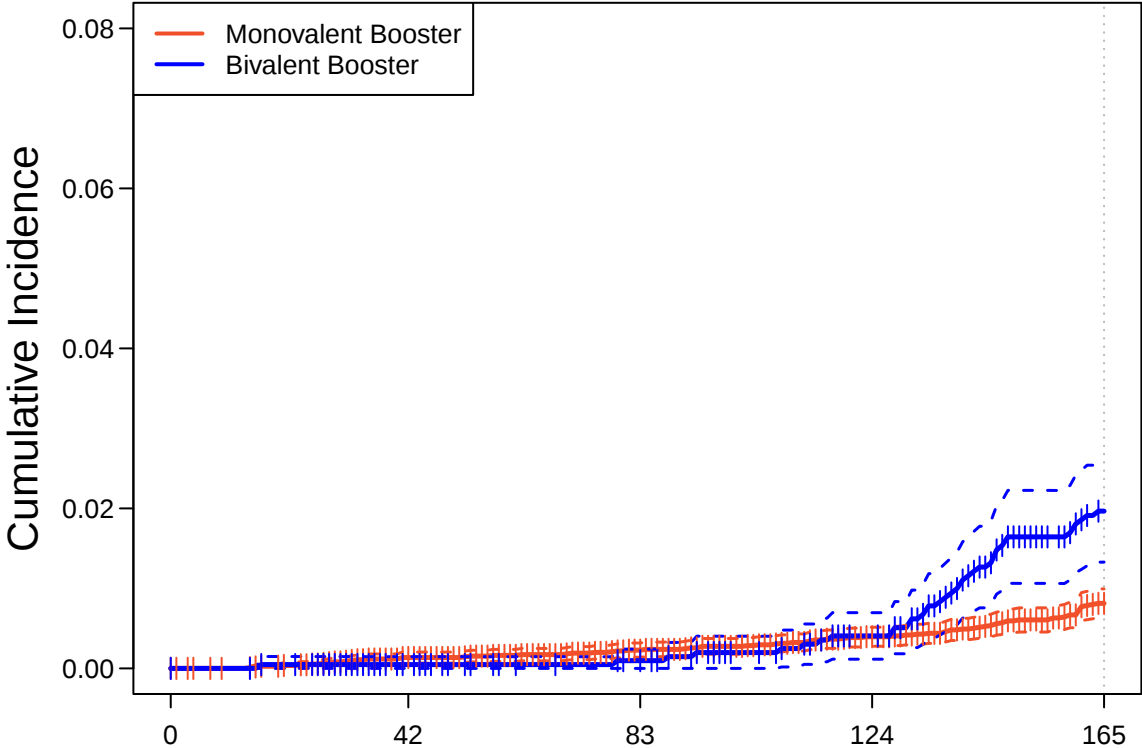
No. at Risk

Monovalent	11128	11027	10705	9749	7405
Bivalent	1988	1927	1909	1883	1763

Total Events

Monovalent	0	15	25	42	77
Bivalent	0	1	2	8	37

MBoost vs BBoost, FPP, CDC14M12, Sensitivity



Time (Days, starting 13 days after M6 vaccination)

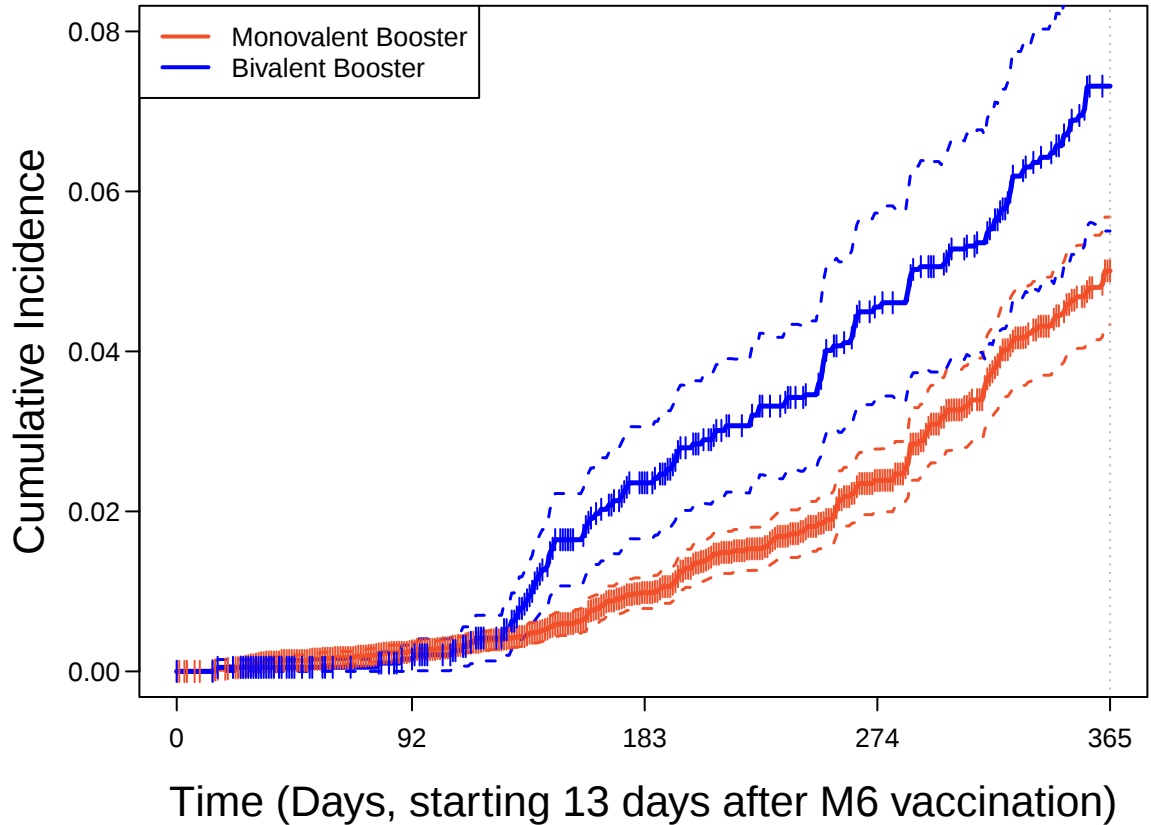
No. at Risk

Monovalent	11128	11027	10705	9749	7405
Bivalent	1988	1927	1909	1883	1763

Total Events

Monovalent	0	15	25	42	77
Bivalent	0	1	2	8	37

MBoost vs BBoost, FPP, CDC14M18, Primary



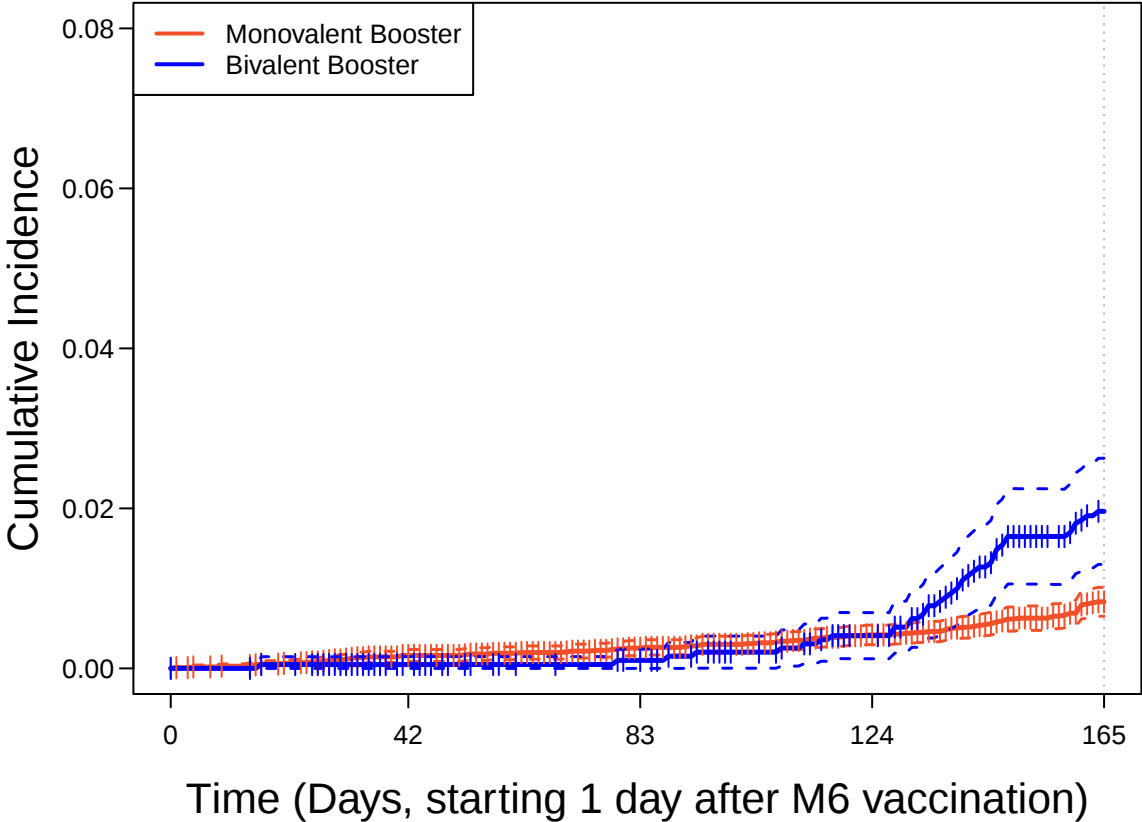
No. at Risk

Monovalent	11128	10538	7168	2370	1988
Bivalent	1987	1906	1778	1638	1568

Total Events

Monovalent	0	28	93	150	209
Bivalent	0	3	44	82	133

MBoost vs BBoost, FM6, CDC1M12, Primary



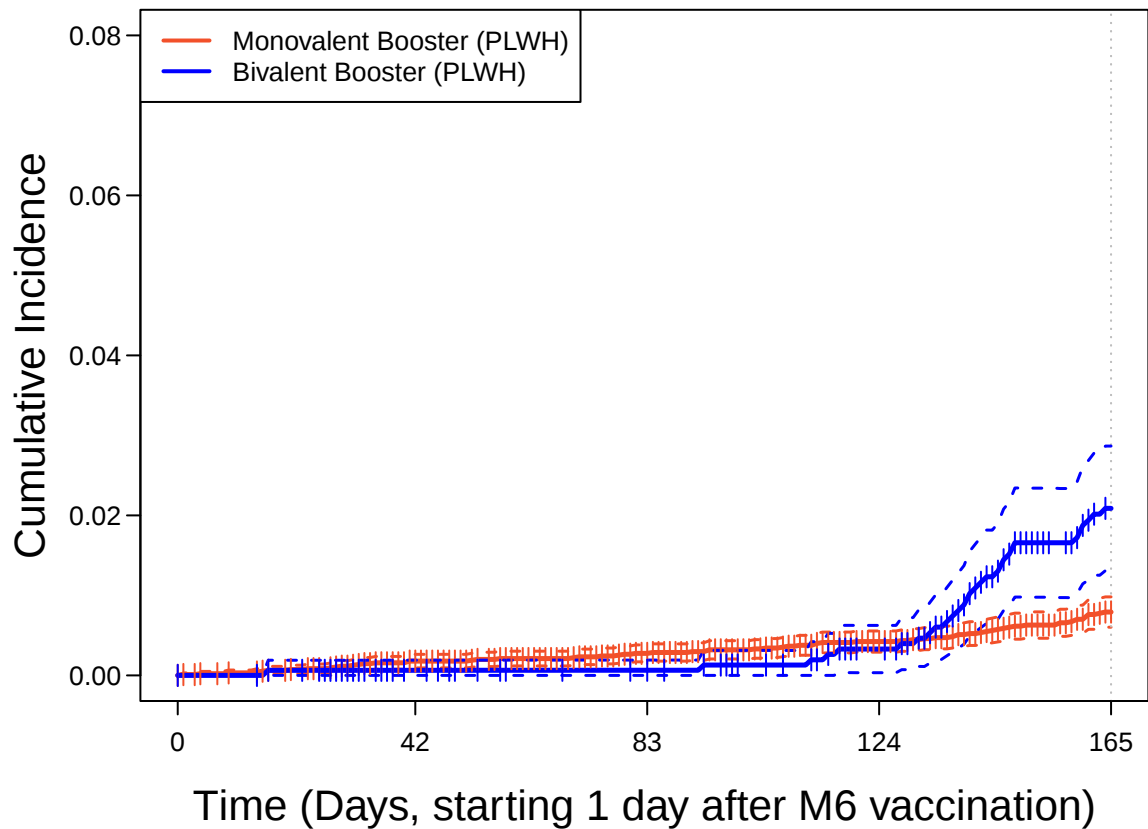
No. at Risk

Monovalent	11211	11110	10787	9826	7464
Bivalent	1996	1935	1917	1891	1771

Total Events

Monovalent	1	18	28	45	80
Bivalent	0	1	2	8	37

MBoost vs BBoost, FM6, CDC1M12, Primary (PLWH)



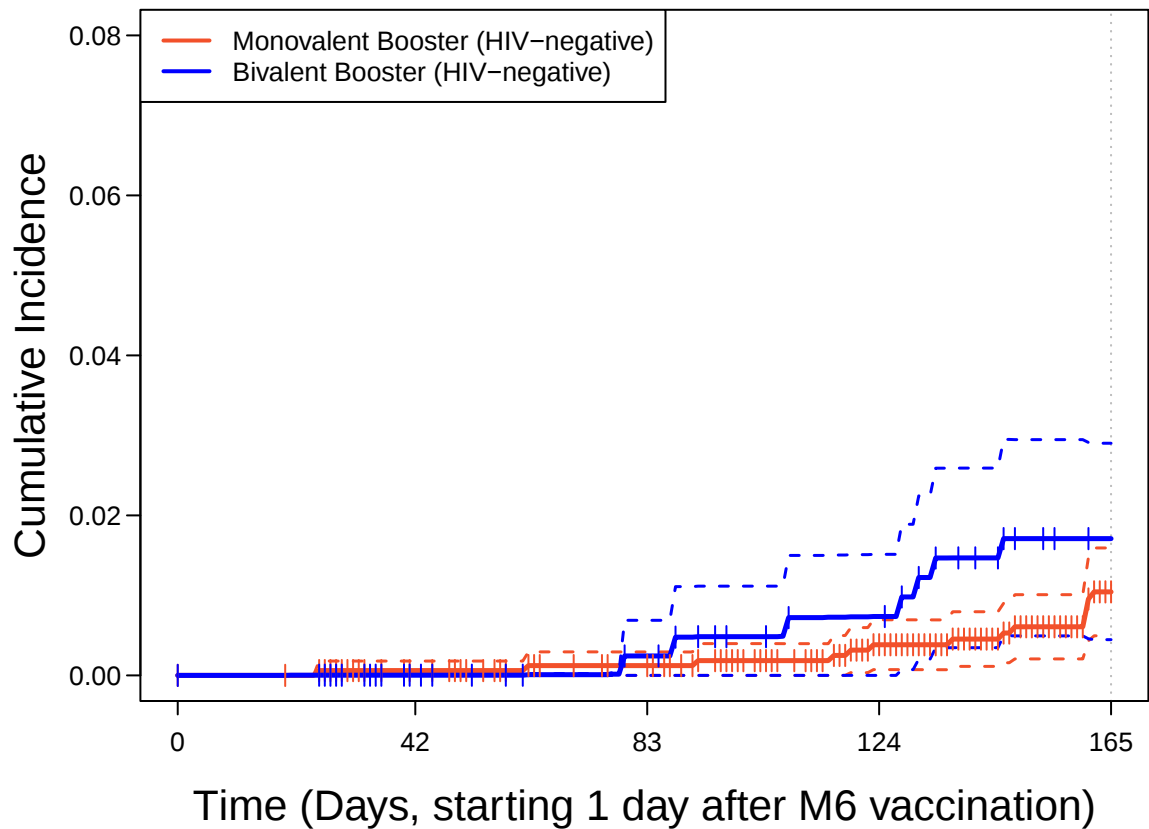
No. at Risk

Monovalent	9561	9482	9190	8352	6408
Bivalent	1546	1510	1498	1480	1377

Total Events

Monovalent	1	17	26	39	66
Bivalent	0	1	1	5	30

MBoost vs BBoost, FM6, CDC1M12, Primary (PLWoH)



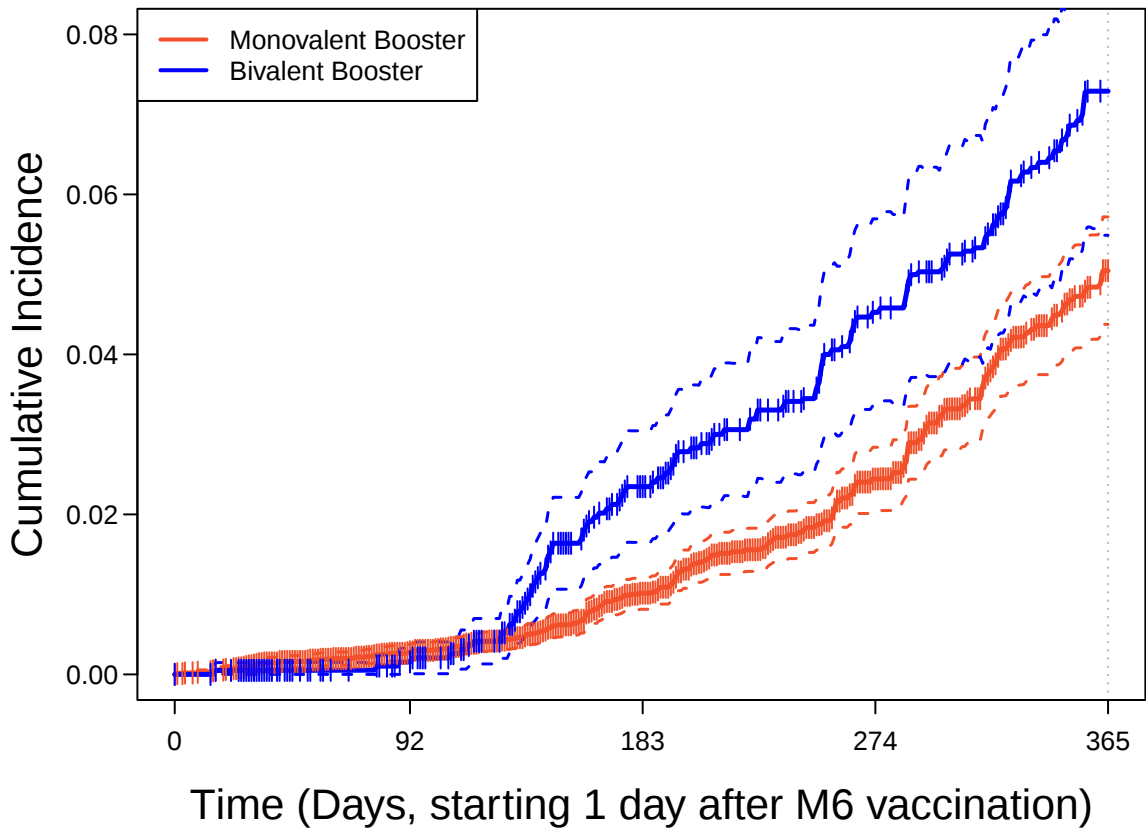
No. at Risk

Monovalent	1650	1628	1597	1474	1056
Bivalent	450	425	419	411	394

Total Events

Monovalent	0	1	2	6	14
Bivalent	0	0	1	3	7

MBoost vs BBoost, FM6, CDC1M18, Primary



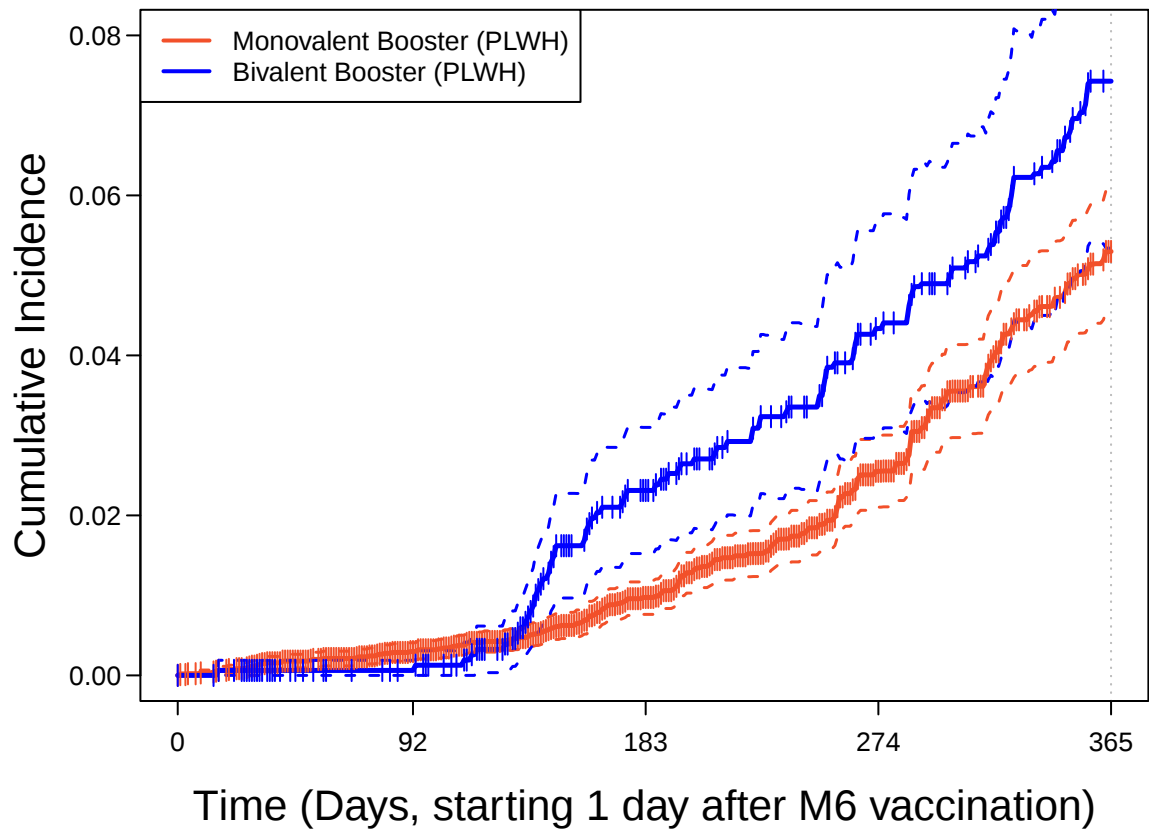
No. at Risk

Monovalent	11211	10619	7231	2389	2003
Bivalent	1996	1915	1787	1647	1577

Total Events

Monovalent	1	31	97	155	214
Bivalent	0	3	44	82	133

MBoost vs BBoost, FM6, CDC1M18, Primary (PLWH)



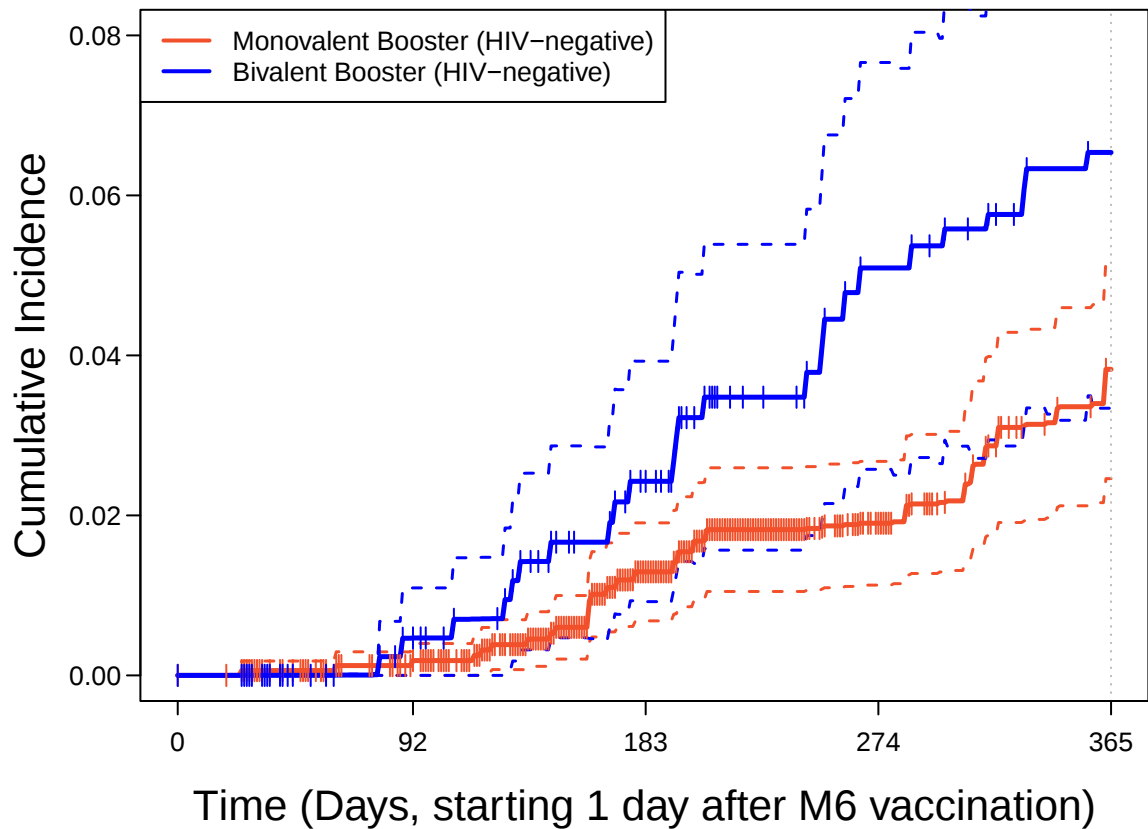
No. at Risk

Monovalent	9561	9042	6299	1974	1626
Bivalent	1546	1498	1399	1303	1243

Total Events

Monovalent	1	28	80	134	185
Bivalent	0	1	34	63	108

MBoost vs BBoost, FM6, CDC1M18, Primary (PLWoH)



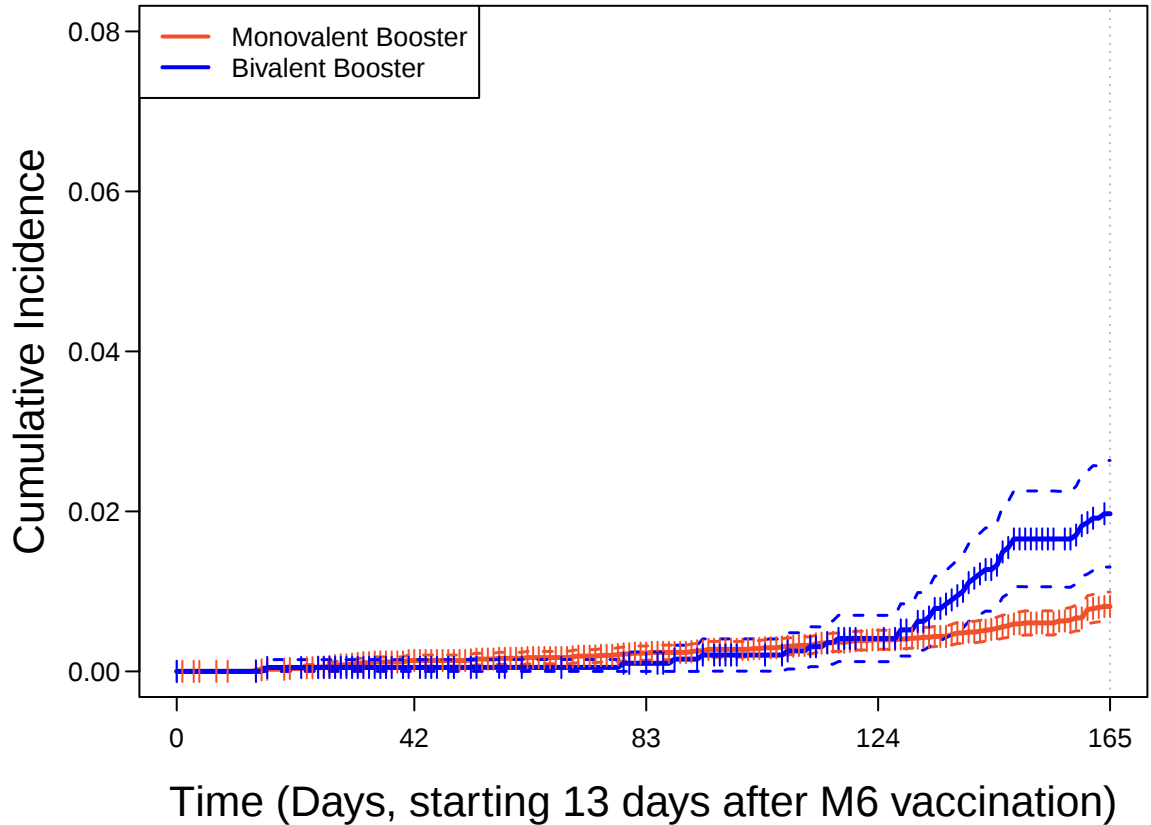
No. at Risk

Monovalent	1650	1577	932	415	377
Bivalent	450	417	388	344	334

Total Events

Monovalent	0	3	17	21	29
Bivalent	0	2	10	19	25

MBoost vs BBoost, FPP, CDC14M12, Primary



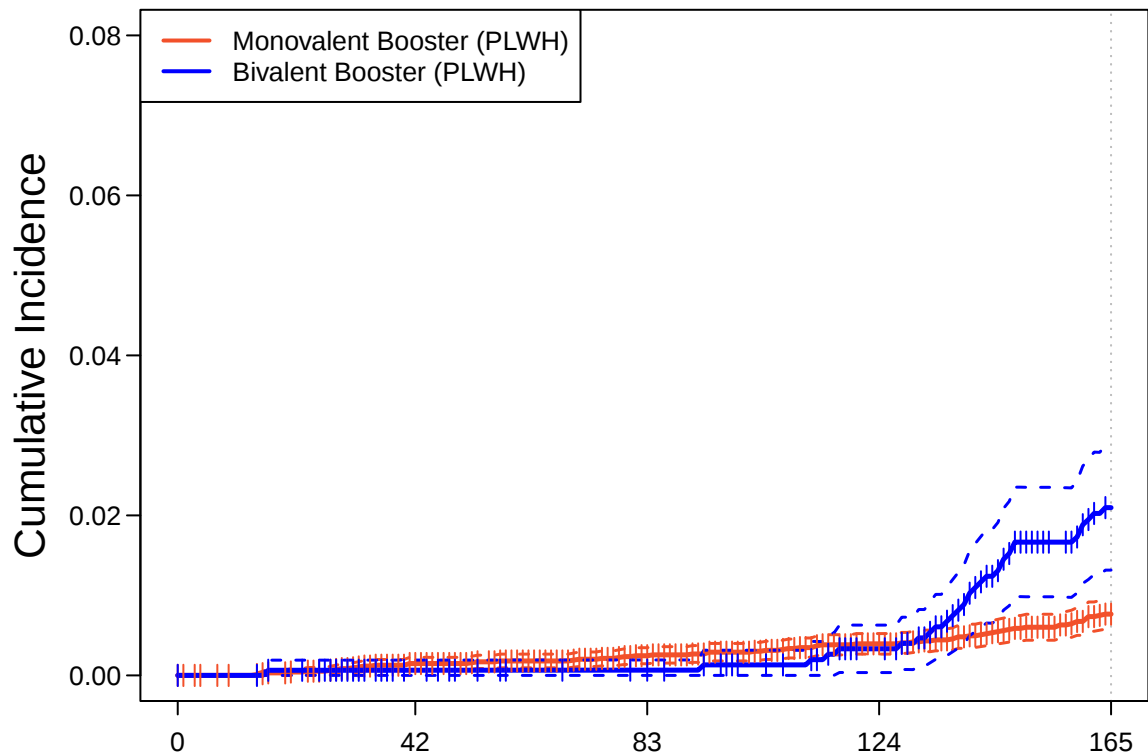
No. at Risk

Monovalent	11128	11027	10705	9749	7405
Bivalent	1988	1927	1909	1883	1763

Total Events

Monovalent	0	15	25	42	77
Bivalent	0	1	2	8	37

MBoost vs BBoost, FPP, CDC14M12, Primary (PLWH)



Time (Days, starting 13 days after M6 vaccination)

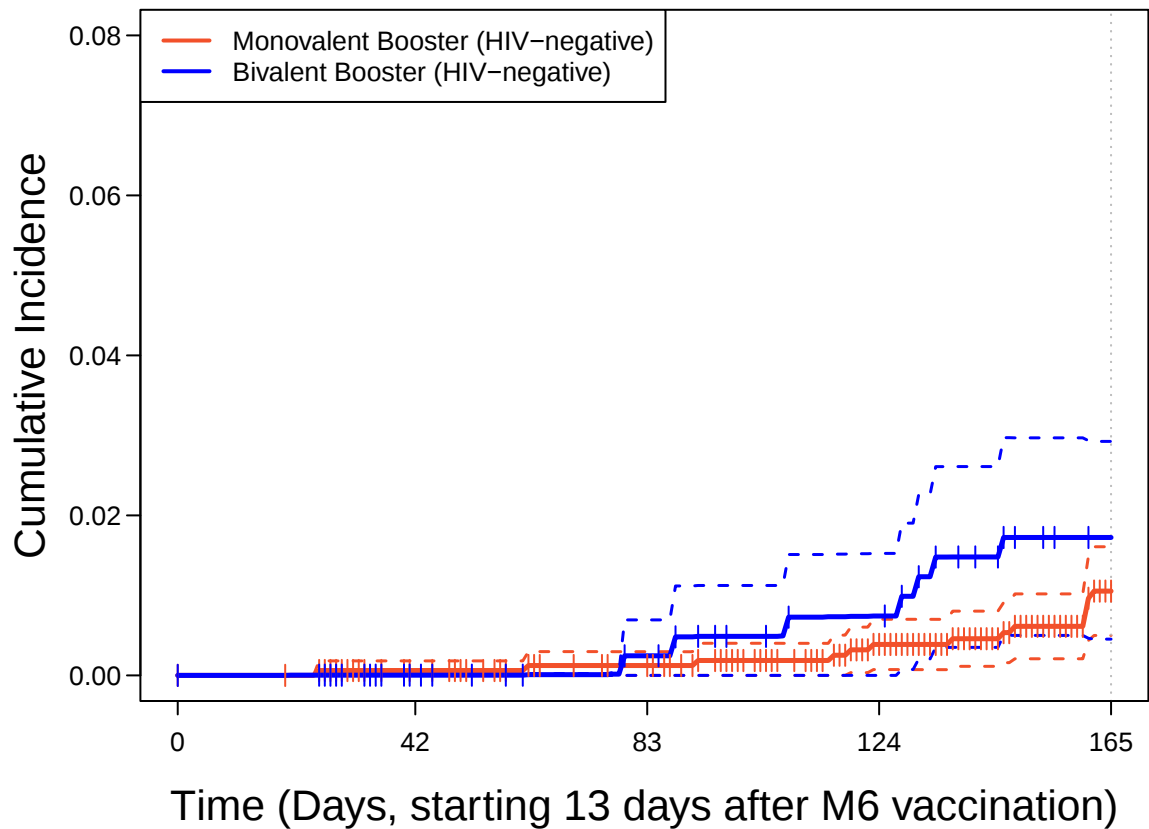
No. at Risk

Monovalent	9495	9416	9125	8289	6358
Bivalent	1541	1505	1493	1475	1372

Total Events

Monovalent	0	14	23	36	63
Bivalent	0	1	1	5	30

MBoost vs BBoost, FPP, CDC14M12, Primary (PLWoH)



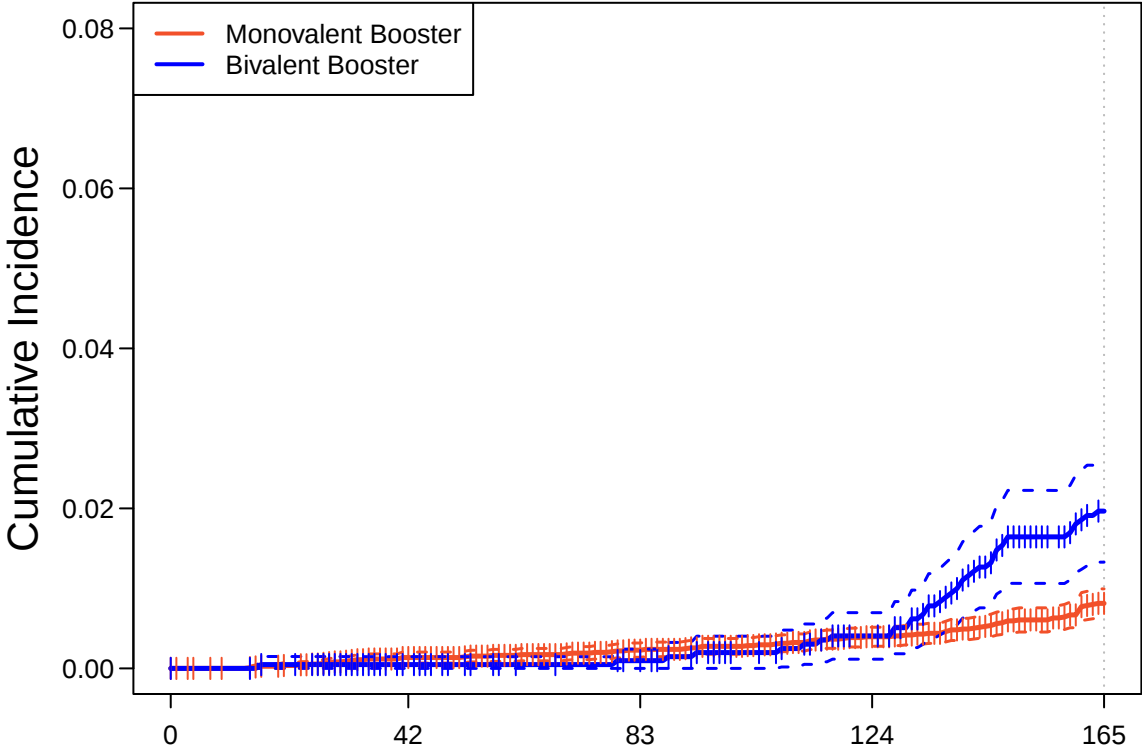
No. at Risk

Monovalent	1633	1611	1580	1460	1047
Bivalent	447	422	416	408	391

Total Events

Monovalent	0	1	2	6	14
Bivalent	0	0	1	3	7

MBoost vs BBoost, FPP, CDC14M12, Sensitivity



Time (Days, starting 13 days after M6 vaccination)

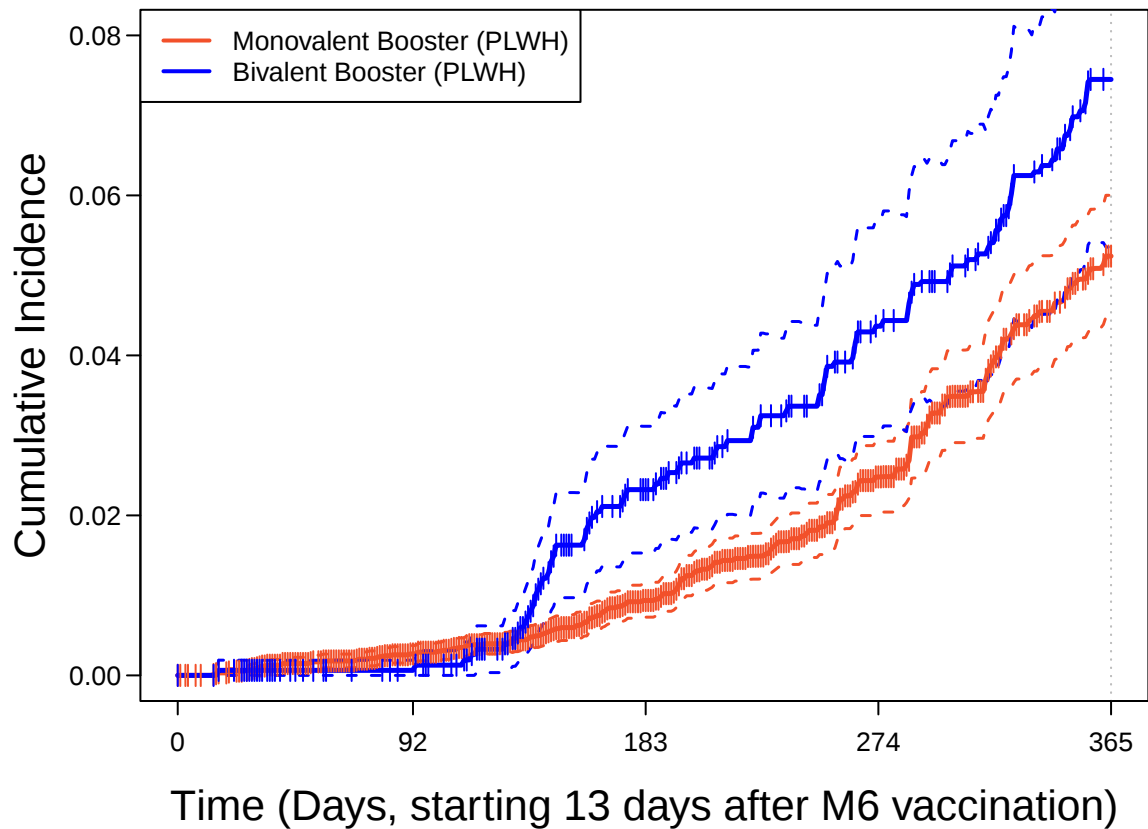
No. at Risk

Monovalent	11128	11027	10705	9749	7405
Bivalent	1988	1927	1909	1883	1763

Total Events

Monovalent	0	15	25	42	77
Bivalent	0	1	2	8	37

MBoost vs BBoost, FPP, CDC14M18, Primary (PLWH)



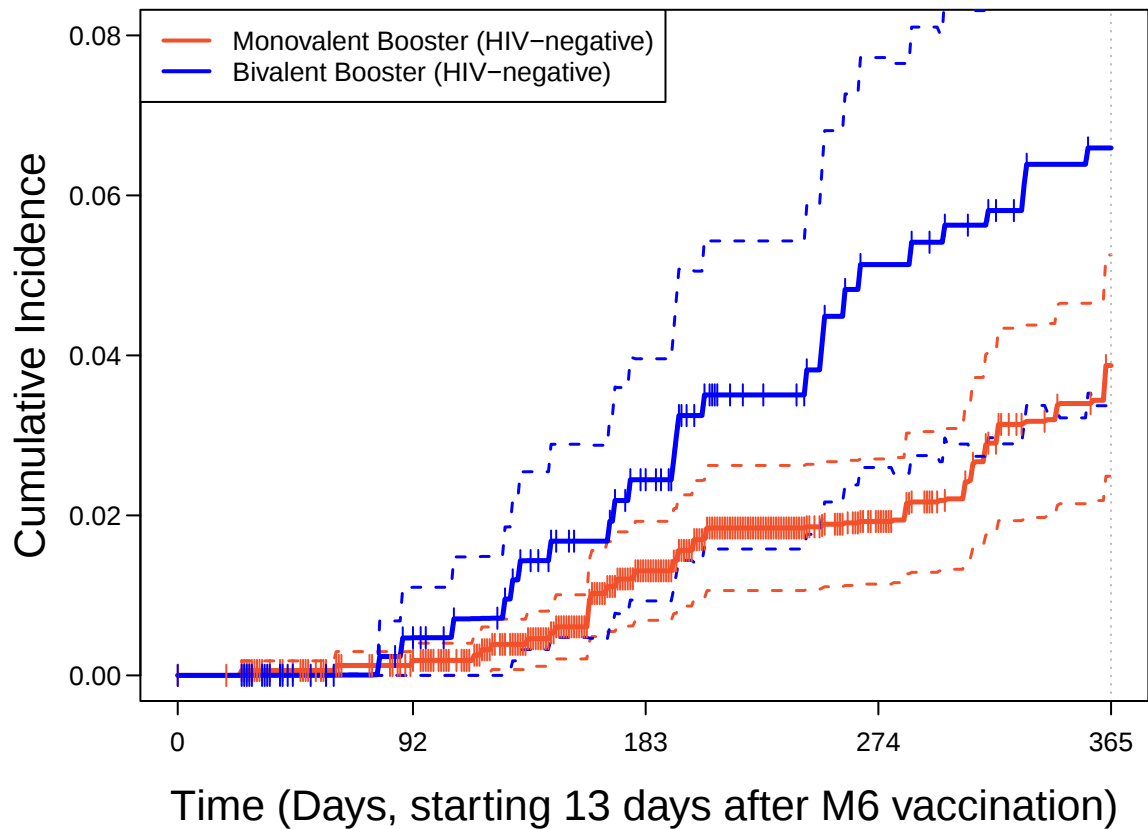
No. at Risk

Monovalent	9495	8977	6248	1960	1616
Bivalent	1540	1492	1393	1297	1237

Total Events

Monovalent	0	25	76	129	180
Bivalent	0	1	34	63	108

MBoost vs BBoost, FPP, CDC14M18, Primary (PLWoH)



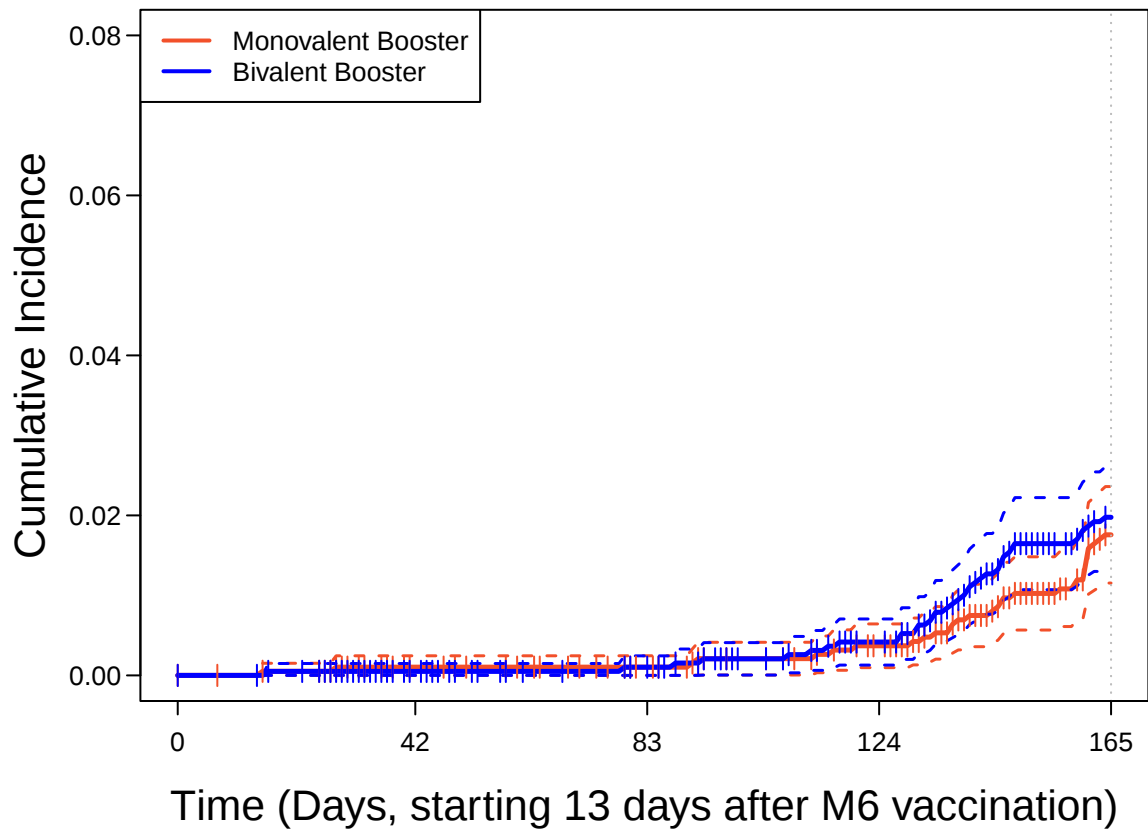
No. at Risk

Monovalent	1633	1561	920	410	372
Bivalent	447	414	385	341	331

Total Events

Monovalent	0	3	17	21	29
Bivalent	0	2	10	19	25

MBoost vs BBoost, RM6, CDC14M12, Primary



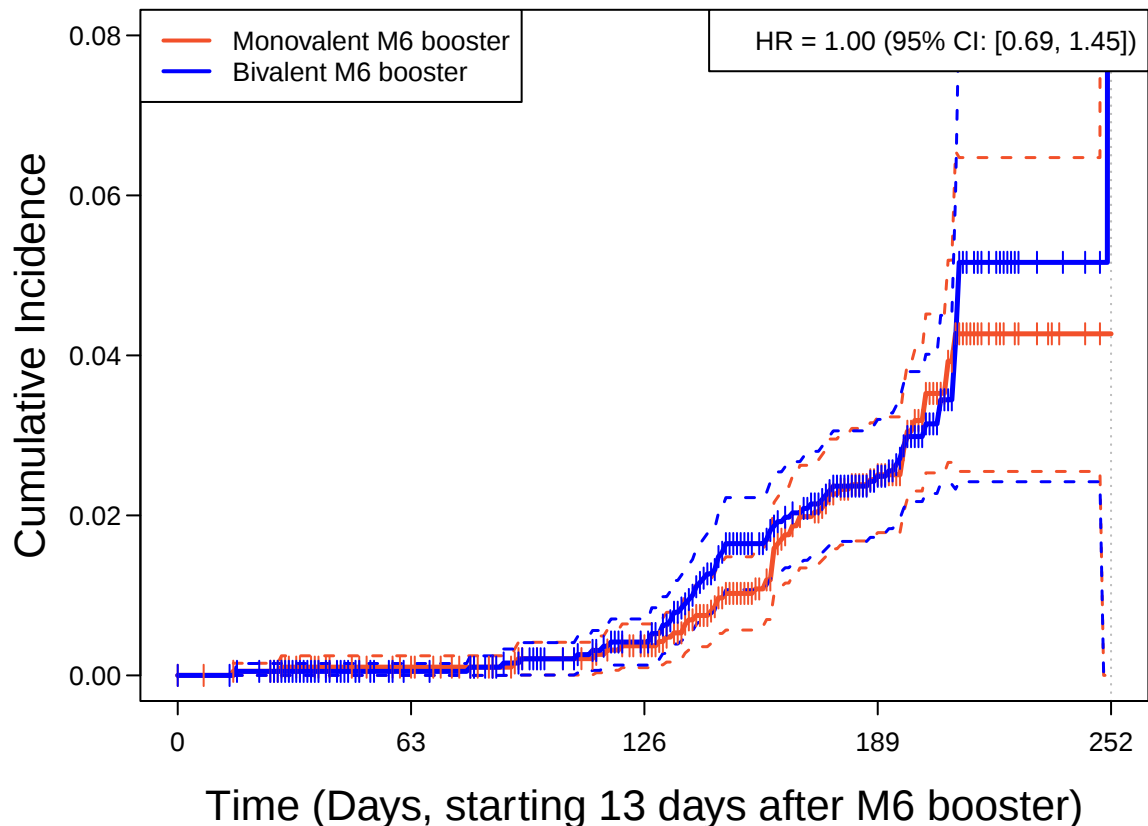
No. at Risk

Monovalent	1949	1896	1880	1860	1742
Bivalent	1996	1935	1917	1891	1771

Total Events

Monovalent	0	2	2	7	32
Bivalent	0	1	2	8	37

COVID-19 incidence over study time



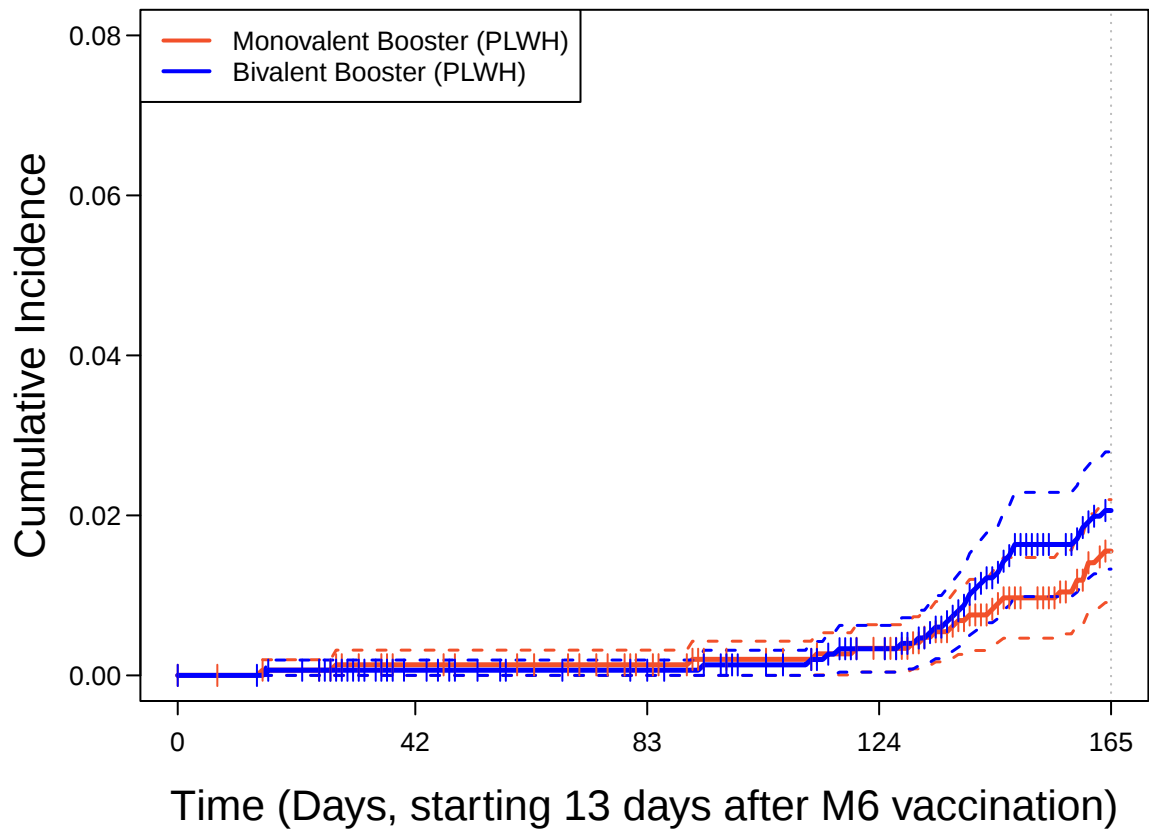
No. at Risk

Monovalent	1949	1889	1859	1538	1
Bivalent	1996	1920	1889	1546	1

Total Events

Monovalent	0	2	7	45	56
Bivalent	0	1	8	46	57

MBoost vs BBoost, RM6, CDC14M12, Primary (PLWH)



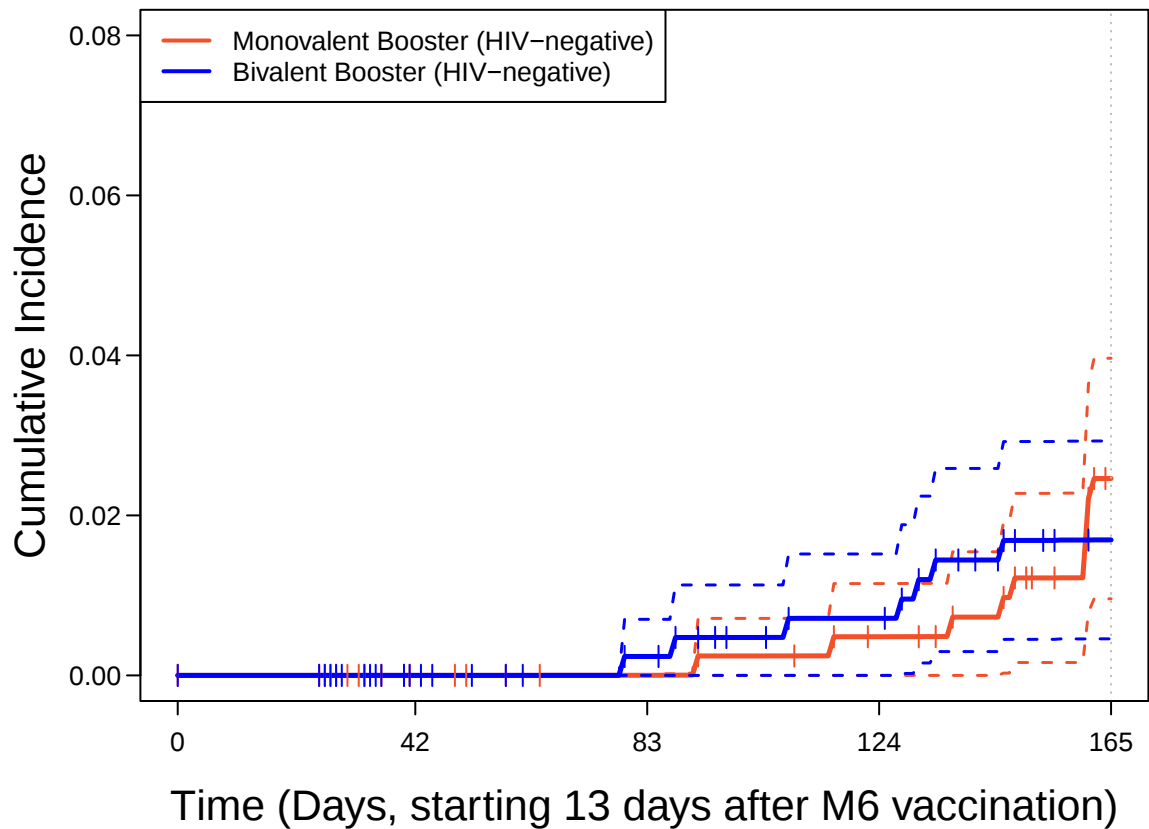
No. at Risk

Monovalent	1510	1473	1462	1446	1346
Bivalent	1546	1510	1498	1480	1377

Total Events

Monovalent	0	2	2	5	22
Bivalent	0	1	1	5	30

MBoost vs BBoost, RM6, CDC14M12, Primary (PLWoH)



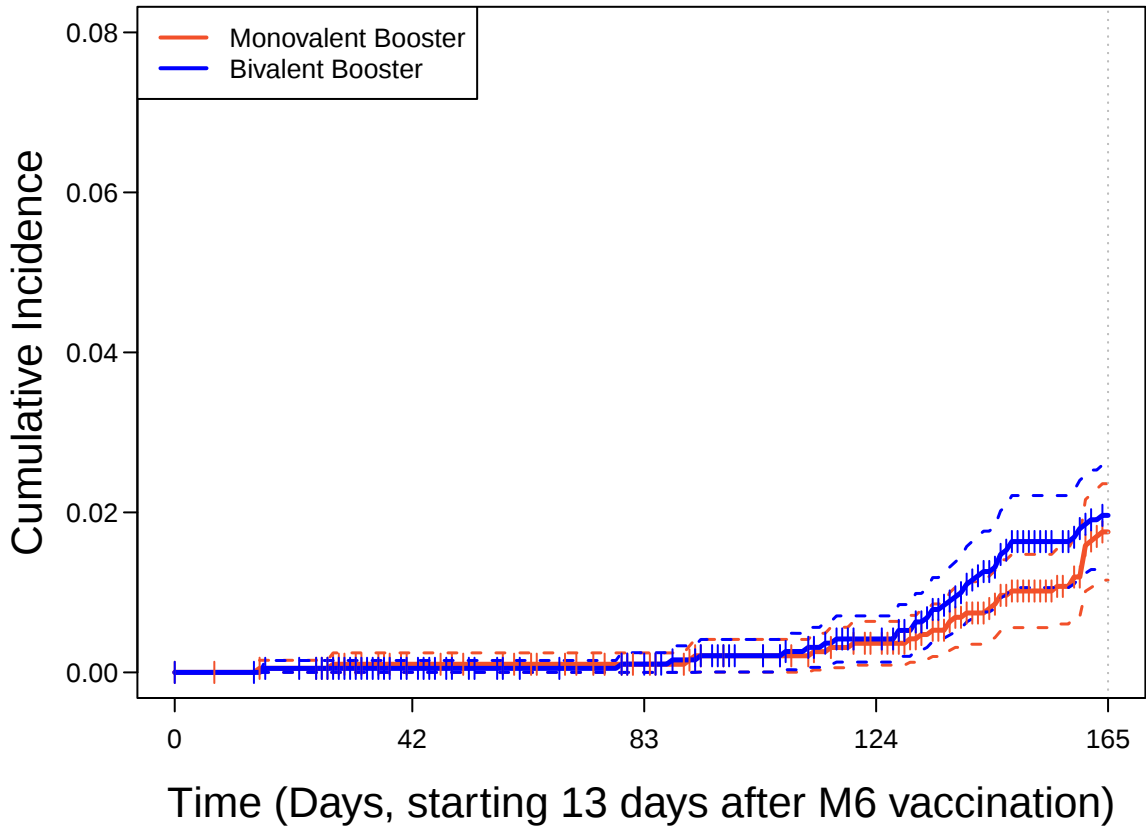
No. at Risk

Monovalent	439	423	418	414	396
Bivalent	450	425	419	411	394

Total Events

Monovalent	0	0	0	2	10
Bivalent	0	0	1	3	7

MBoost vs BBoost, RM6, CDC14M12, Sensitivity



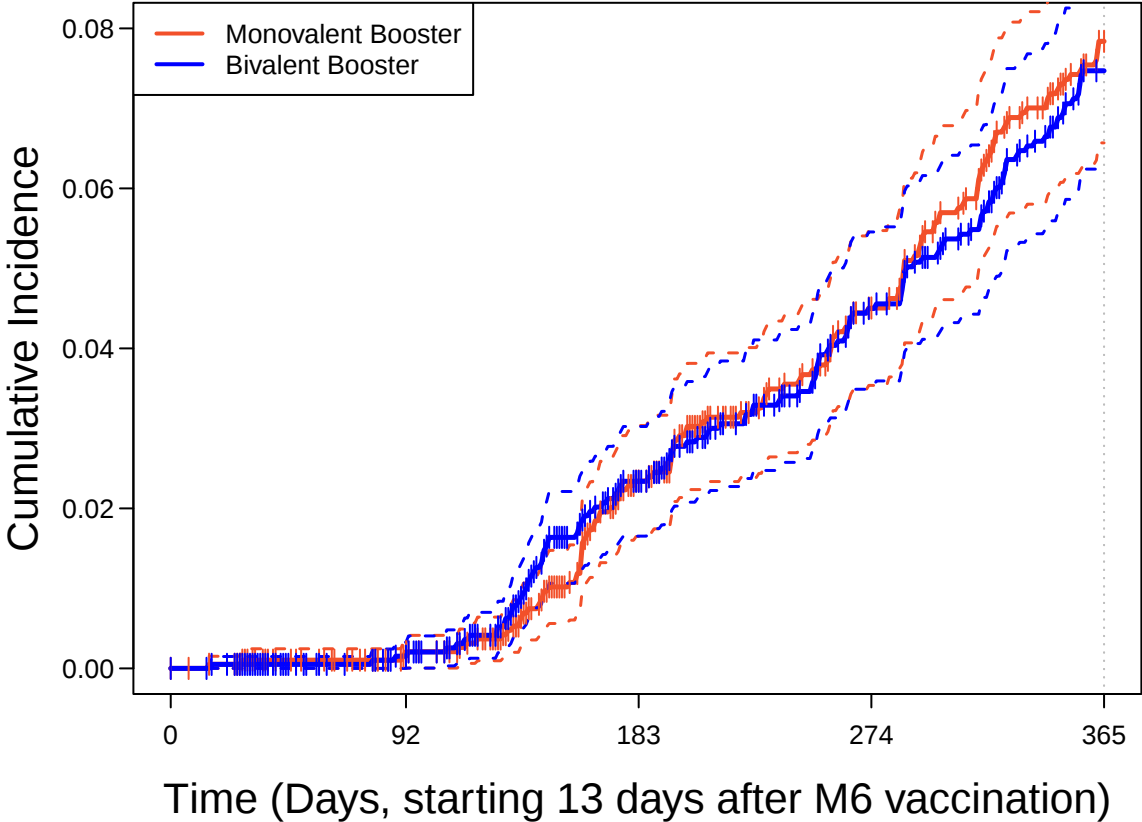
No. at Risk

Monovalent	1949	1896	1880	1860	1742
Bivalent	1996	1935	1917	1891	1771

Total Events

Monovalent	0	2	2	7	32
Bivalent	0	1	2	8	37

MBoost vs BBoost, RM6, CDC14M18, Primary



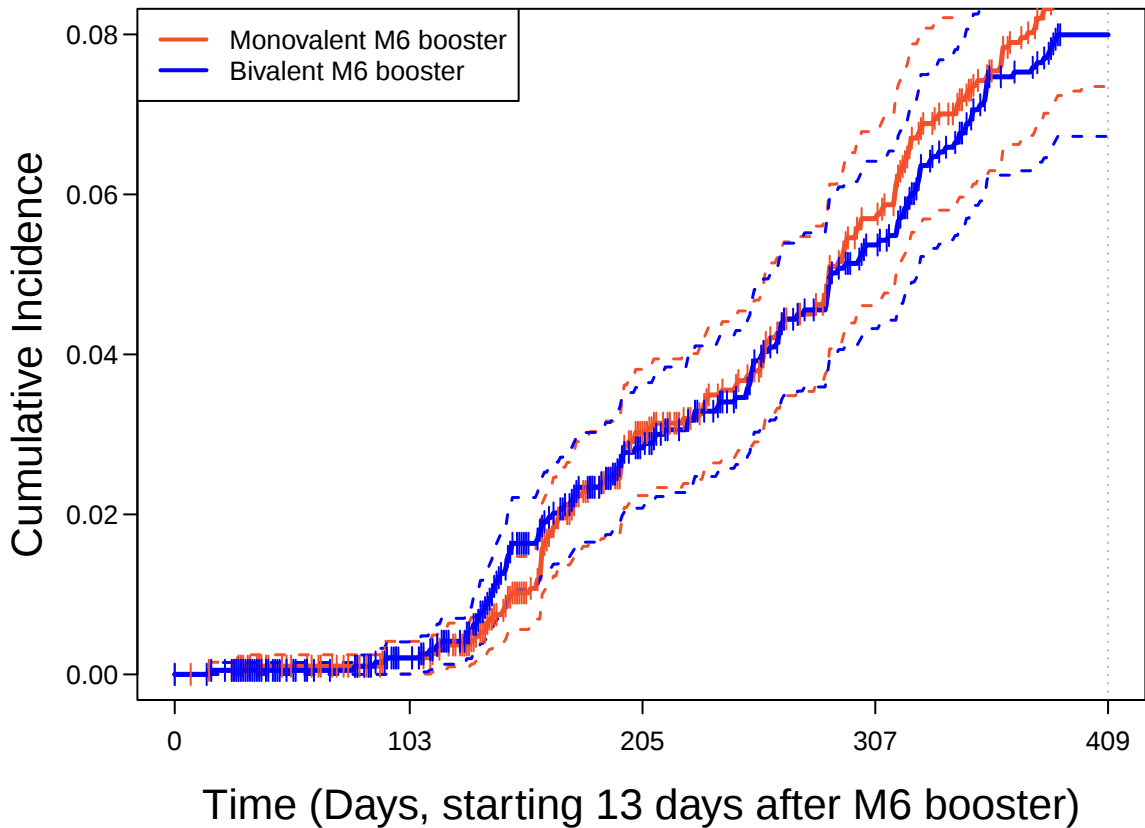
No. at Risk

Monovalent	1949	1877	1752	1615	1537
Bivalent	1996	1915	1787	1647	1577

Total Events

Monovalent	0	4	43	80	136
Bivalent	0	3	44	82	133

COVID-19 incidence over study time



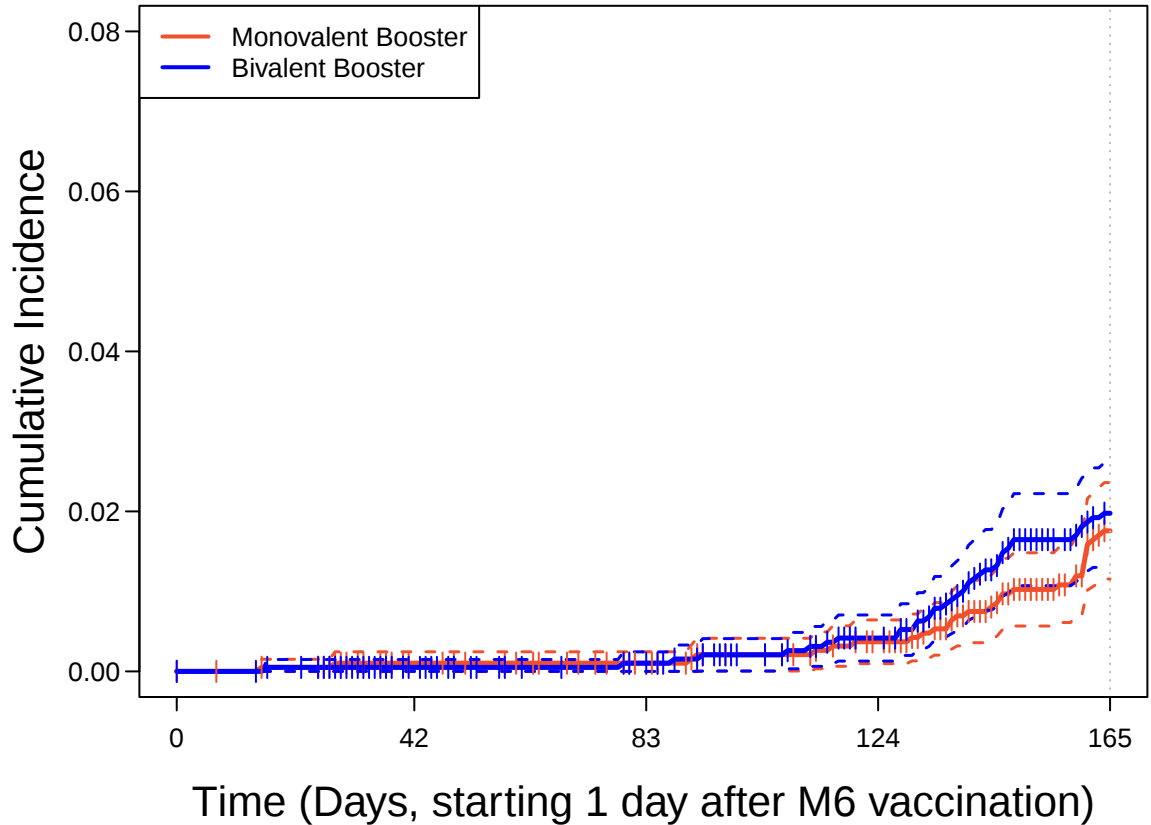
No. at Risk

Monovalent	1949	1874	1693	1585	1519
Bivalent	1996	1908	1725	1625	1567

Total Events

Monovalent	0	4	55	100	151
Bivalent	0	4	53	97	142

MBoost vs BBoost, RM6, CDC1M12, Primary



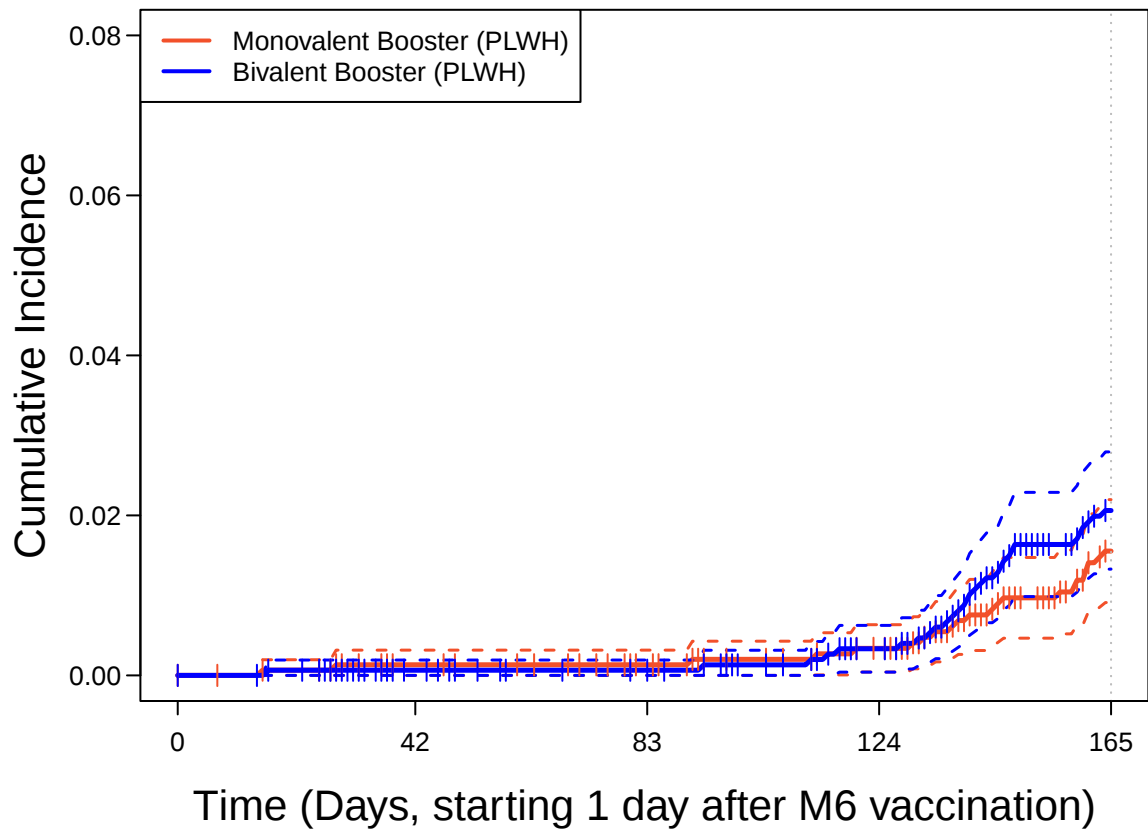
No. at Risk

Monovalent	1949	1896	1880	1860	1742
Bivalent	1996	1935	1917	1891	1771

Total Events

Monovalent	0	2	2	7	32
Bivalent	0	1	2	8	37

MBoost vs BBoost, RM6, CDC1M12, Primary (PLWH)



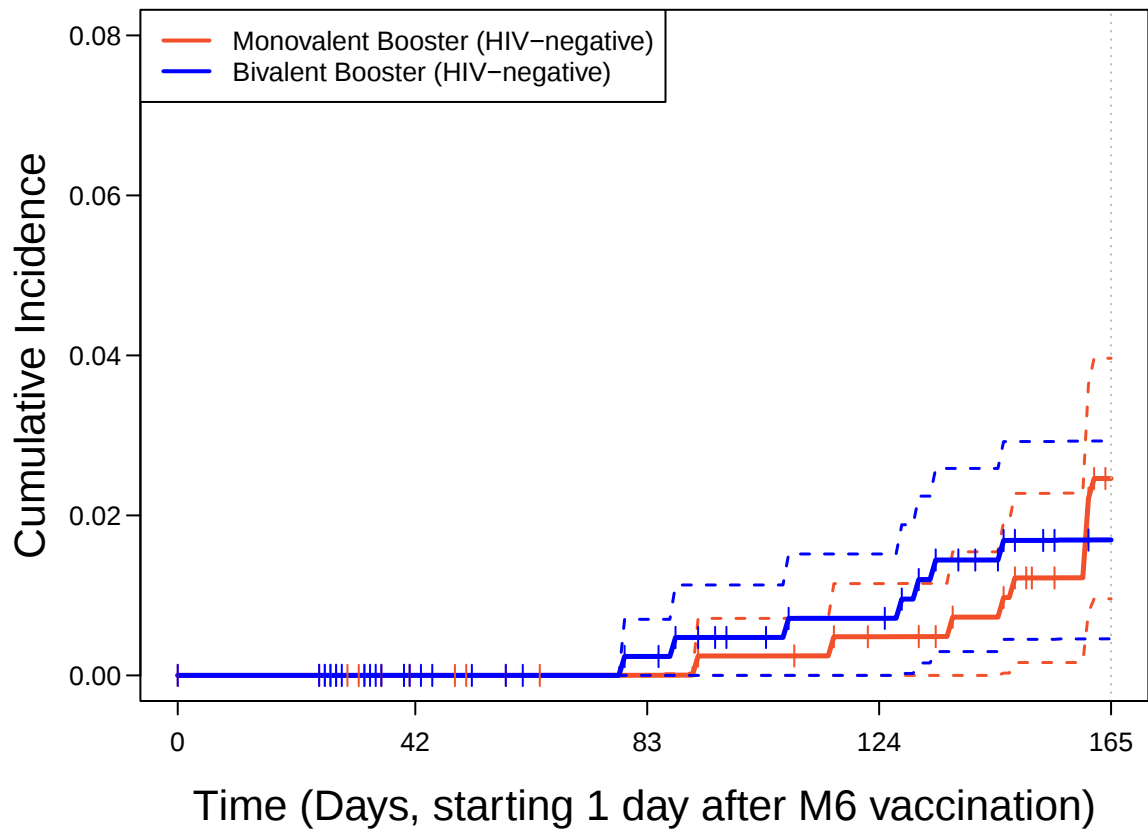
No. at Risk

Monovalent	1510	1473	1462	1446	1346
Bivalent	1546	1510	1498	1480	1377

Total Events

Monovalent	0	2	2	5	22
Bivalent	0	1	1	5	30

MBoost vs BBoost, RM6, CDC1M12, Primary (PLWoH)



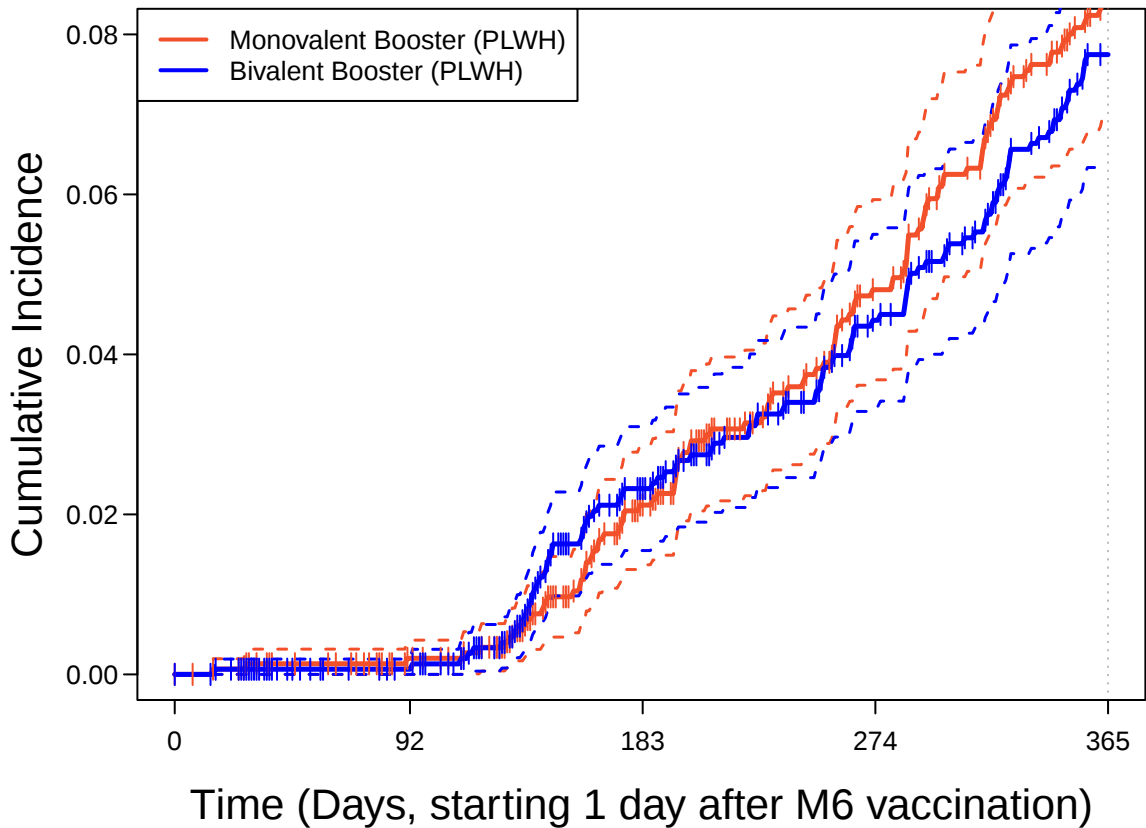
No. at Risk

Monovalent	439	423	418	414	396
Bivalent	450	425	419	411	394

Total Events

Monovalent	0	0	0	2	10
Bivalent	0	0	1	3	7

MBoost vs BBoost, RM6, CDC1M18, Primary (PLWH)



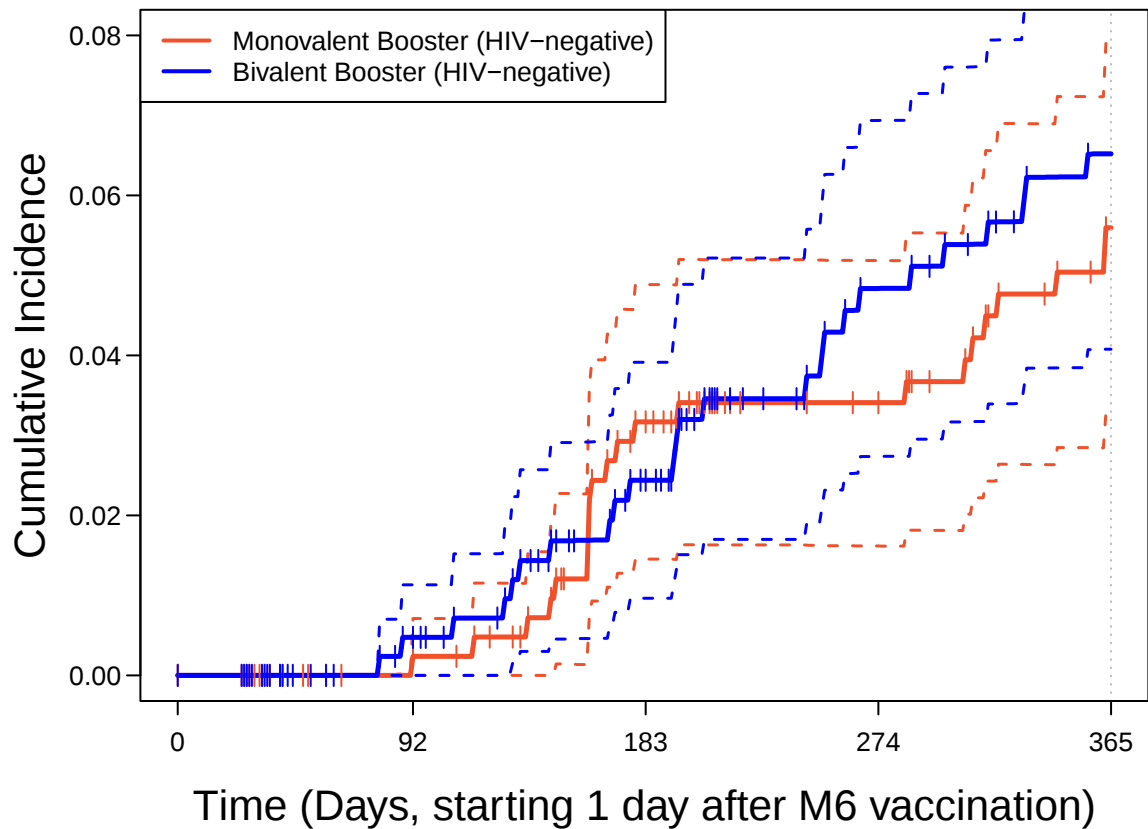
No. at Risk

Monovalent	1510	1459	1357	1256	1193
Bivalent	1546	1498	1399	1303	1243

Total Events

Monovalent	0	3	30	66	114
Bivalent	0	1	34	63	108

MBoost vs BBoost, RM6, CDC1M18, Primary (PLWoH)



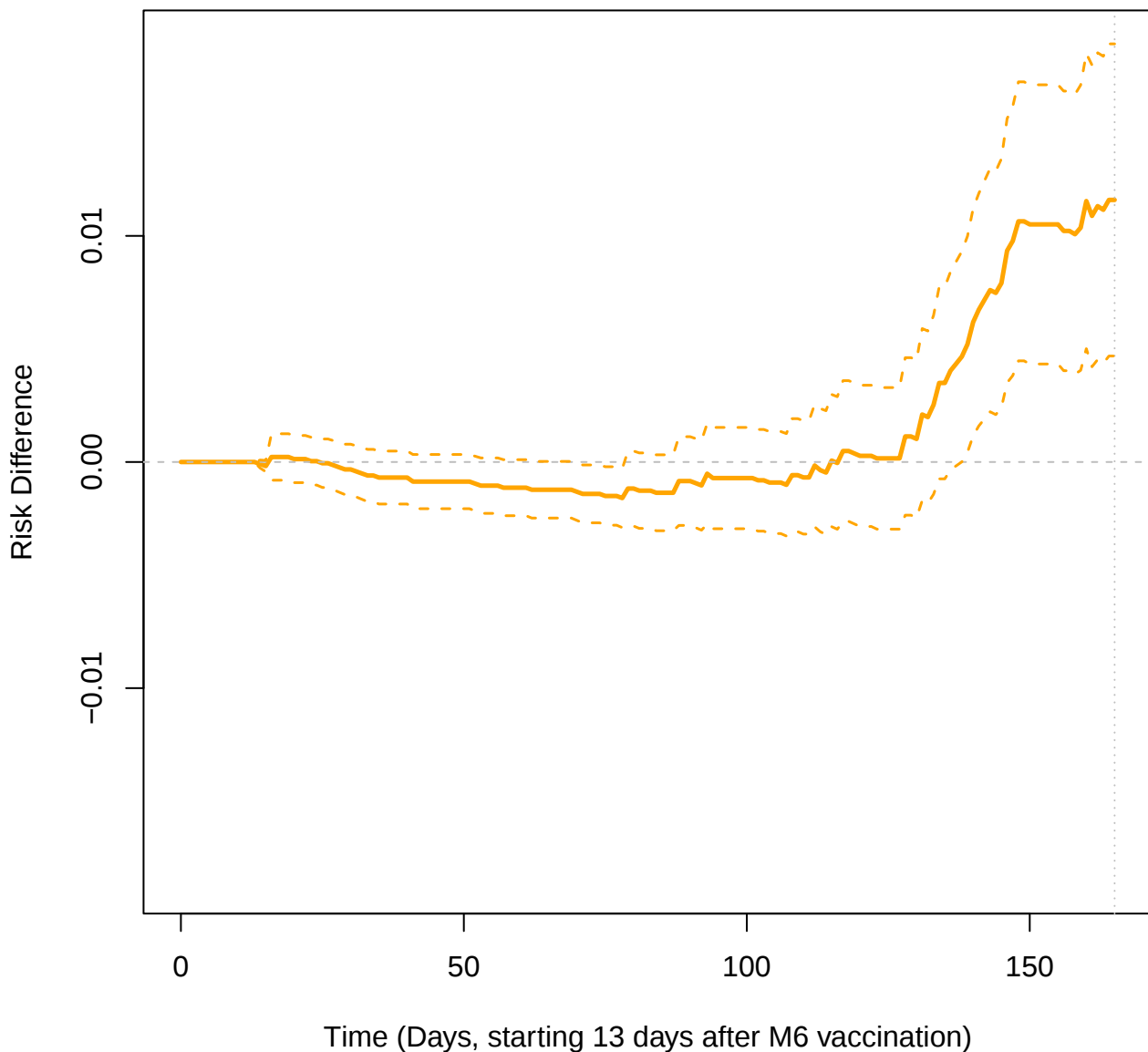
No. at Risk

Monovalent	439	418	395	359	344
Bivalent	450	417	388	344	334

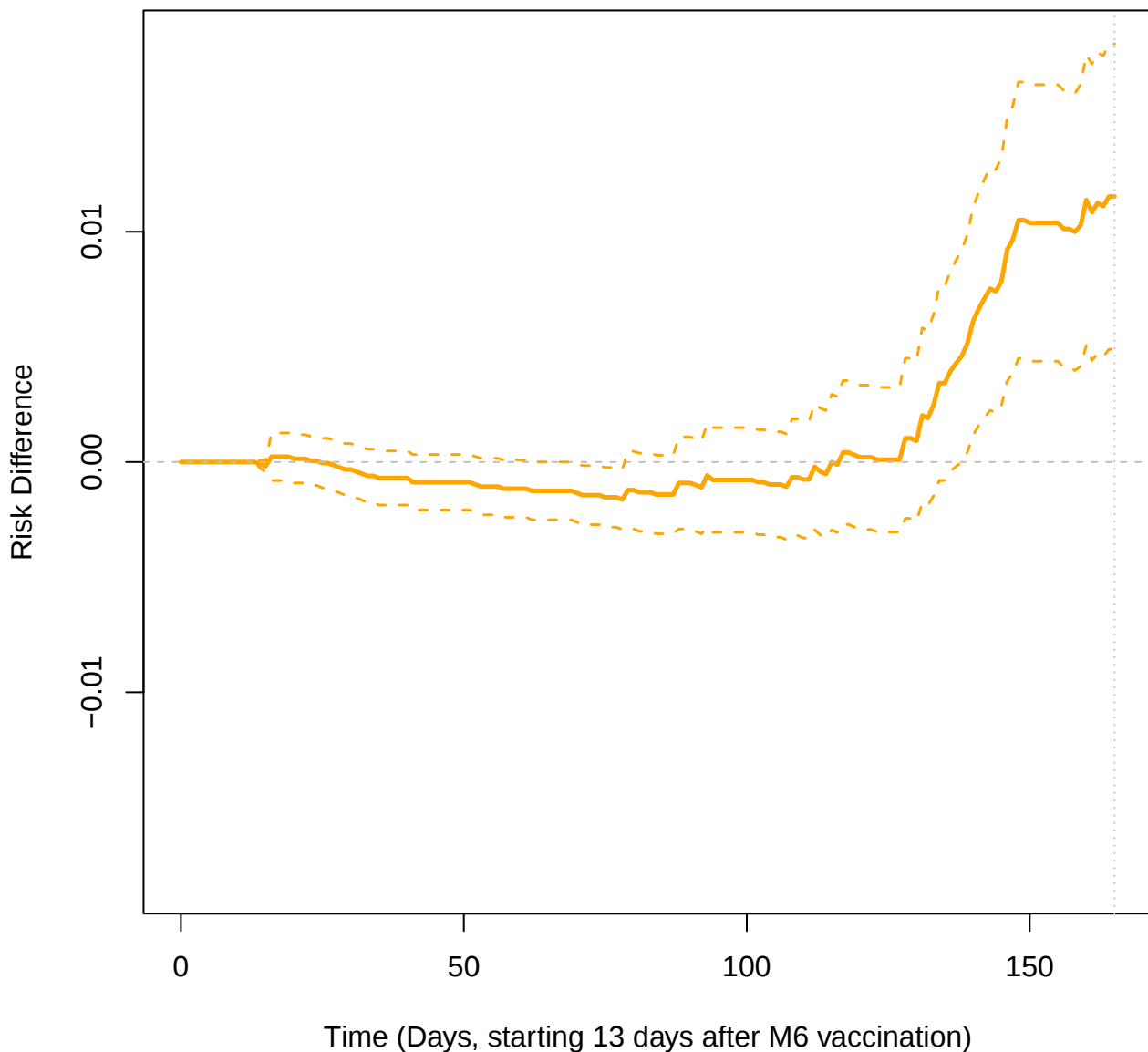
Total Events

Monovalent	0	1	13	14	22
Bivalent	0	2	10	19	25

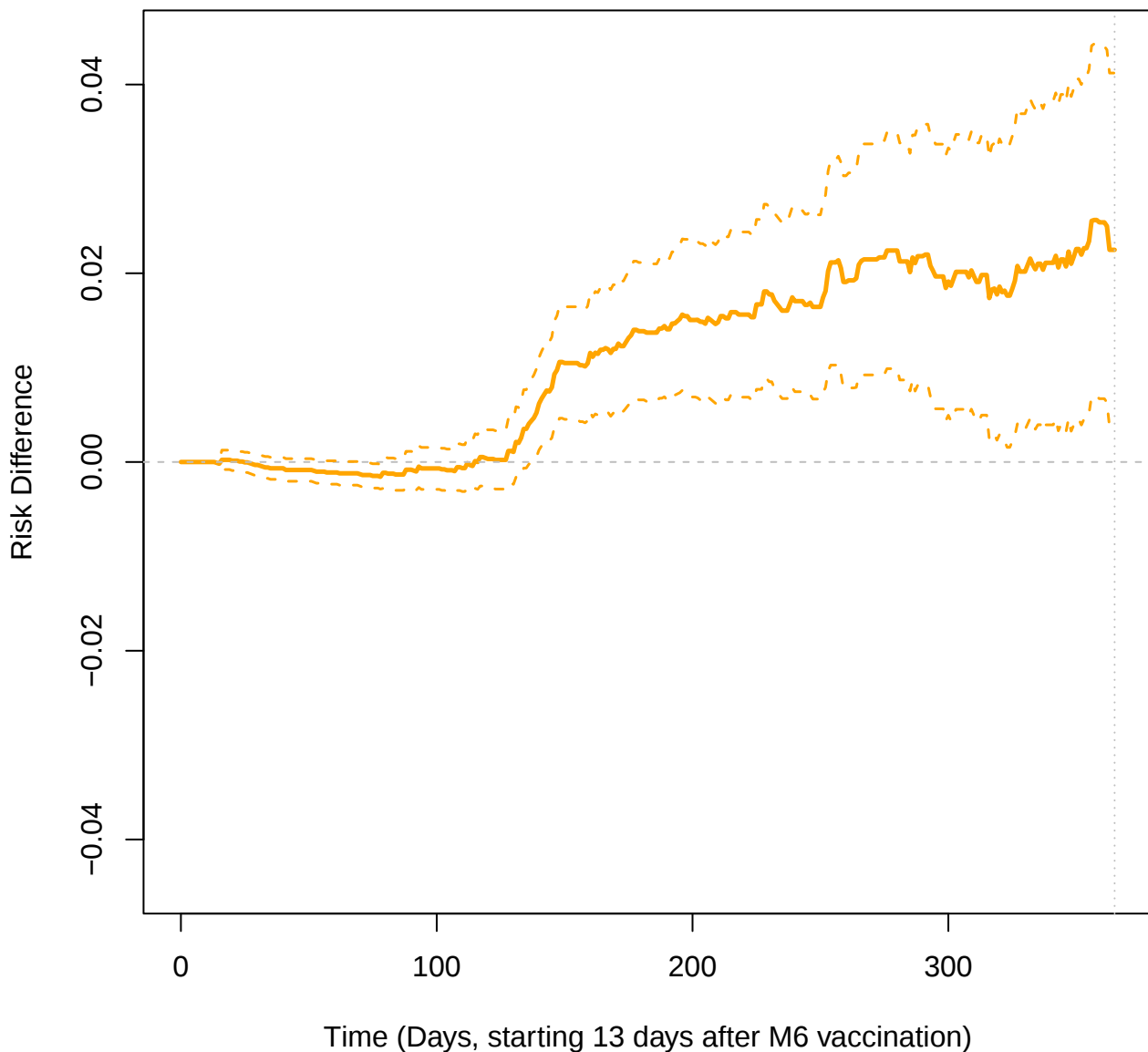
MBoost vs BBoost, FPP, CDC14M12, Primary



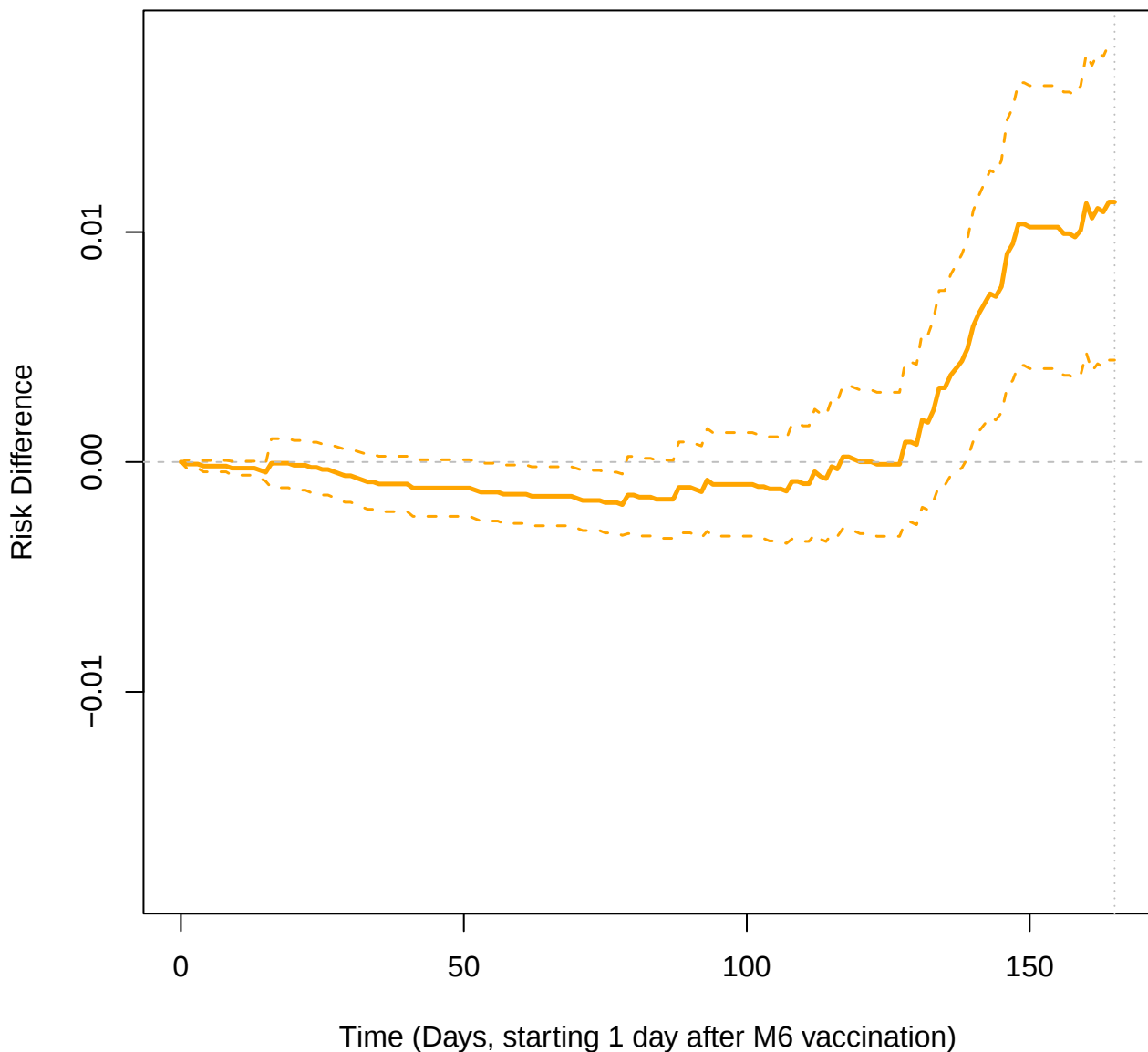
MBoost vs BBoost, FPP, CDC14M12, Sensitivity



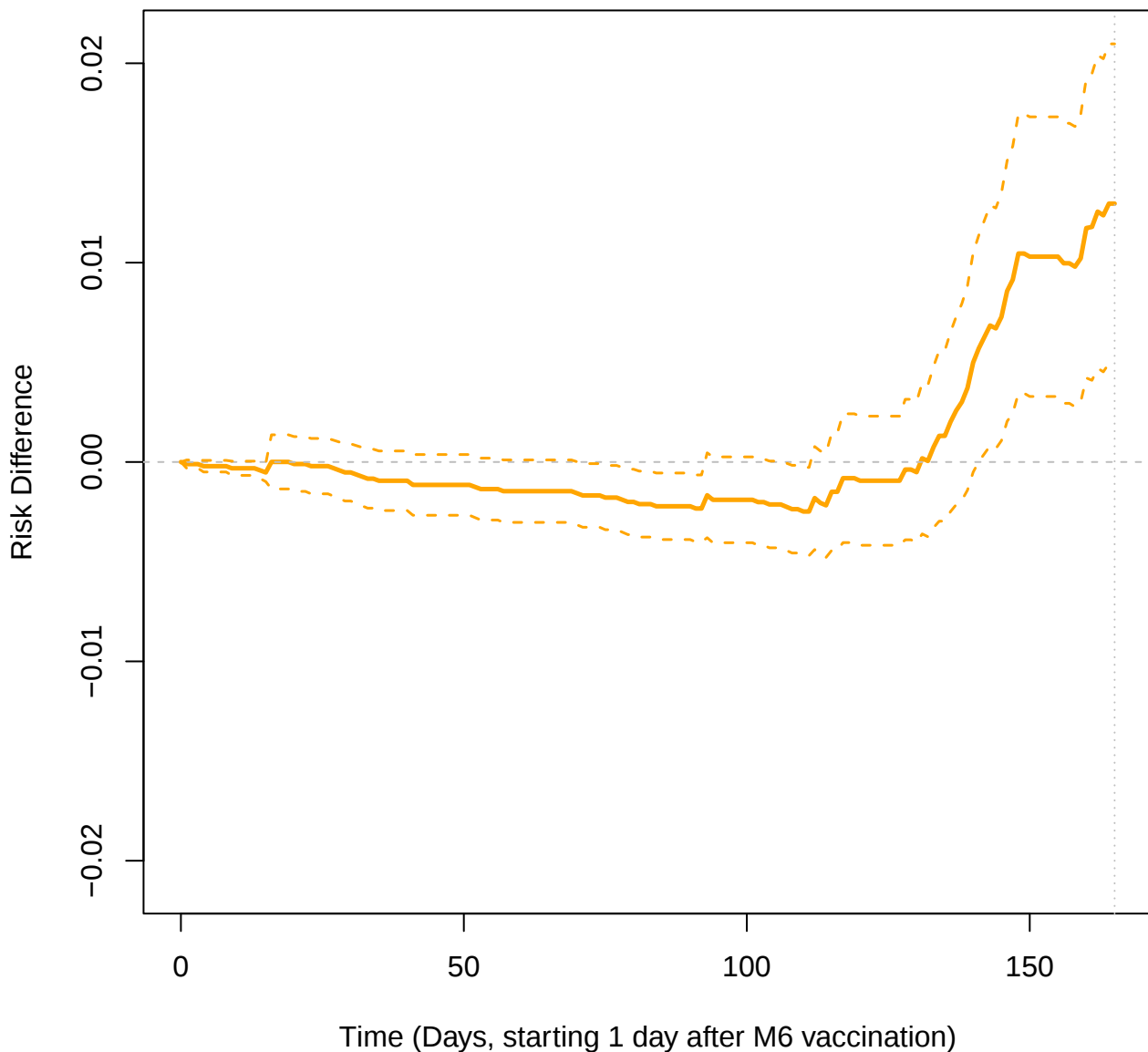
MBoost vs BBoost, FPP, CDC14M18, Primary



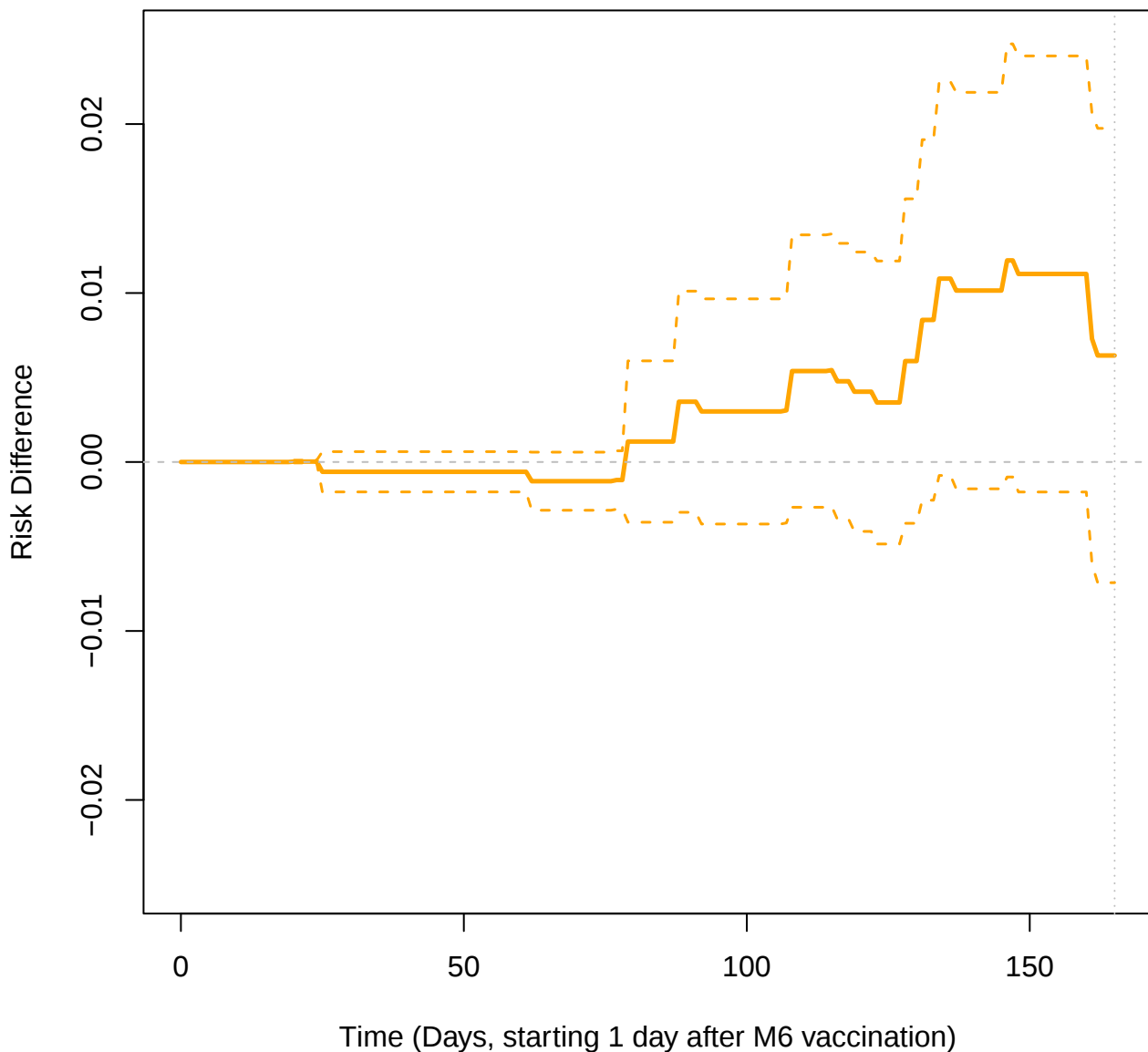
MBoost vs BBoost, FM6, CDC1M12, Primary



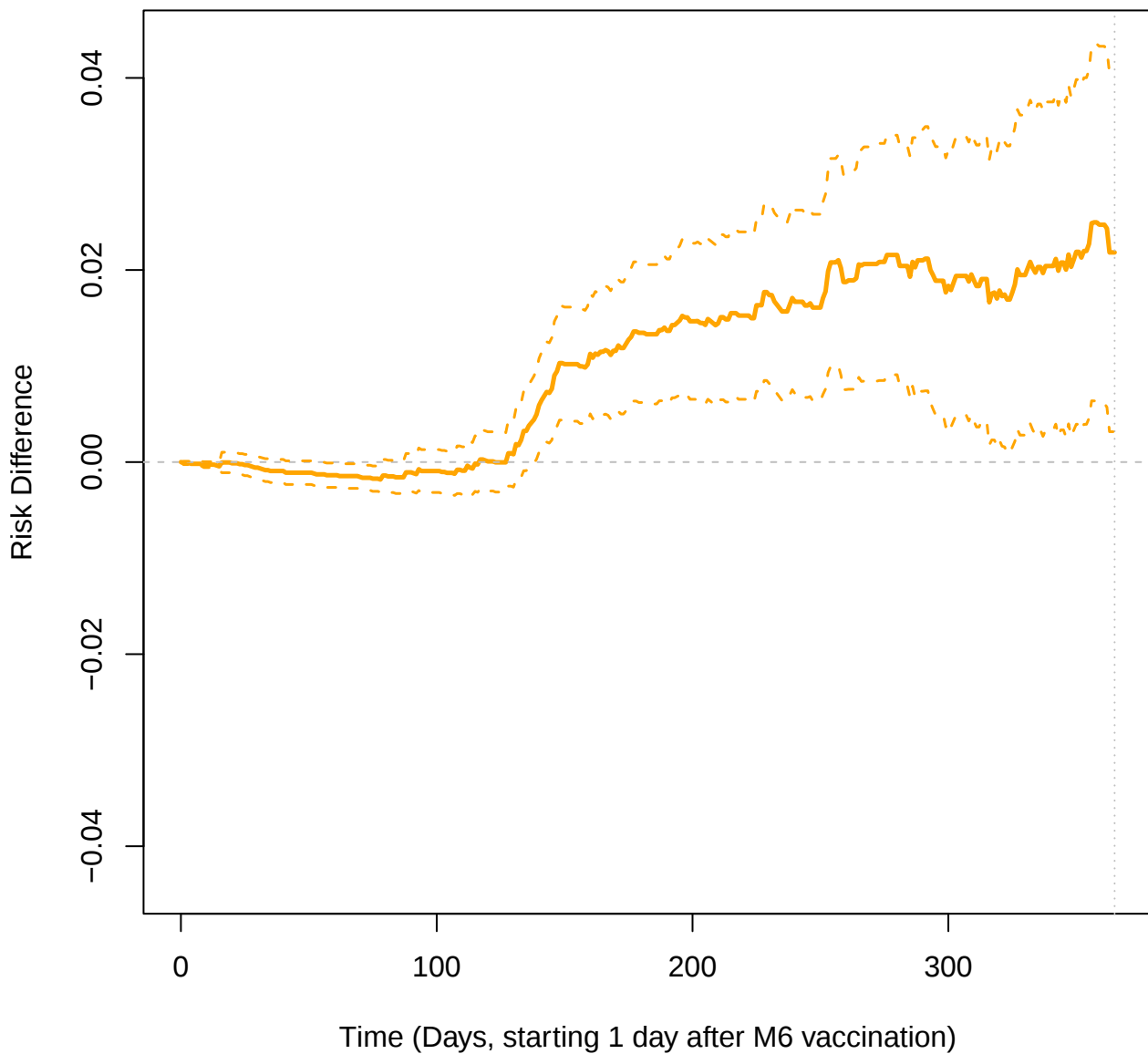
MBoost vs BBoost, FM6, CDC1M12, Primary (PLWH)



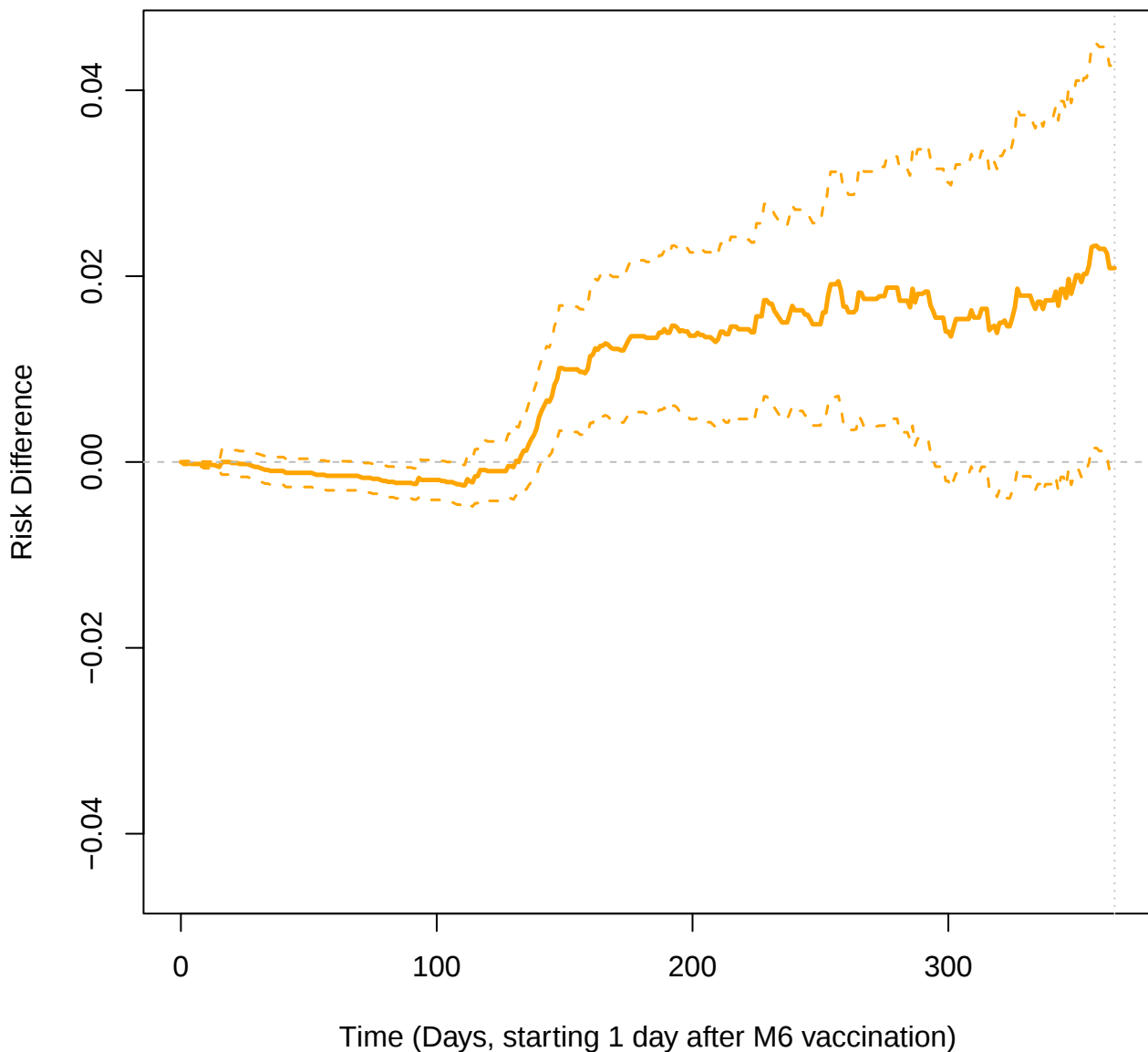
MBoost vs BBoost, FM6, CDC1M12, Primary (PLWoH)



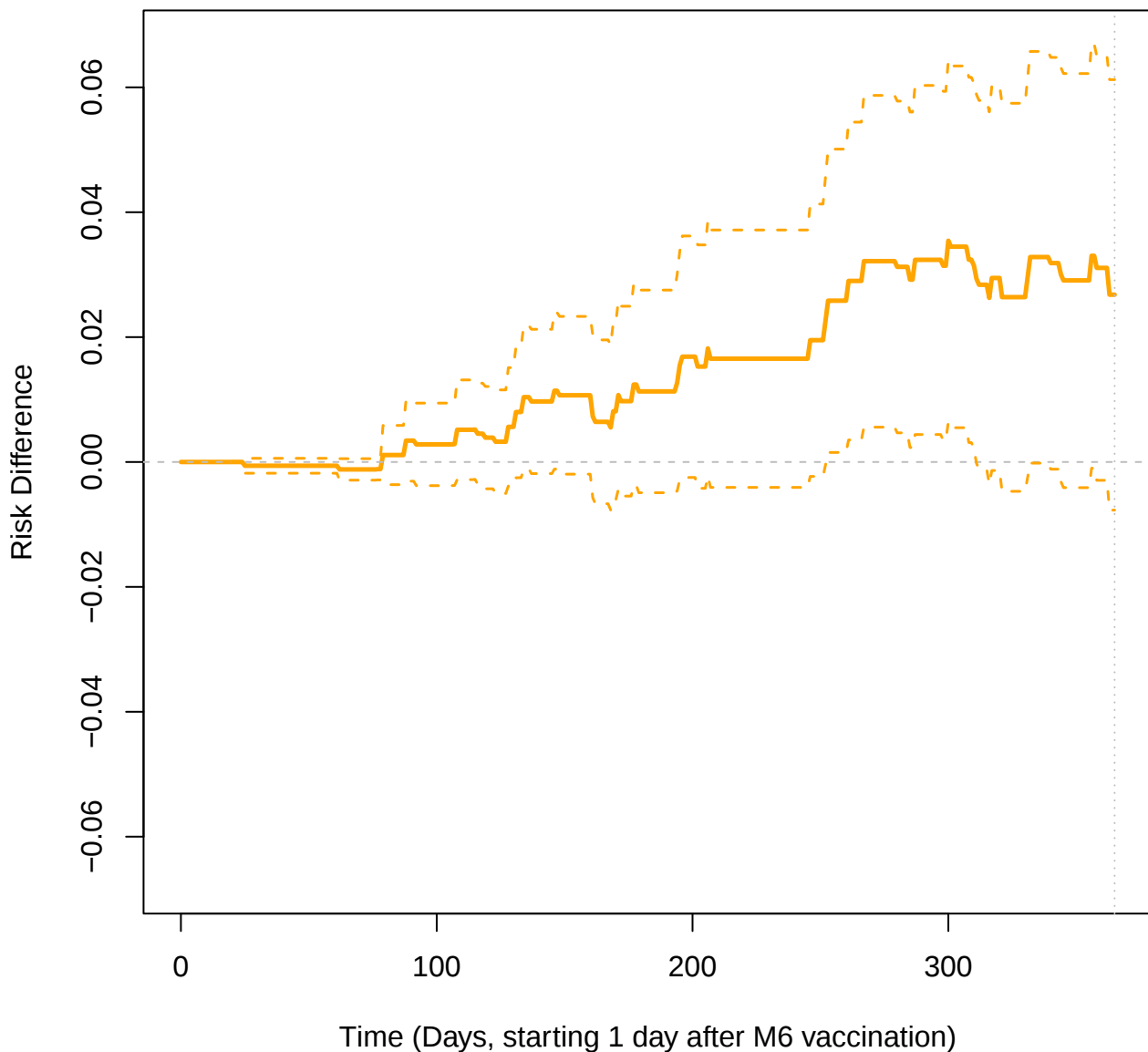
MBoost vs BBoost, FM6, CDC1M18, Primary



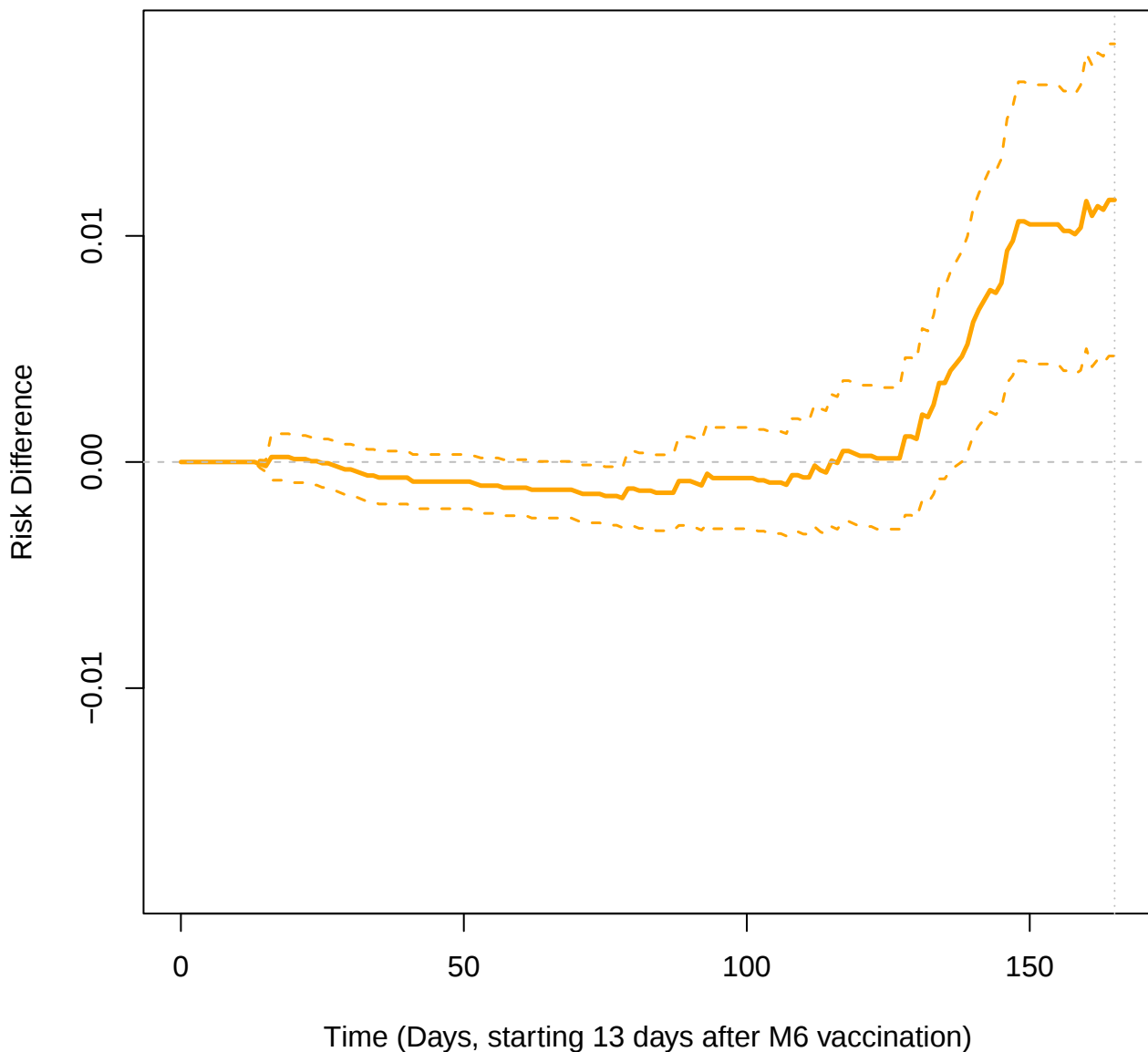
MBoost vs BBoost, FM6, CDC1M18, Primary (PLWH)



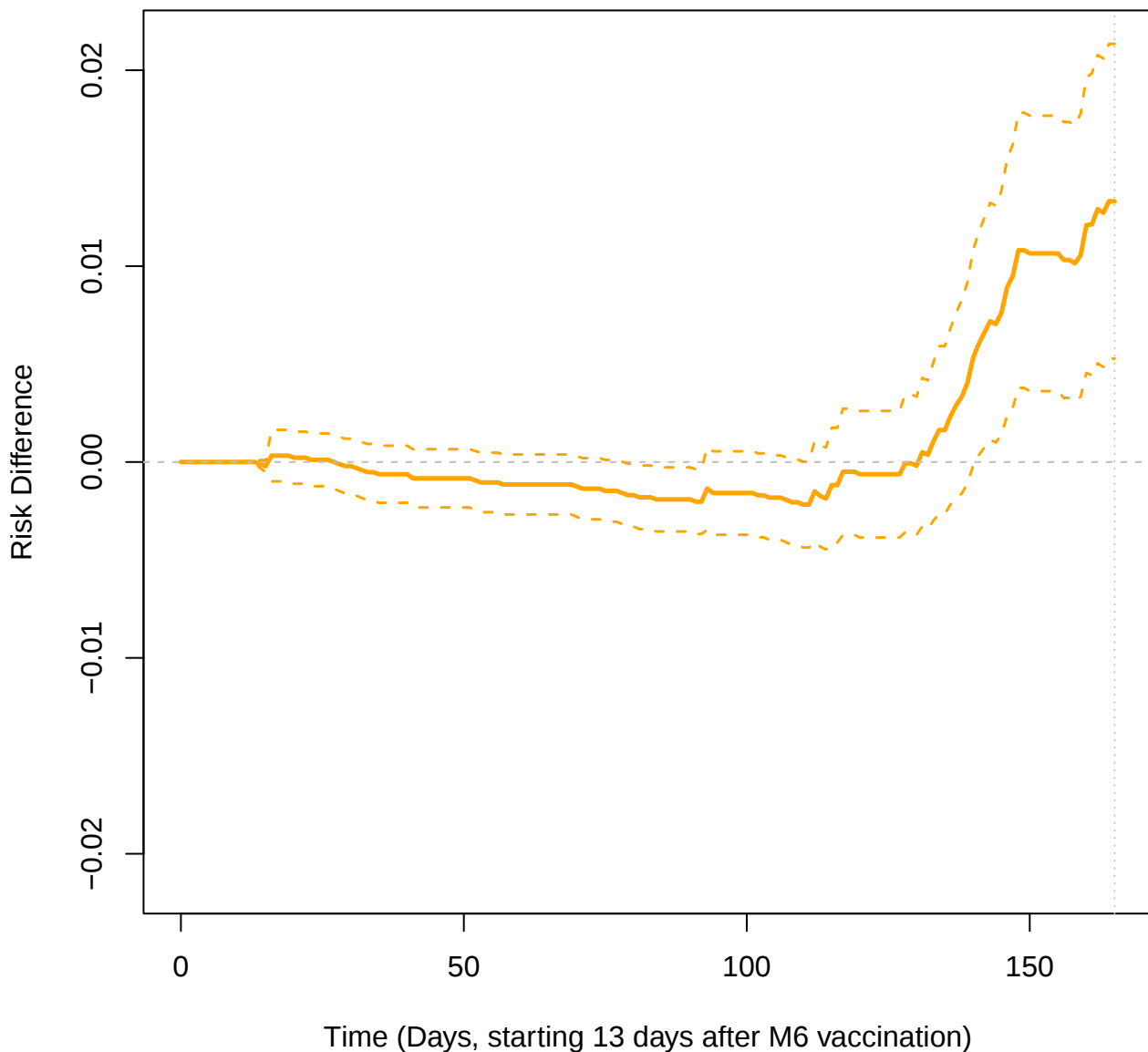
MBoost vs BBoost, FM6, CDC1M18, Primary (PLWoH)



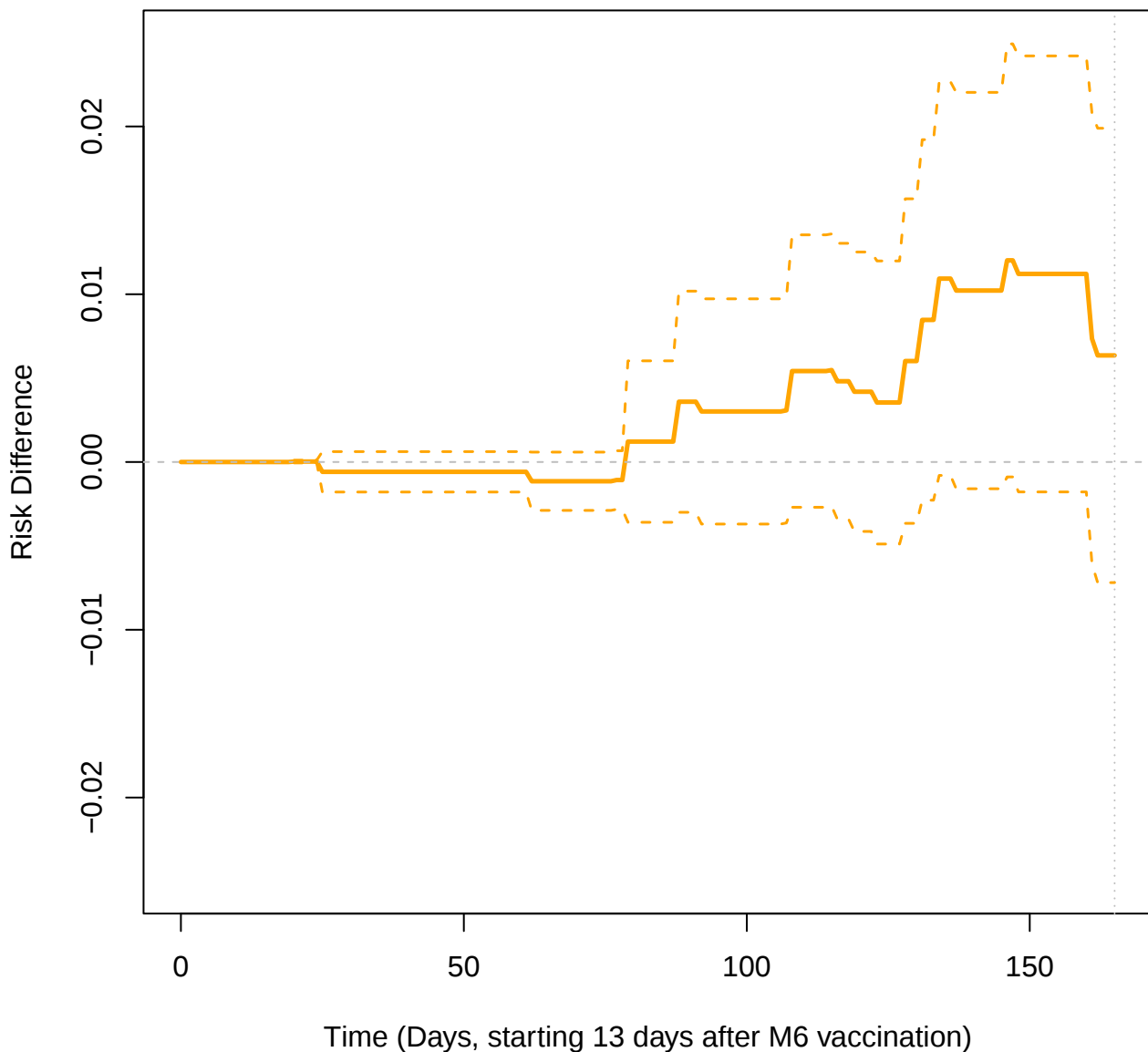
MBoost vs BBoost, FPP, CDC14M12, Primary



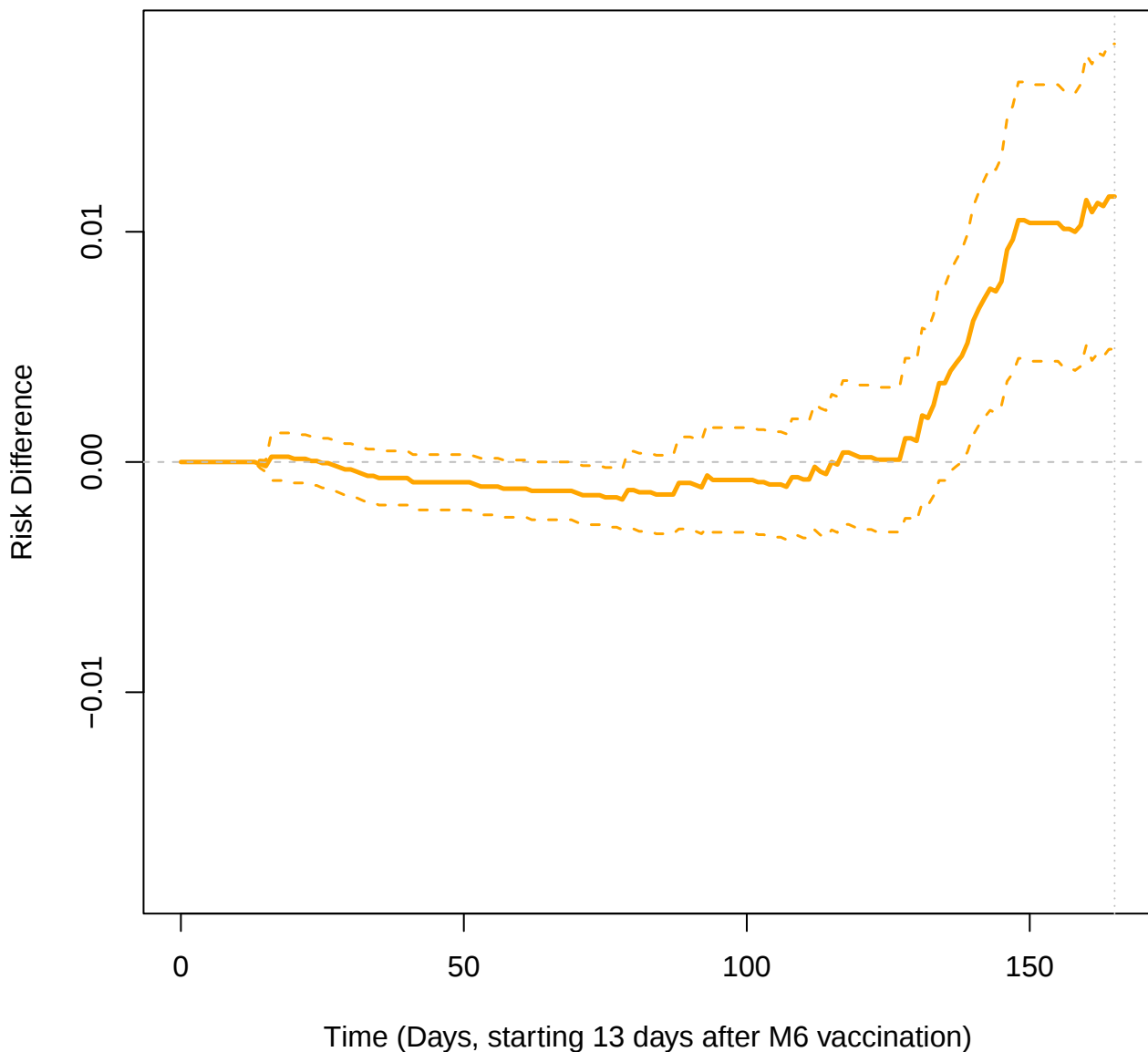
MBoost vs BBoost, FPP, CDC14M12, Primary (PLWH)



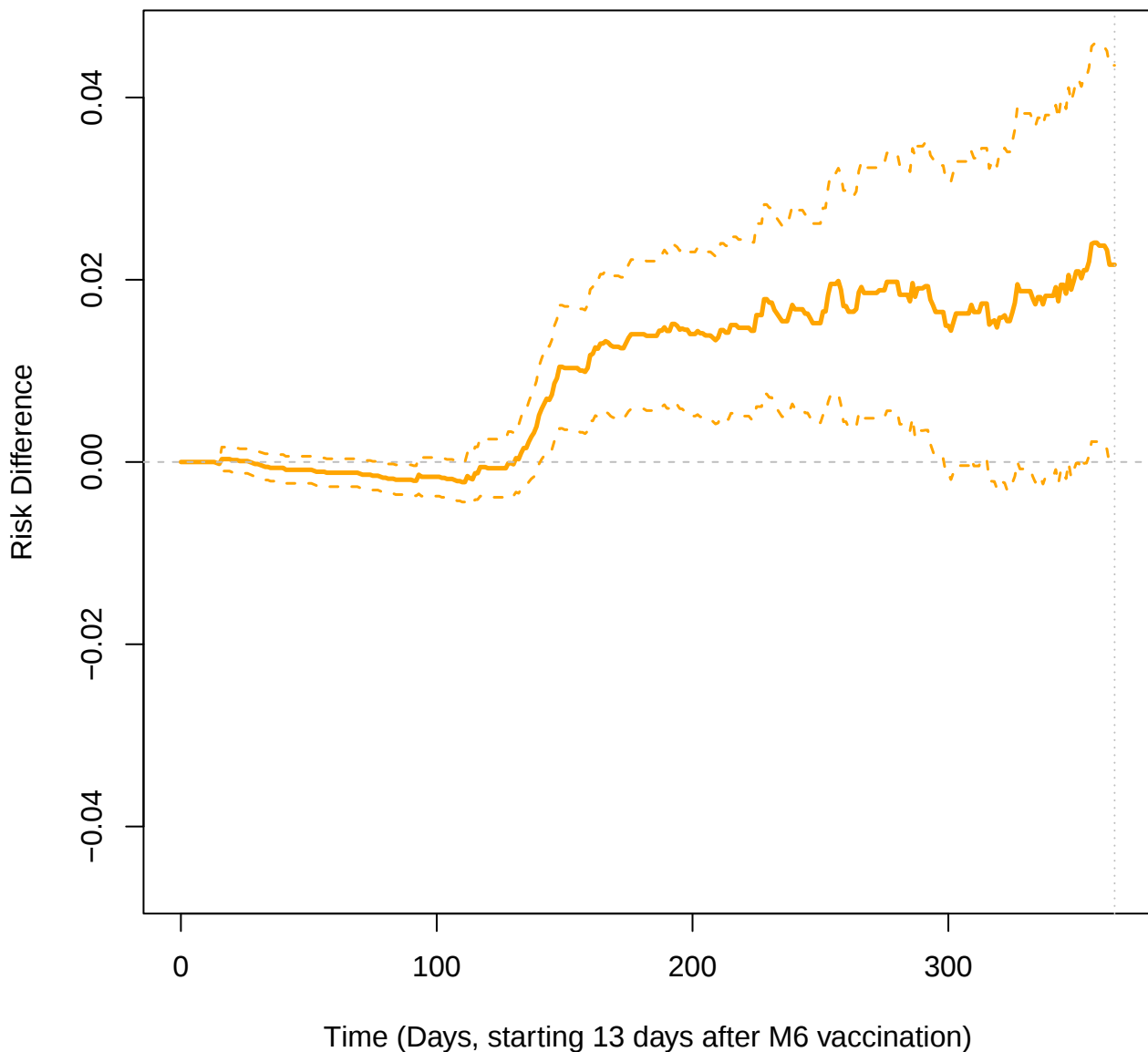
MBoost vs BBoost, FPP, CDC14M12, Primary (PLWoH)



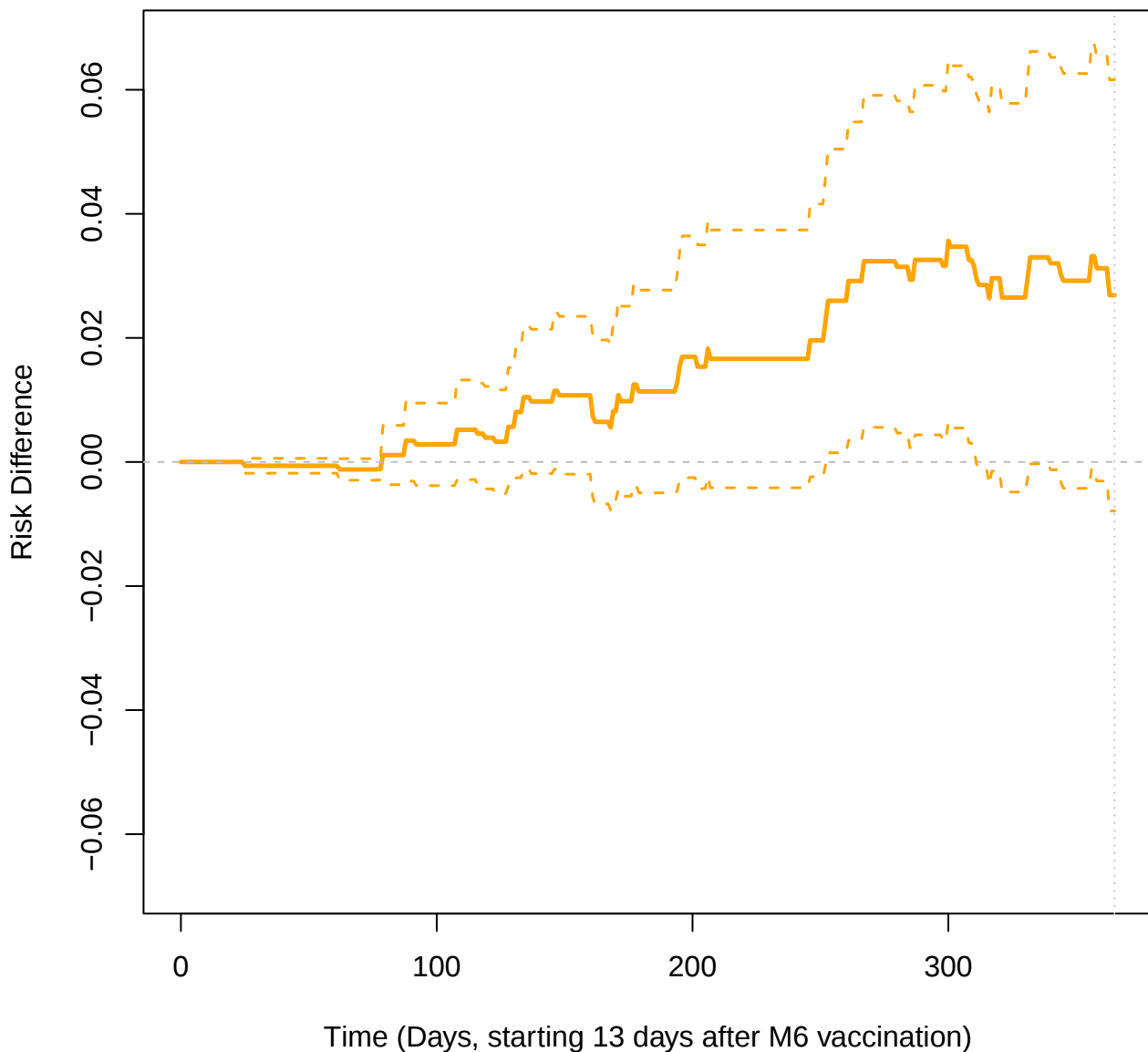
MBoost vs BBoost, FPP, CDC14M12, Sensitivity



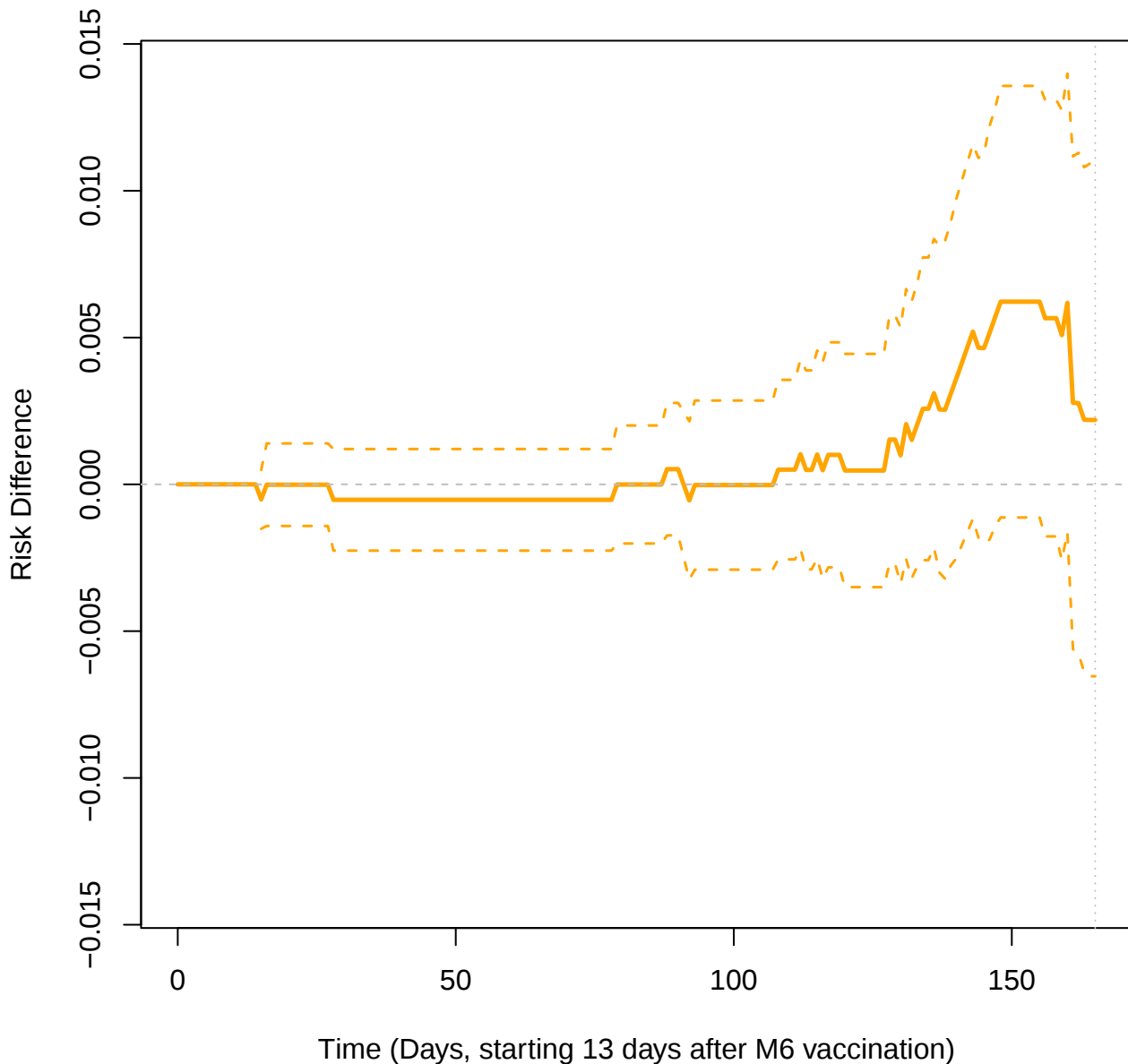
MBoost vs BBoost, FPP, CDC14M18, Primary (PLWH)



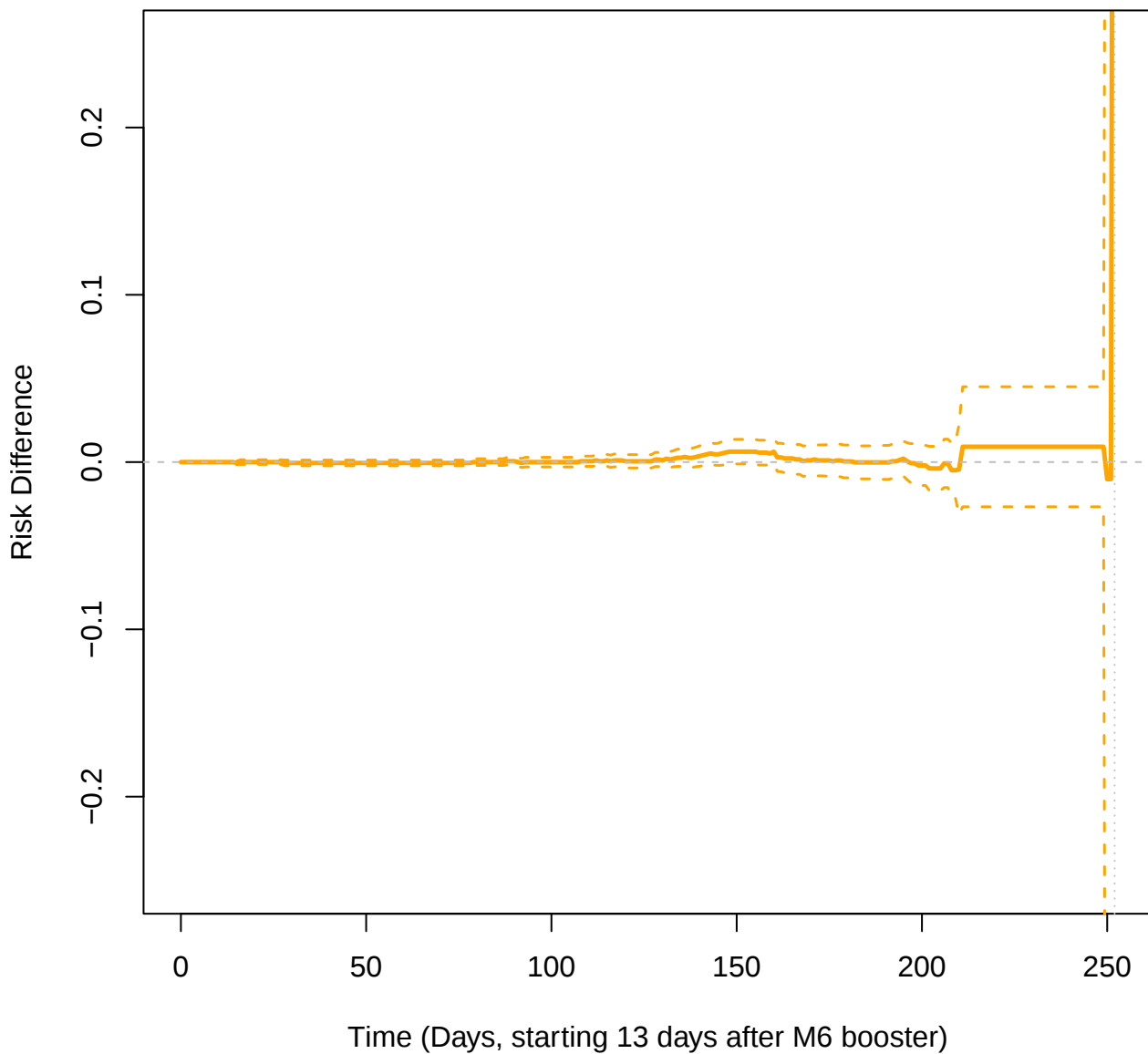
MBoost vs BBoost, FPP, CDC14M18, Primary (PLWoH)



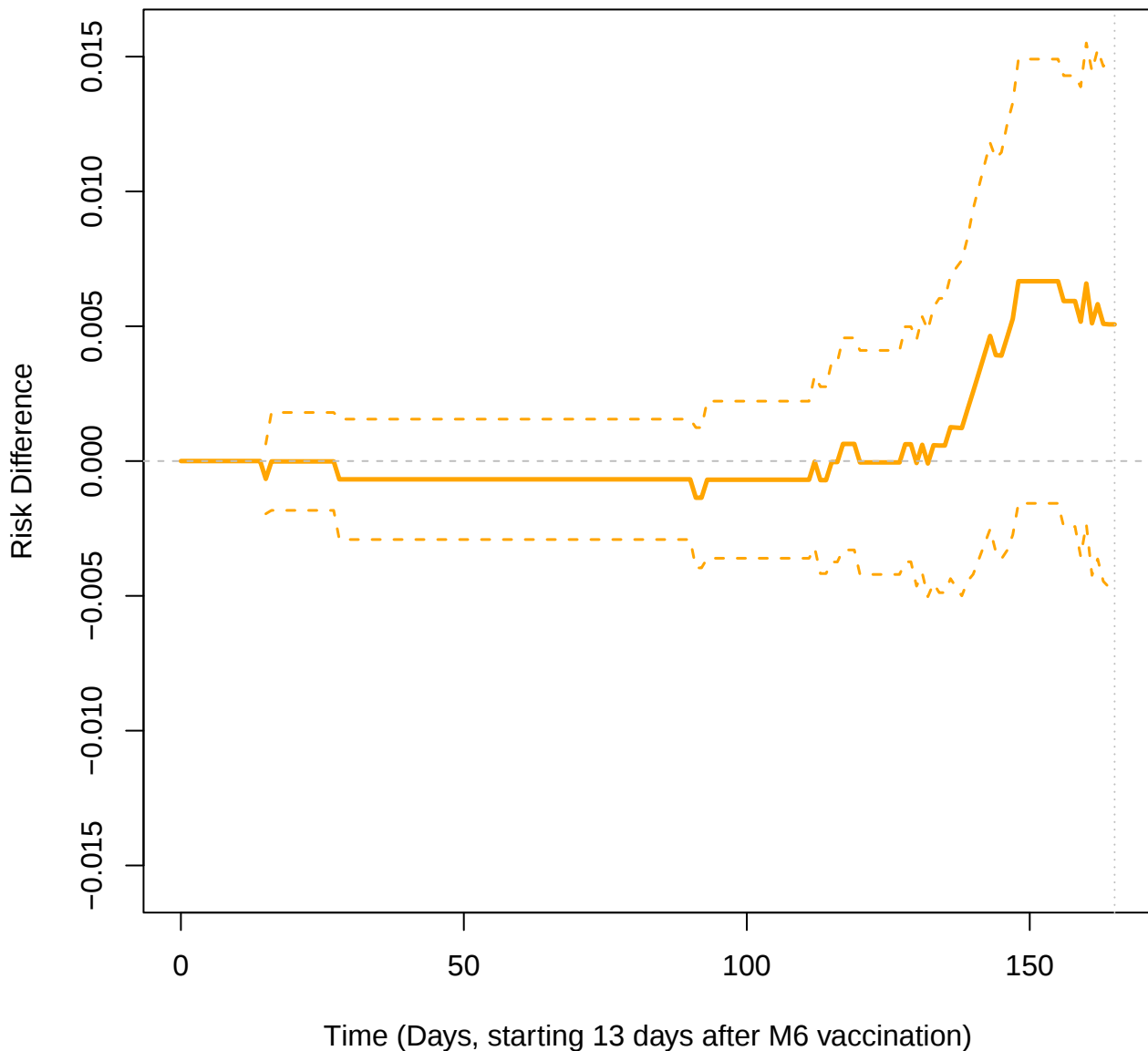
MBoost vs BBoost, RM6, CDC14M12, Primary



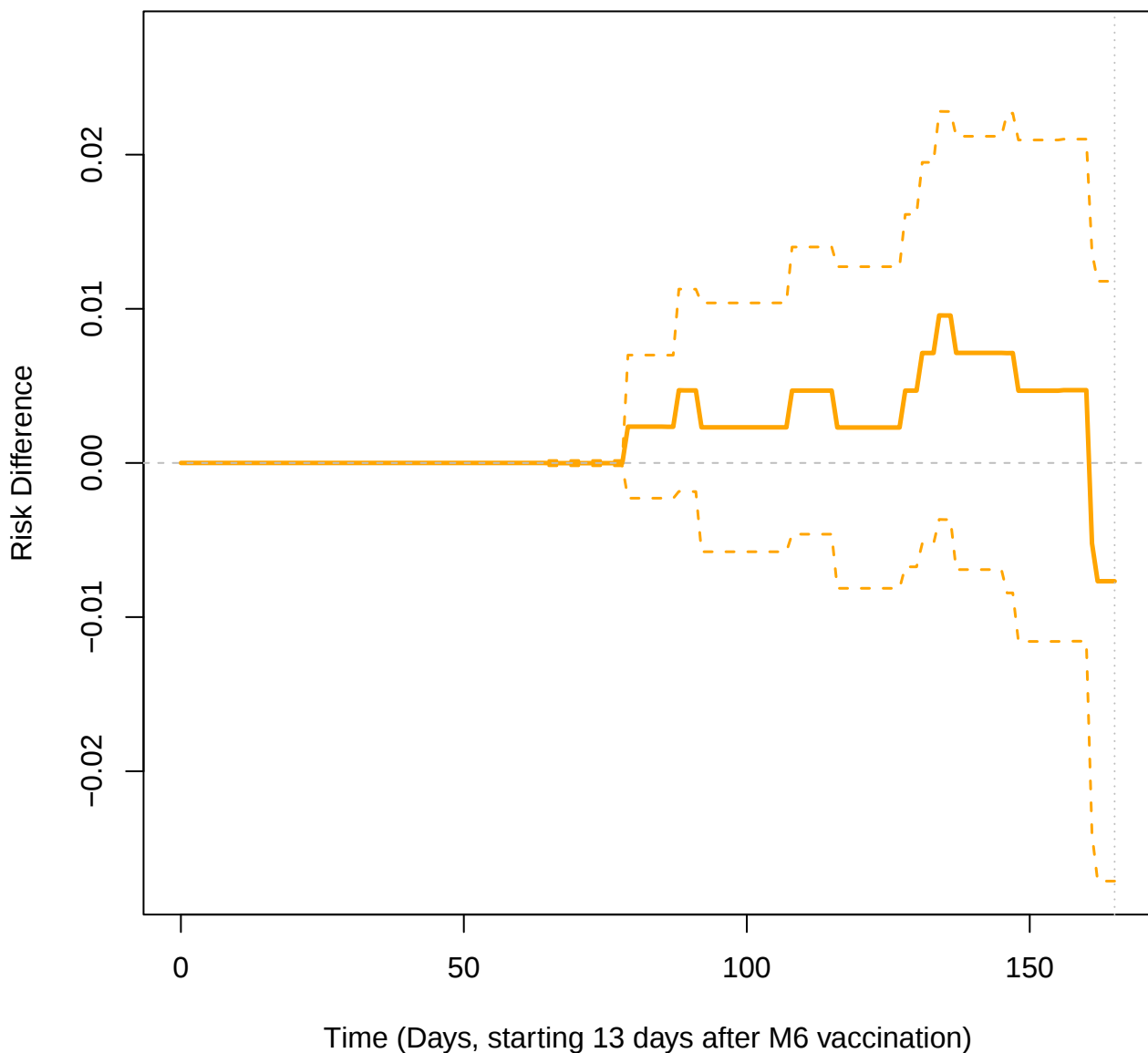
COVID-19 incidence over study time



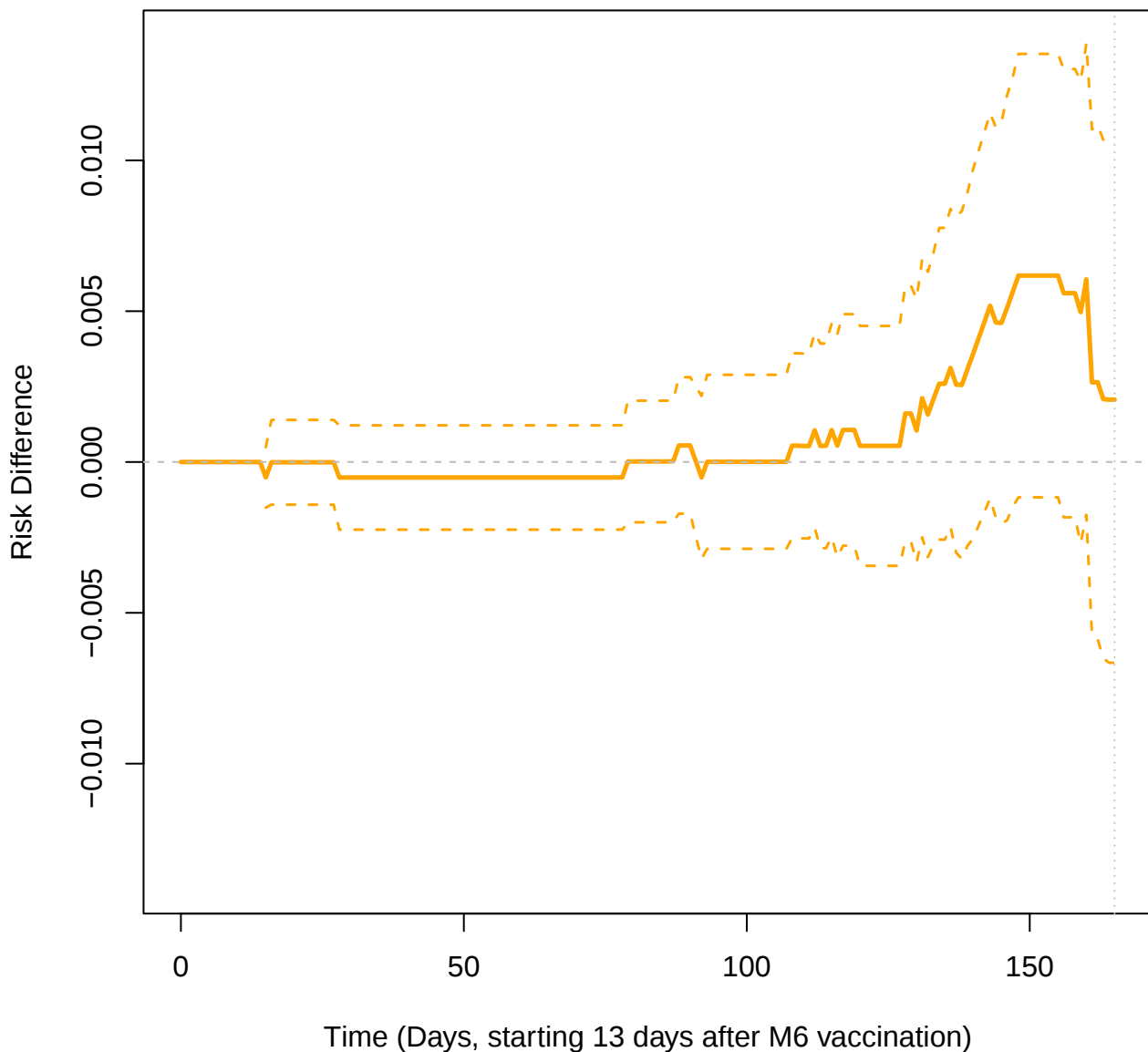
MBoost vs BBoost, RM6, CDC14M12, Primary (PLWH)



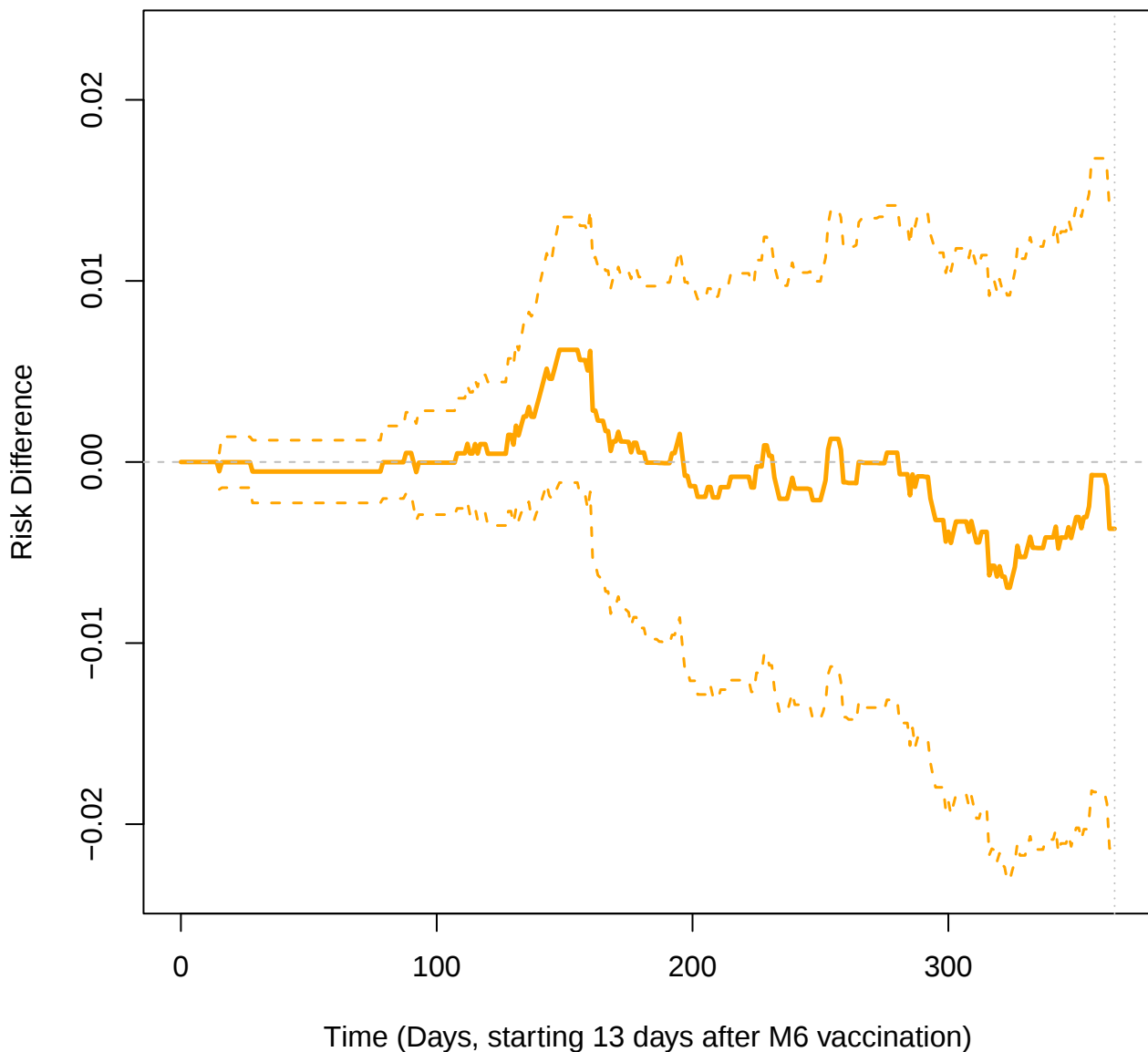
MBoost vs BBoost, RM6, CDC14M12, Primary (PLWoH)



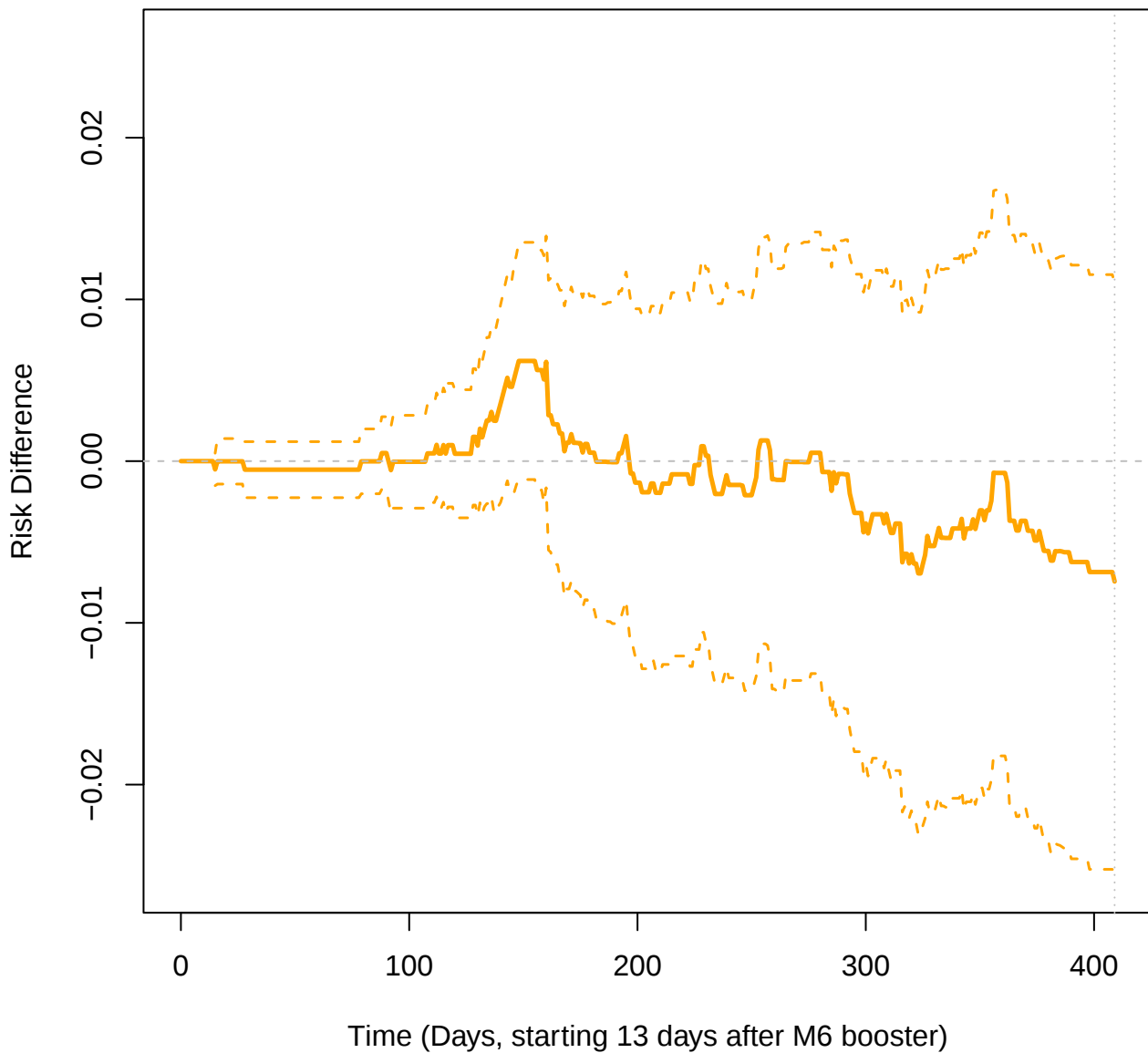
MBoost vs BBoost, RM6, CDC14M12, Sensitivity



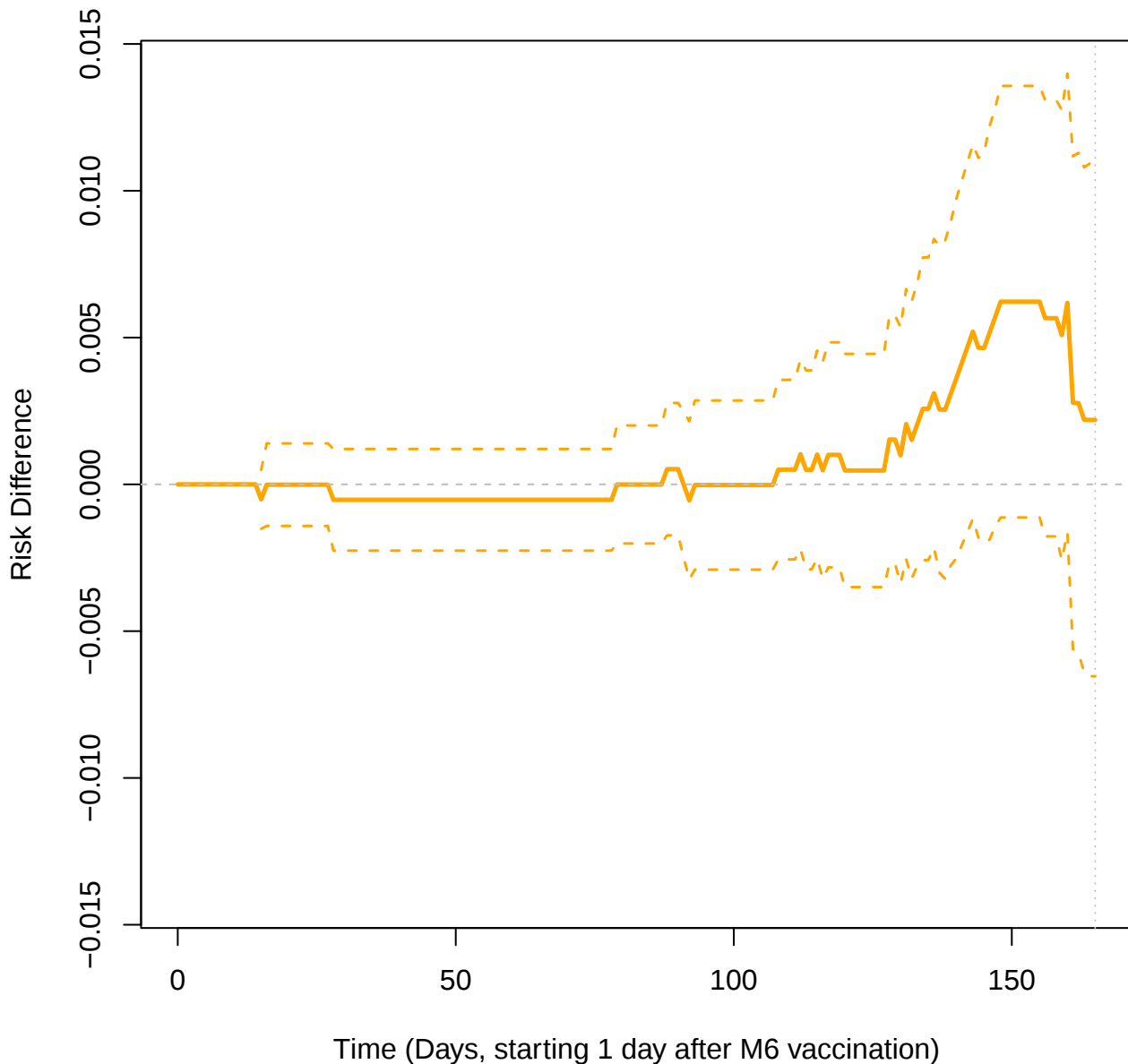
MBoost vs BBoost, RM6, CDC14M18, Primary



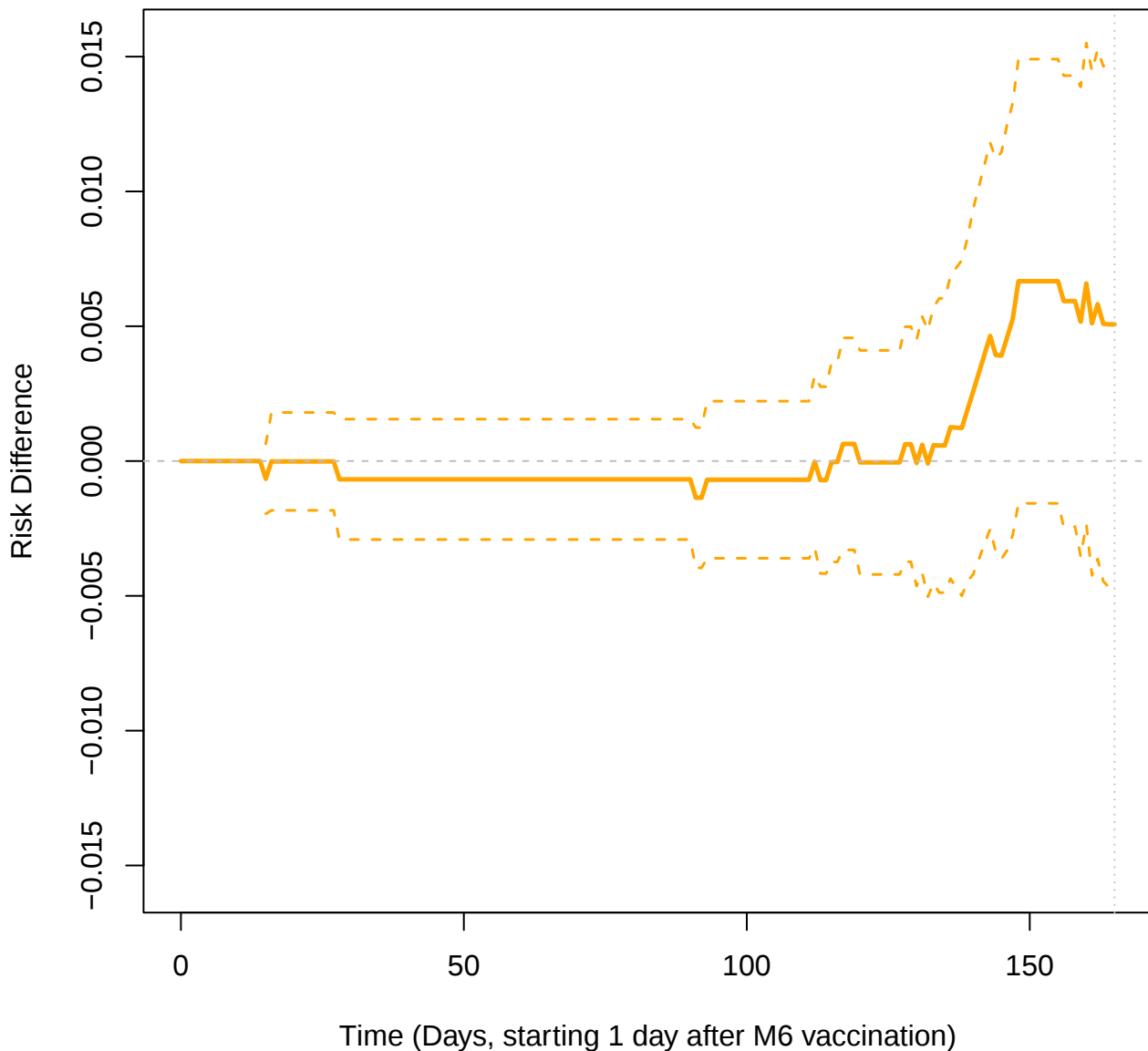
COVID-19 incidence over study time



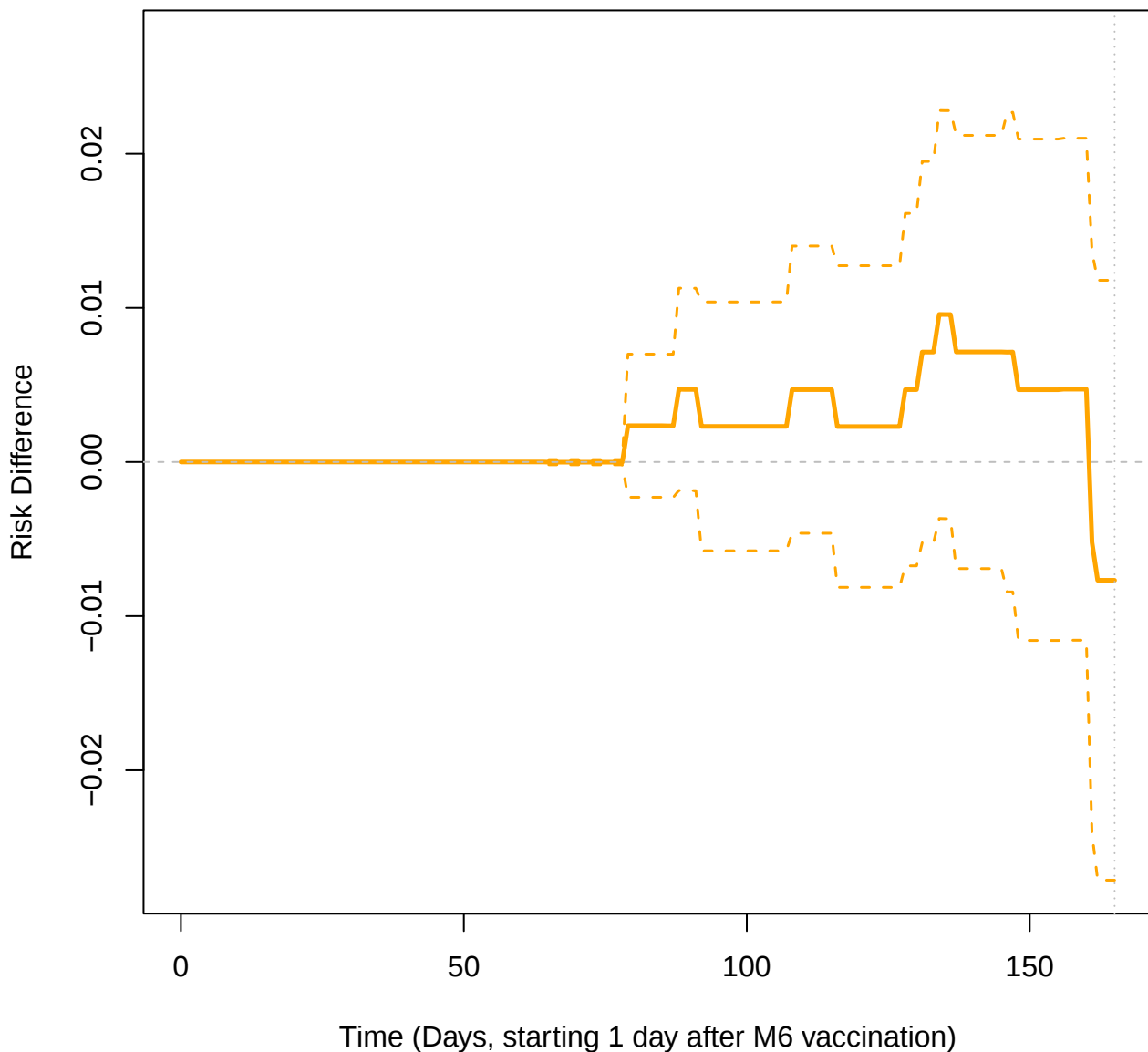
MBoost vs BBoost, RM6, CDC1M12, Primary



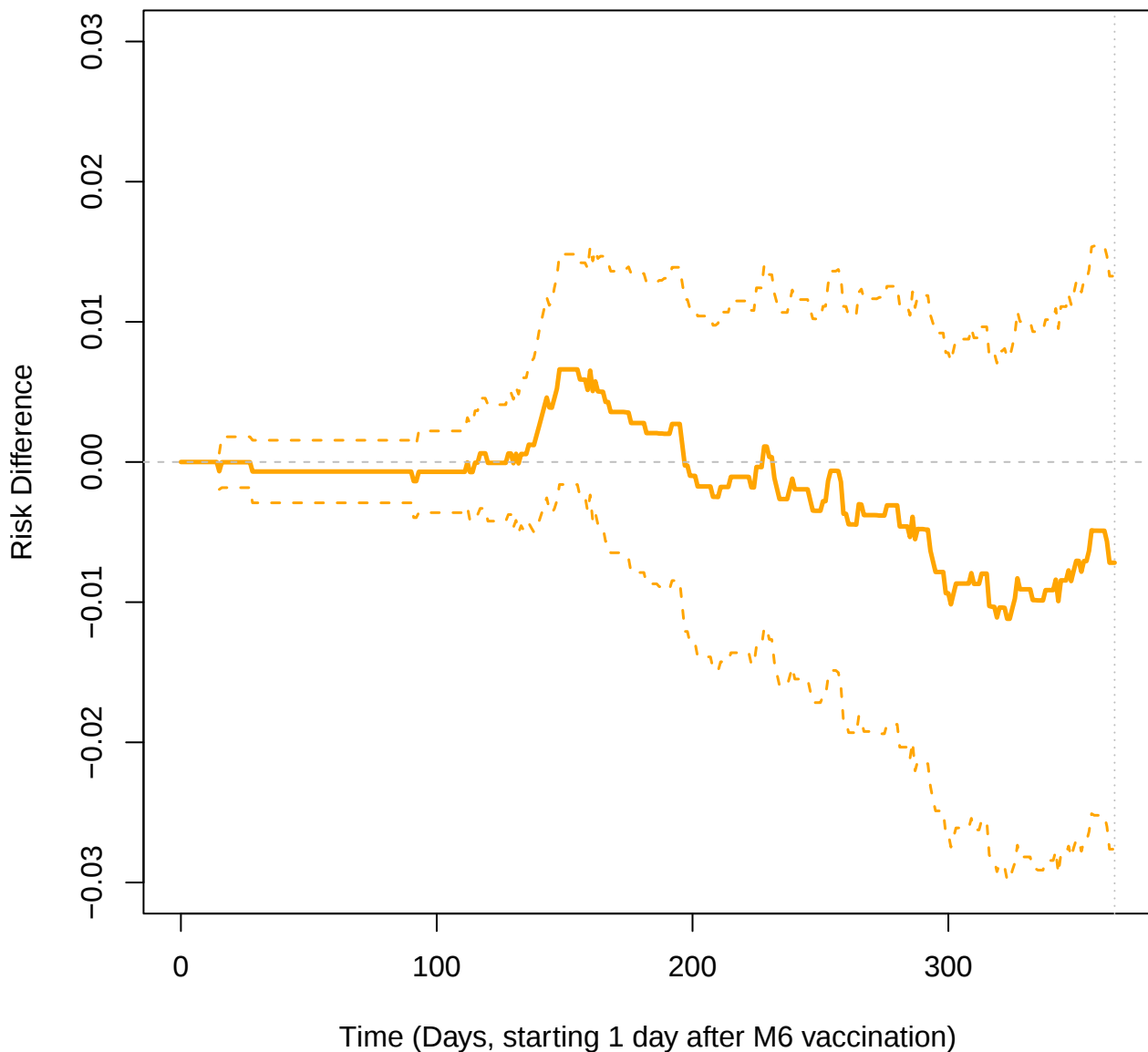
MBoost vs BBoost, RM6, CDC1M12, Primary (PLWH)



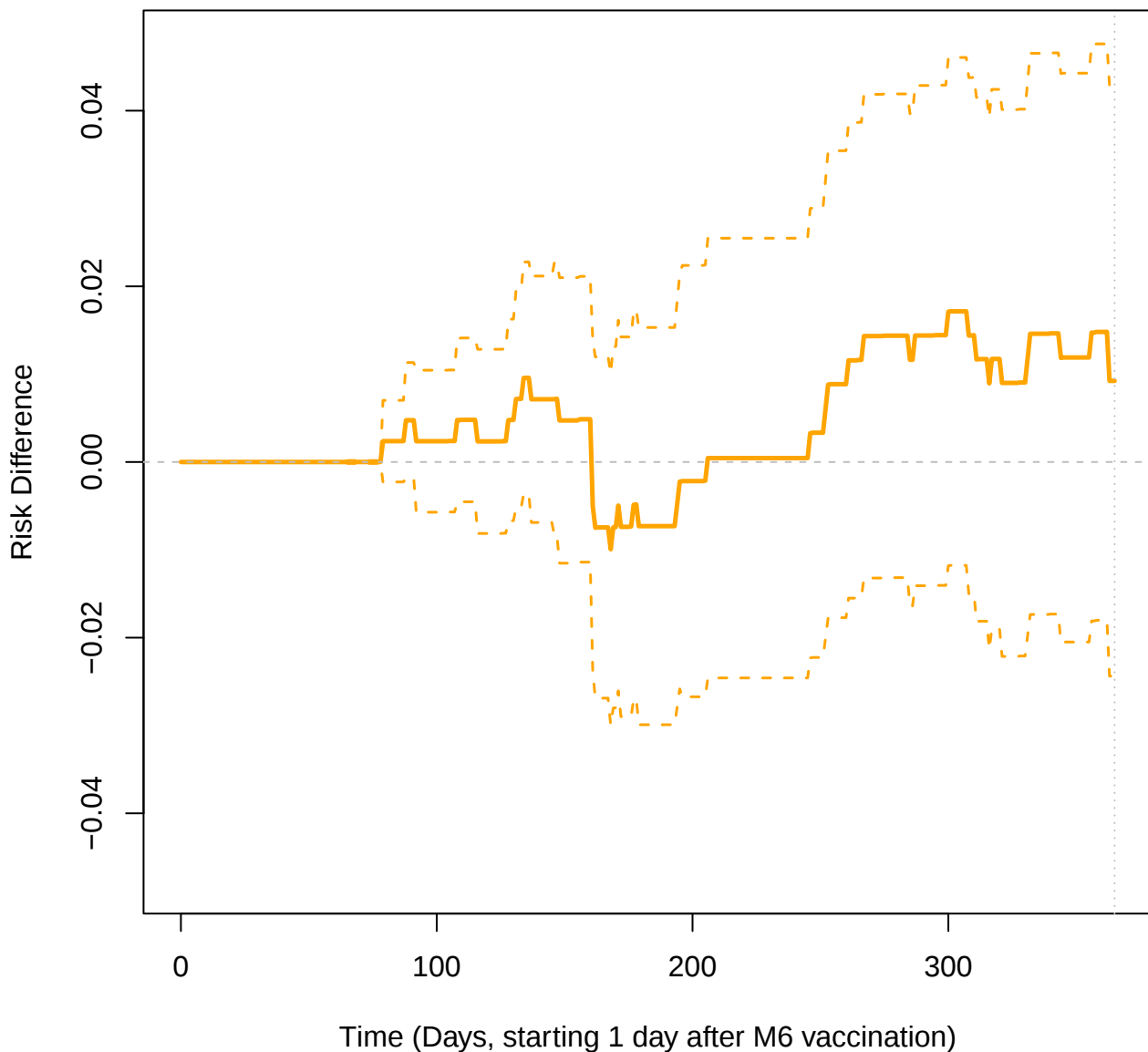
MBoost vs BBoost, RM6, CDC1M12, Primary (PLWoH)



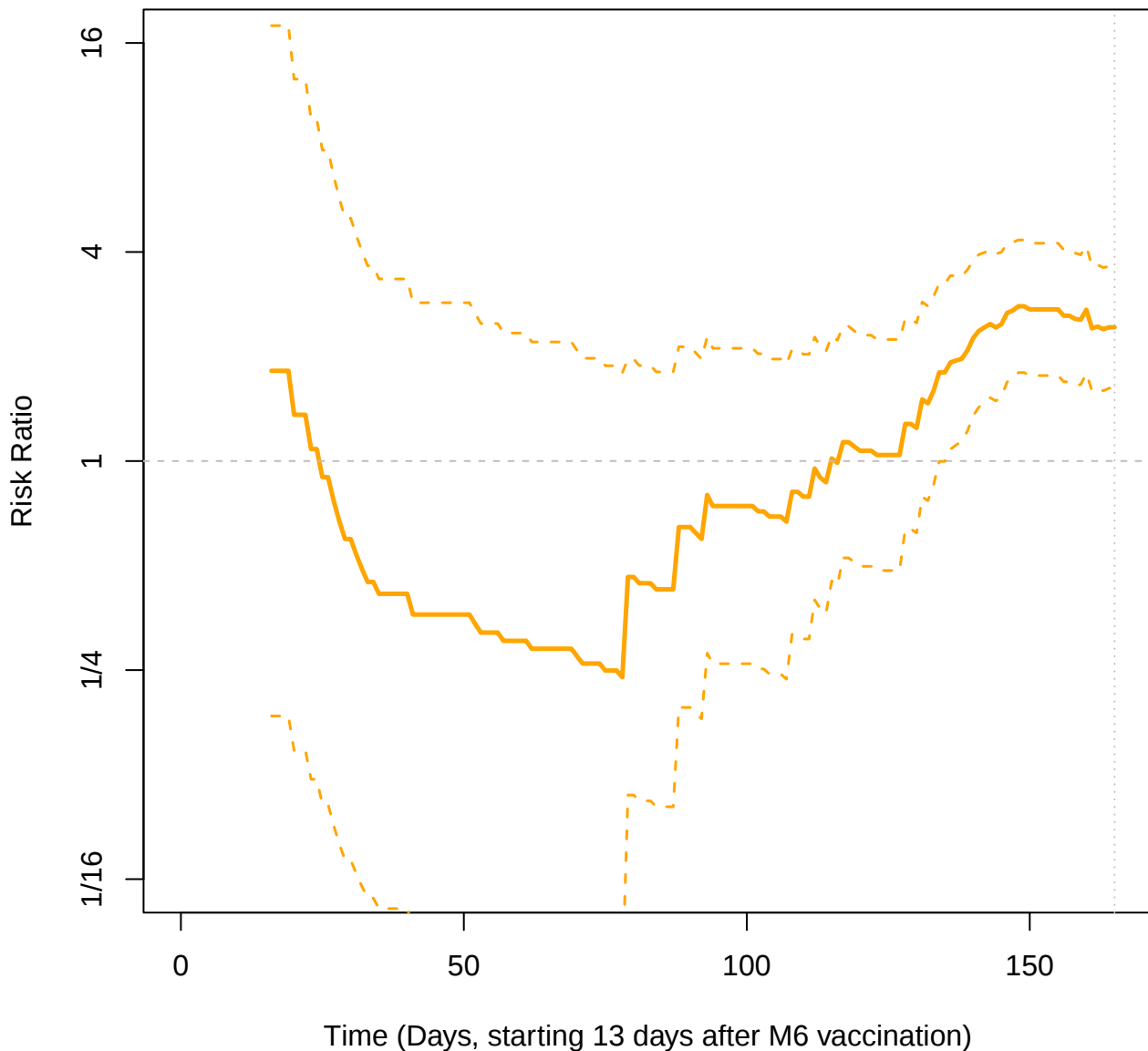
MBoost vs BBoost, RM6, CDC1M18, Primary (PLWH)



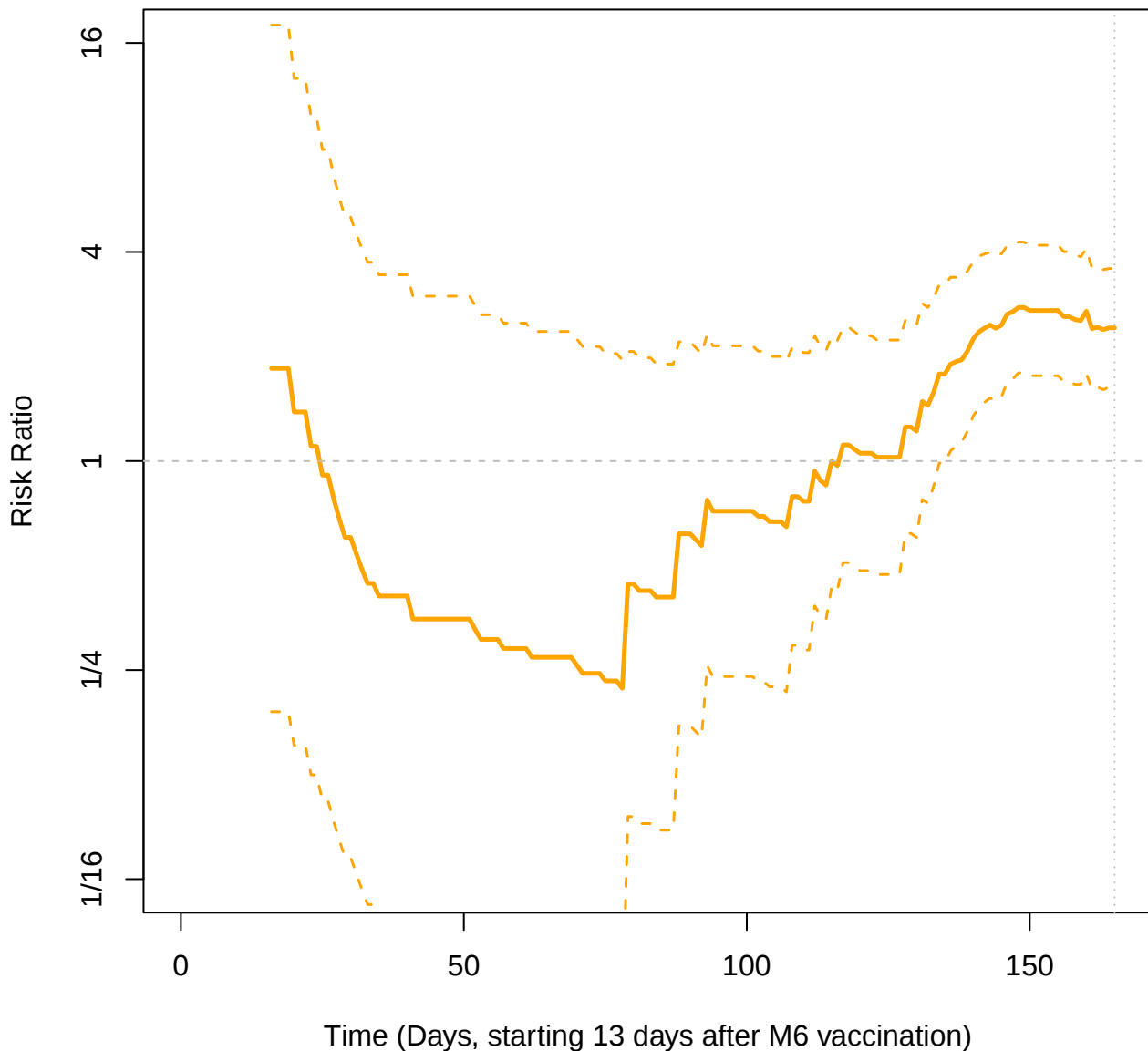
MBoost vs BBoost, RM6, CDC1M18, Primary (PLWoH)



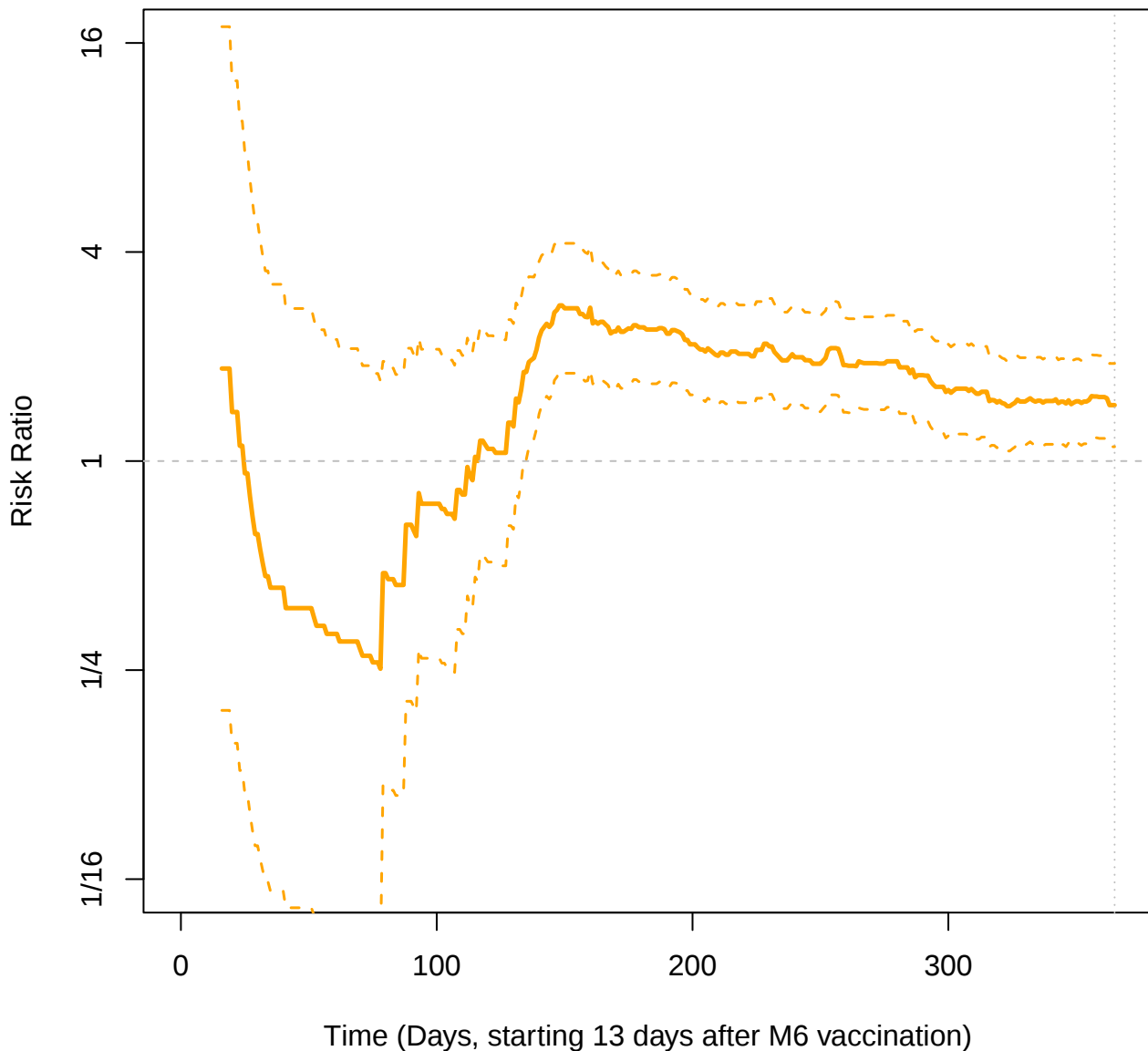
MBoost vs BBoost, FPP, CDC14M12, Primary



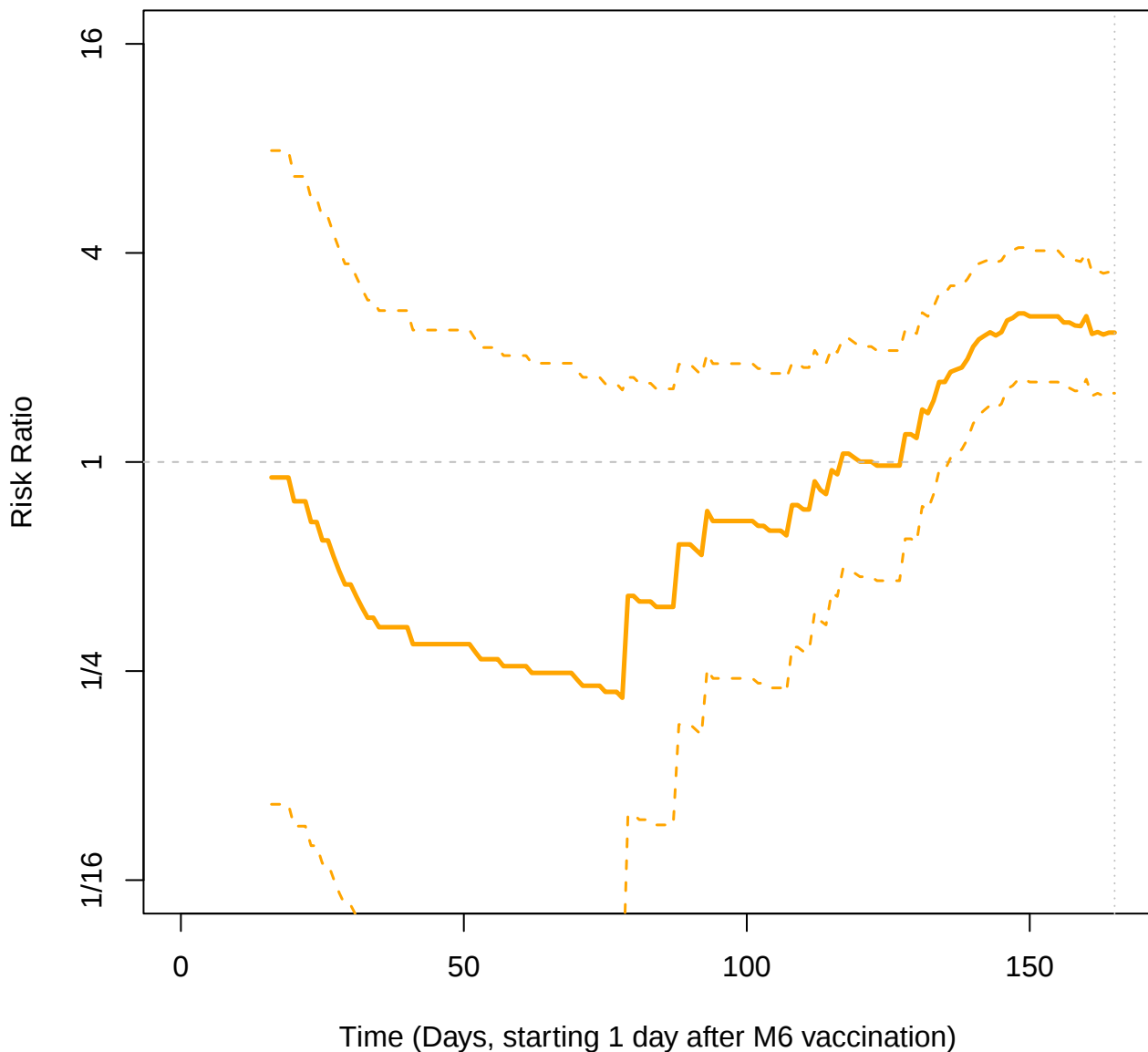
MBoost vs BBoost, FPP, CDC14M12, Sensitivity



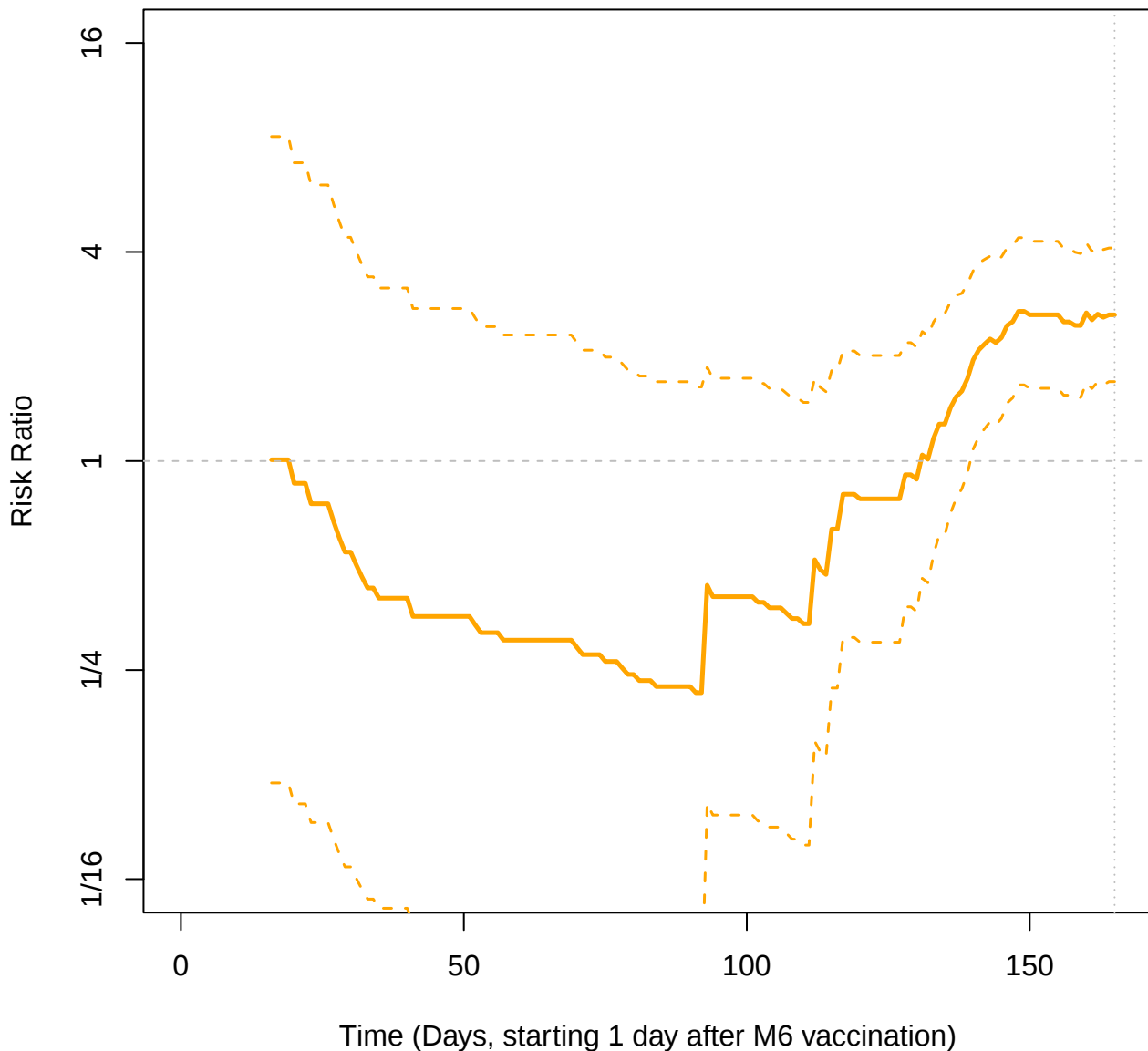
MBoost vs BBoost, FPP, CDC14M18, Primary



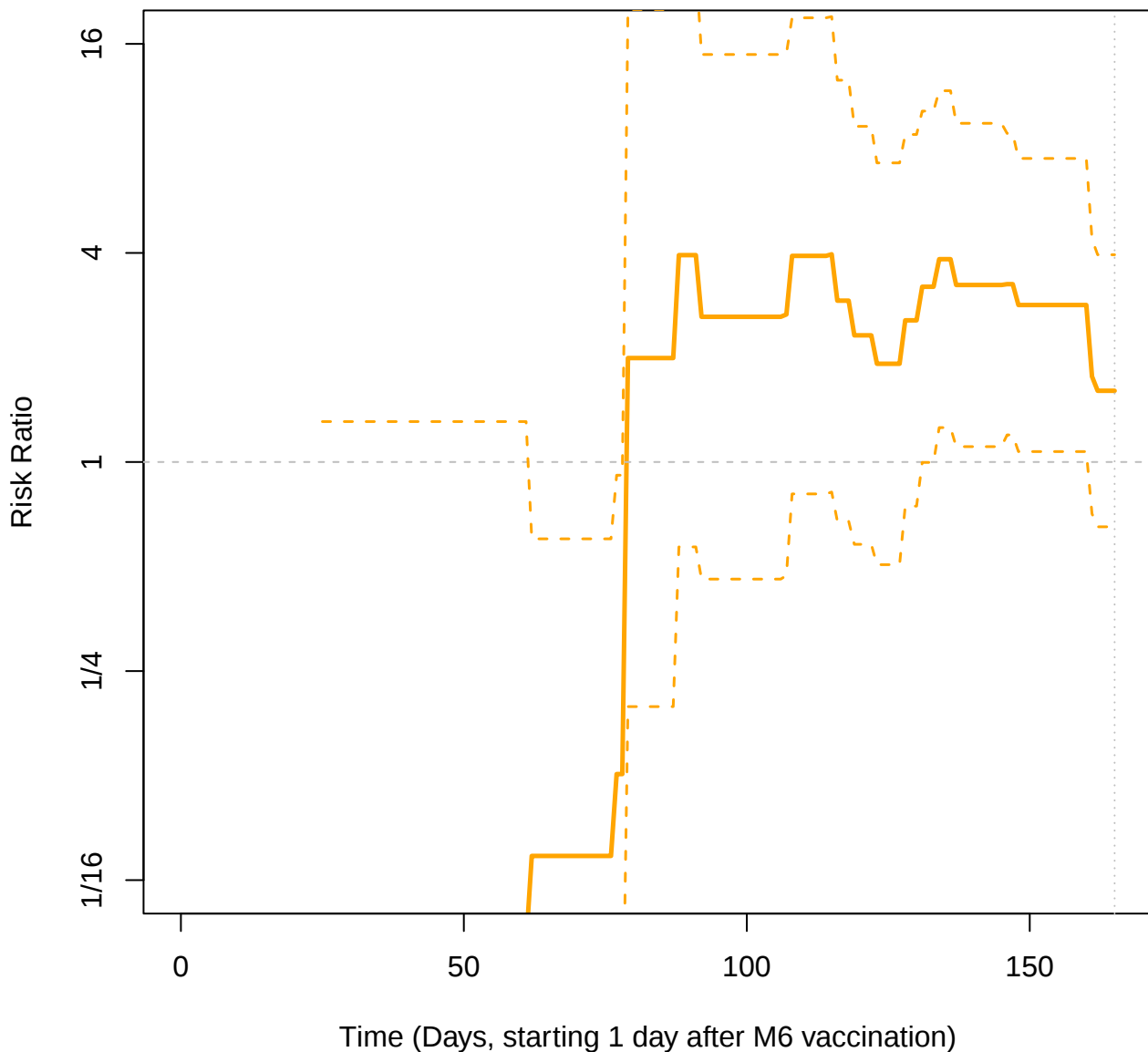
MBoost vs BBoost, FM6, CDC1M12, Primary



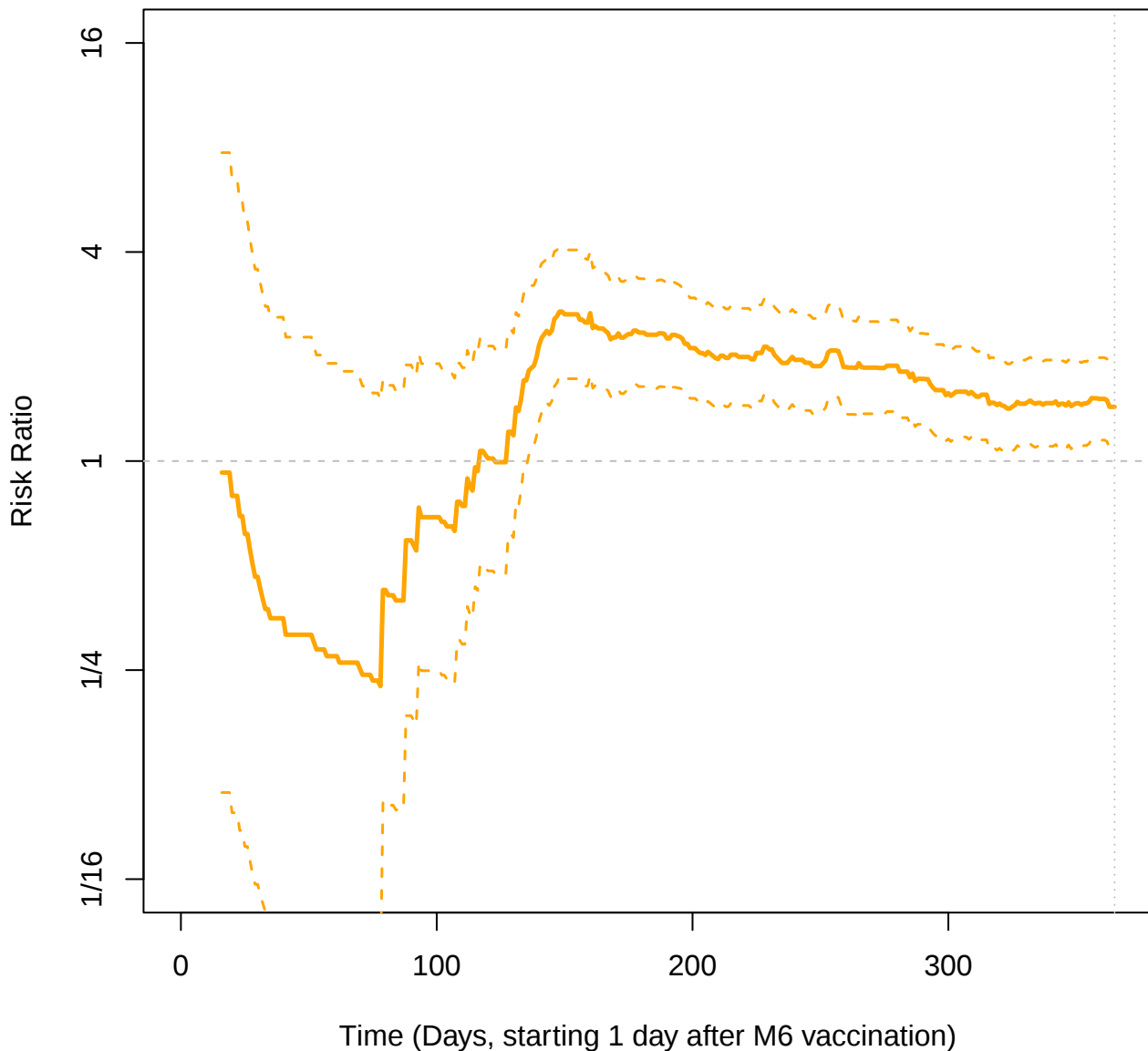
MBoost vs BBoost, FM6, CDC1M12, Primary (PLWH)



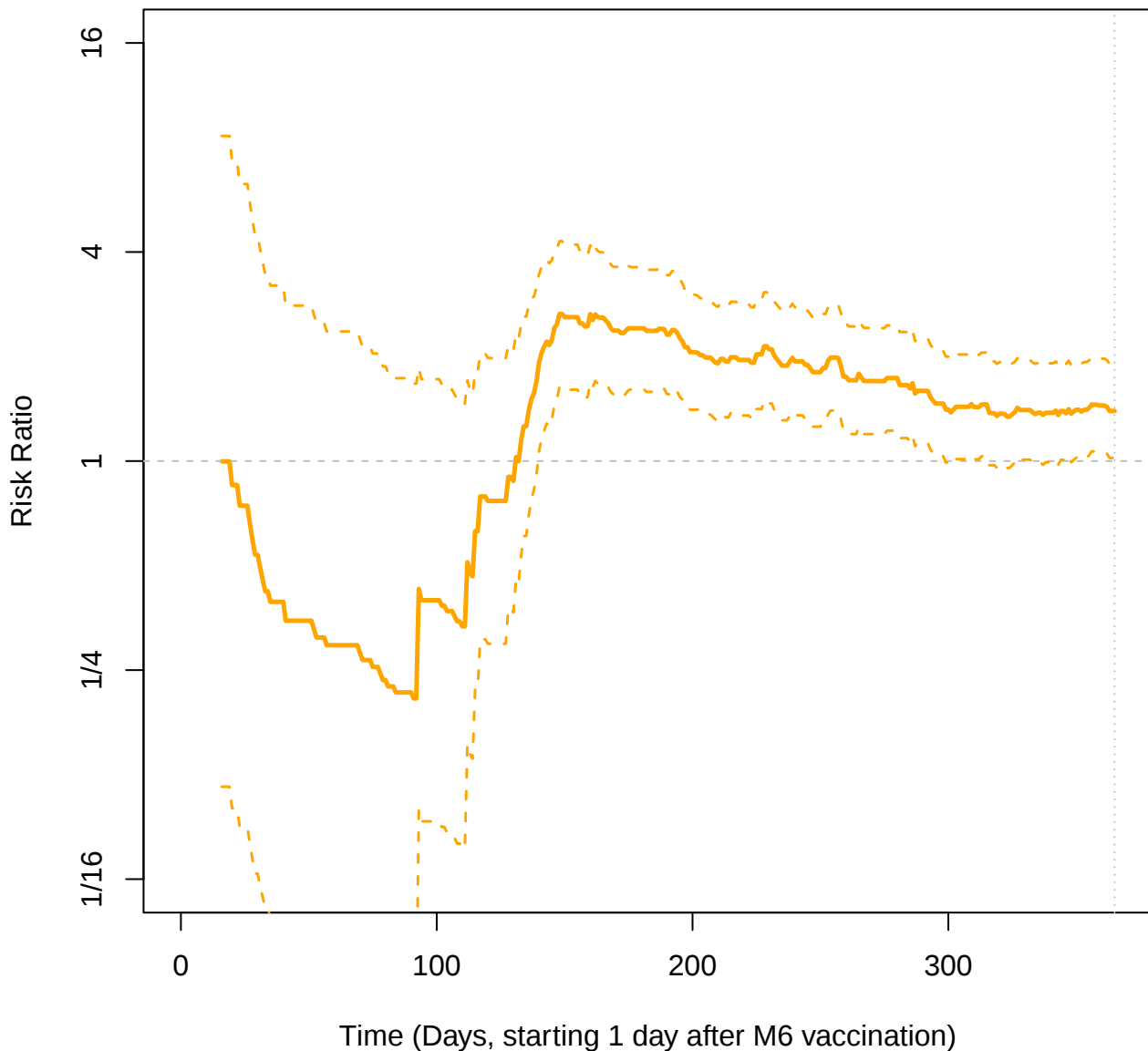
MBoost vs BBoost, FM6, CDC1M12, Primary (PLWoH)



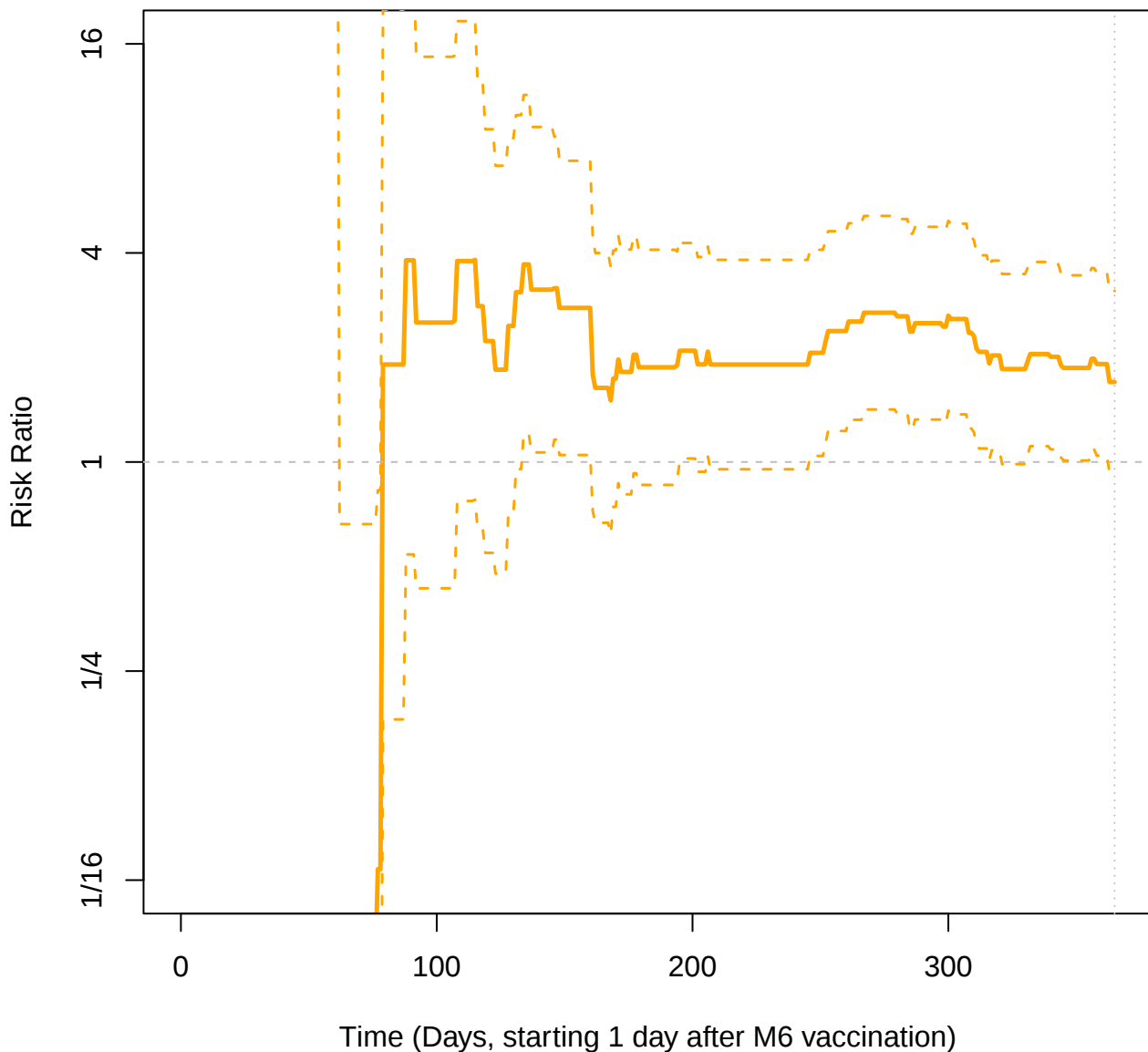
MBoost vs BBoost, FM6, CDC1M18, Primary



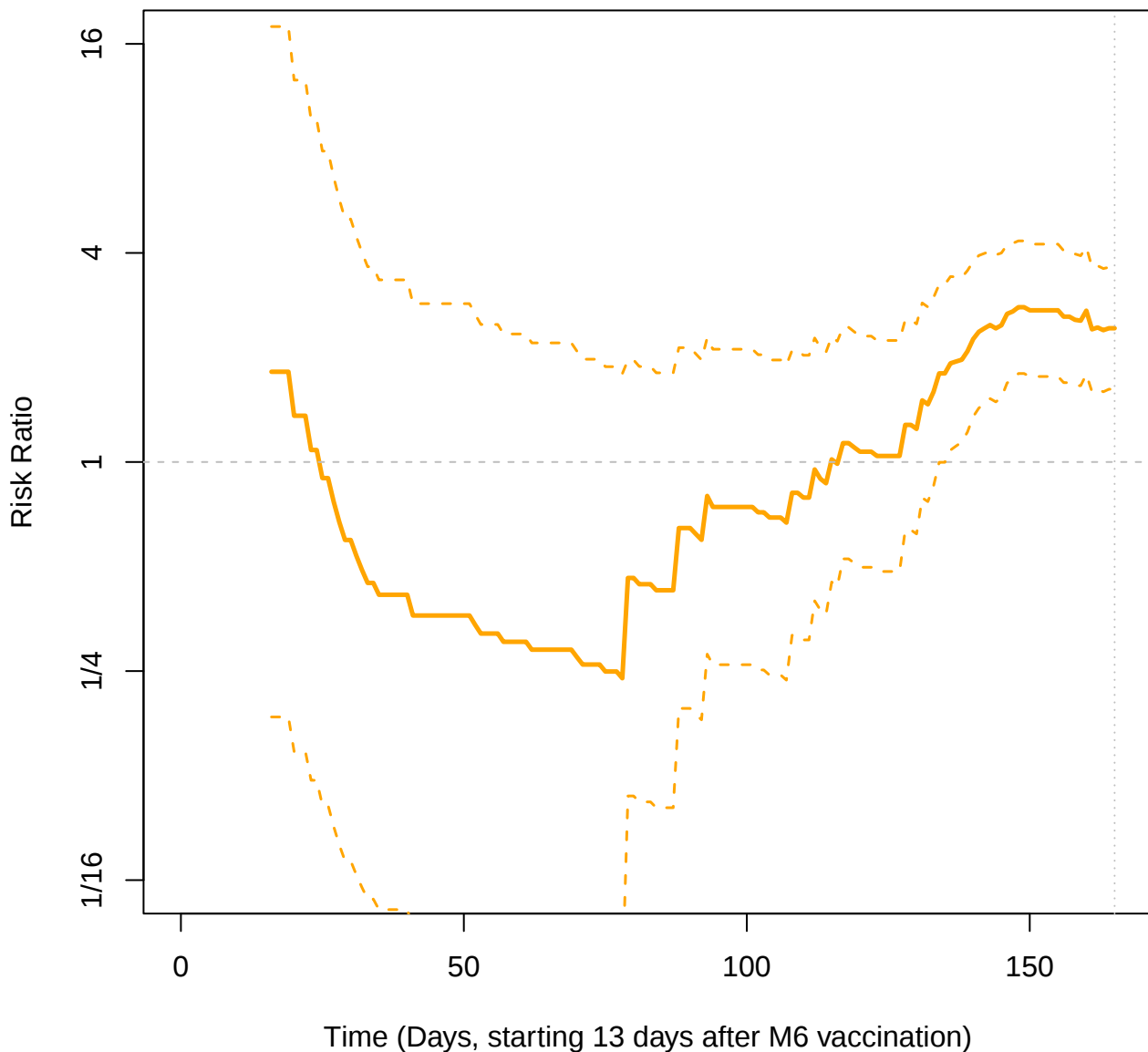
MBoost vs BBoost, FM6, CDC1M18, Primary (PLWH)



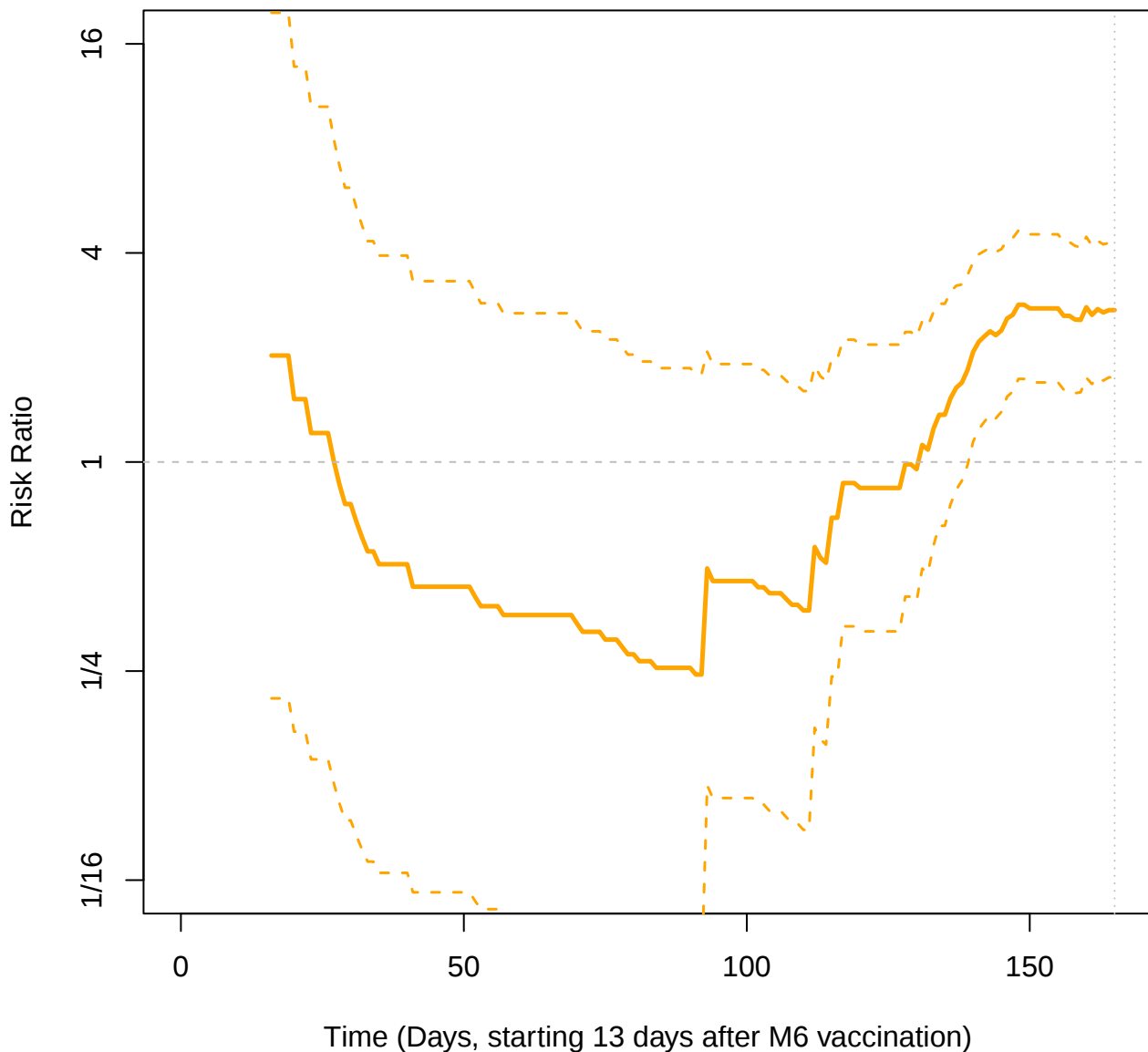
MBoost vs BBoost, FM6, CDC1M18, Primary (PLWoH)



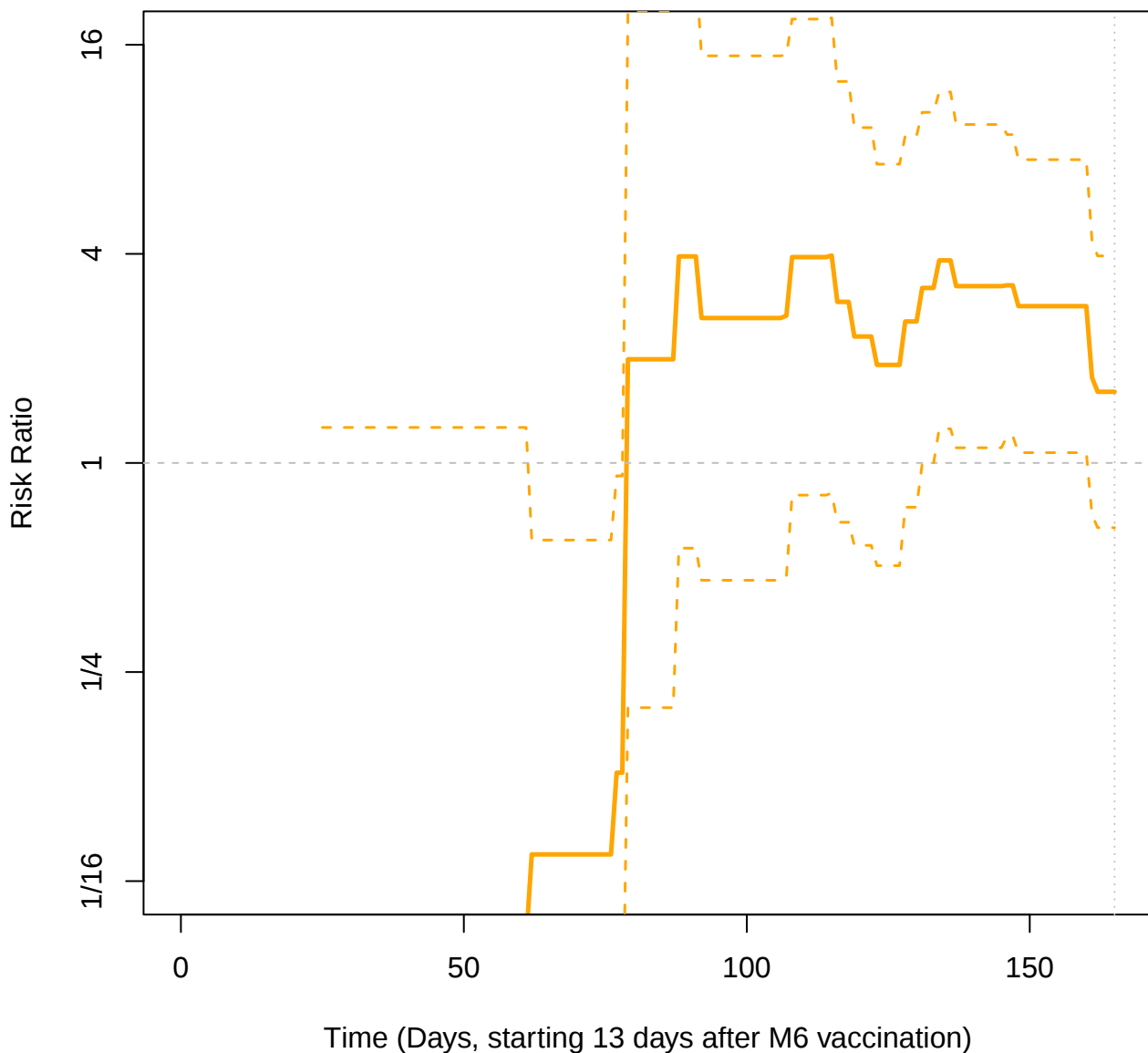
MBoost vs BBoost, FPP, CDC14M12, Primary



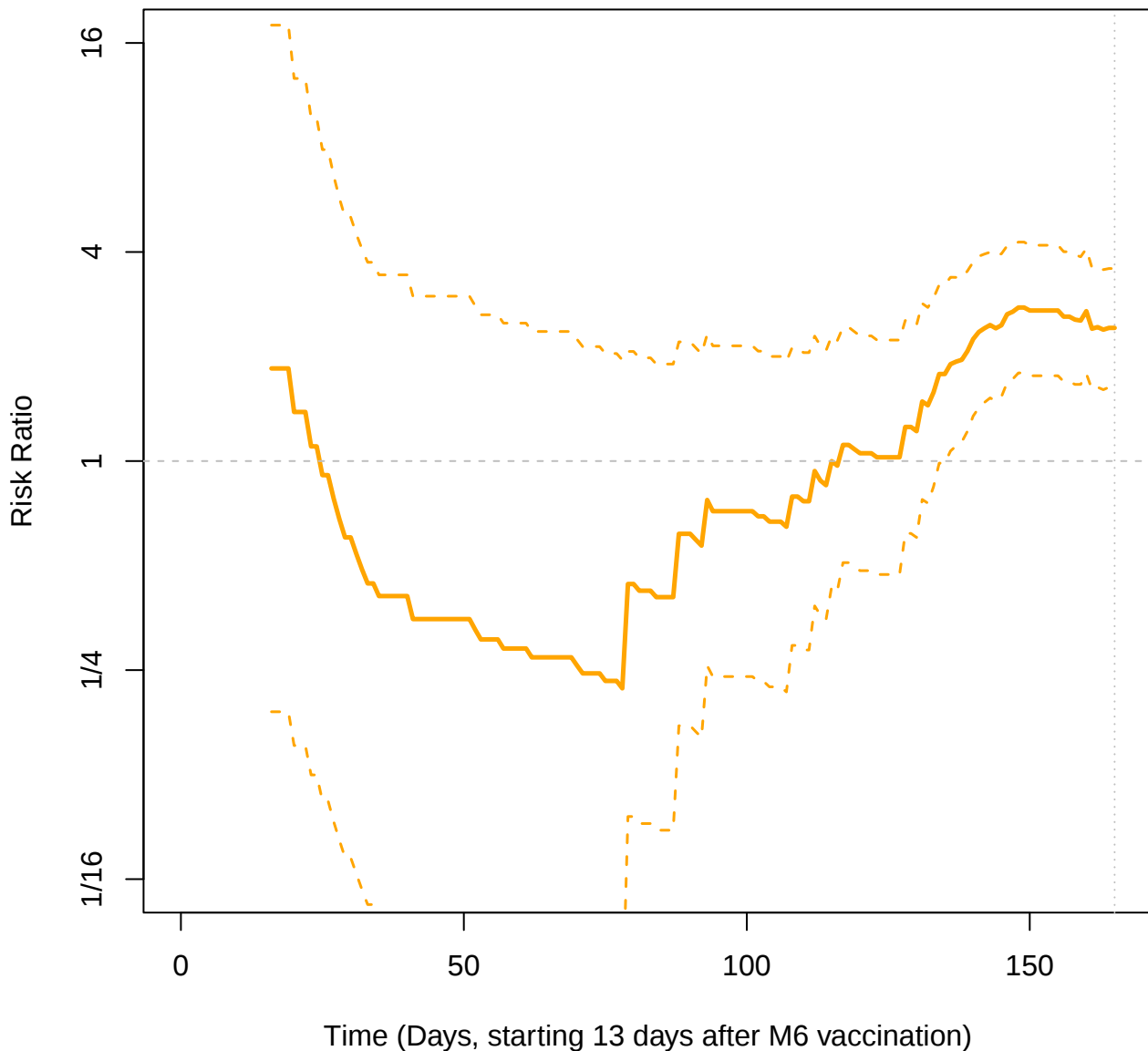
MBoost vs BBoost, FPP, CDC14M12, Primary (PLWH)



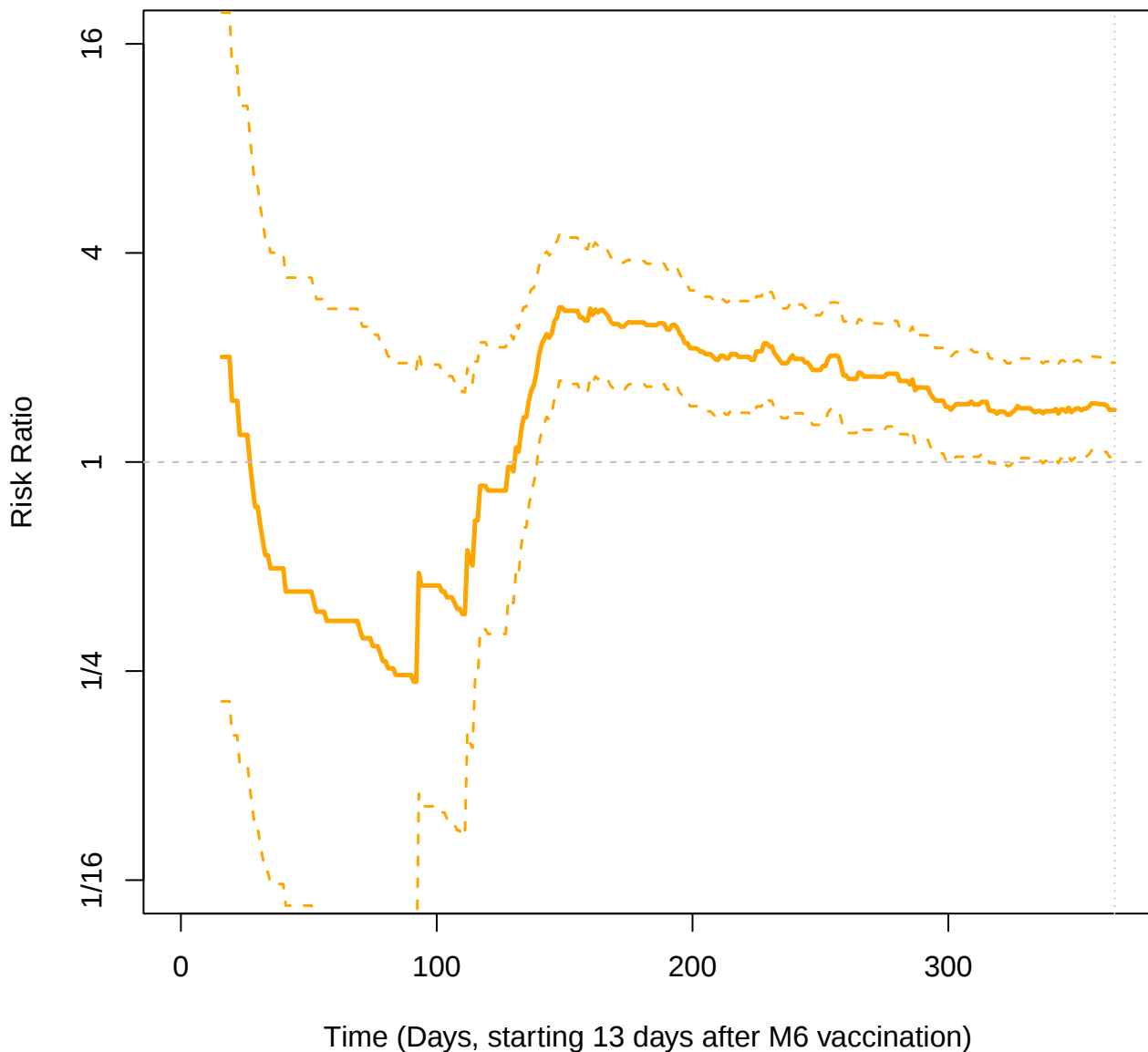
MBoost vs BBoost, FPP, CDC14M12, Primary (PLWoH)



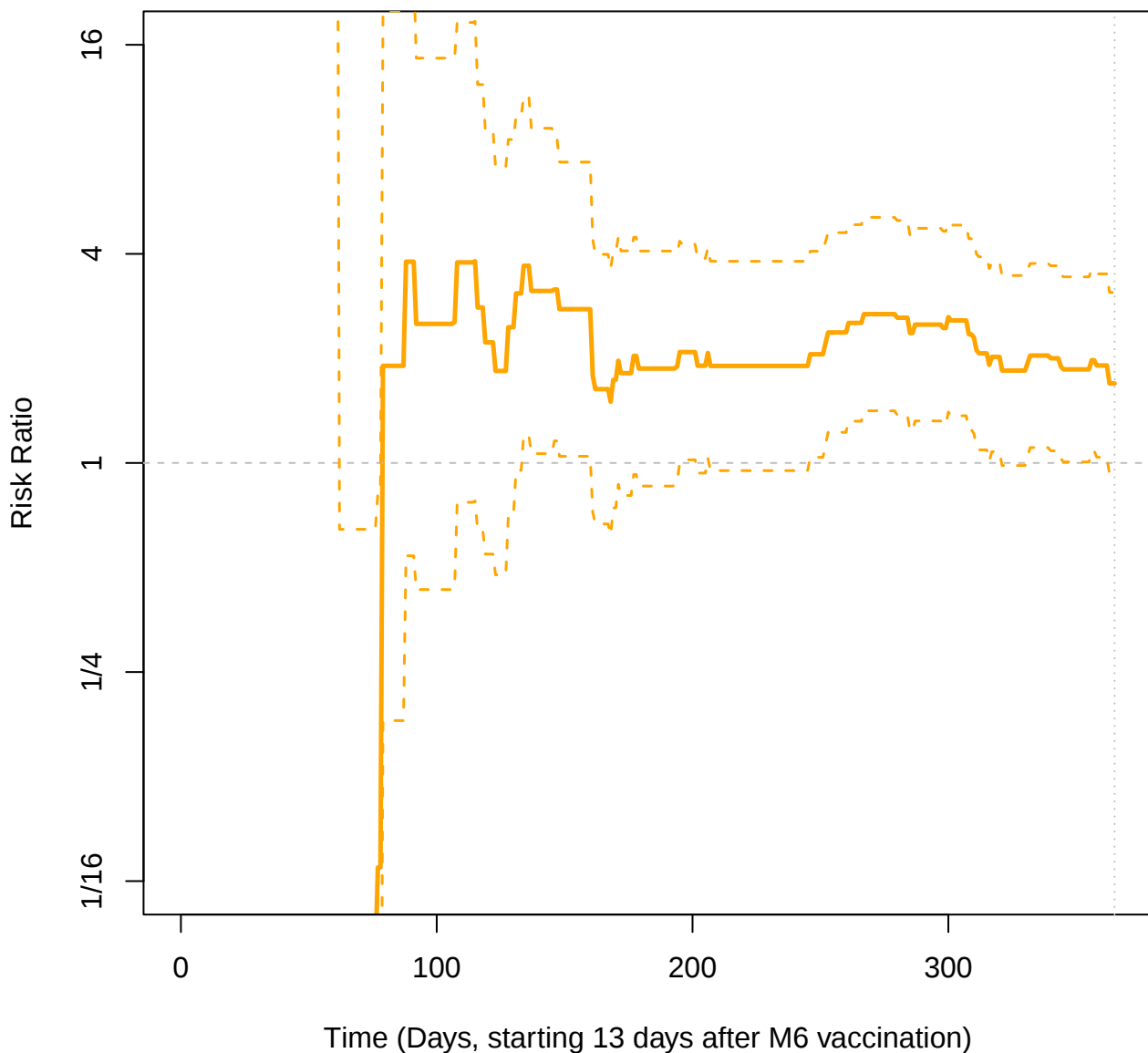
MBoost vs BBoost, FPP, CDC14M12, Sensitivity



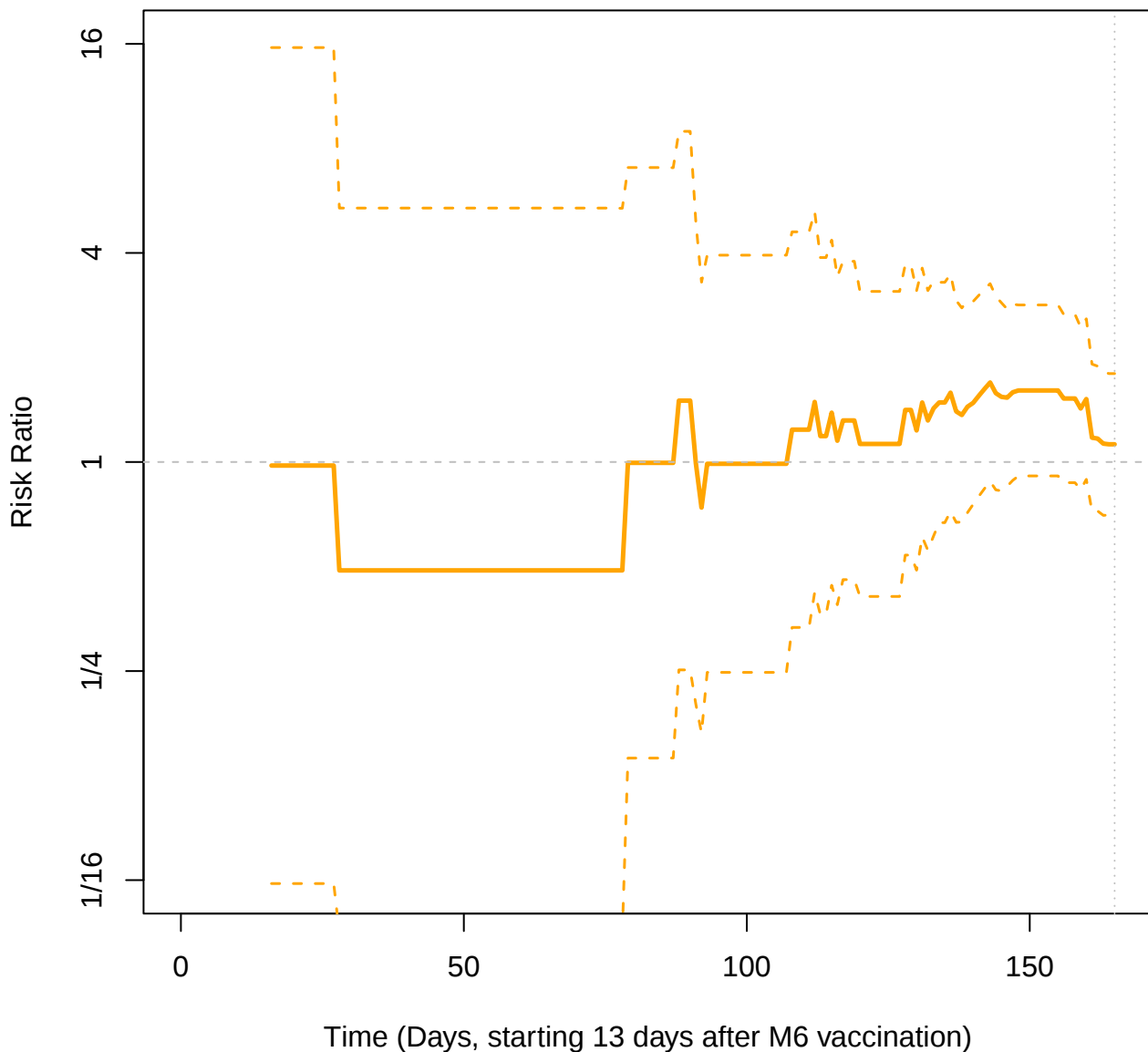
MBoost vs BBoost, FPP, CDC14M18, Primary (PLWH)



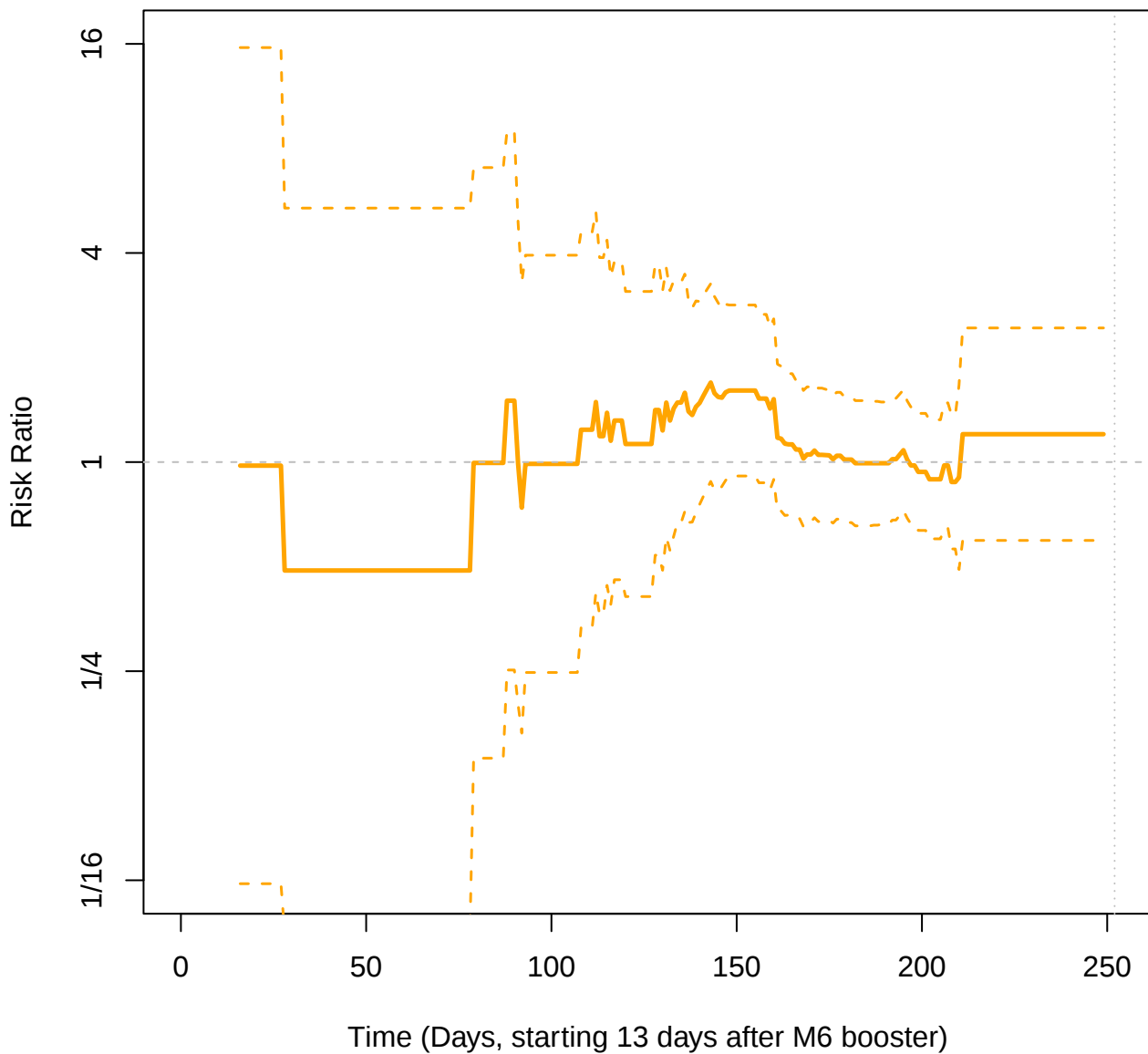
MBoost vs BBoost, FPP, CDC14M18, Primary (PLWoH)



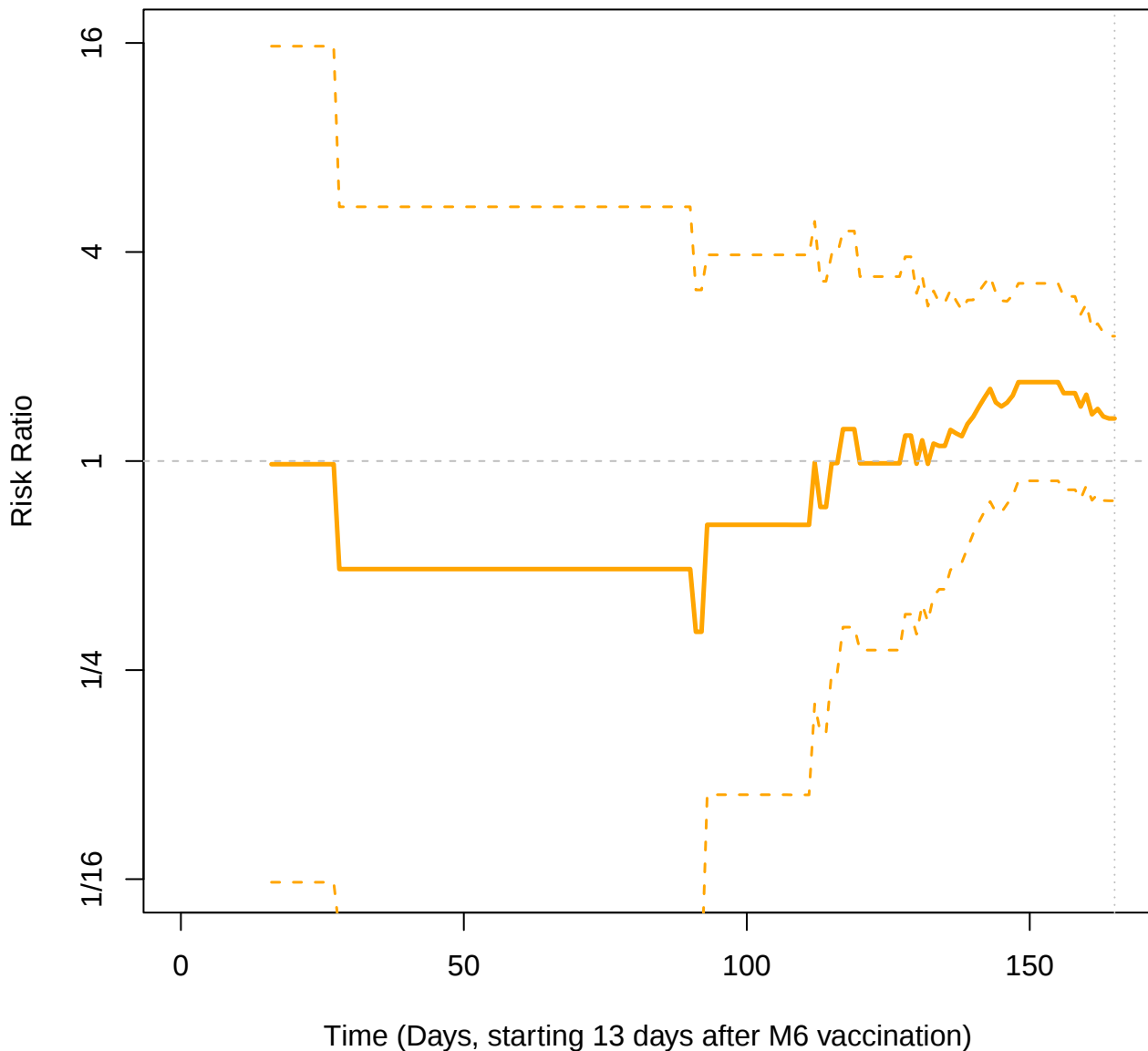
MBoost vs BBoost, RM6, CDC14M12, Primary



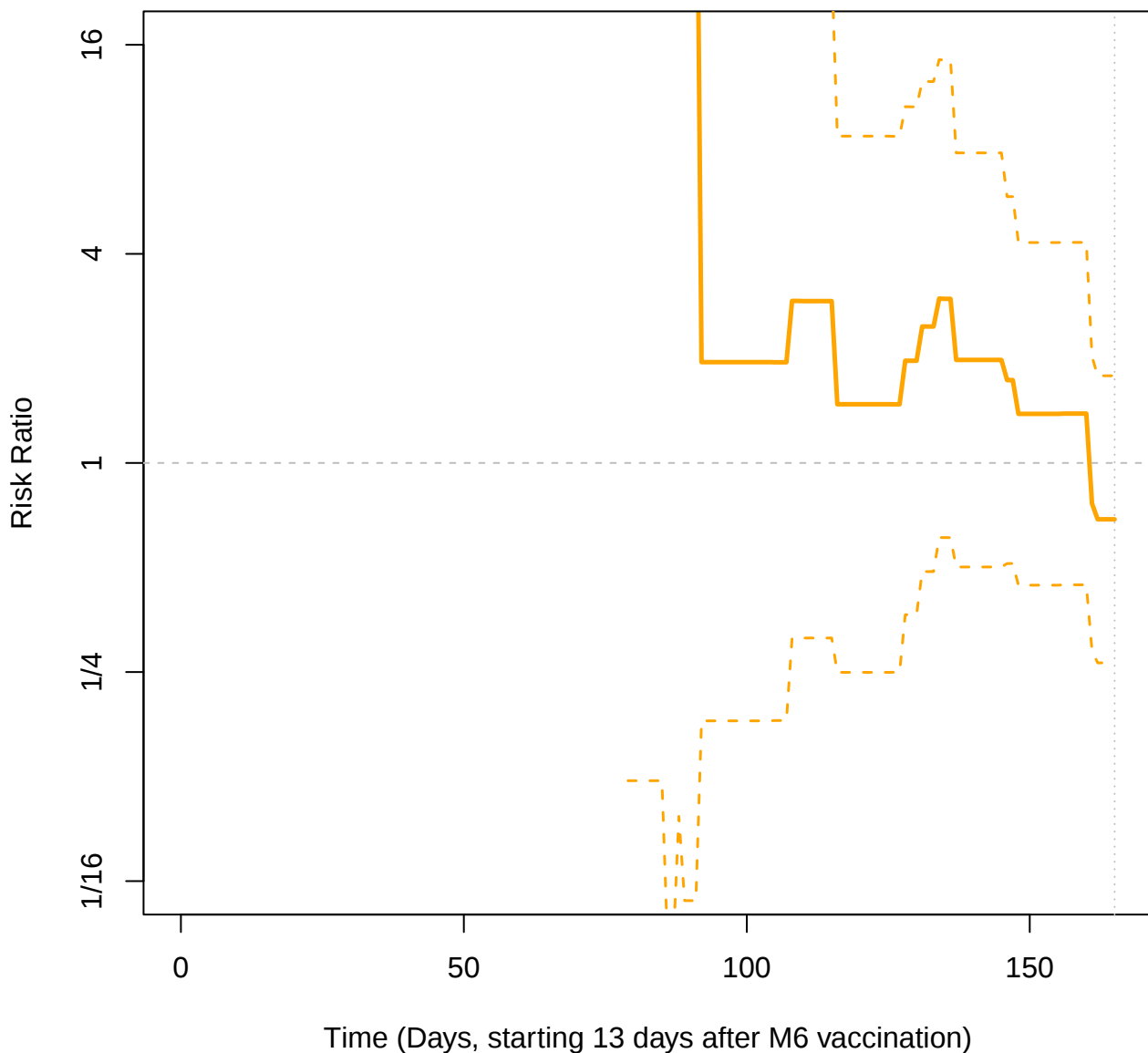
COVID-19 incidence over study time



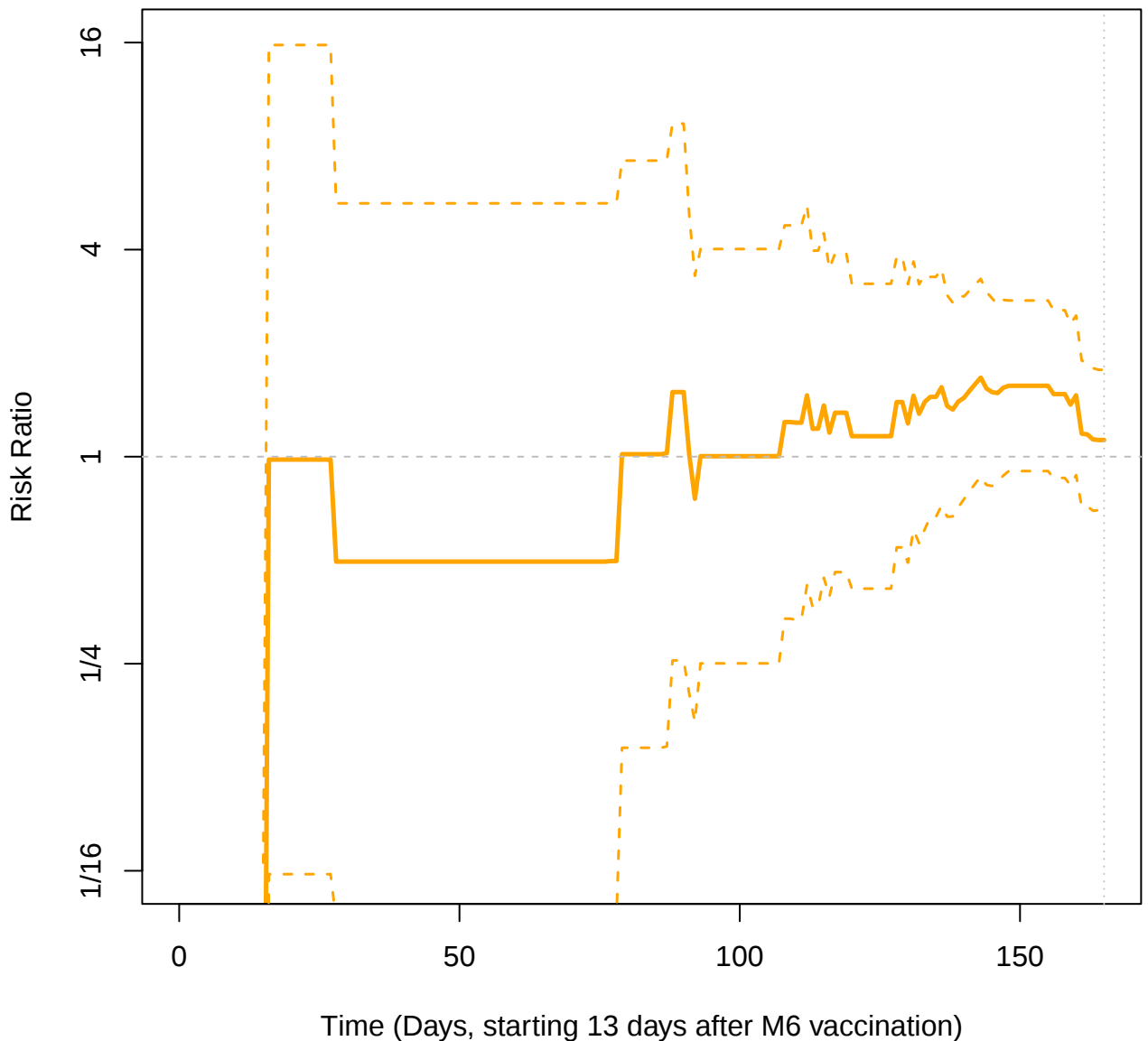
MBoost vs BBoost, RM6, CDC14M12, Primary (PLWH)



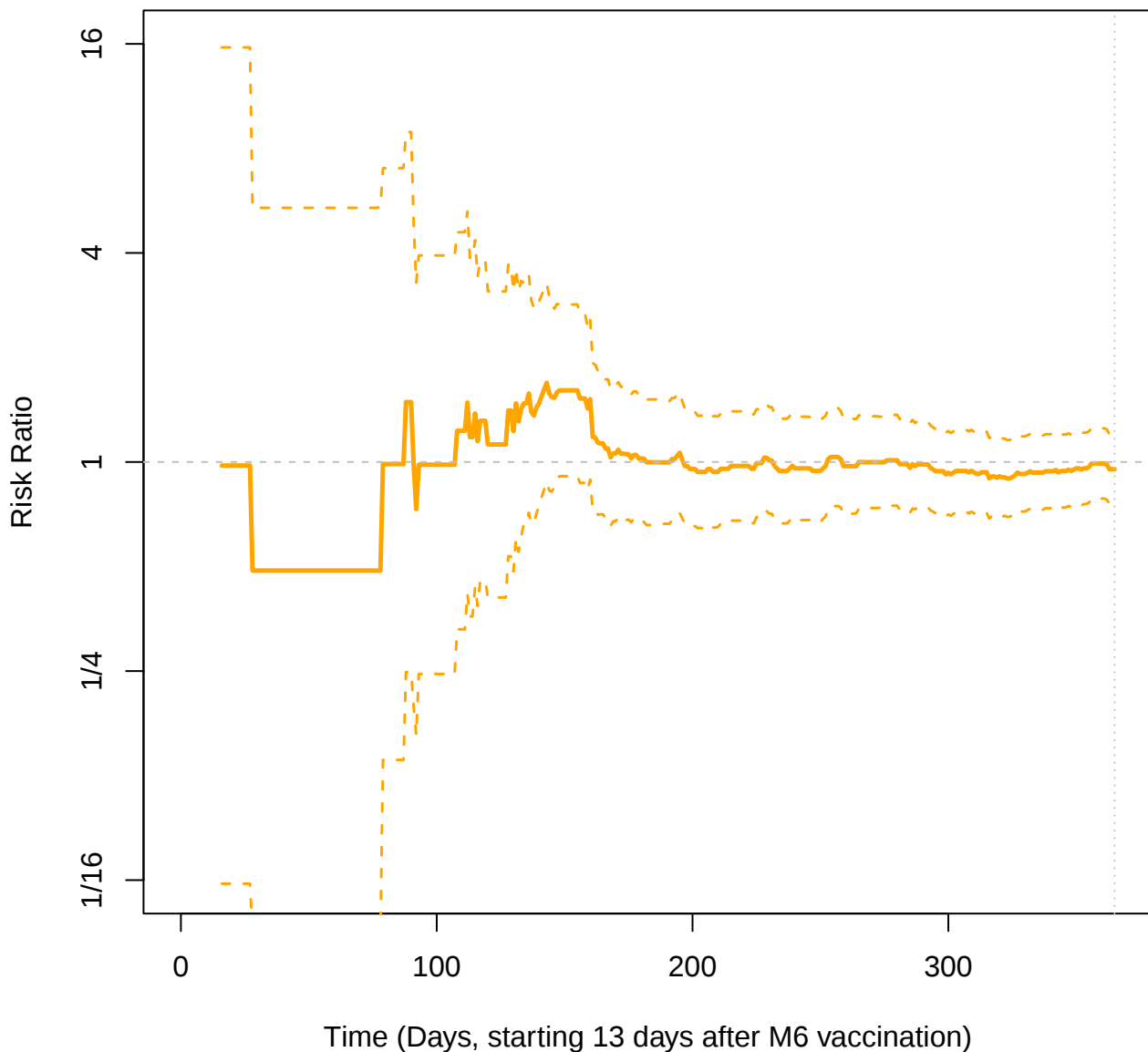
MBoost vs BBoost, RM6, CDC14M12, Primary (PLWoH)



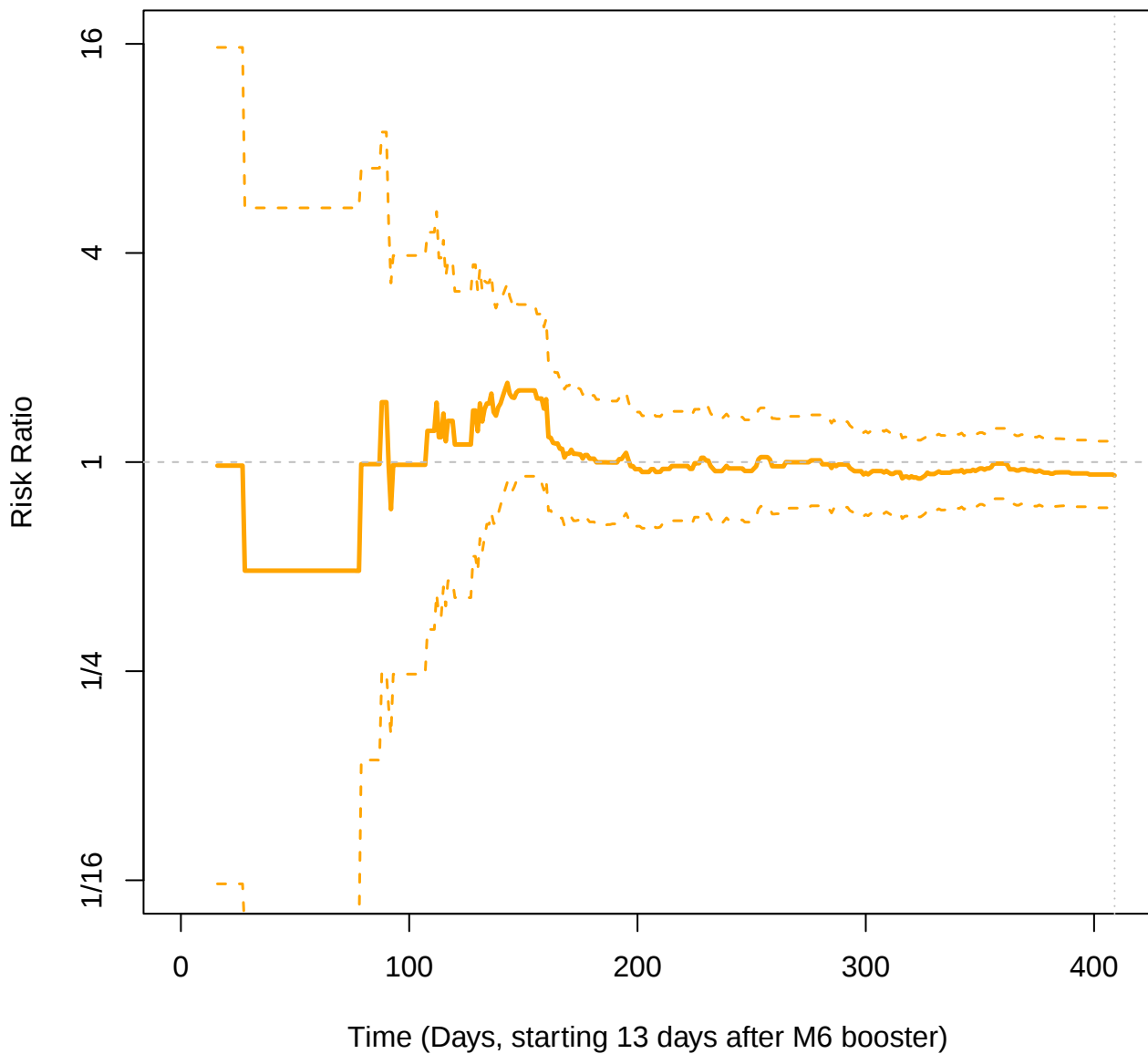
MBoost vs BBoost, RM6, CDC14M12, Sensitivity



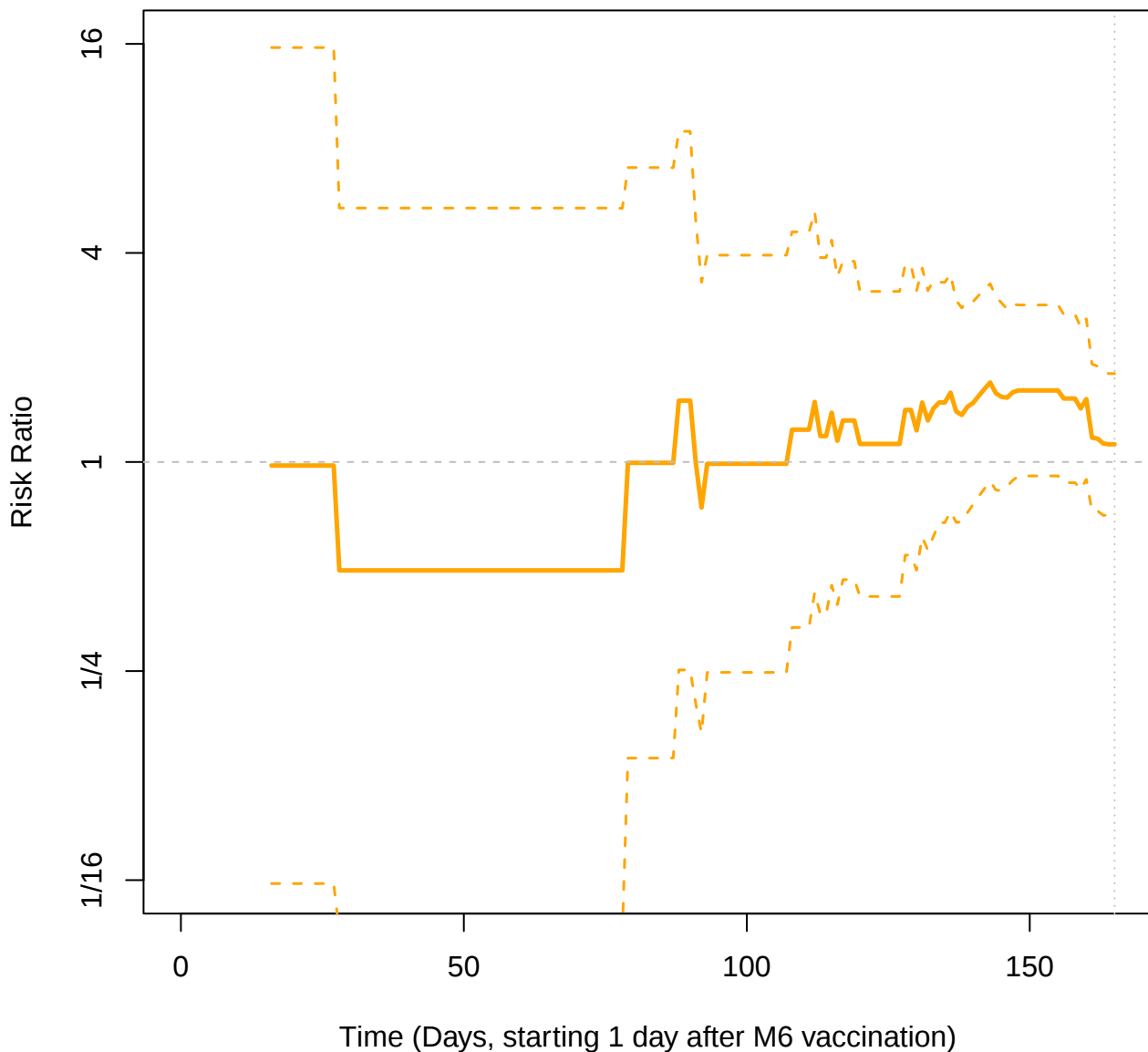
MBoost vs BBoost, RM6, CDC14M18, Primary



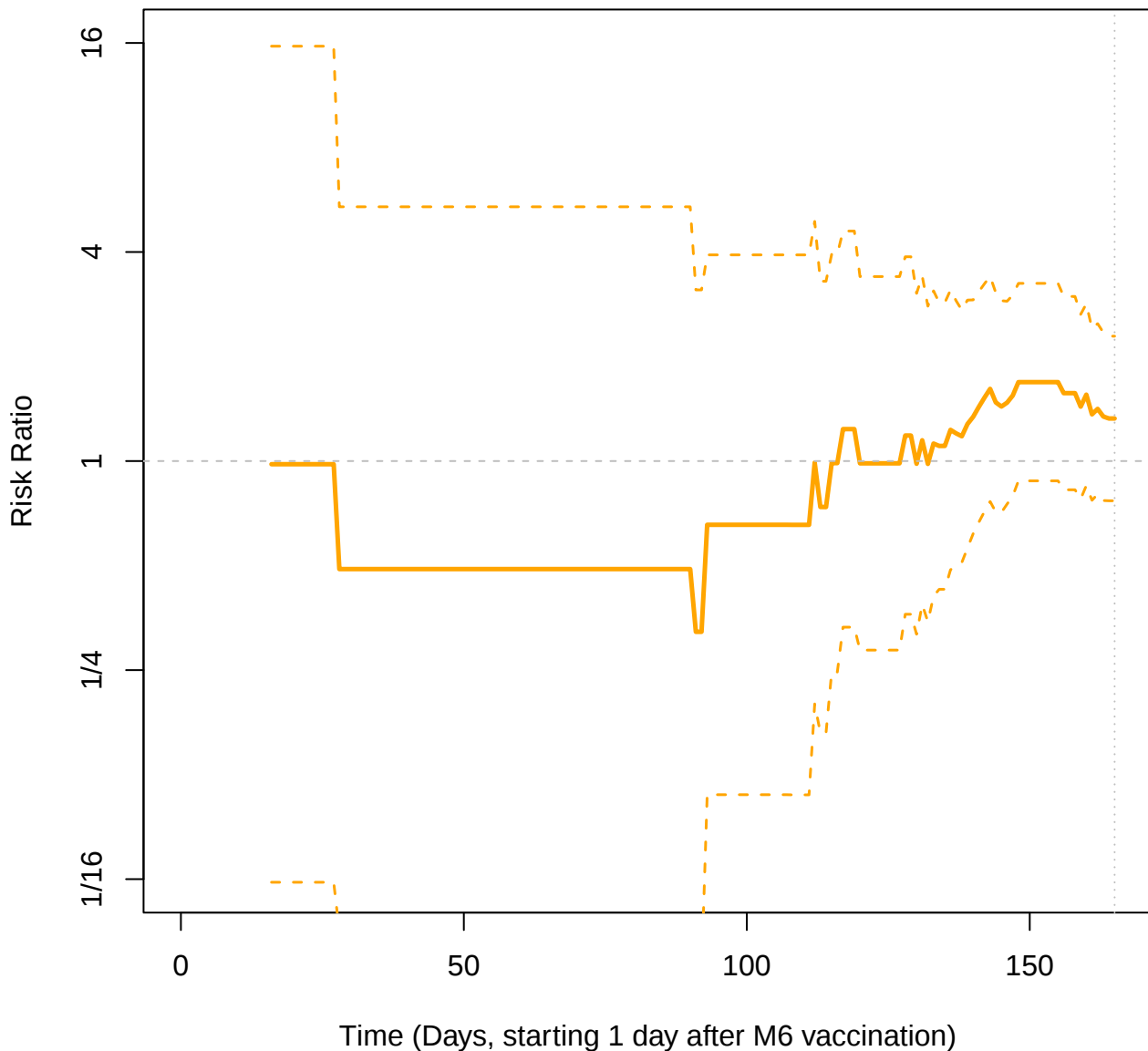
COVID-19 incidence over study time



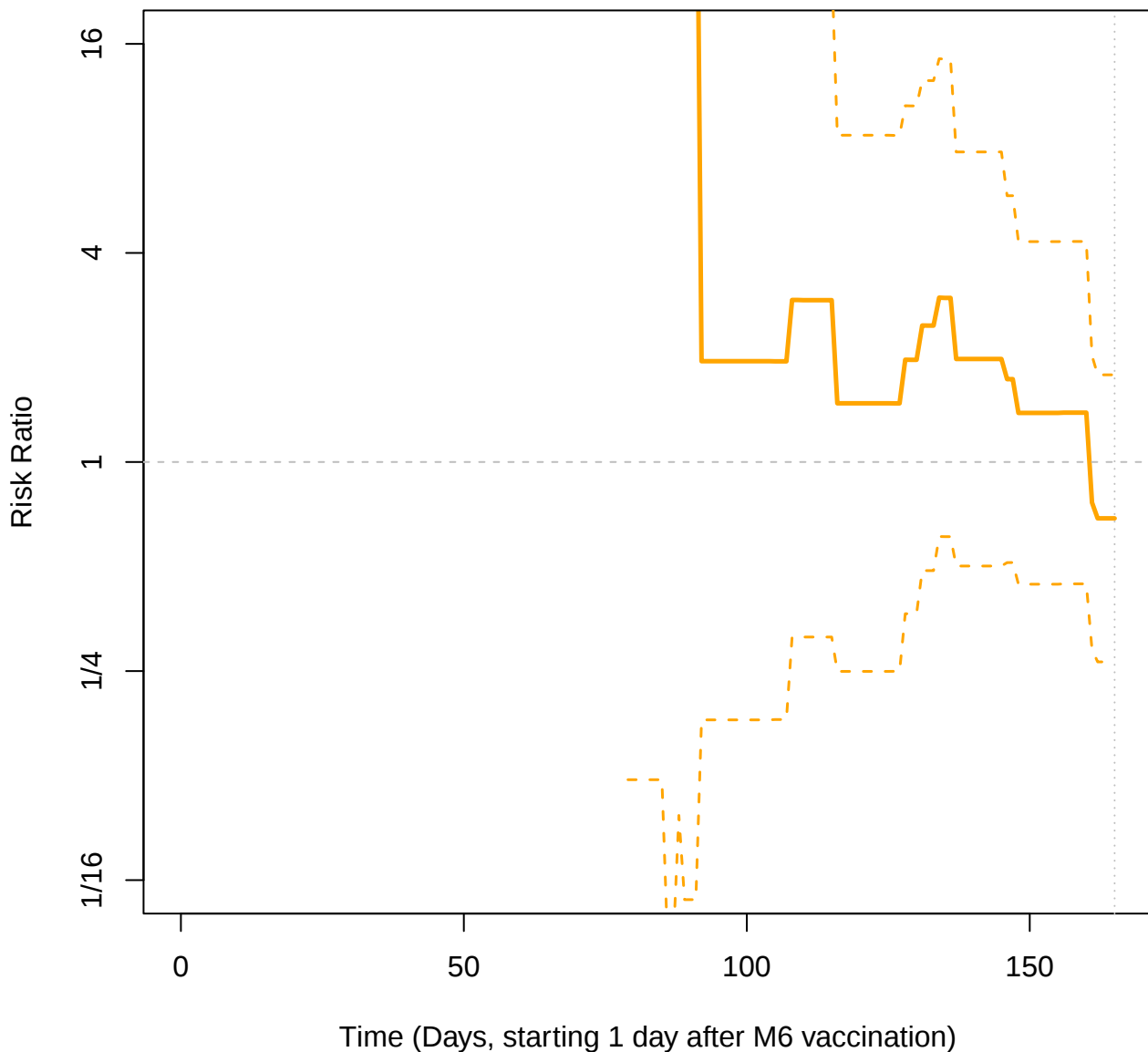
MBoost vs BBoost, RM6, CDC1M12, Primary



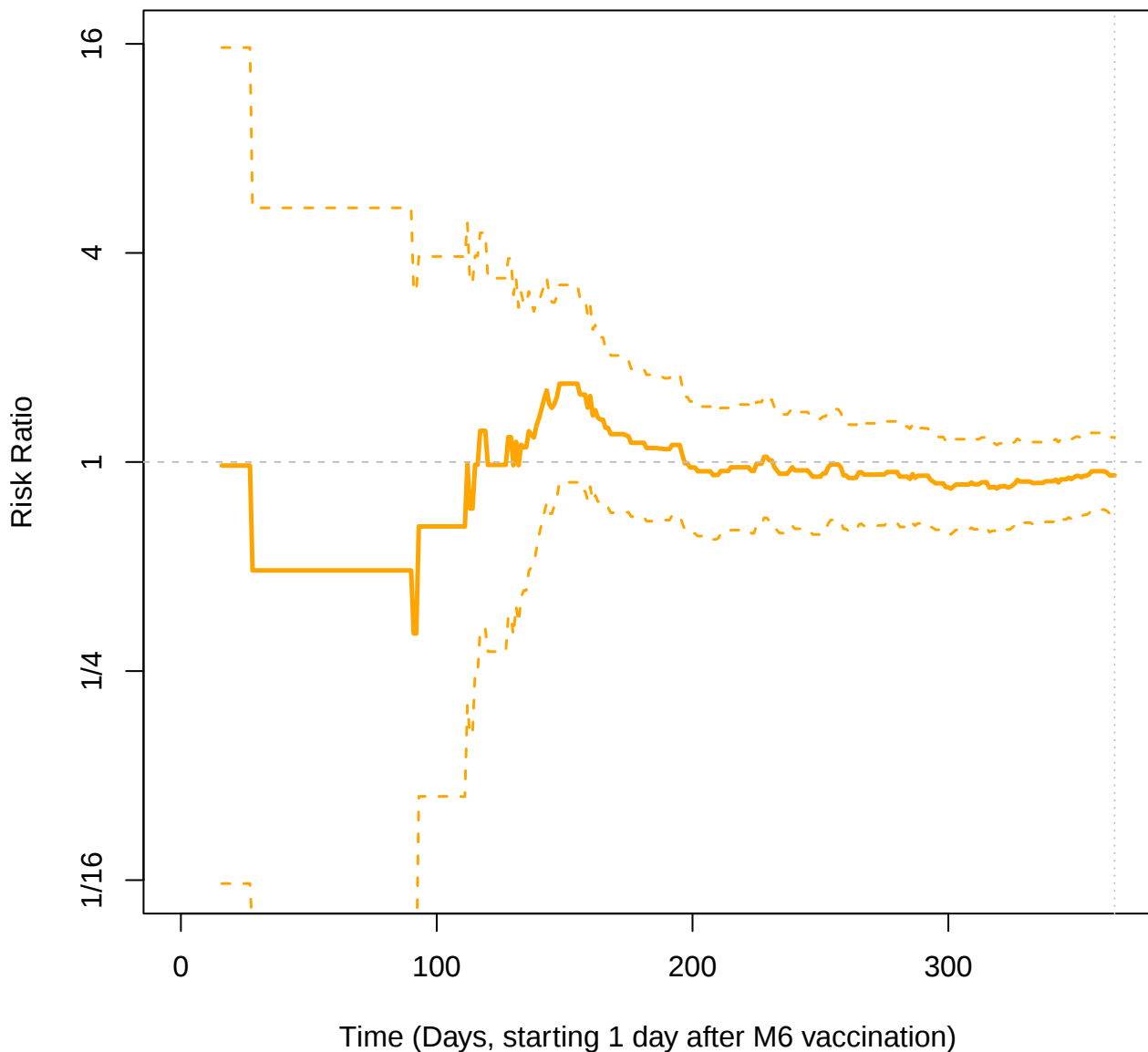
MBoost vs BBoost, RM6, CDC1M12, Primary (PLWH)



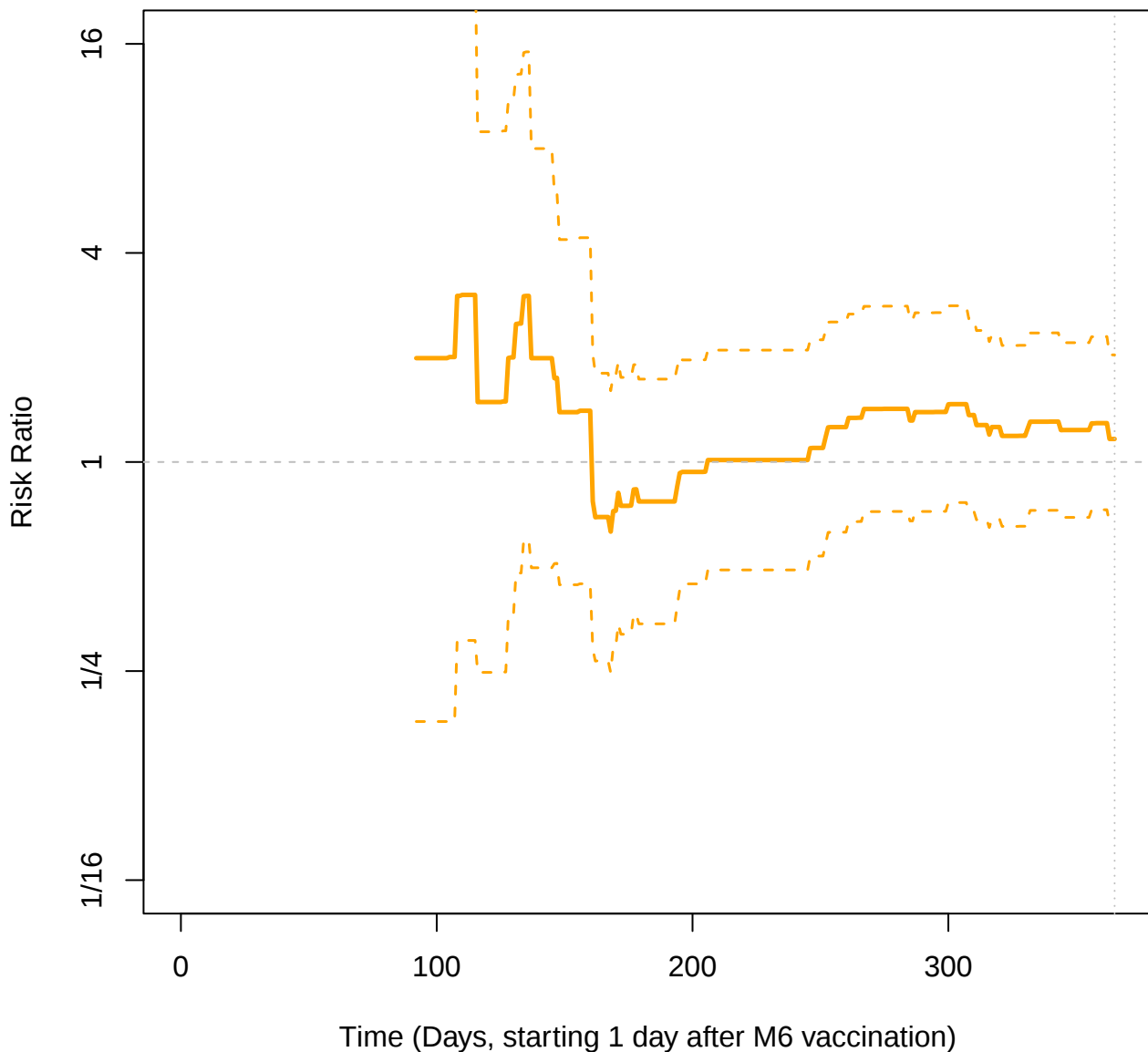
MBoost vs BBoost, RM6, CDC1M12, Primary (PLWoH)



MBoost vs BBoost, RM6, CDC1M18, Primary (PLWH)



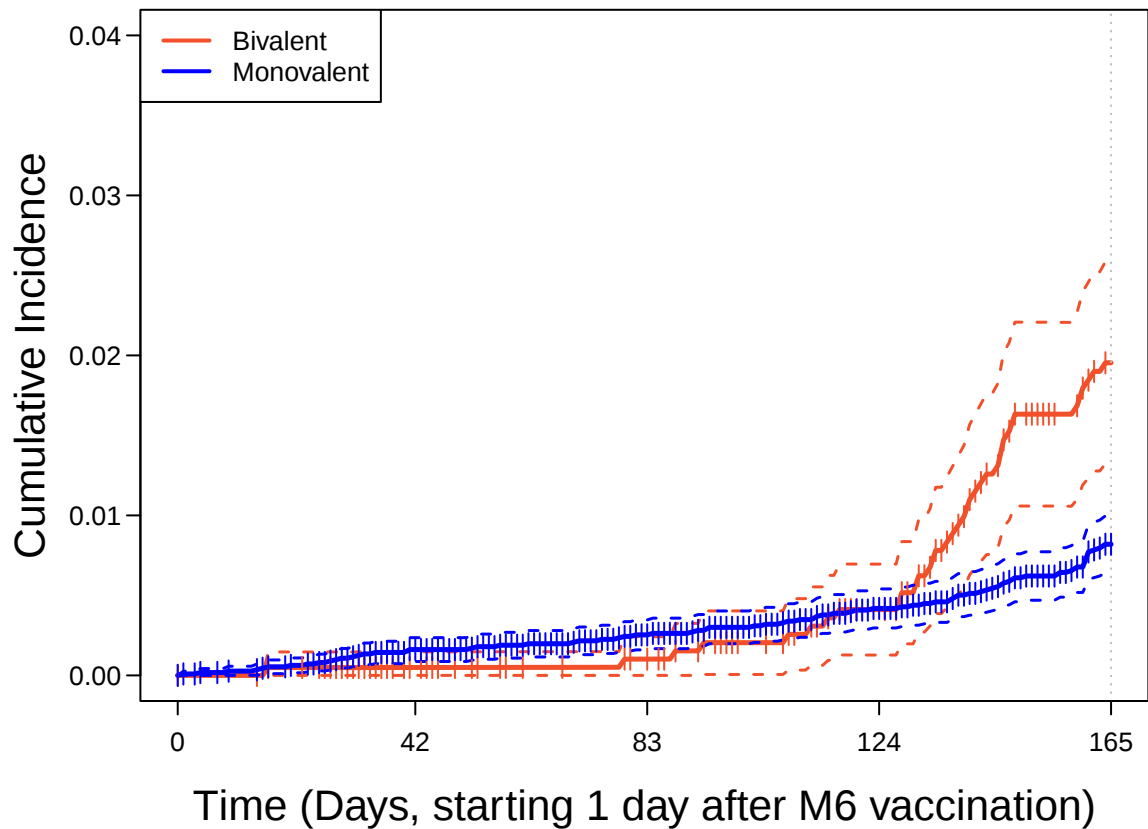
MBoost vs BBoost, RM6, CDC1M18, Primary (PLWoH)



Part 3 — M12 Figures

126 figures — M12-Figs/

MBoost vs BBoost, FM6, CDC1M18, Primary



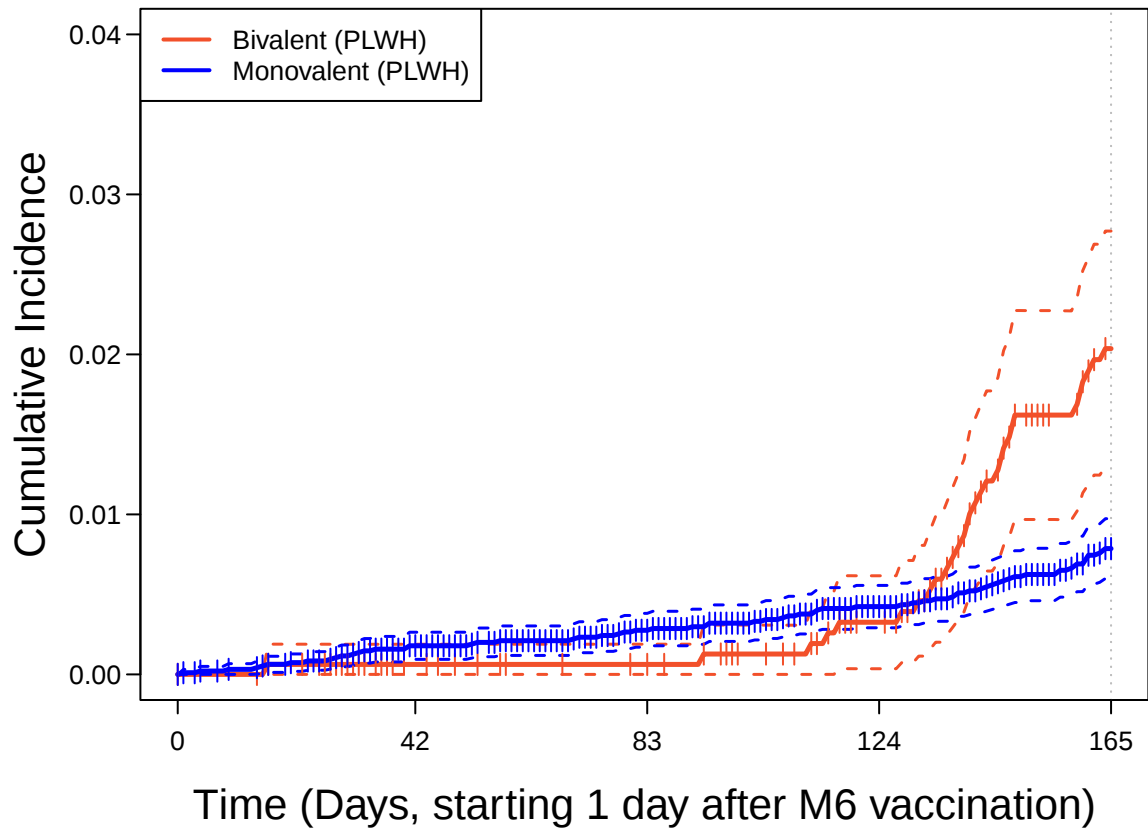
No. at Risk

Bivalent	1995	1934	1918	1891	1803
Monovalent	11211	11110	10790	9873	8356

Total Events

Bivalent	0	1	2	8	37
Monovalent	1	18	28	45	81

MBoost vs BBoost, FM6, CDC1M18, Primary (PLWH)



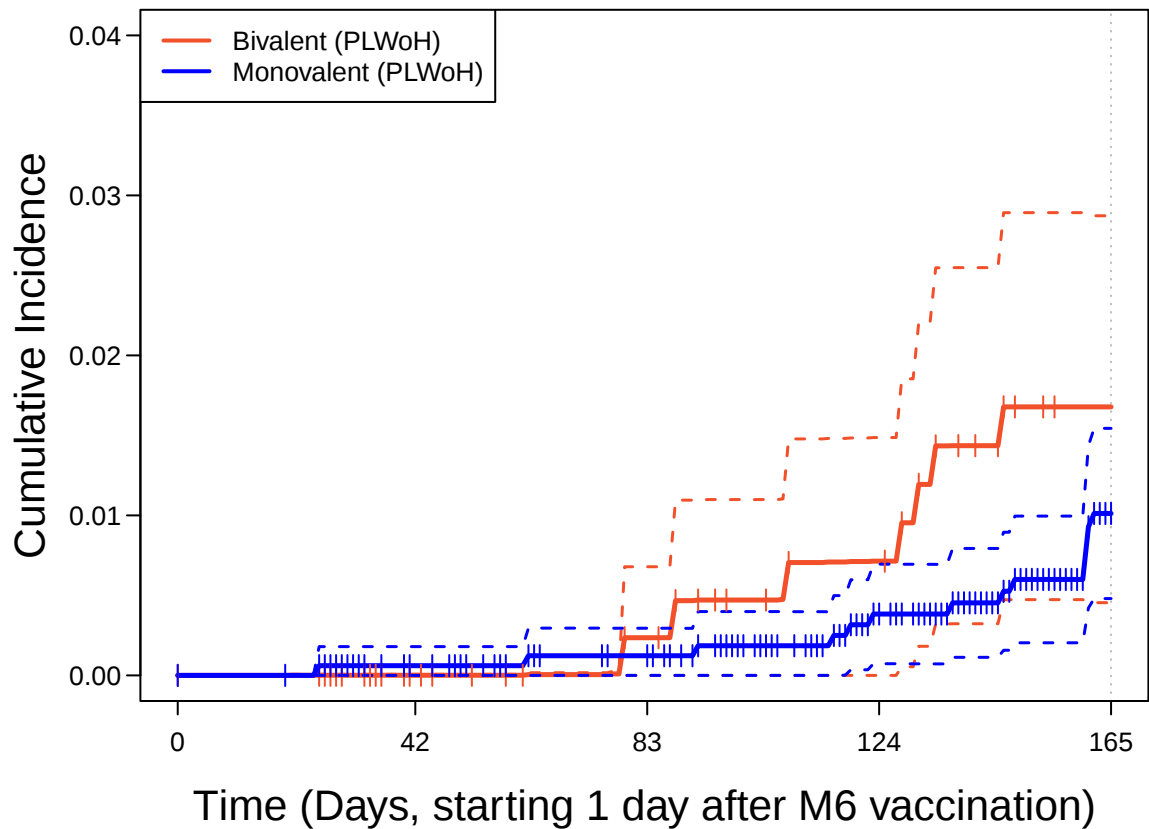
No. at Risk

Bivalent	1546	1510	1500	1481	1408
Monovalent	9561	9482	9192	8394	7209

Total Events

Bivalent	0	1	1	5	30
Monovalent	1	17	26	39	67

MBoost vs BBoost, FM6, CDC1M18, Primary (PLWoH)



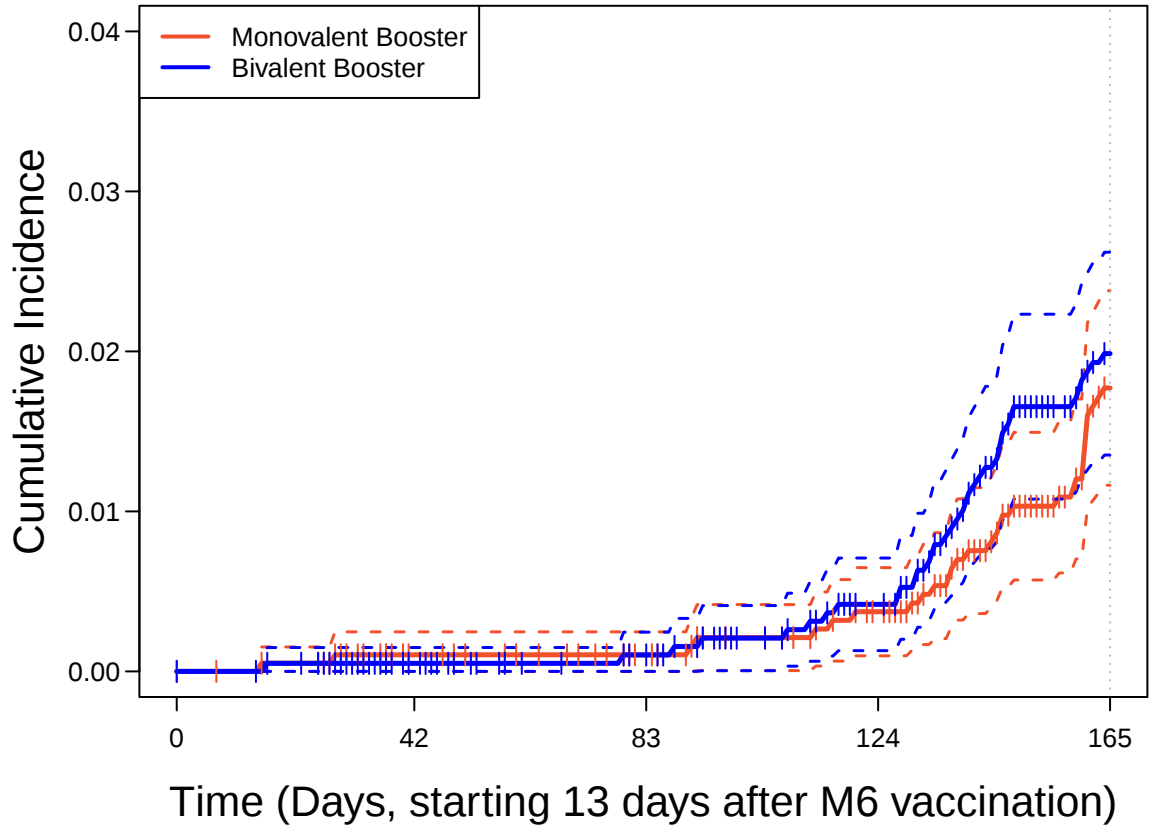
No. at Risk

Bivalent	449	424	418	410	395
Monovalent	1650	1628	1598	1479	1147

Total Events

Bivalent	0	0	1	3	7
Monovalent	0	1	2	6	14

MBoost vs BBoost, FPP, CDC14M12, Primary



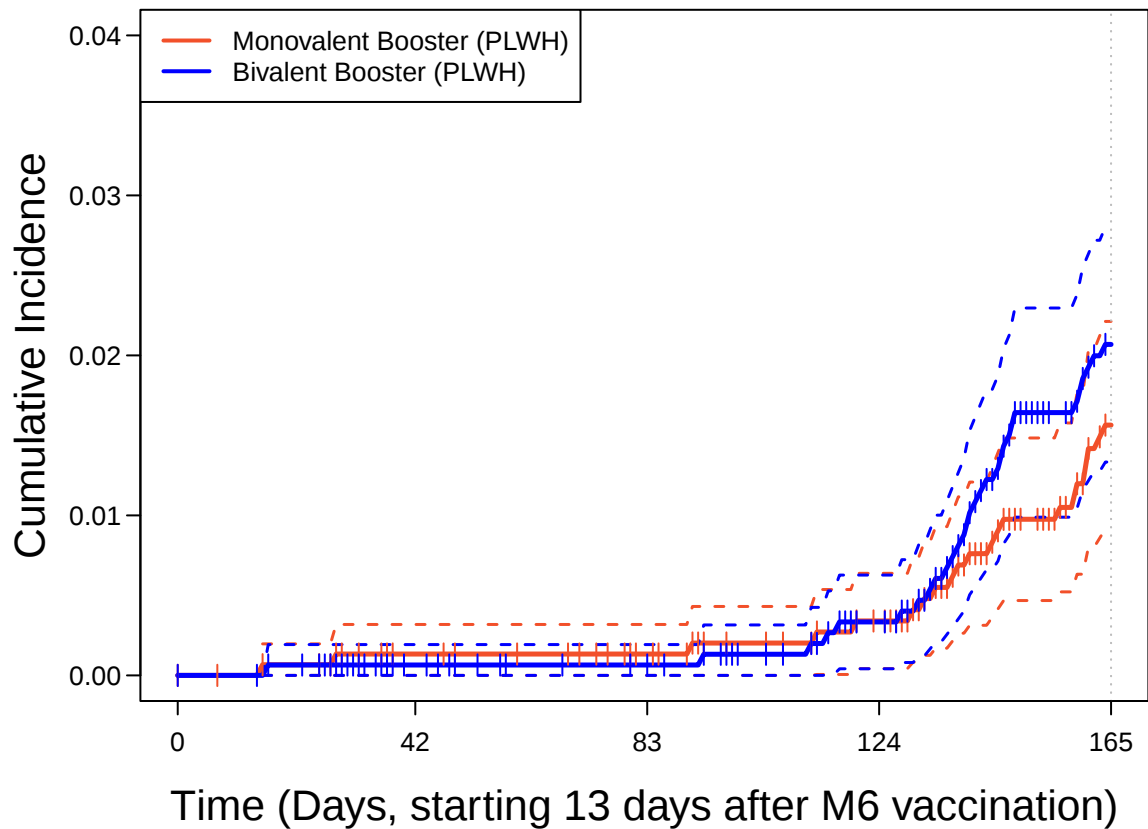
No. at Risk

Monovalent	1933	1880	1865	1845	1727
Bivalent	1988	1927	1909	1883	1763

Total Events

Monovalent	0	2	2	7	32
Bivalent	0	1	2	8	37

MBoost vs BBoost, FPP, CDC14M12, Primary (PLWH)



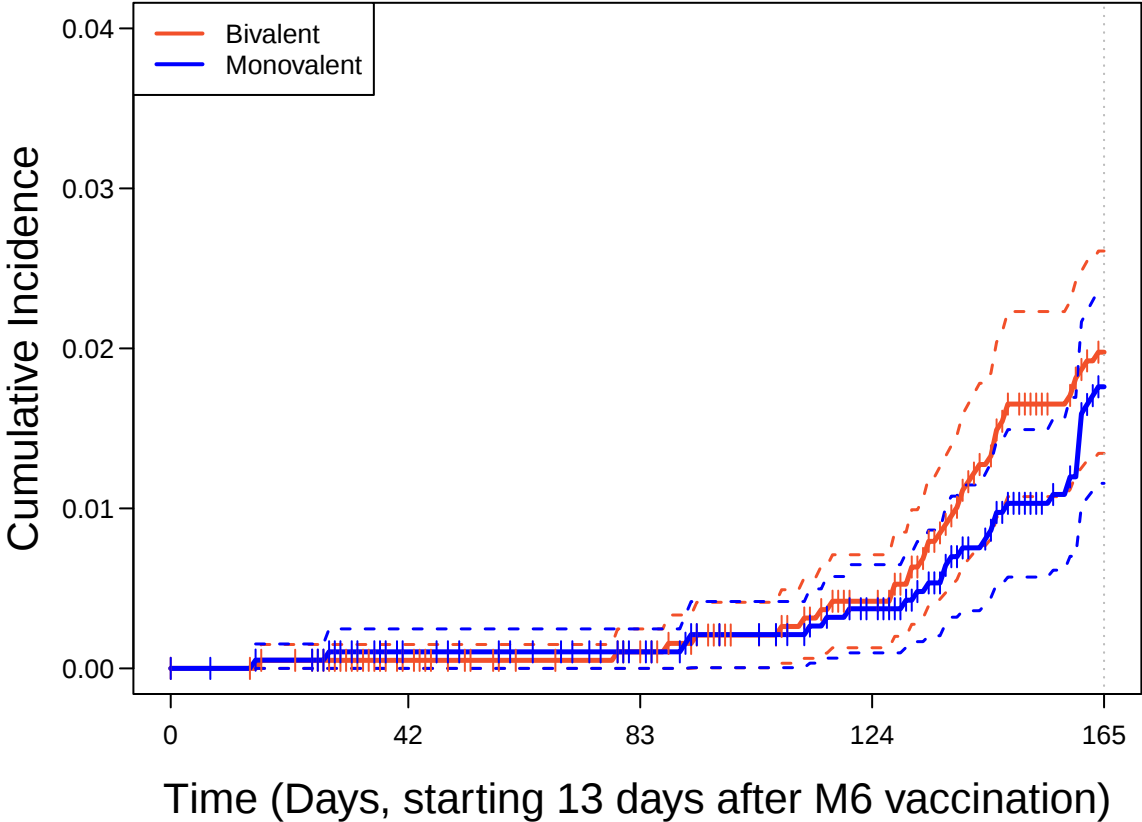
No. at Risk

Monovalent	1499	1462	1452	1436	1336
Bivalent	1541	1505	1493	1475	1372

Total Events

Monovalent	0	2	2	5	22
Bivalent	0	1	1	5	30

MBoost vs BBoost, FPP, CDC14M18, Primary



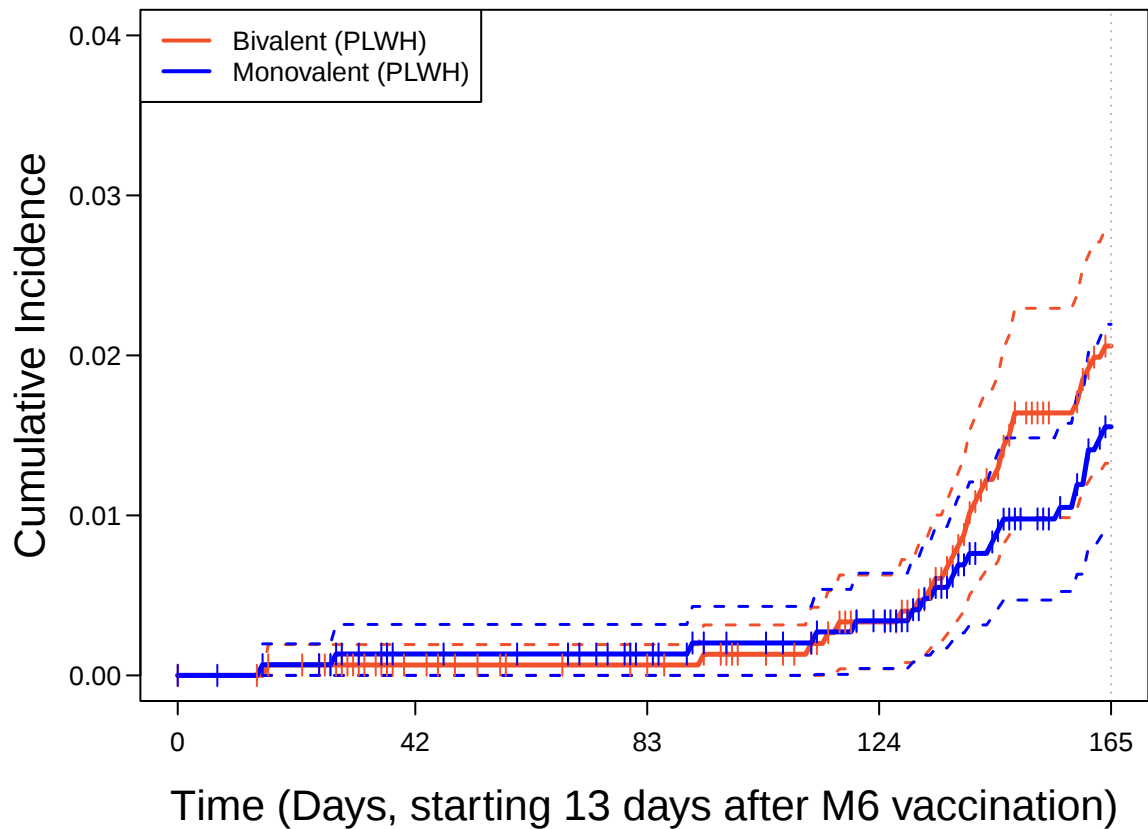
No. at Risk

Bivalent	1986	1925	1909	1882	1794
Monovalent	1933	1880	1866	1847	1755

Total Events

Bivalent	0	1	2	8	37
Monovalent	0	2	2	7	32

MBoost vs BBoost, FPP, CDC14M18, Primary (PLWH)



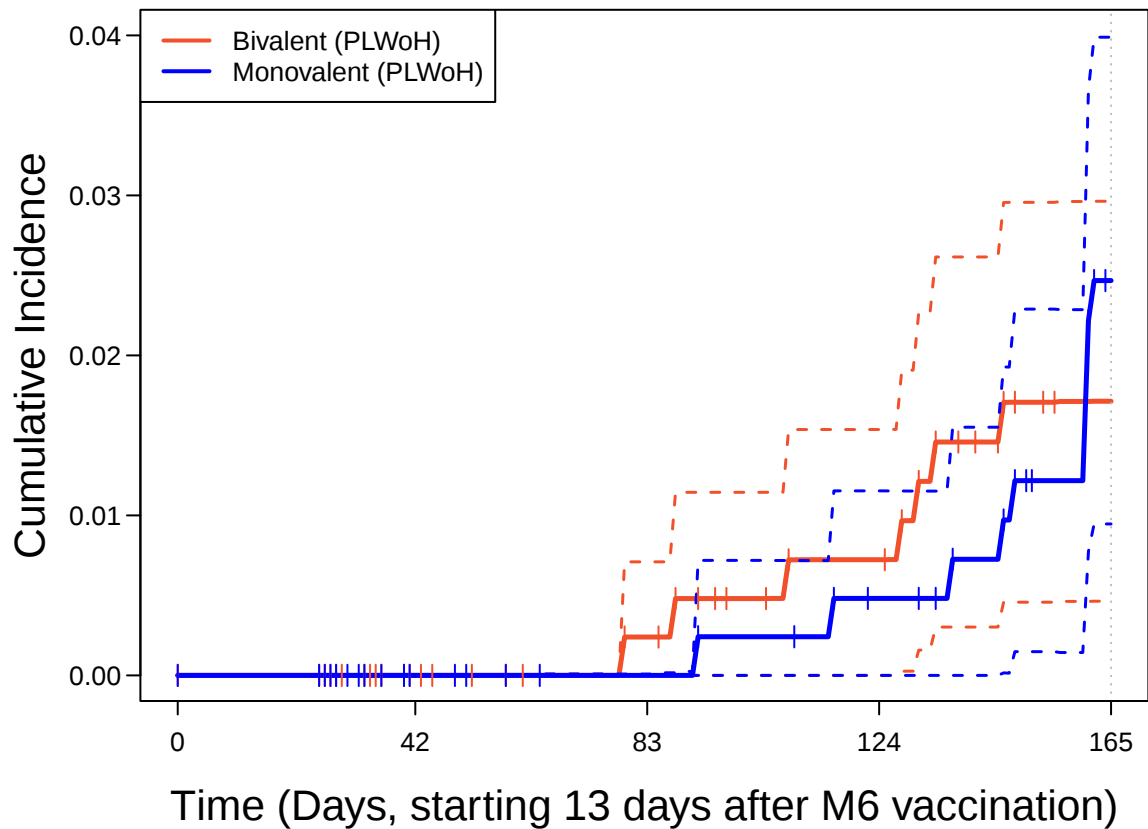
No. at Risk

Bivalent	1540	1504	1494	1475	1402
Monovalent	1499	1462	1453	1438	1363

Total Events

Bivalent	0	1	1	5	30
Monovalent	0	2	2	5	22

MBoost vs BBoost, FPP, CDC14M18, Primary (PLWoH)



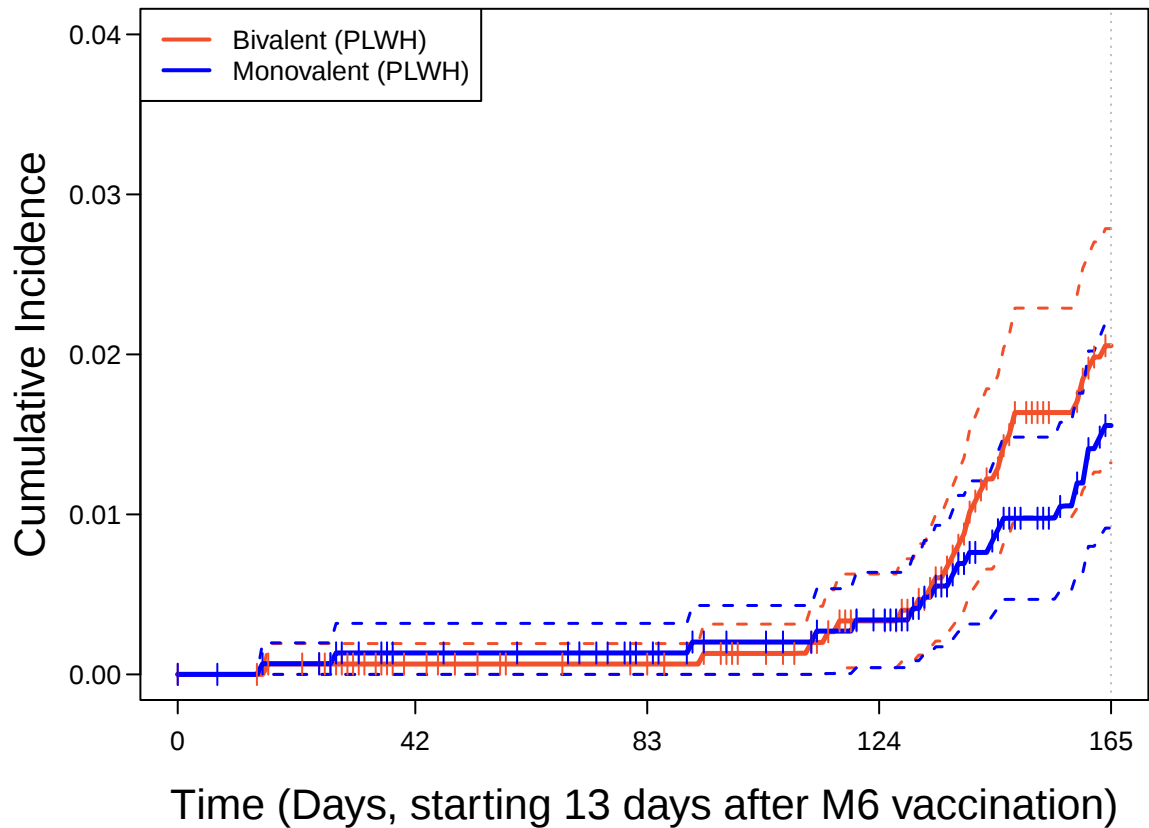
No. at Risk

Bivalent	446	421	415	407	392
Monovalent	434	418	413	409	392

Total Events

Bivalent	0	0	1	3	7
Monovalent	0	0	0	2	10

MBoost vs BBoost, FPP, CDC14M18, Sensitivity (PLWH)



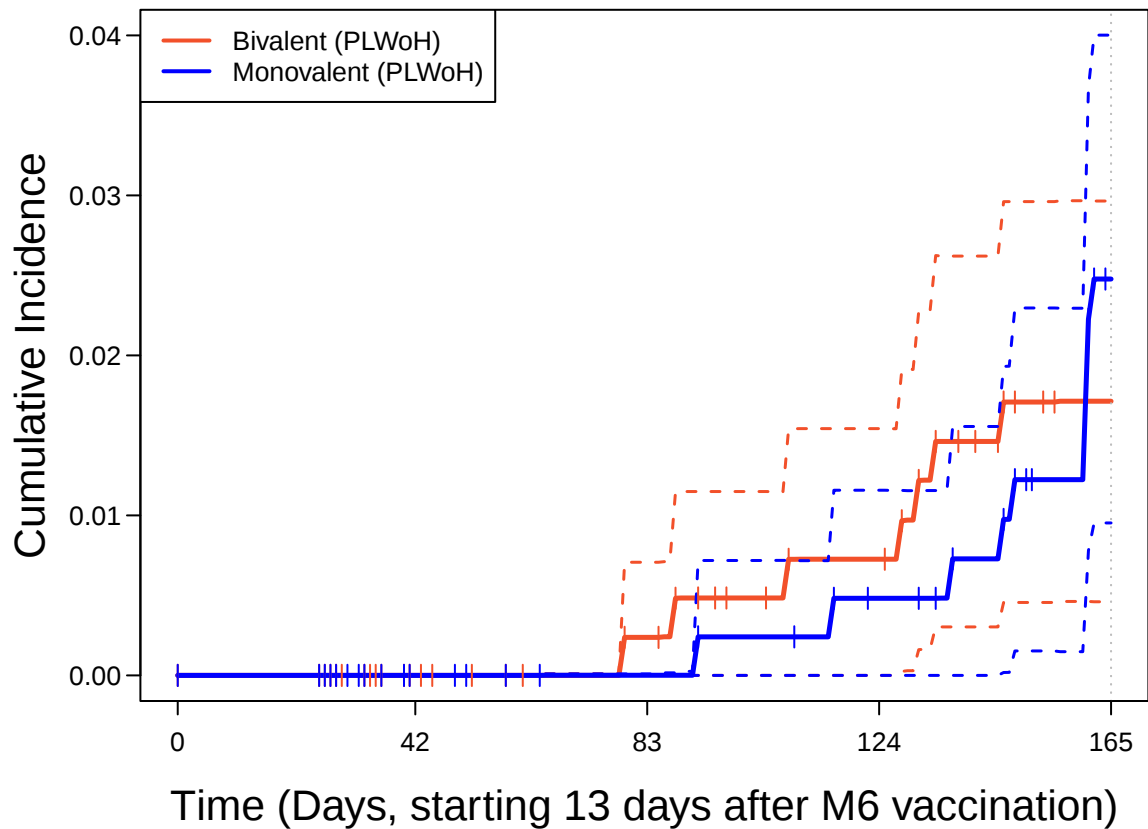
No. at Risk

Bivalent	1540	1504	1494	1475	1402
Monovalent	1499	1462	1453	1438	1363

Total Events

Bivalent	0	1	1	5	30
Monovalent	0	2	2	5	22

MBoost vs BBoost, FPP, CDC14M18, Sensitivity (PLWoH)



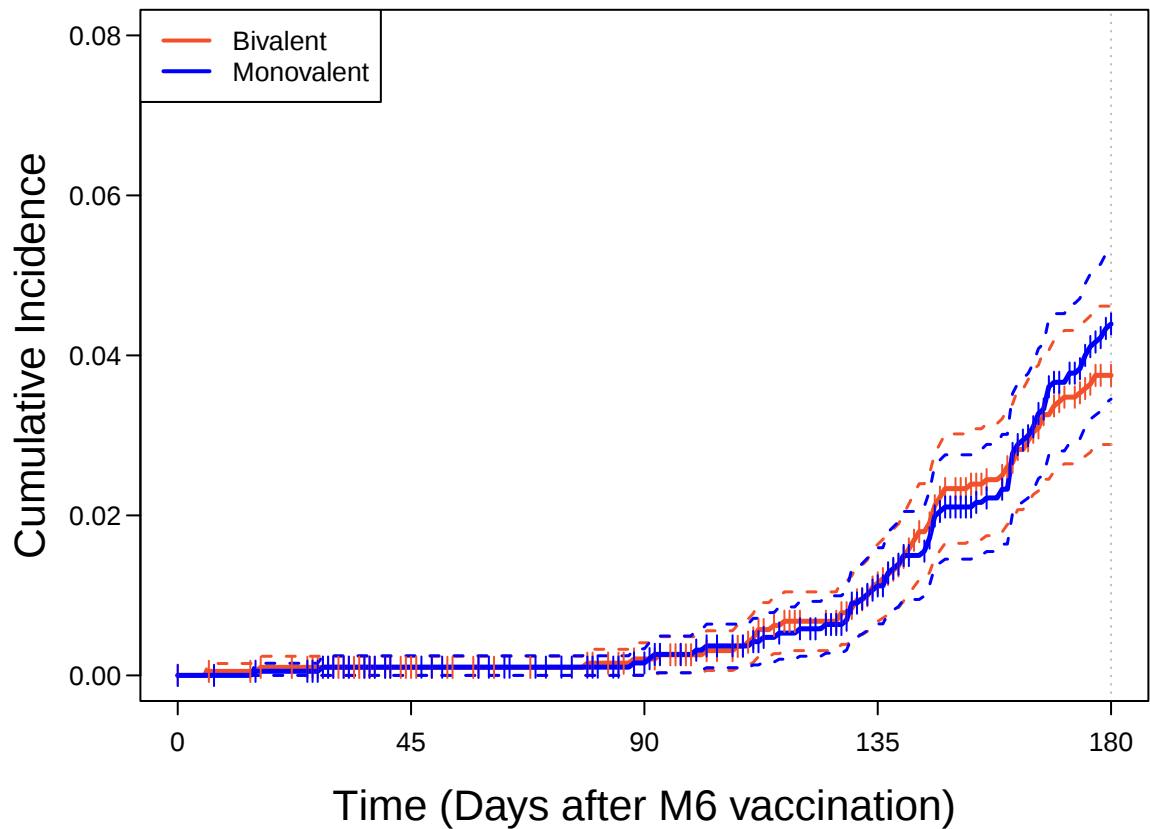
No. at Risk

Bivalent	446	421	415	407	392
Monovalent	434	418	413	409	392

Total Events

Bivalent	0	0	1	3	7
Monovalent	0	0	0	2	10

MBoost vs BBoost, RM6, ANYINF, Primary



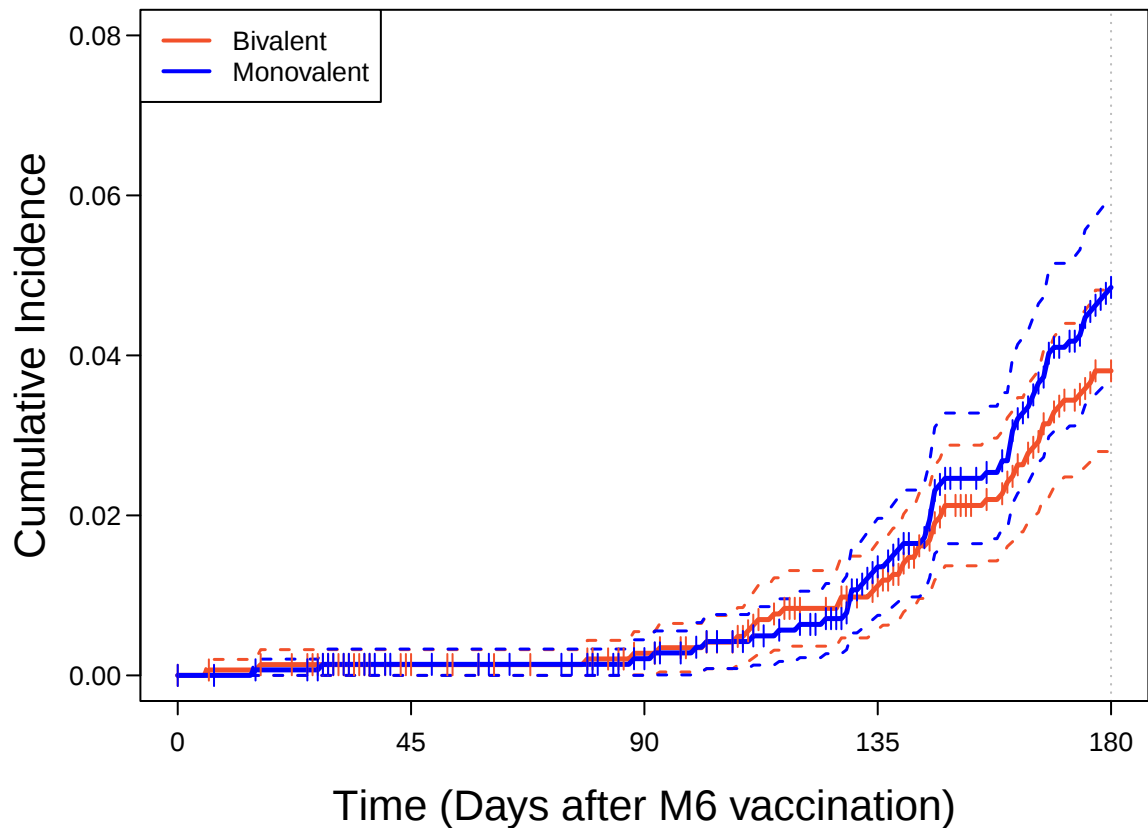
No. at Risk

Bivalent	1995	1930	1913	1867	1756
Monovalent	1949	1896	1878	1833	1710

Total Events

Bivalent	0	2	4	22	70
Monovalent	0	2	3	21	80

MBoost vs BBoost, RM6, ANYINF, Primary, Hybrid Immunity



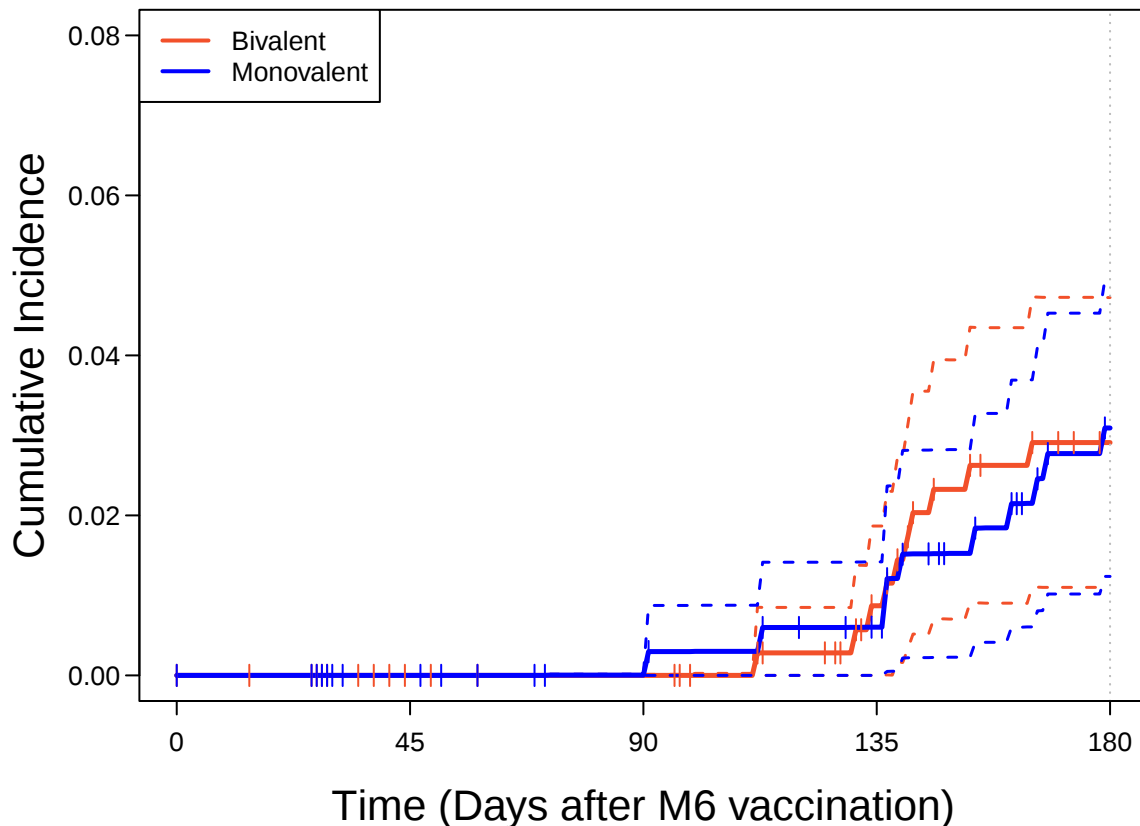
No. at Risk

Bivalent	1483	1438	1425	1395	1307
Monovalent	1451	1416	1404	1366	1269

Total Events

Bivalent	0	2	4	16	53
Monovalent	0	2	3	19	66

MBoost vs BBoost, RM6, ANYINF, Primary, Vaccine Immunity



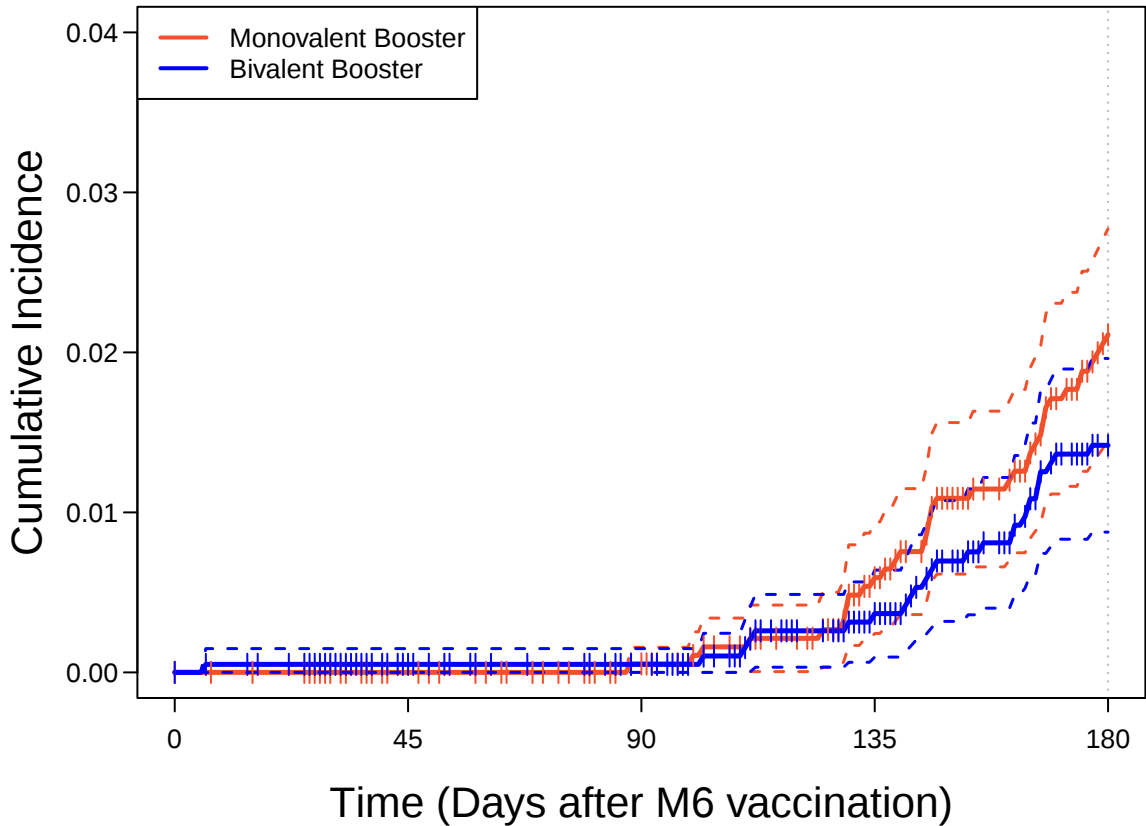
No. at Risk

Bivalent	365	351	349	338	324
Monovalent	352	340	335	329	314

Total Events

Bivalent	0	0	0	3	10
Monovalent	0	0	0	2	10

MBoost vs BBoost, RM6, ASYMINF, Primary



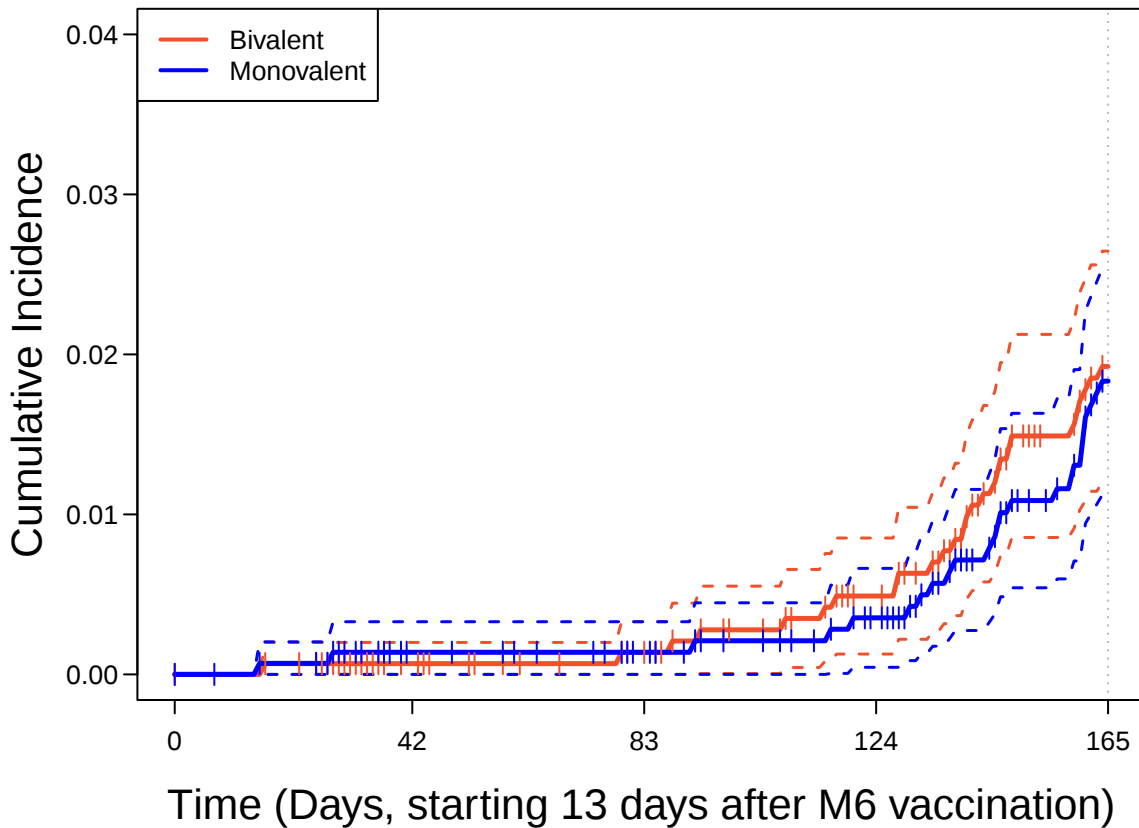
No. at Risk

Monovalent	1949	1896	1878	1833	1710
Bivalent	1995	1930	1913	1867	1756

Total Events

Monovalent	0	0	1	11	38
Bivalent	0	1	1	7	26

MBoost vs BBoost, RM6, CD14M18, Primary, Hybrid Immunit



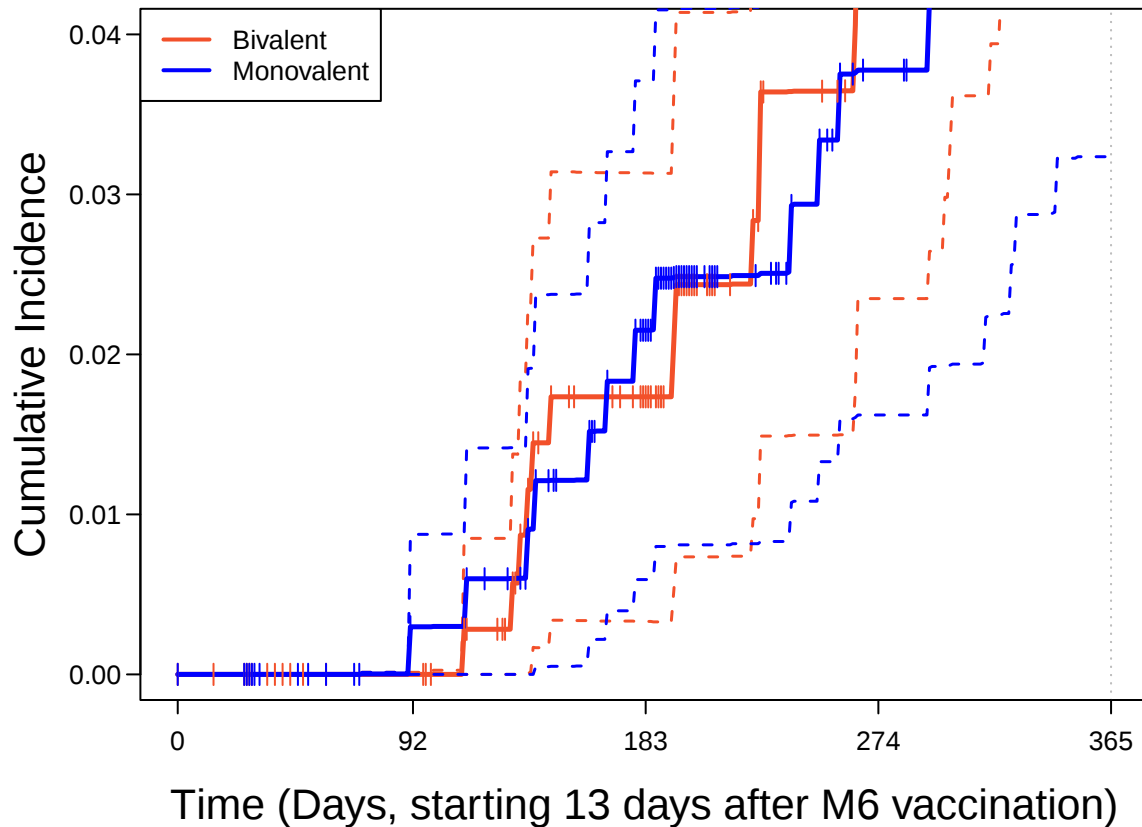
No. at Risk

Bivalent	1483	1441	1430	1410	1344
Monovalent	1451	1416	1407	1392	1320

Total Events

Bivalent	0	1	2	7	27
Monovalent	0	2	2	5	25

MBoost vs BBoost, RM6, CD14M18, Primary, Vaccine Immuni



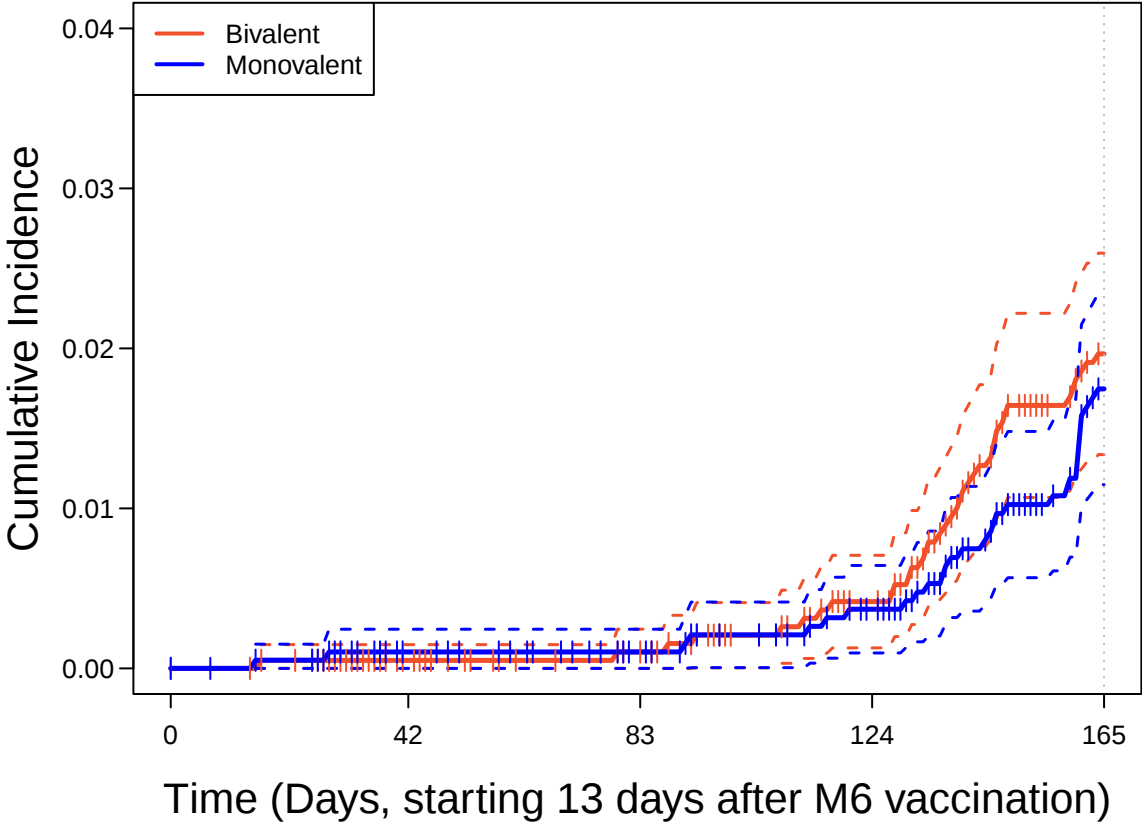
No. at Risk

Bivalent	365	349	322	231	184
Monovalent	352	334	313	221	168

Total Events

Bivalent	0	0	6	14	23
Monovalent	0	1	7	11	16

MBoost vs BBoost, RM6, CD14M18, Primary



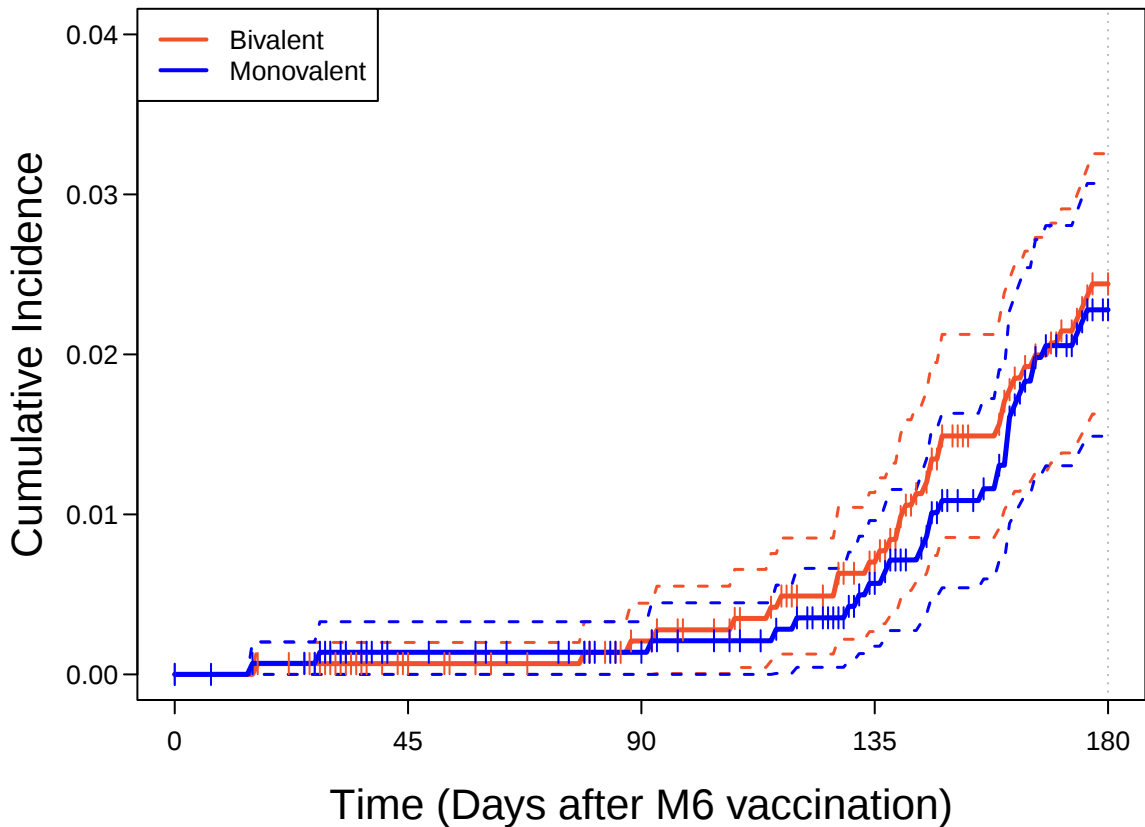
No. at Risk

Bivalent	1995	1934	1918	1891	1803
Monovalent	1949	1896	1881	1862	1770

Total Events

Bivalent	0	1	2	8	37
Monovalent	0	2	2	7	32

MBoost vs BBoost, RM6, CD1M18, Primary, Hybrid Immunity



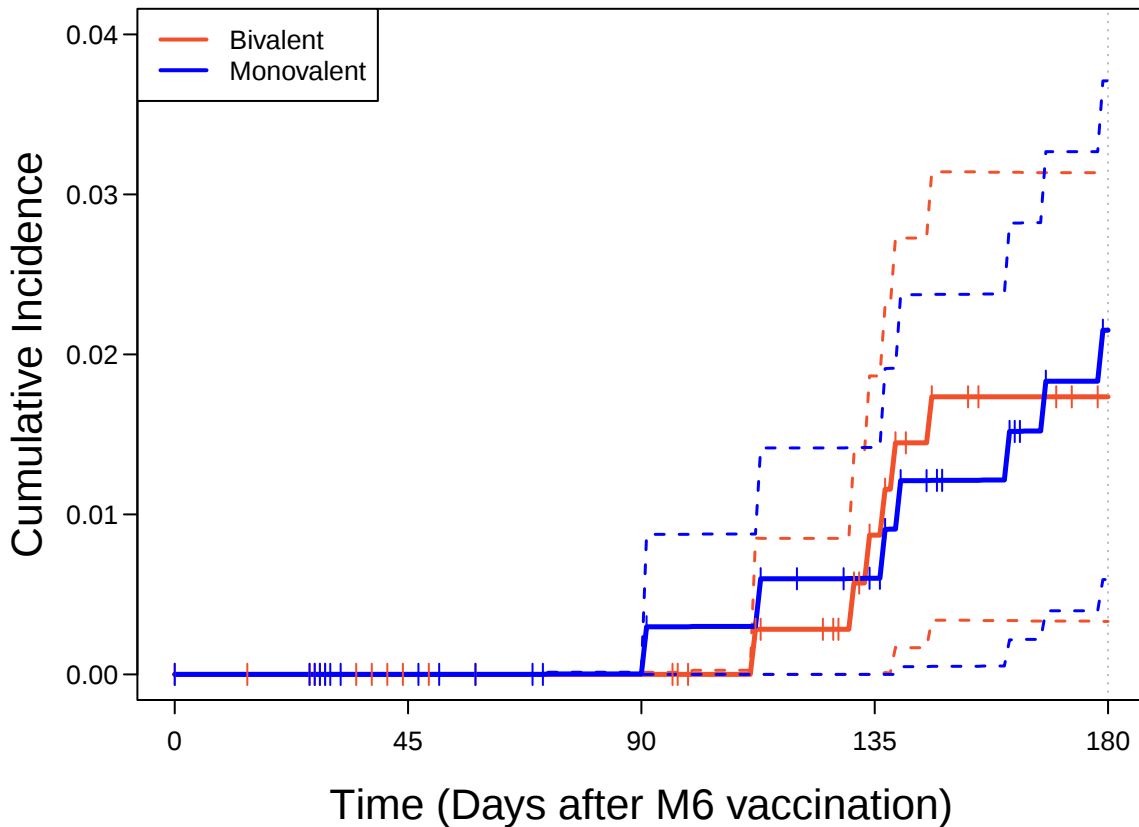
No. at Risk

Bivalent	1483	1439	1426	1400	1326
Monovalent	1451	1416	1405	1376	1303

Total Events

Bivalent	0	1	3	10	34
Monovalent	0	2	2	8	31

MBoost vs BBoost, RM6, CD1M18, Primary, Vaccine Immunit



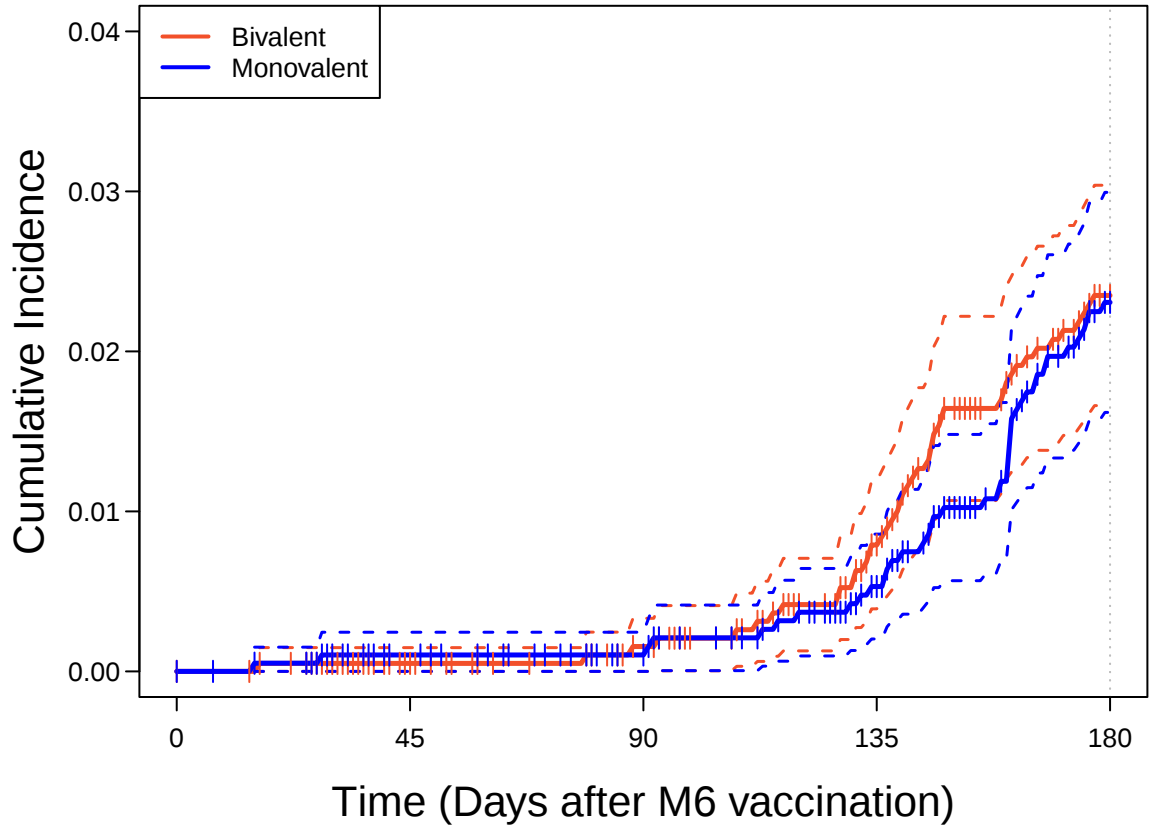
No. at Risk

Bivalent	365	351	349	338	328
Monovalent	352	340	335	329	317

Total Events

Bivalent	0	0	0	3	6
Monovalent	0	0	0	2	7

MBoost vs BBoost, RM6, CD1M18, Primary



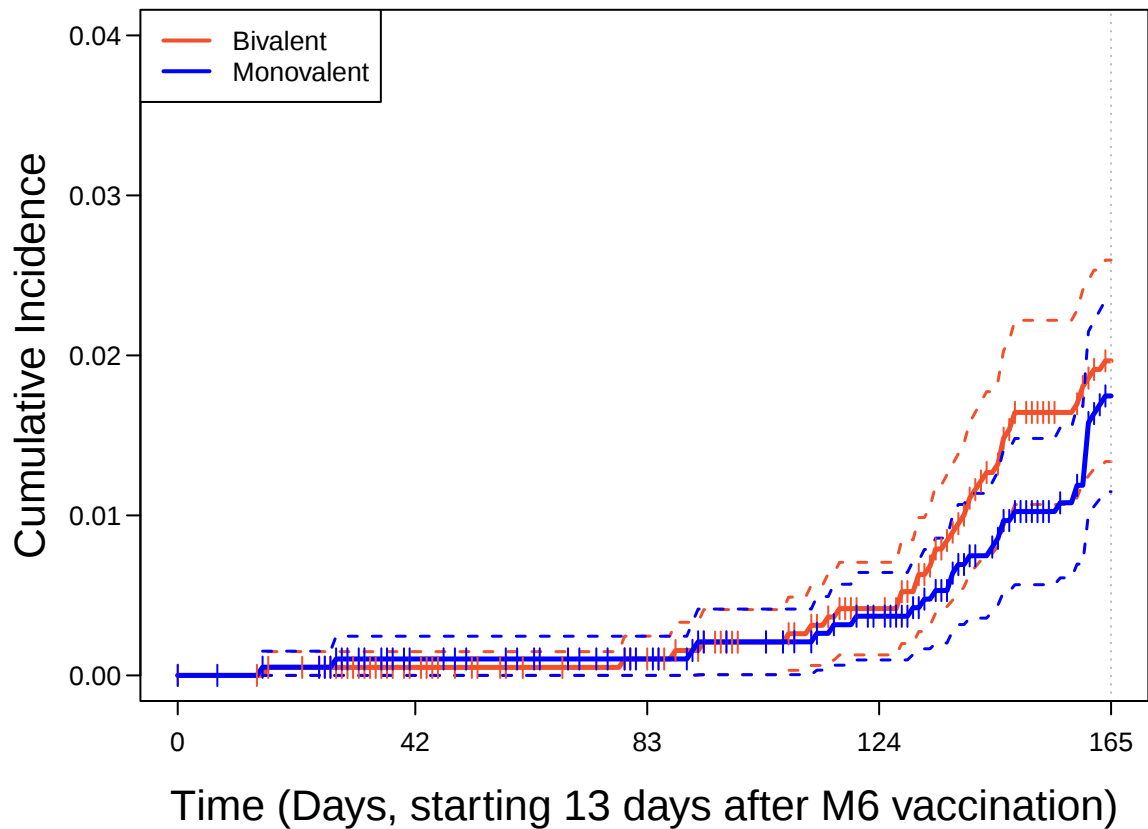
No. at Risk

Bivalent	1995	1931	1914	1873	1782
Monovalent	1949	1896	1879	1843	1747

Total Events

Bivalent	0	1	3	15	44
Monovalent	0	2	2	10	42

MBoost vs BBoost, RM6, CDC14M12, Primary



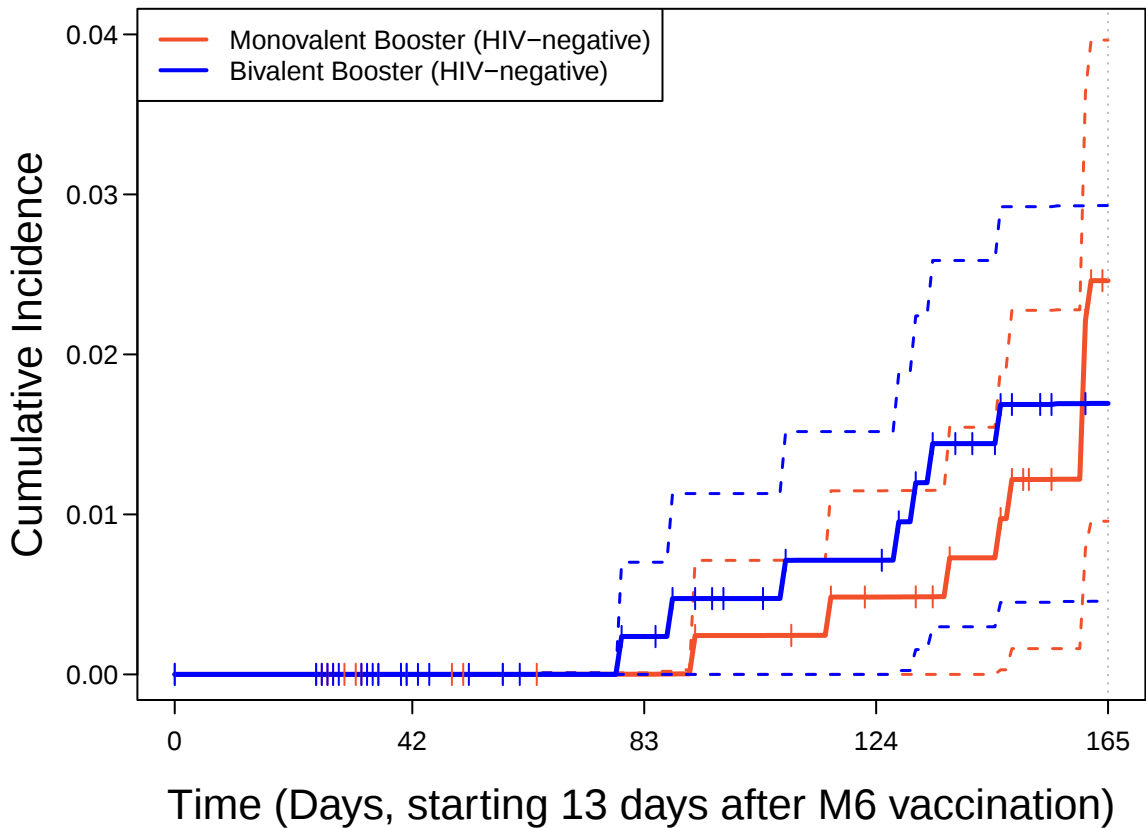
No. at Risk

Bivalent	1995	1934	1918	1891	1803
Monovalent	1949	1896	1881	1862	1770

Total Events

Bivalent	0	1	2	8	37
Monovalent	0	2	2	7	32

MBoost vs BBoost, RM6, CDC14M12, Primary (PLWoH)



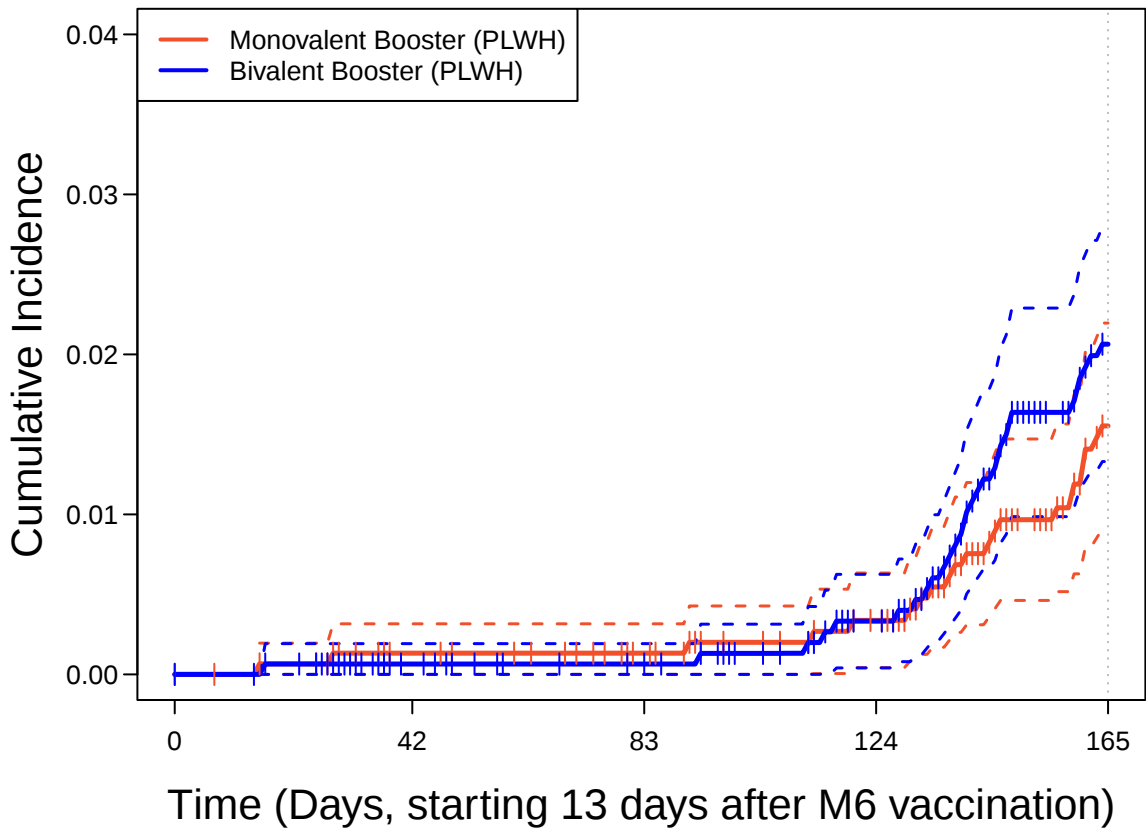
No. at Risk

Monovalent	439	423	418	414	396
Bivalent	450	425	419	411	394

Total Events

Monovalent	0	0	0	2	10
Bivalent	0	0	1	3	7

MBoost vs BBoost, RM6, CDC14M12, Sensitivity (PLWH)



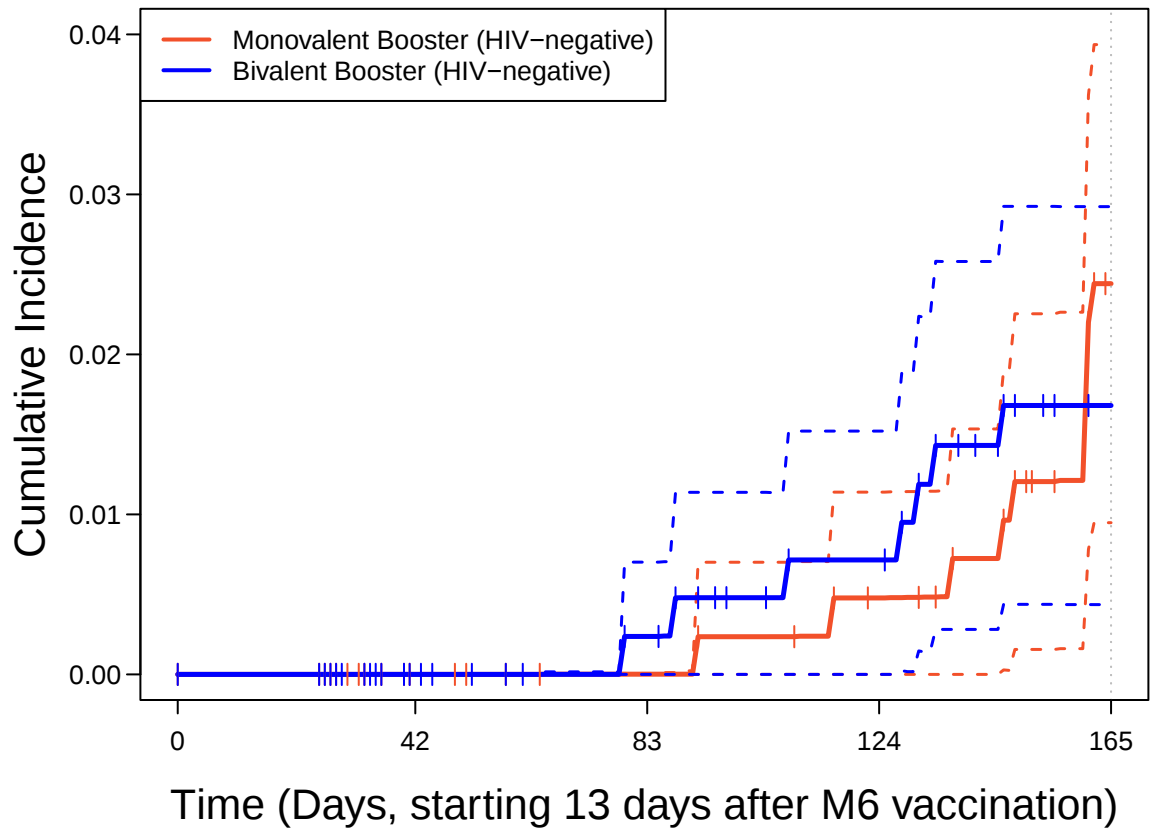
No. at Risk

Monovalent	1510	1473	1462	1446	1346
Bivalent	1546	1510	1498	1480	1377

Total Events

Monovalent	0	2	2	5	22
Bivalent	0	1	1	5	30

MBoost vs BBoost, RM6, CDC14M12, Sensitivity (PLWoH)



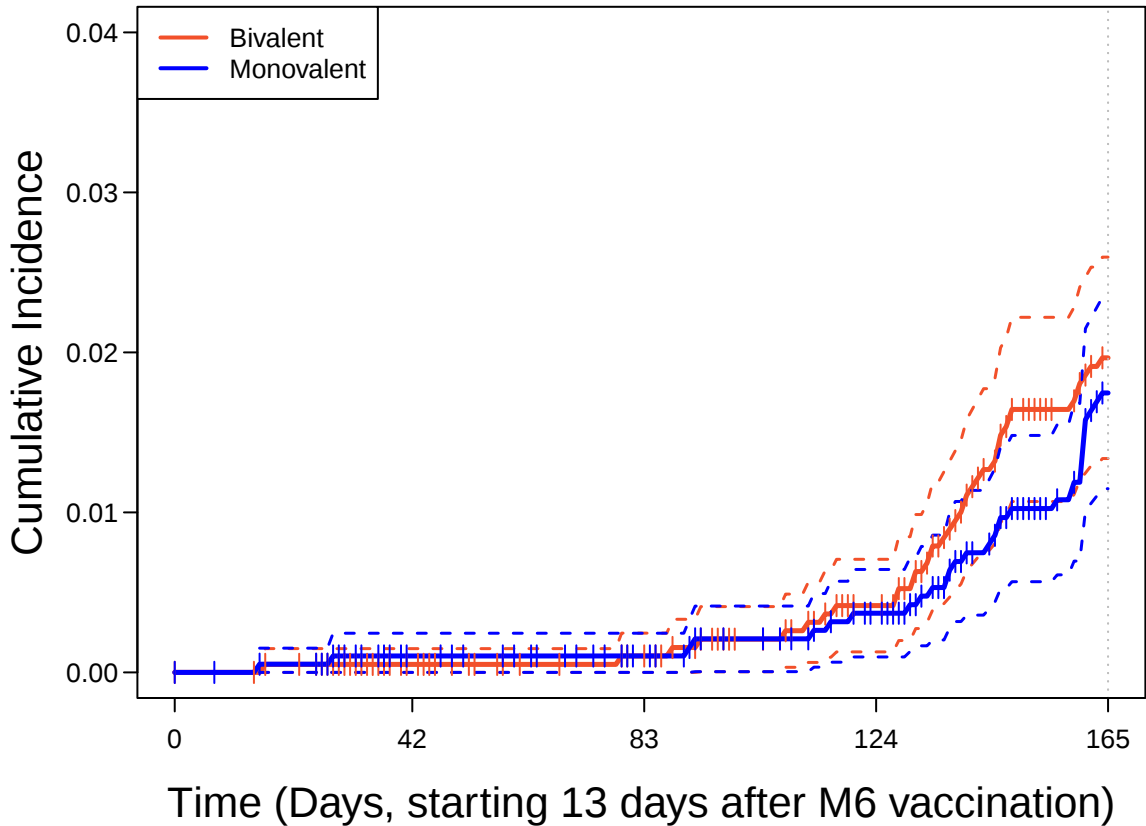
No. at Risk

Monovalent	439	423	418	414	396
Bivalent	450	425	419	411	394

Total Events

Monovalent	0	0	0	2	10
Bivalent	0	0	1	3	7

MBoost vs BBoost, RM6, CDC14M18, Primary



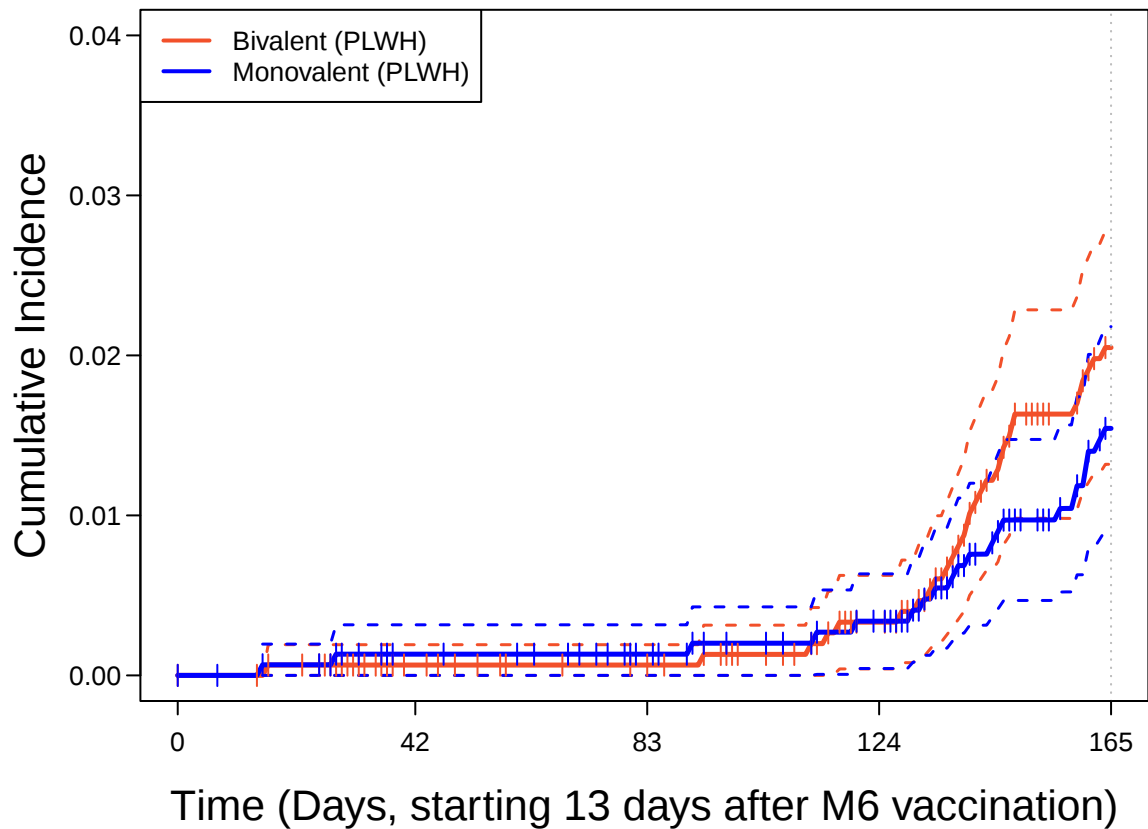
No. at Risk

Bivalent	1995	1934	1918	1891	1803
Monovalent	1949	1896	1881	1862	1770

Total Events

Bivalent	0	1	2	8	37
Monovalent	0	2	2	7	32

MBoost vs BBoost, RM6, CDC14M18, Primary (PLWH)



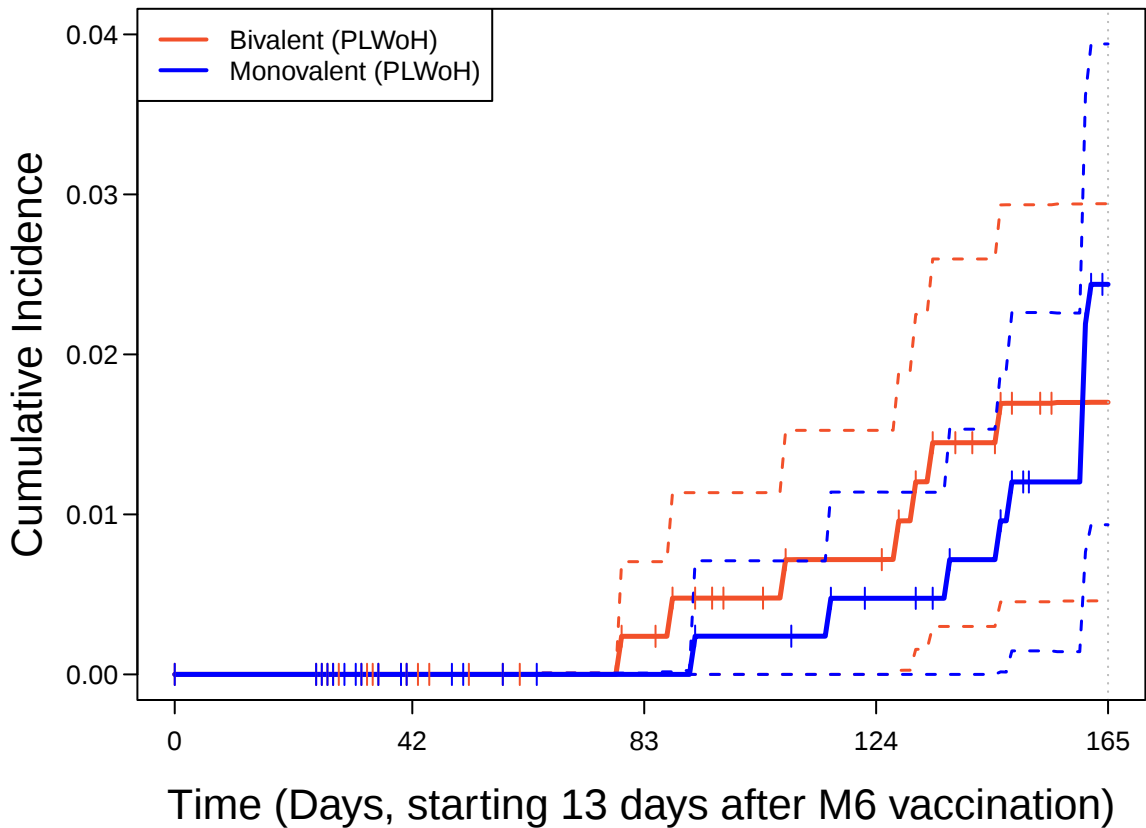
No. at Risk

Bivalent	1546	1510	1500	1481	1408
Monovalent	1510	1473	1463	1448	1373

Total Events

Bivalent	0	1	1	5	30
Monovalent	0	2	2	5	22

MBoost vs BBoost, RM6, CDC14M18, Primary (PLWoH)



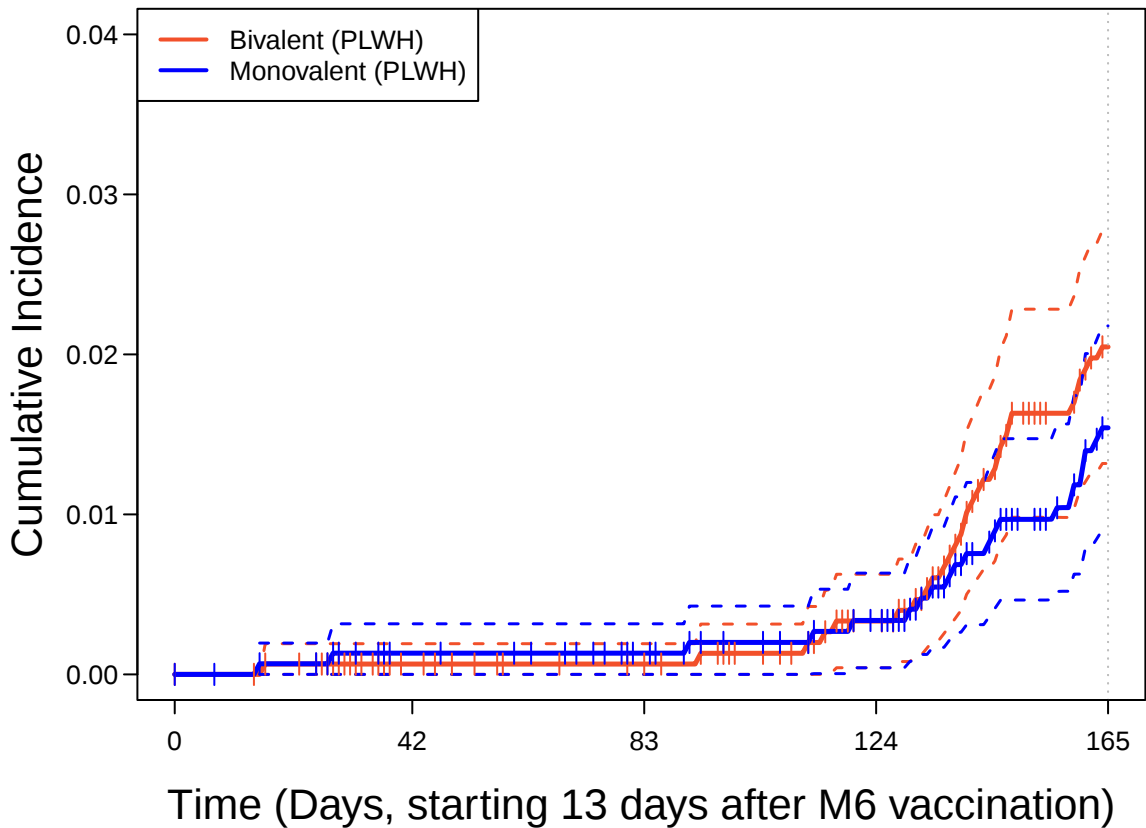
No. at Risk

Bivalent	449	424	418	410	395
Monovalent	439	423	418	414	397

Total Events

Bivalent	0	0	1	3	7
Monovalent	0	0	0	2	10

MBoost vs BBoost, RM6, CDC14M18, Sensitivity (PLWH)



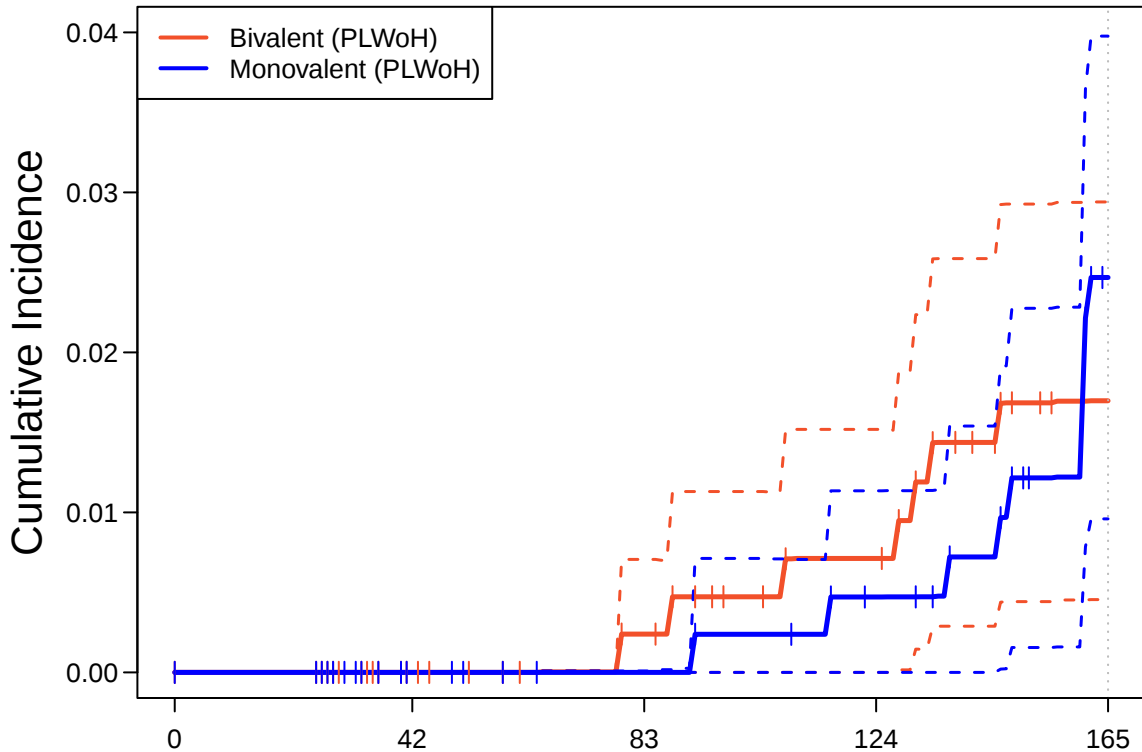
No. at Risk

Bivalent	1546	1510	1500	1481	1408
Monovalent	1510	1473	1463	1448	1373

Total Events

Bivalent	0	1	1	5	30
Monovalent	0	2	2	5	22

MBoost vs BBoost, RM6, CDC14M18, Sensitivity (PLWoH)



Time (Days, starting 13 days after M6 vaccination)

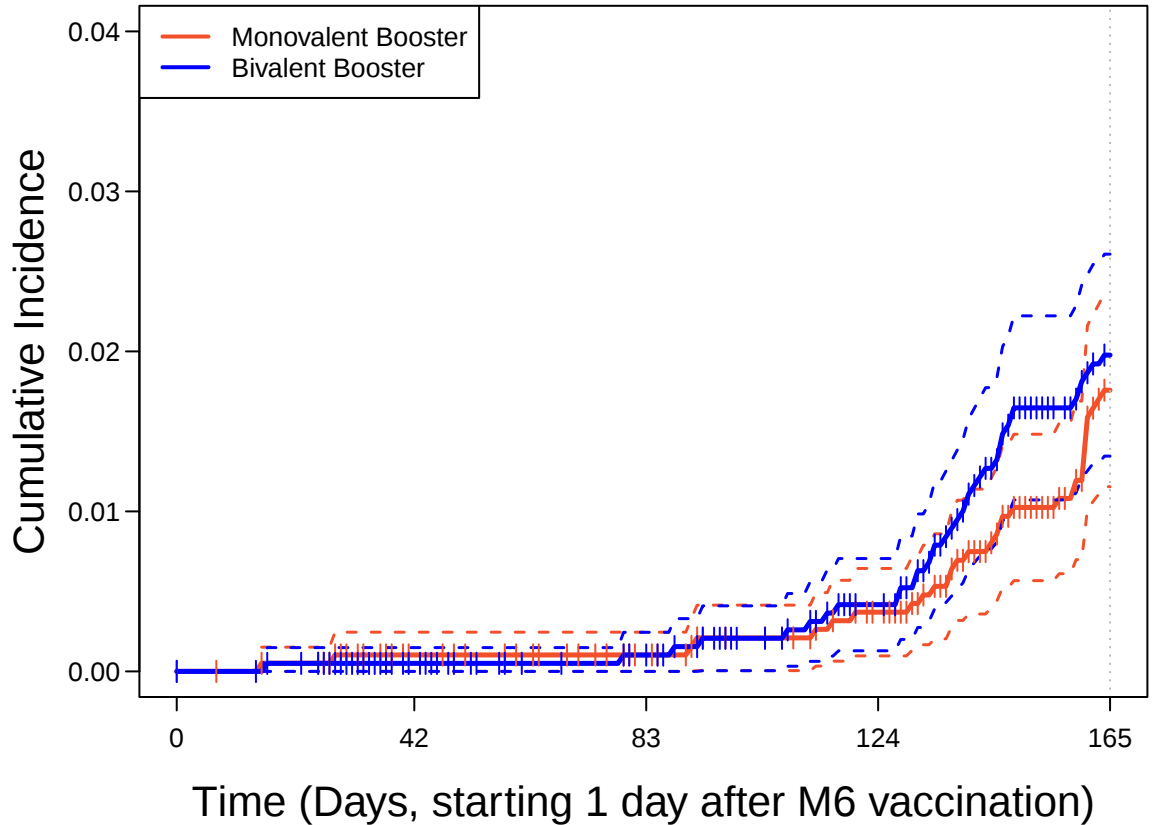
No. at Risk

Bivalent	449	424	418	410	395
Monovalent	439	423	418	414	397

Total Events

Bivalent	0	0	1	3	7
Monovalent	0	0	0	2	10

MBoost vs BBoost, RM6, CDC1M12, Primary



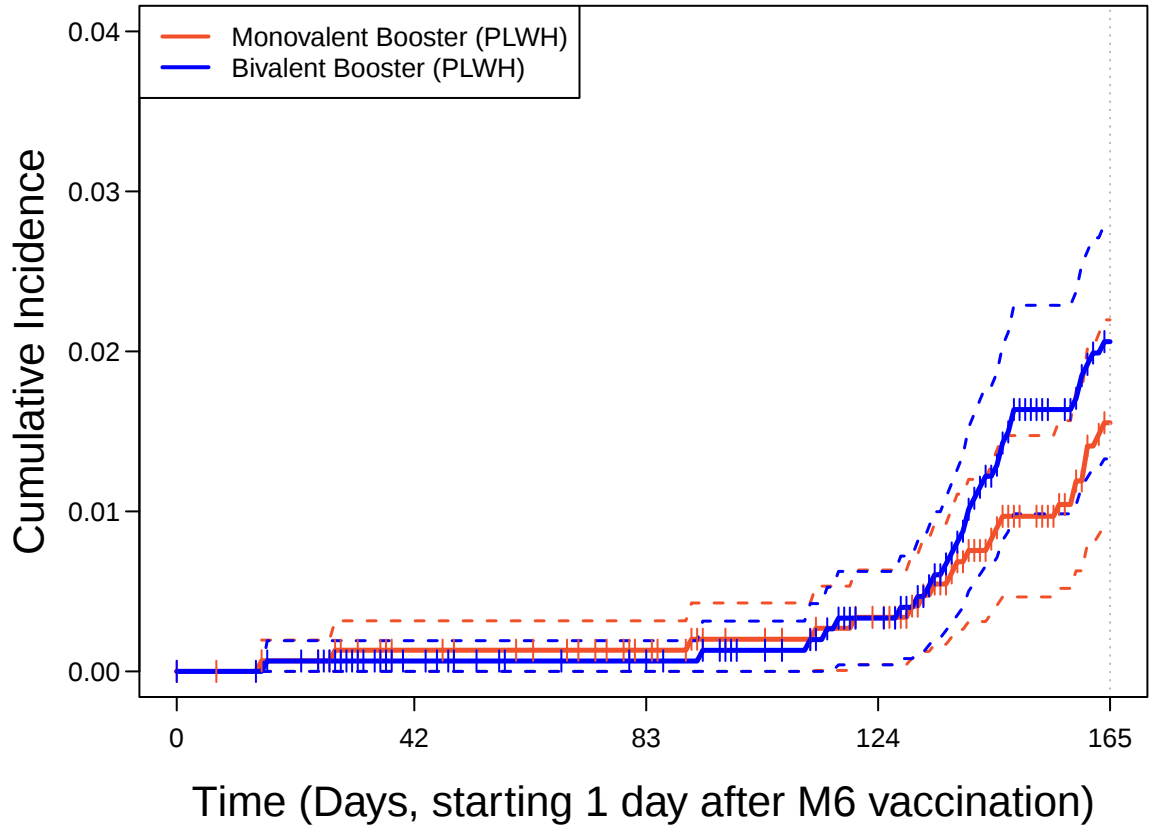
No. at Risk

Monovalent	1949	1896	1880	1860	1742
Bivalent	1996	1935	1917	1891	1771

Total Events

Monovalent	0	2	2	7	32
Bivalent	0	1	2	8	37

MBoost vs BBoost, RM6, CDC1M12, Primary (PLWH)



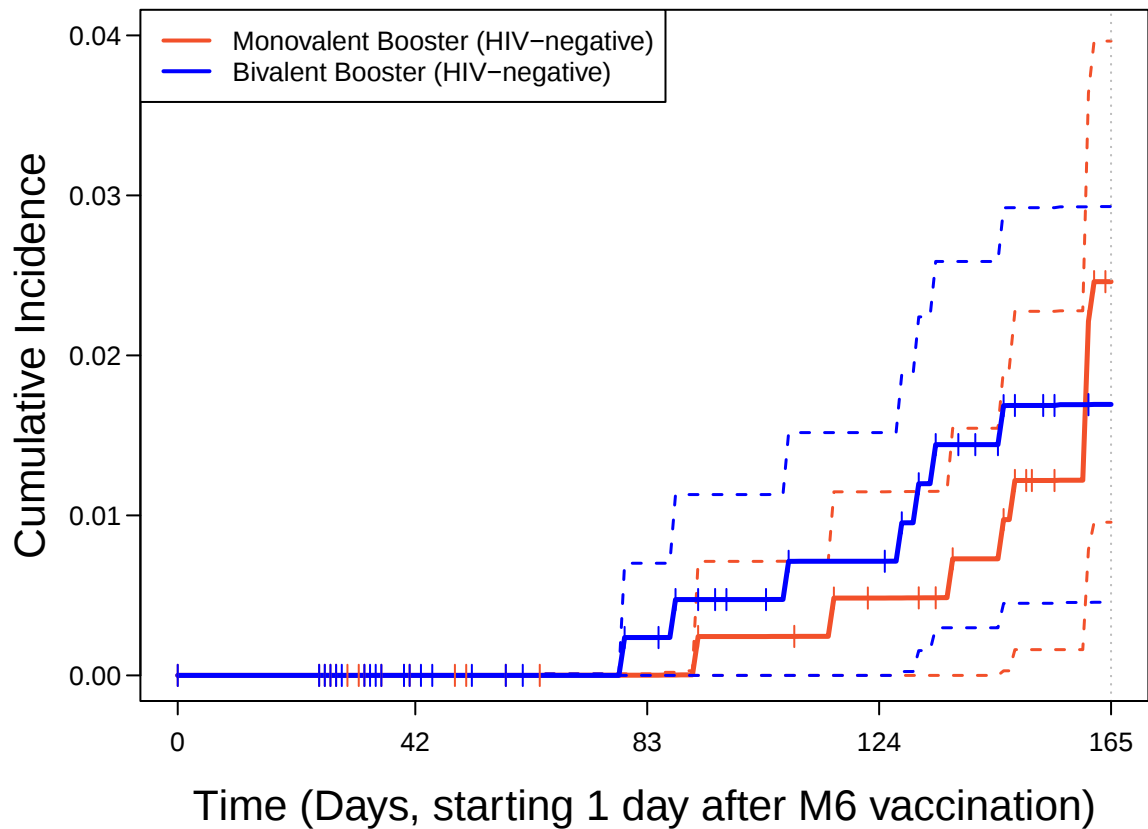
No. at Risk

Monovalent	1510	1473	1462	1446	1346
Bivalent	1546	1510	1498	1480	1377

Total Events

Monovalent	0	2	2	5	22
Bivalent	0	1	1	5	30

MBoost vs BBoost, RM6, CDC1M12, Primary (PLWoH)



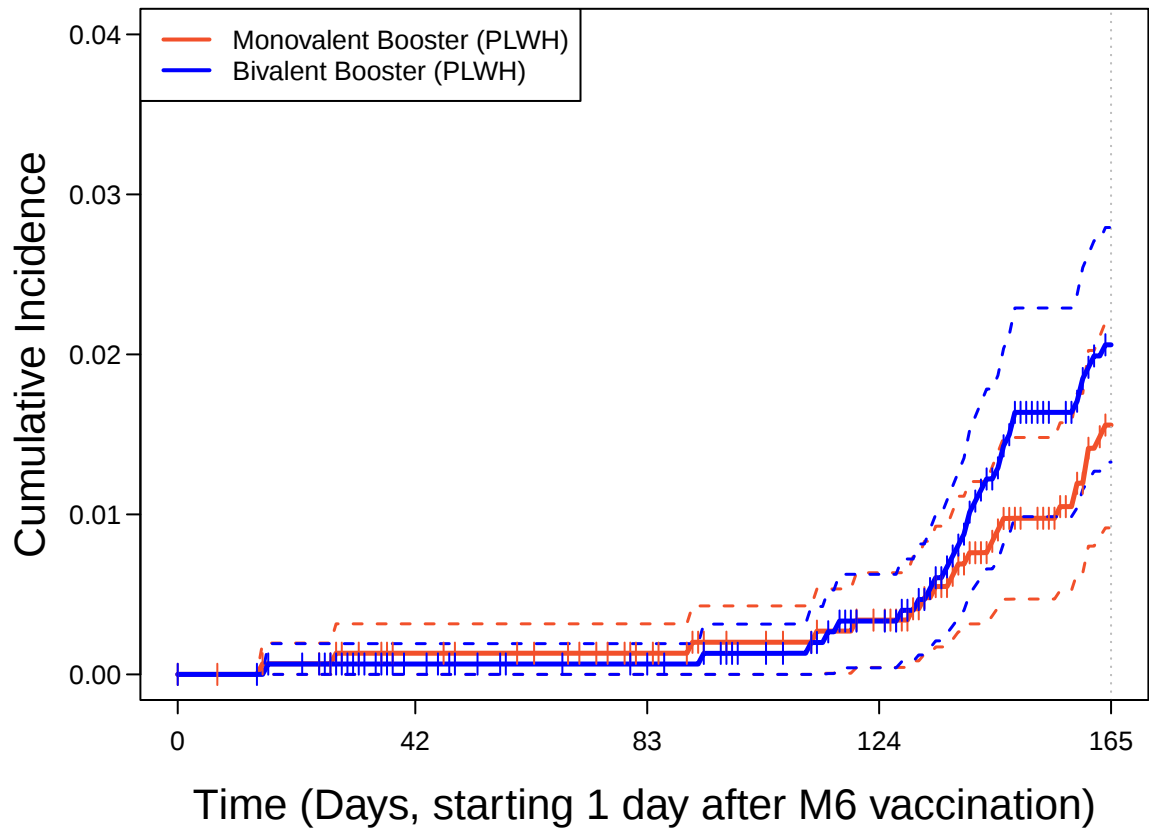
No. at Risk

Monovalent	439	423	418	414	396
Bivalent	450	425	419	411	394

Total Events

Monovalent	0	0	0	2	10
Bivalent	0	0	1	3	7

MBoost vs BBoost, RM6, CDC1M12, Sensitivity (PLWH)



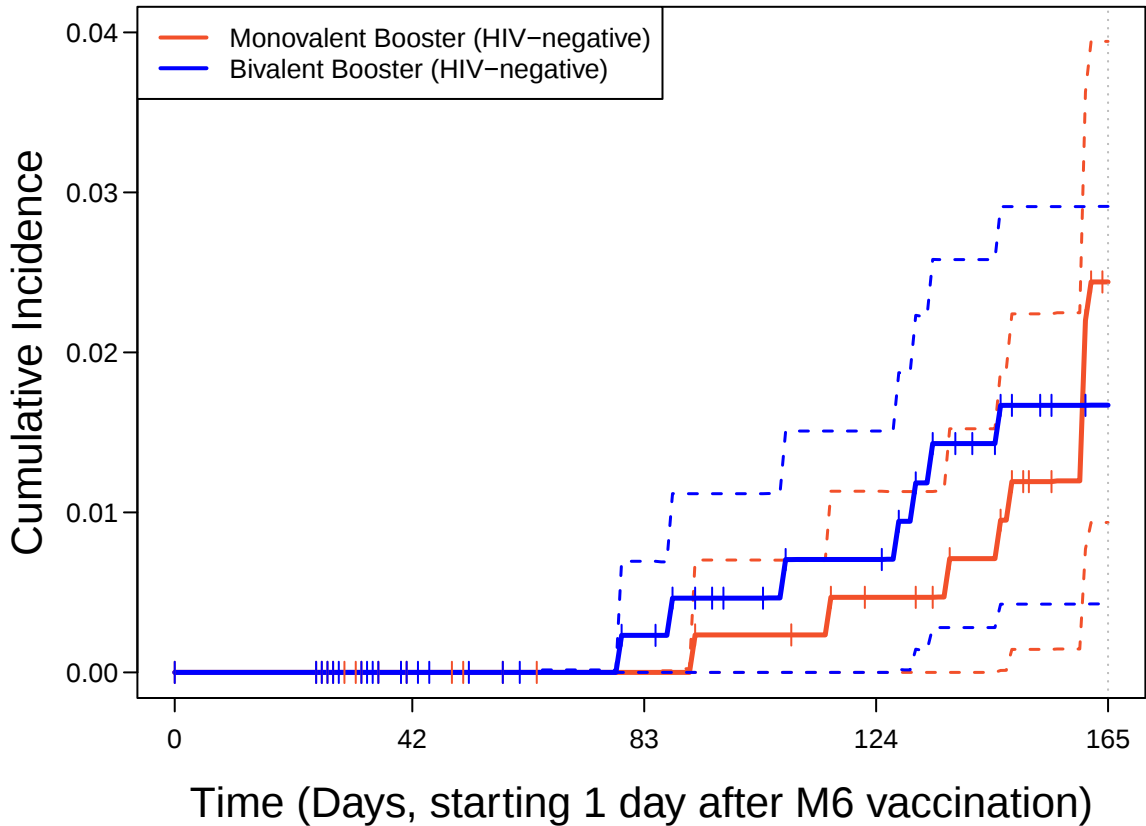
No. at Risk

Monovalent	1510	1473	1462	1446	1346
Bivalent	1546	1510	1498	1480	1377

Total Events

Monovalent	0	2	2	5	22
Bivalent	0	1	1	5	30

MBoost vs BBoost, RM6, CDC1M12, Sensitivity (PLWoH)



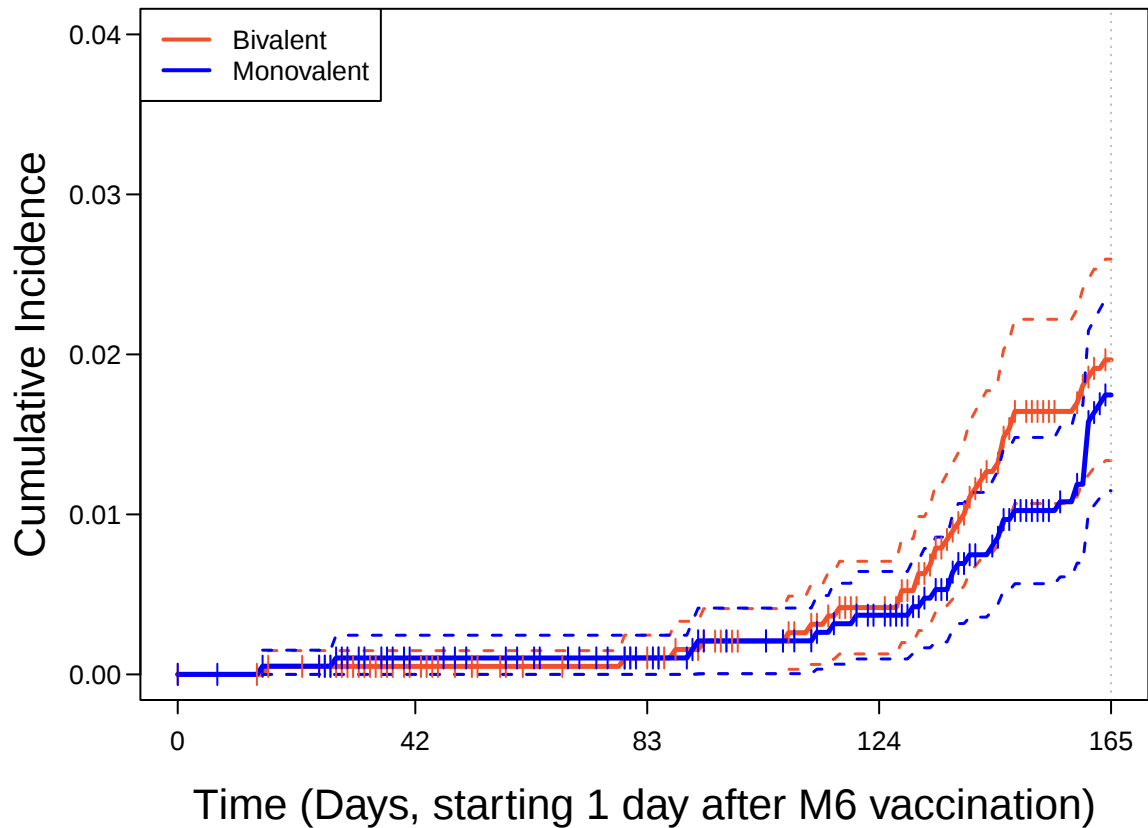
No. at Risk

Monovalent	439	423	418	414	396
Bivalent	450	425	419	411	394

Total Events

Monovalent	0	0	0	2	10
Bivalent	0	0	1	3	7

MBoost vs BBoost, RM6, CDC1M18, Primary



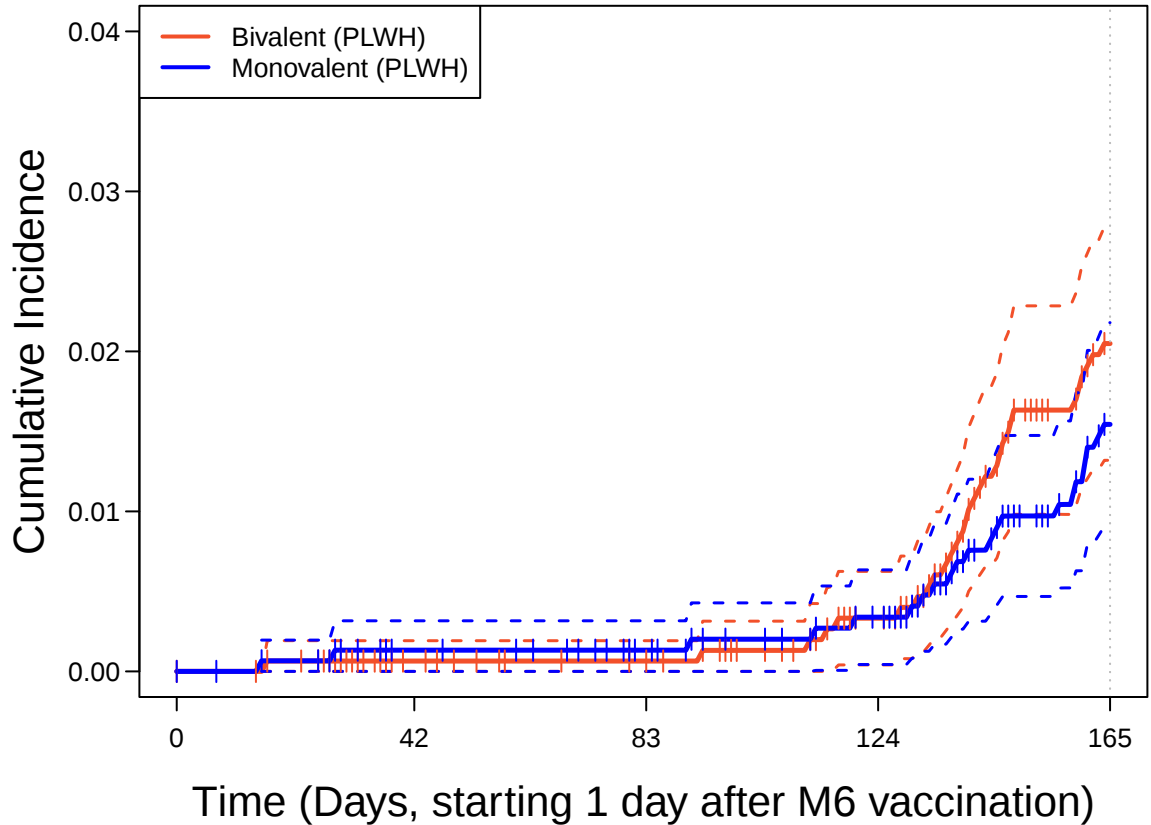
No. at Risk

Bivalent	1995	1934	1918	1891	1803
Monovalent	1949	1896	1881	1862	1770

Total Events

Bivalent	0	1	2	8	37
Monovalent	0	2	2	7	32

MBoost vs BBoost, RM6, CDC1M18, Primary (PLWH)



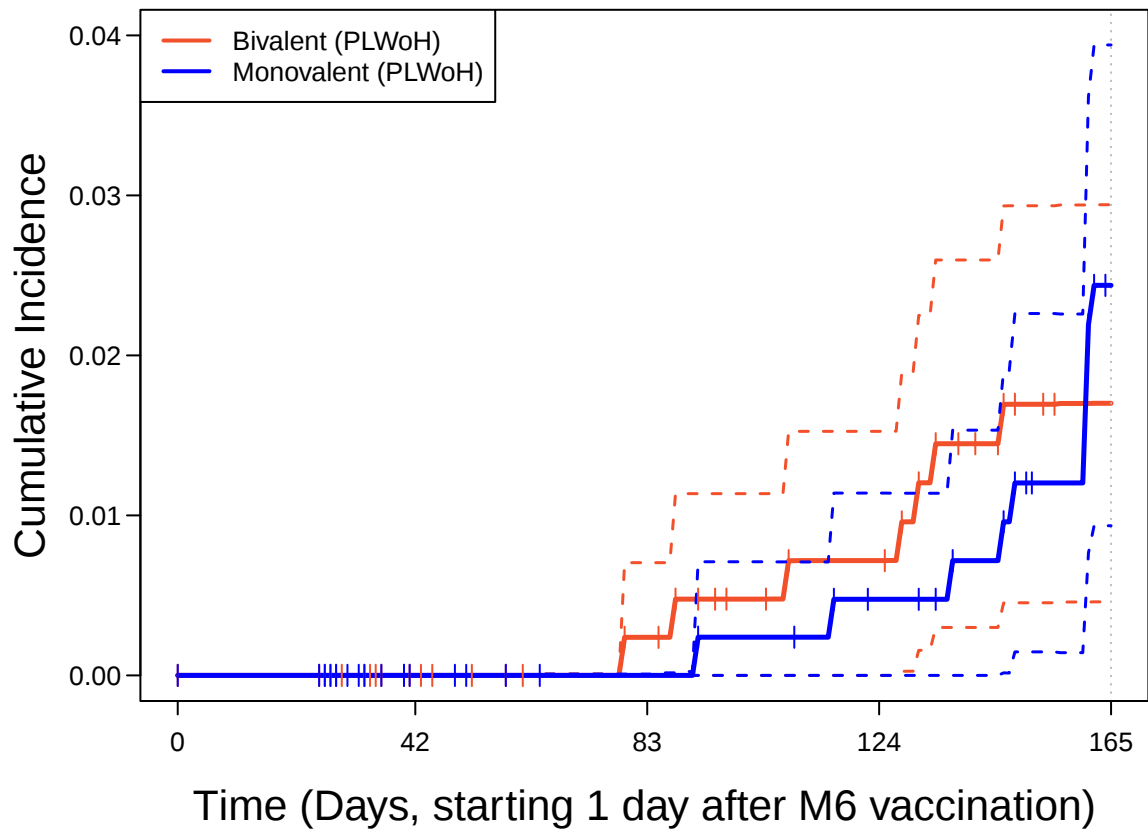
No. at Risk

Bivalent	1546	1510	1500	1481	1408
Monovalent	1510	1473	1463	1448	1373

Total Events

Bivalent	0	1	1	5	30
Monovalent	0	2	2	5	22

MBoost vs BBoost, RM6, CDC1M18, Primary (PLWoH)



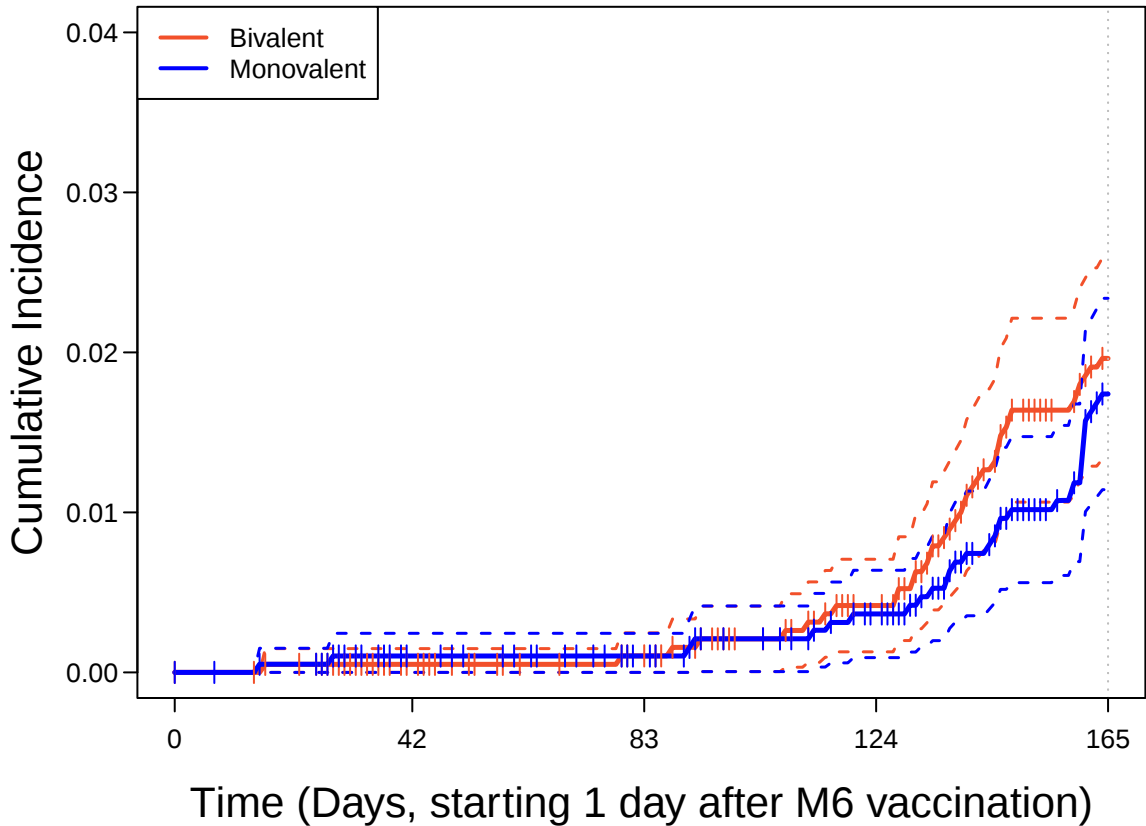
No. at Risk

Bivalent	449	424	418	410	395
Monovalent	439	423	418	414	397

Total Events

Bivalent	0	0	1	3	7
Monovalent	0	0	0	2	10

MBoost vs BBoost, RM6, CDC1M18, Sensitivity



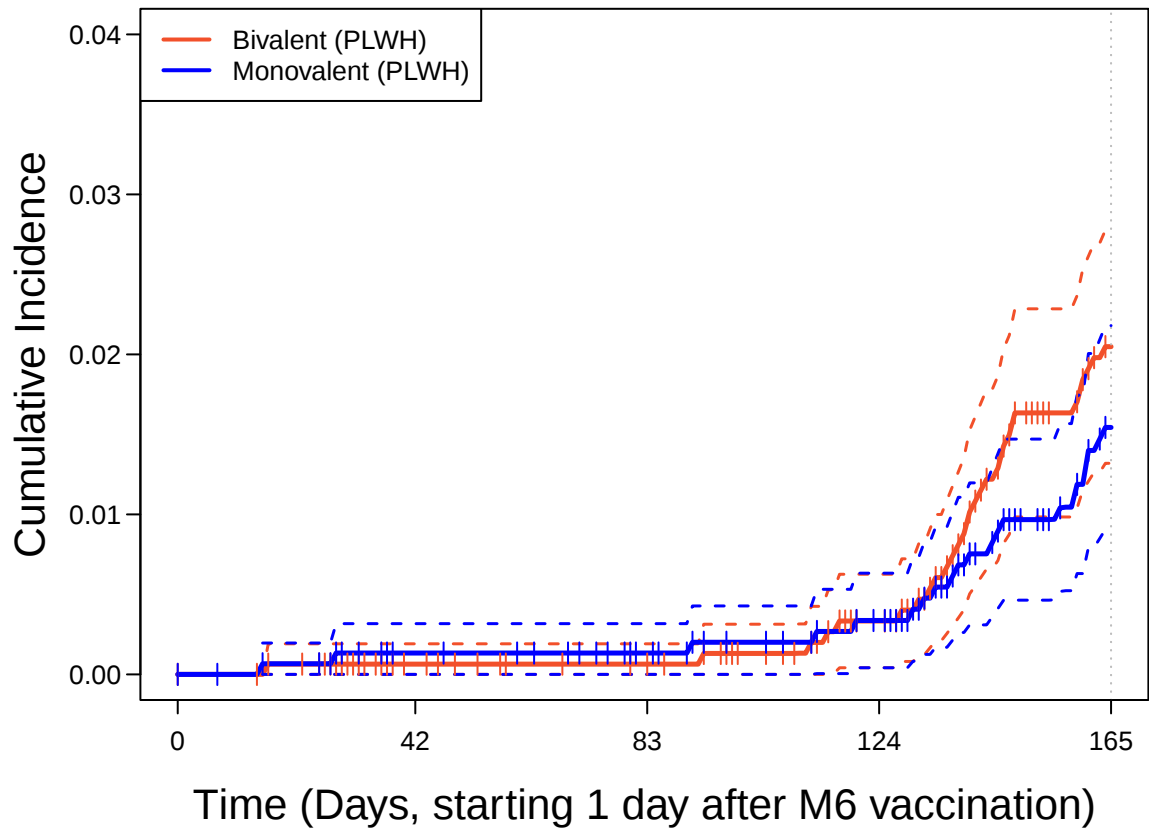
No. at Risk

Bivalent	1995	1934	1918	1891	1803
Monovalent	1949	1896	1881	1862	1770

Total Events

Bivalent	0	1	2	8	37
Monovalent	0	2	2	7	32

MBoost vs BBoost, RM6, CDC1M18, Sensitivity (PLWH)



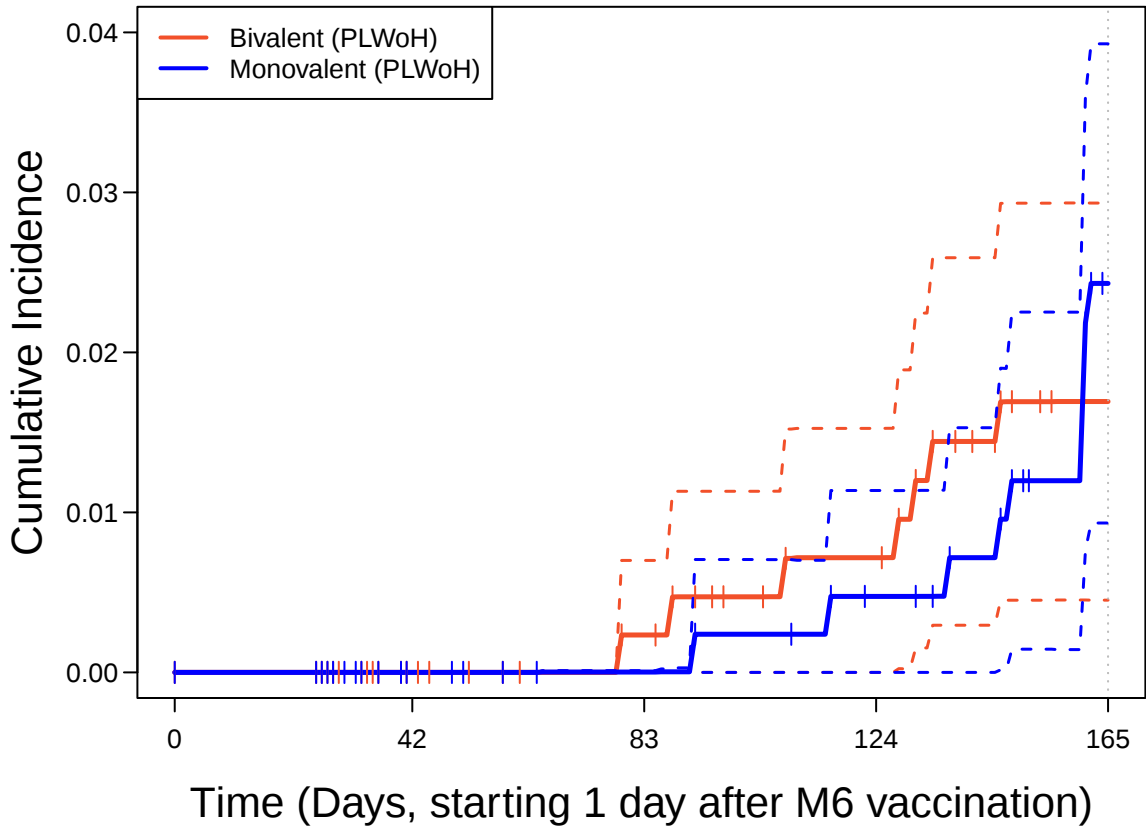
No. at Risk

Bivalent	1546	1510	1500	1481	1408
Monovalent	1510	1473	1463	1448	1373

Total Events

Bivalent	0	1	1	5	30
Monovalent	0	2	2	5	22

MBoost vs BBoost, RM6, CDC1M18, Sensitivity (PLWoH)



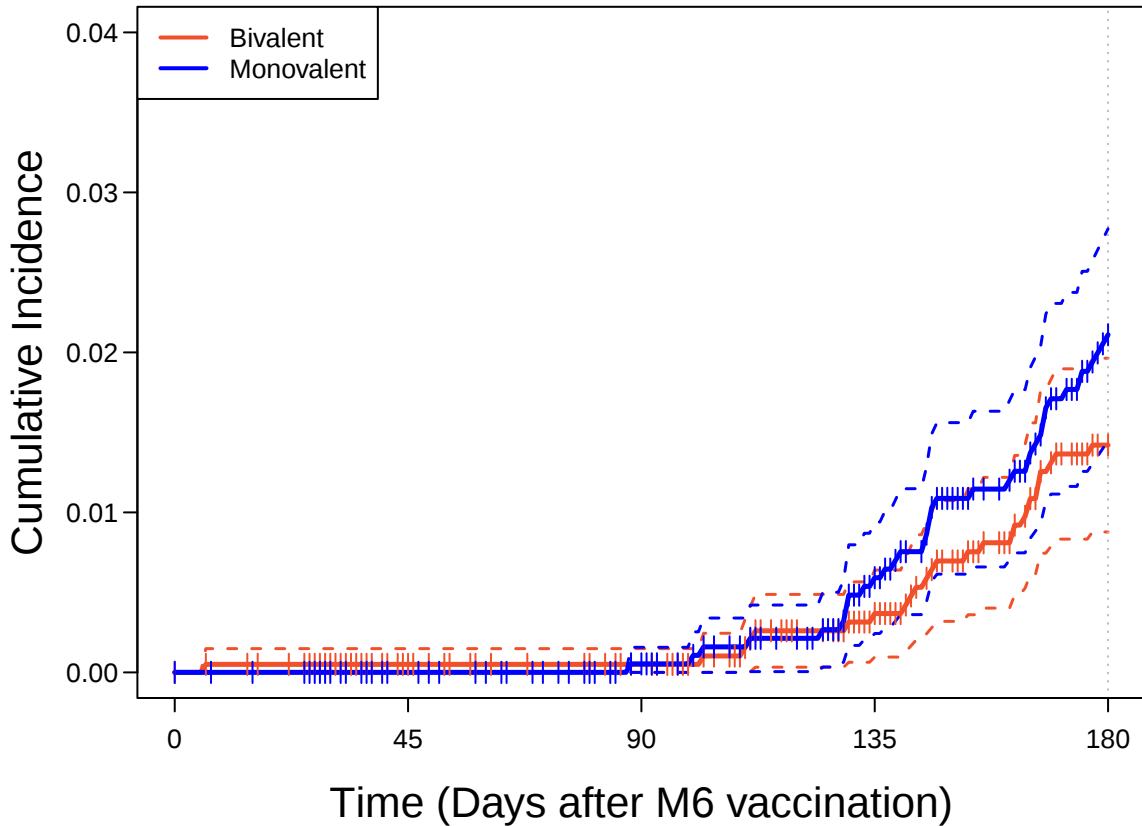
No. at Risk

Bivalent	449	424	418	410	395
Monovalent	439	423	418	414	397

Total Events

Bivalent	0	0	1	3	7
Monovalent	0	0	0	2	10

MBoost vs BBoost, RM6, SUBCINF, Primary



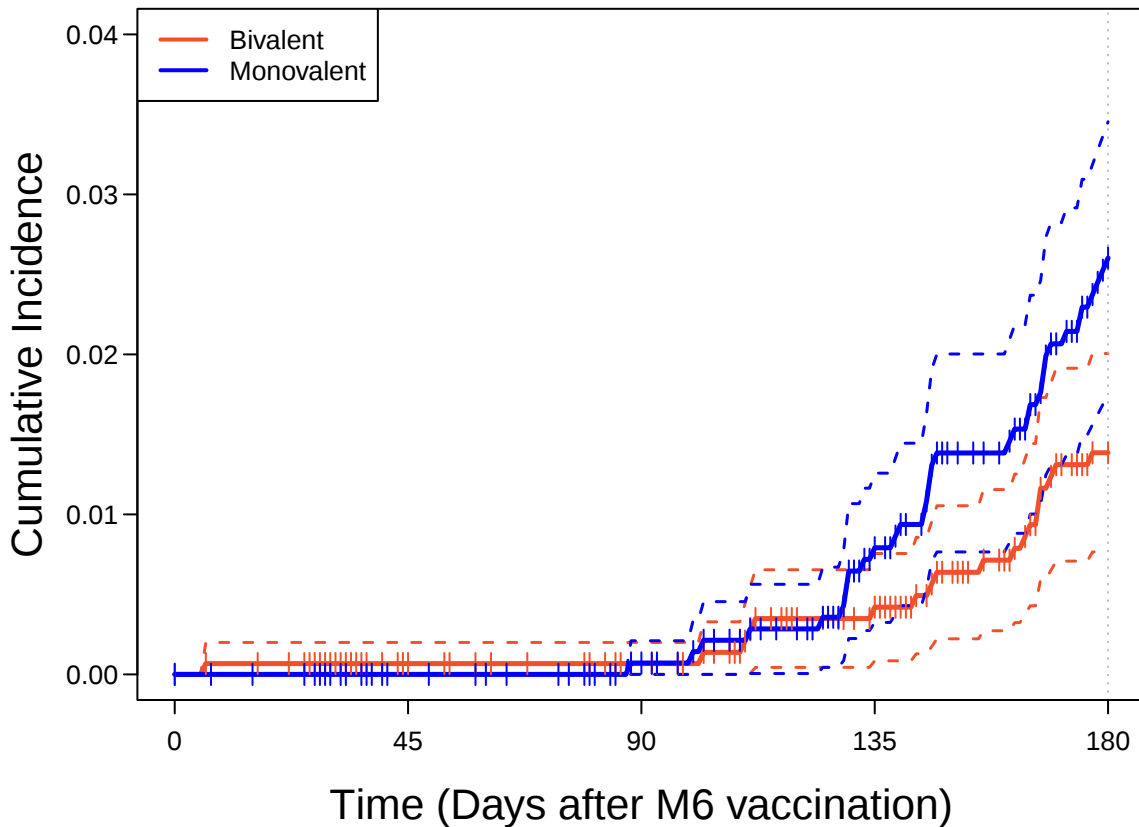
No. at Risk

Bivalent	1995	1930	1913	1867	1756
Monovalent	1949	1896	1878	1833	1710

Total Events

Bivalent	0	1	1	7	26
Monovalent	0	0	1	11	38

MBoost vs BBoost, RM6, SUBCINF, Primary, Hybrid Immunit



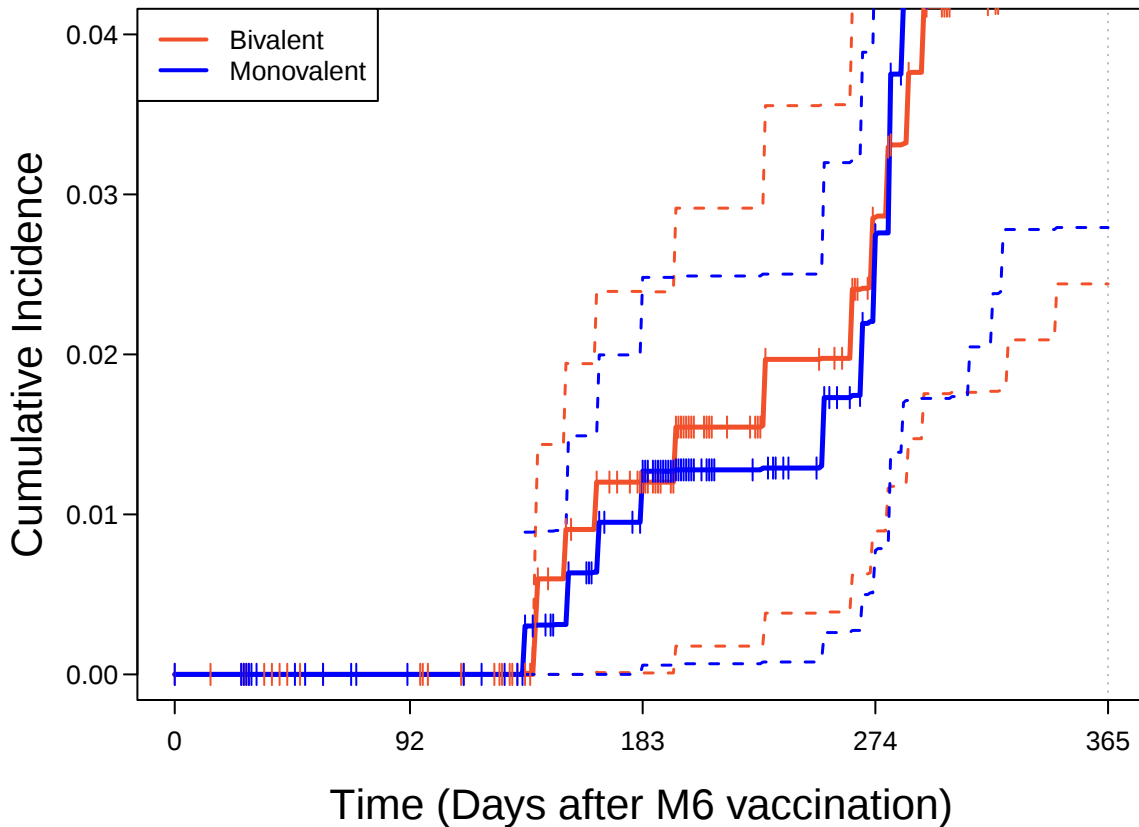
No. at Risk

Bivalent	1483	1438	1425	1395	1307
Monovalent	1451	1416	1404	1366	1269

Total Events

Bivalent	0	1	1	6	19
Monovalent	0	0	1	11	35

MBoost vs BBoost, RM6, SUBCINF, Primary, Vaccine Immuni



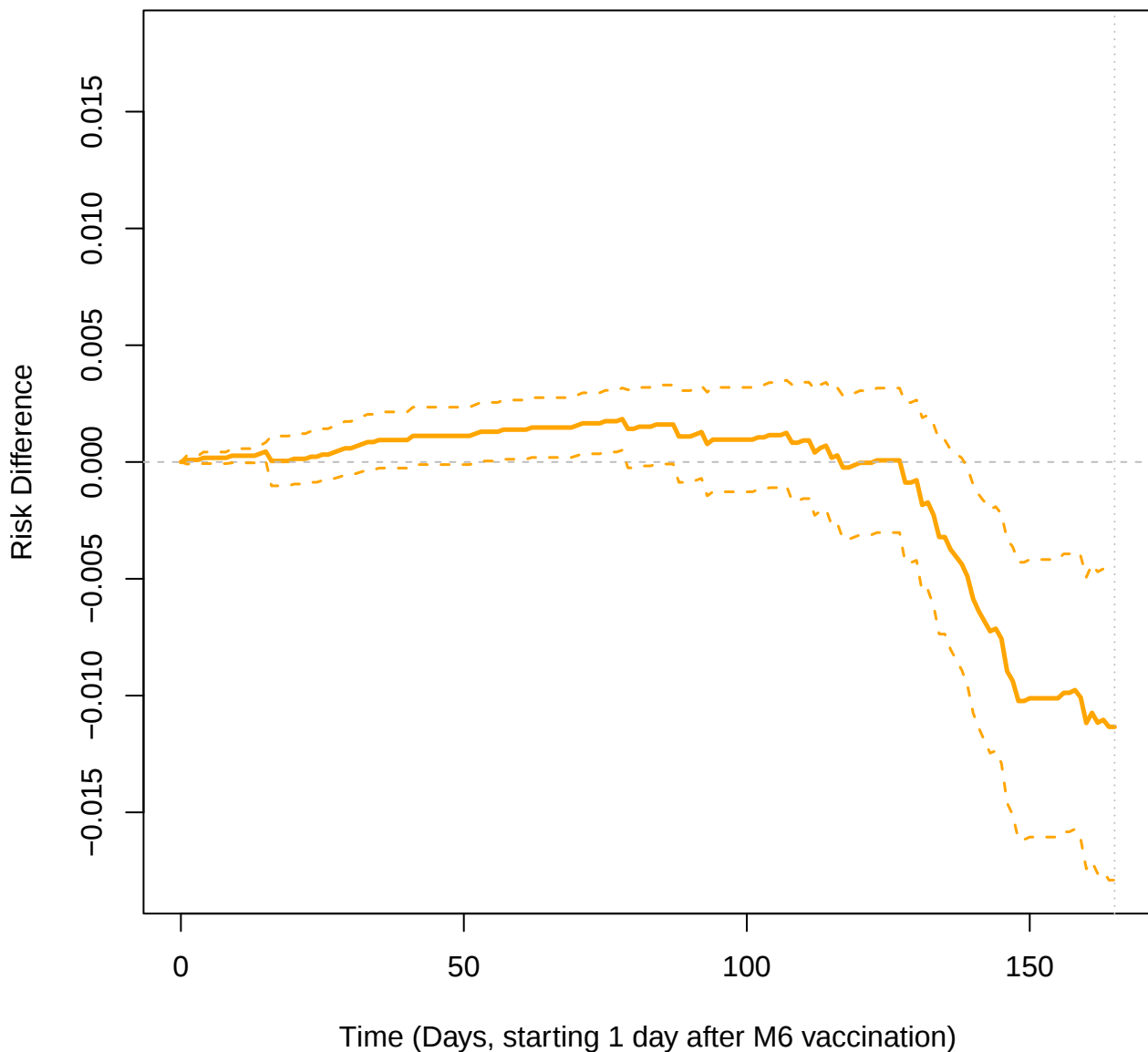
No. at Risk

Bivalent	365	349	319	224	173
Monovalent	352	334	311	216	158

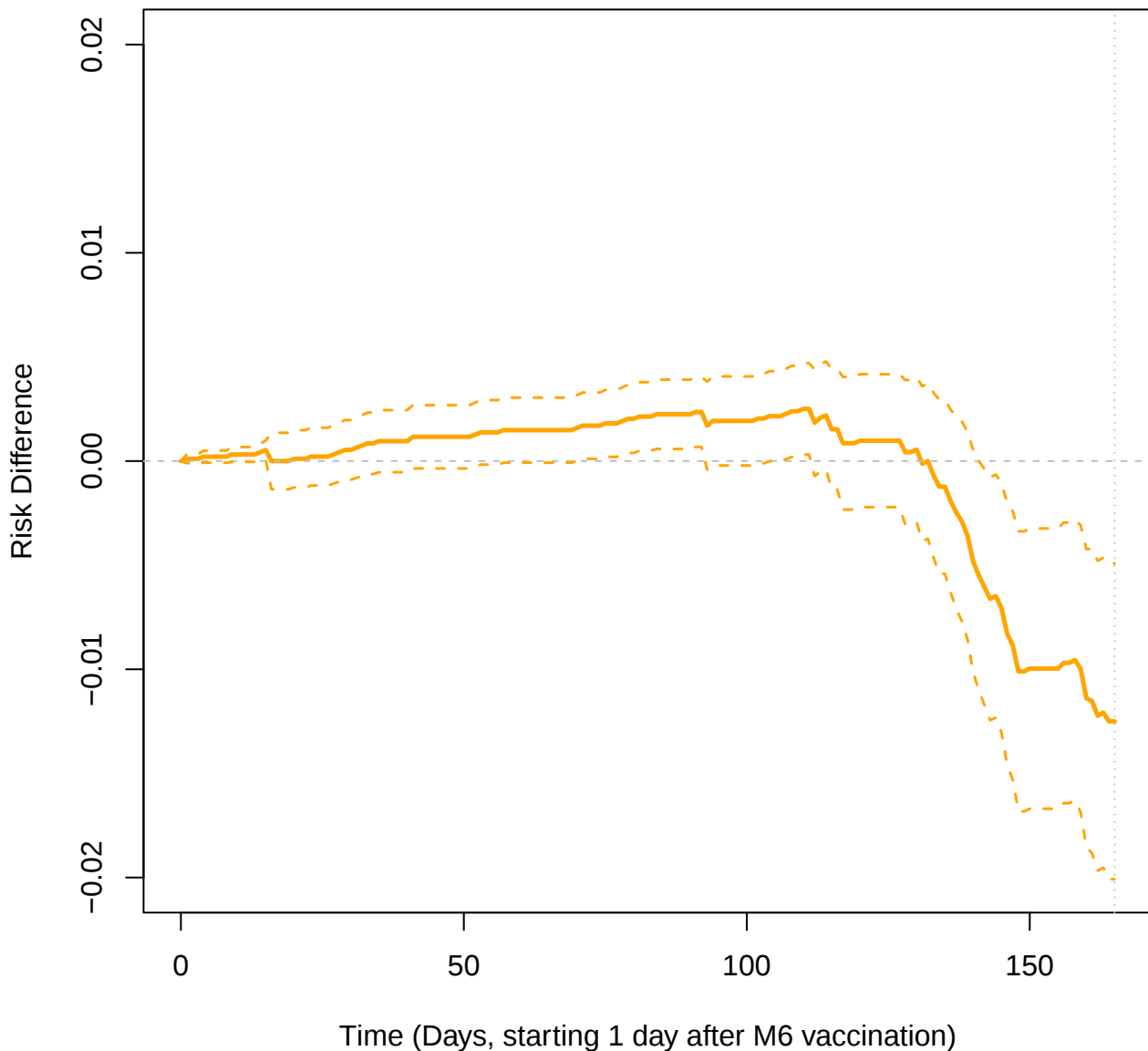
Total Events

Bivalent	0	0	4	8	13
Monovalent	0	0	4	7	13

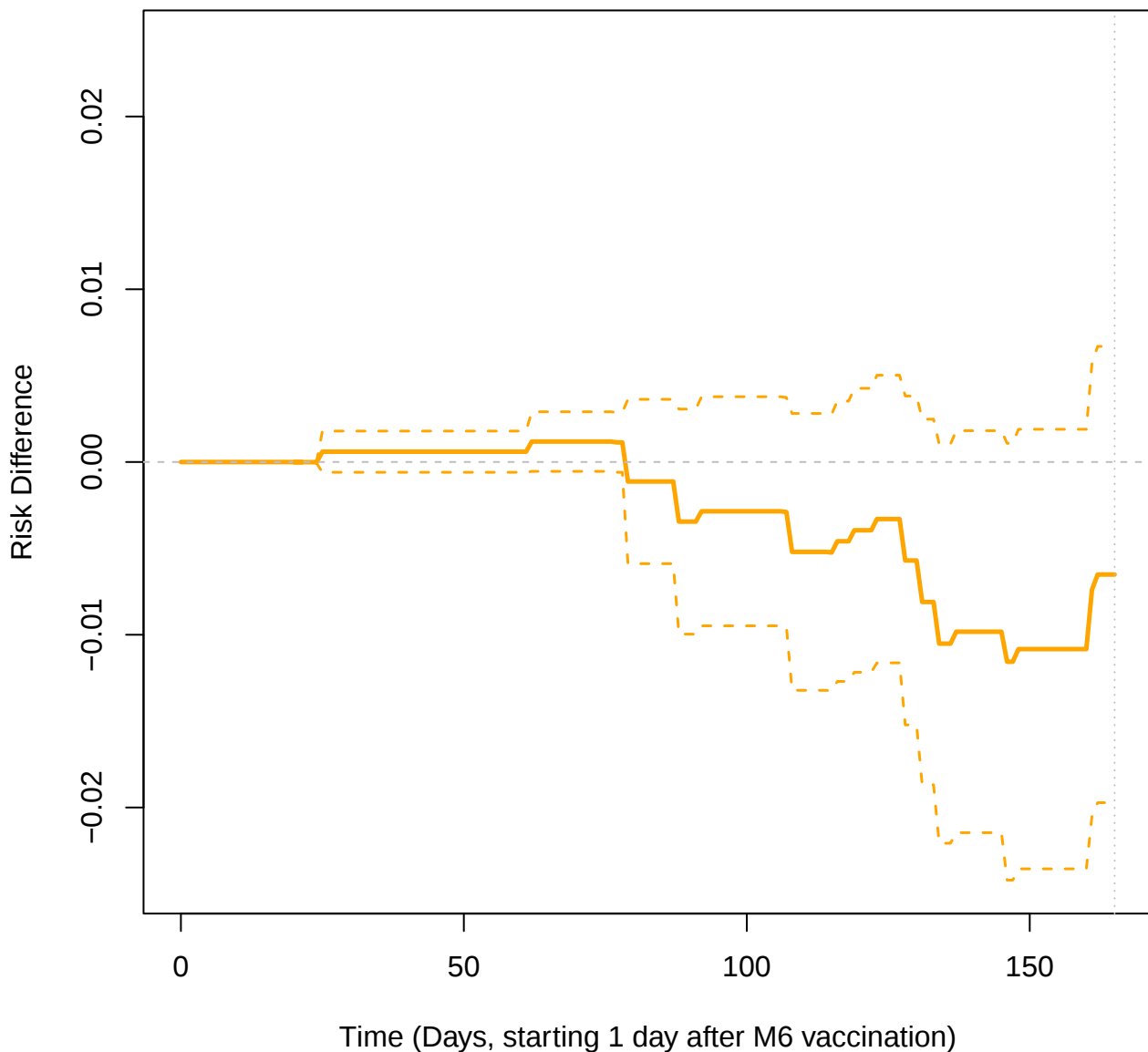
MBoost vs BBoost, FM6, CDC1M18, Primary



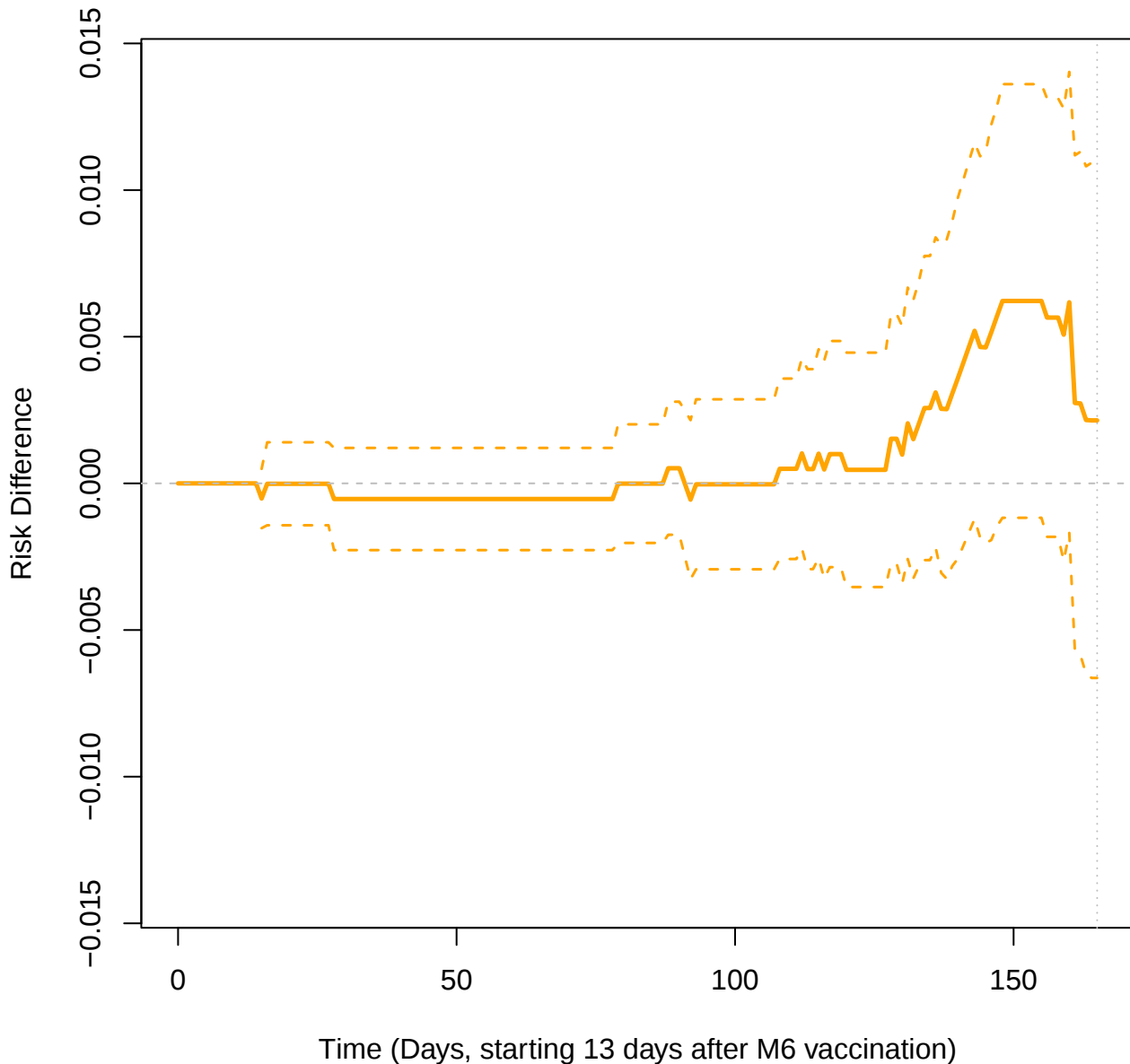
MBoost vs BBoost, FM6, CDC1M18, Primary (PLWH)



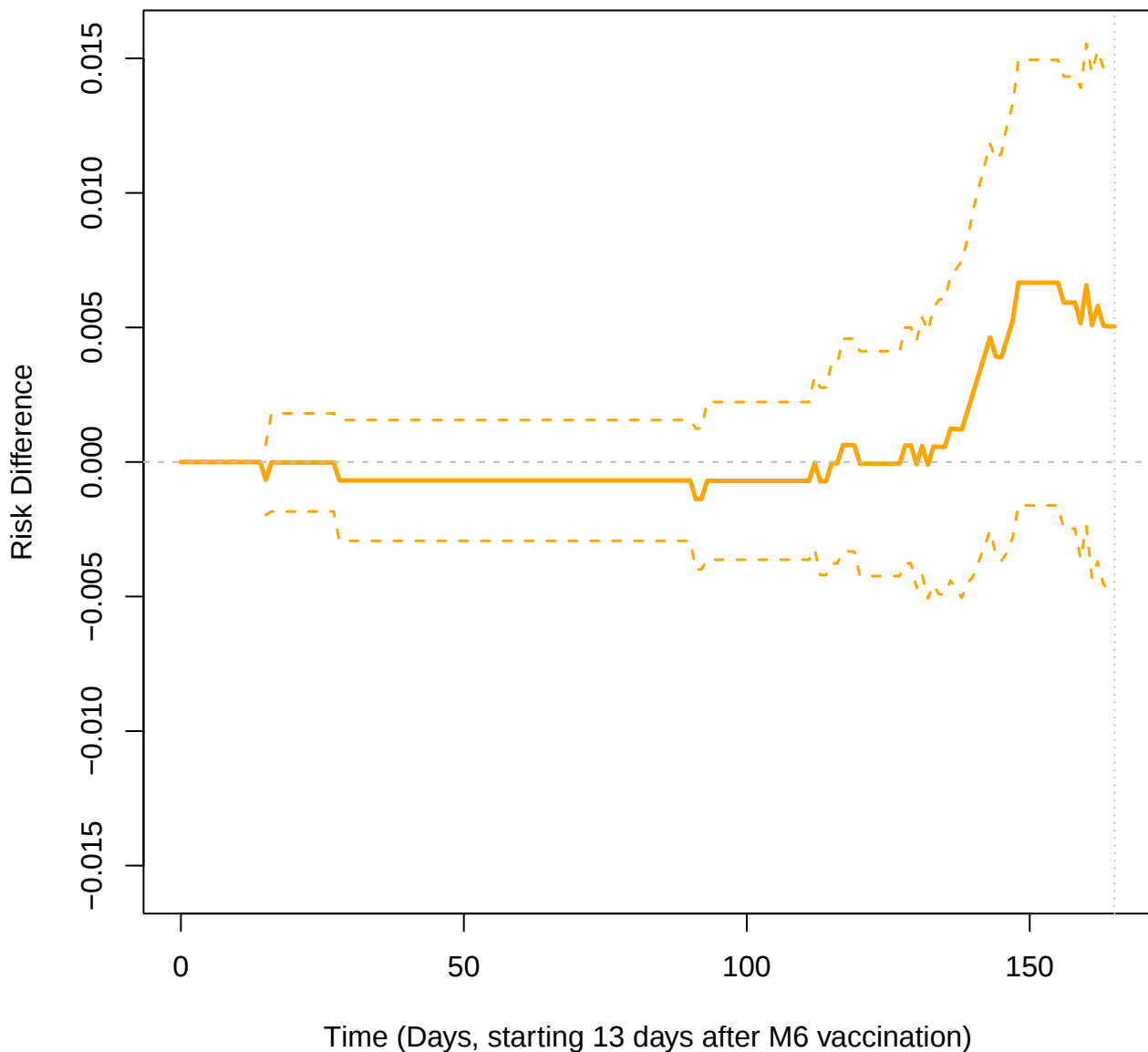
MBoost vs BBoost, FM6, CDC1M18, Primary (PLWoH)



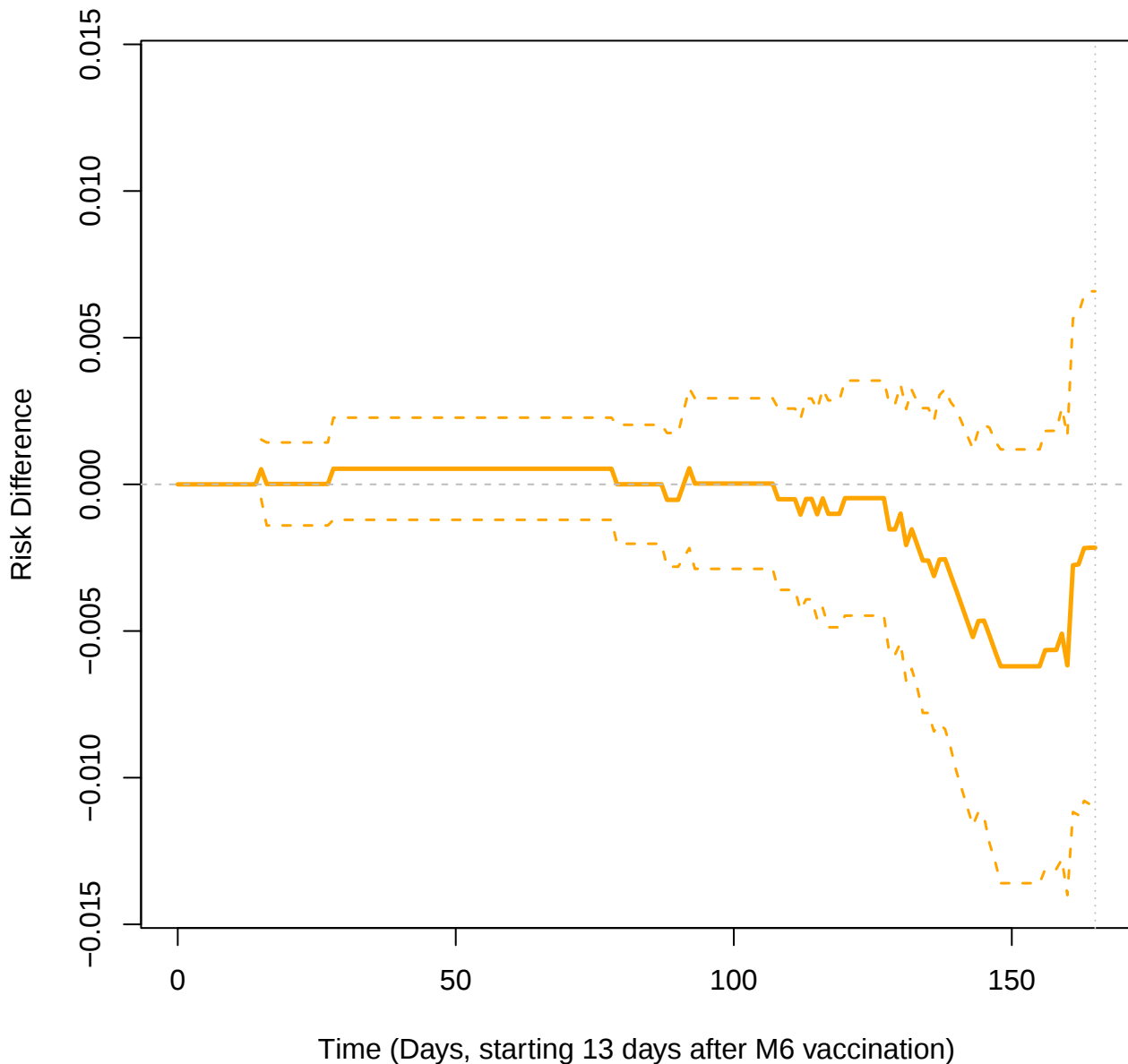
MBoost vs BBoost, FPP, CDC14M12, Primary



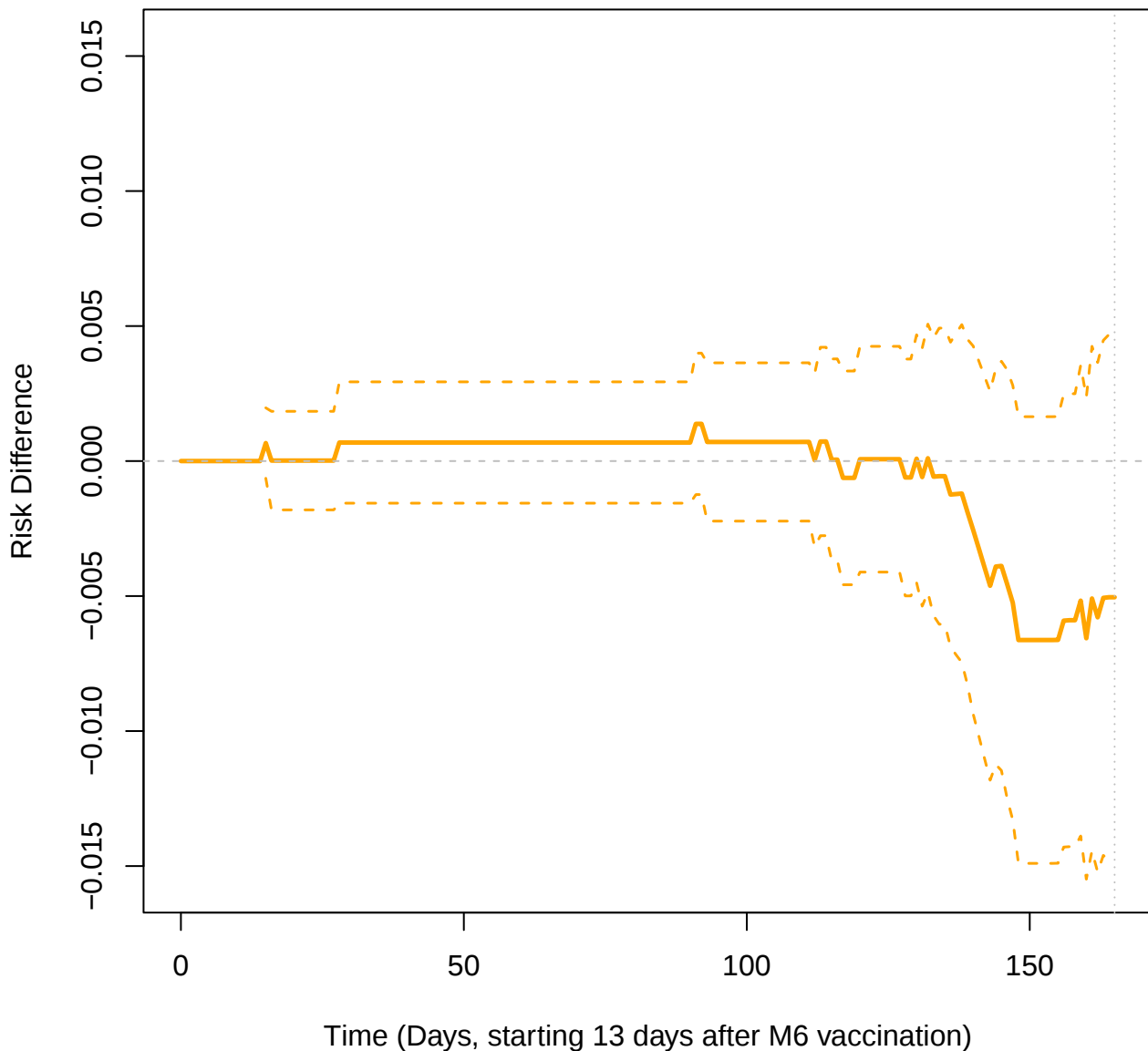
MBoost vs BBoost, FPP, CDC14M12, Primary (PLWH)



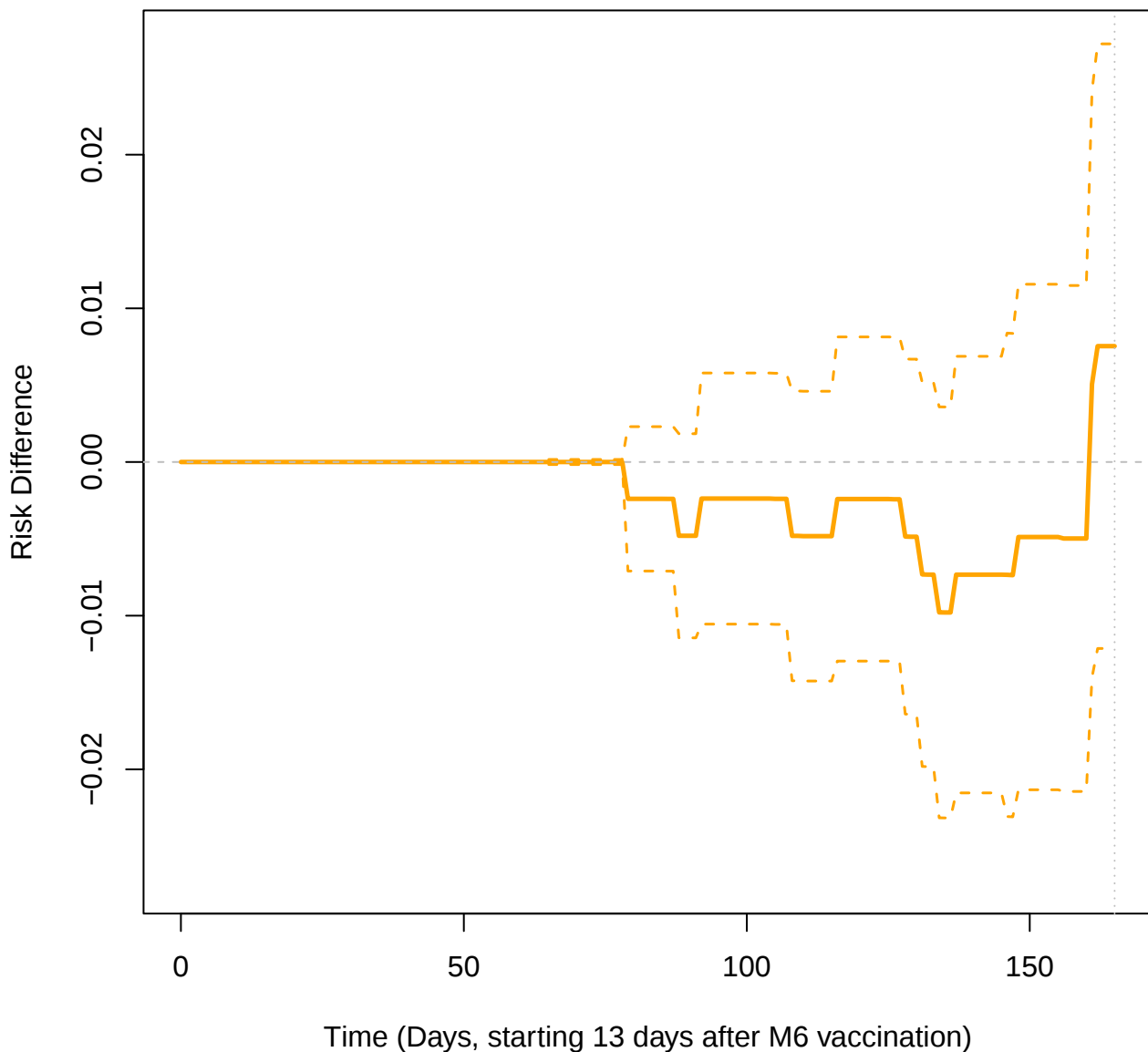
MBoost vs BBoost, FPP, CDC14M18, Primary



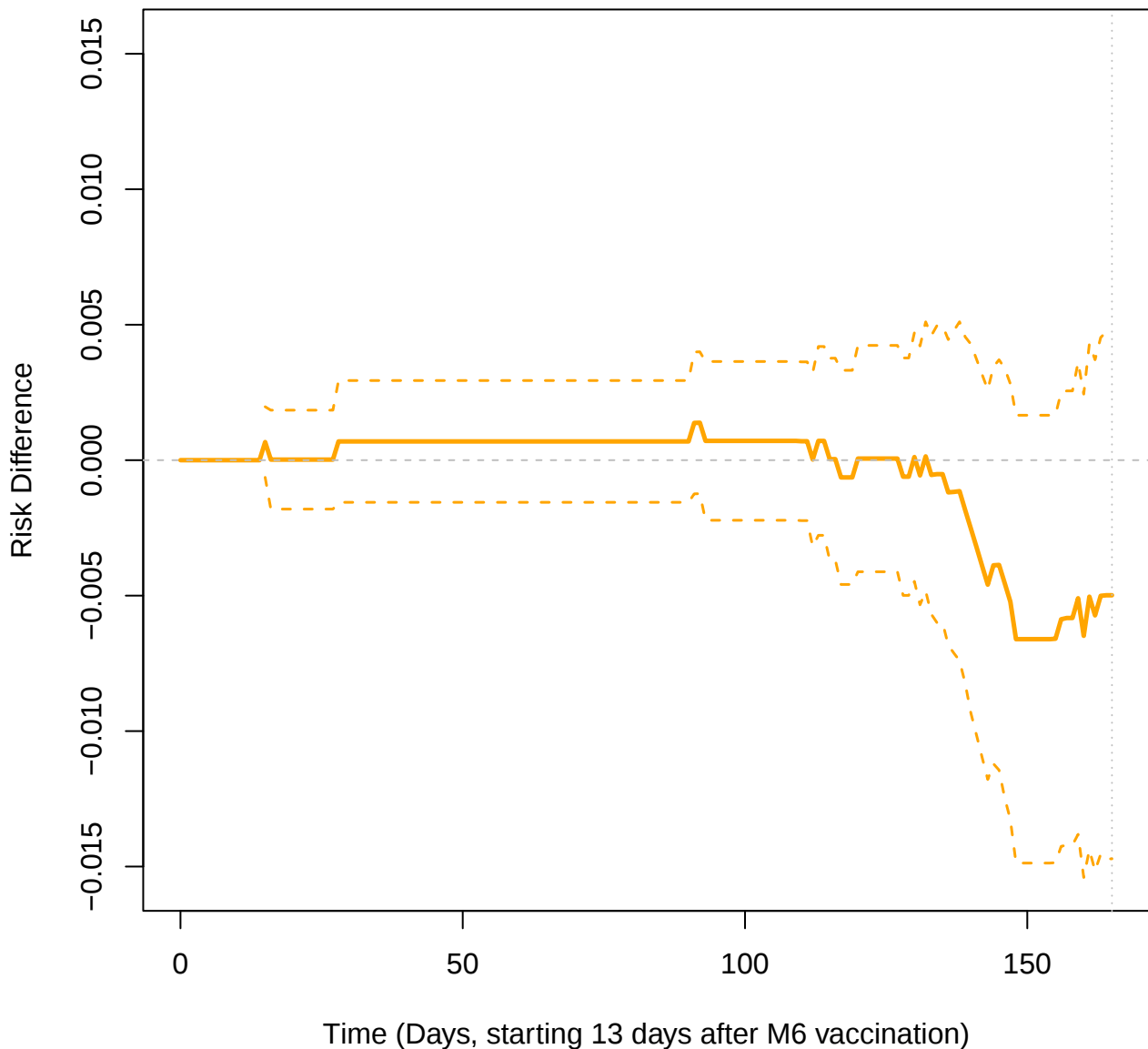
MBoost vs BBoost, FPP, CDC14M18, Primary (PLWH)



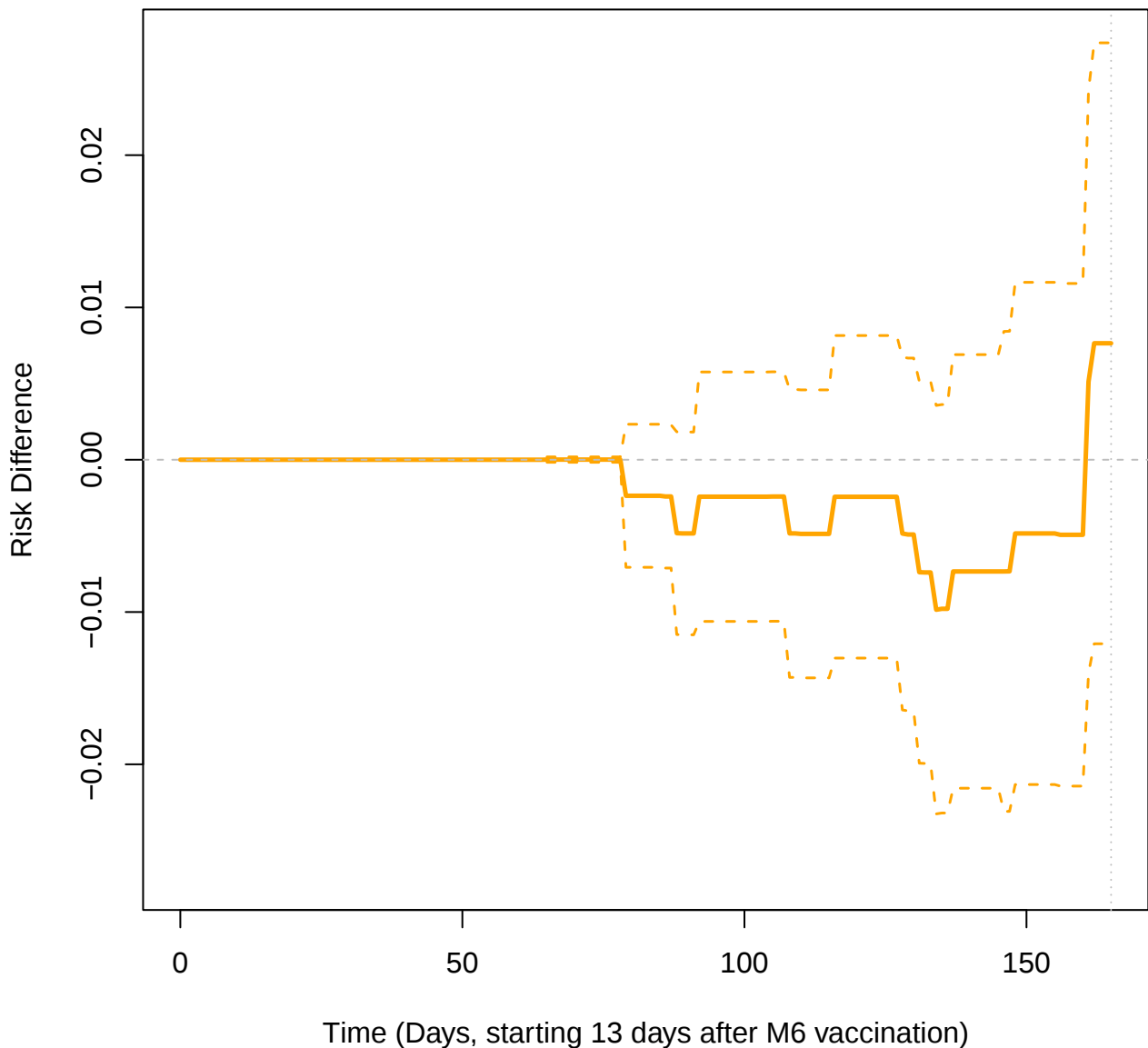
MBoost vs BBoost, FPP, CDC14M18, Primary (PLWoH)



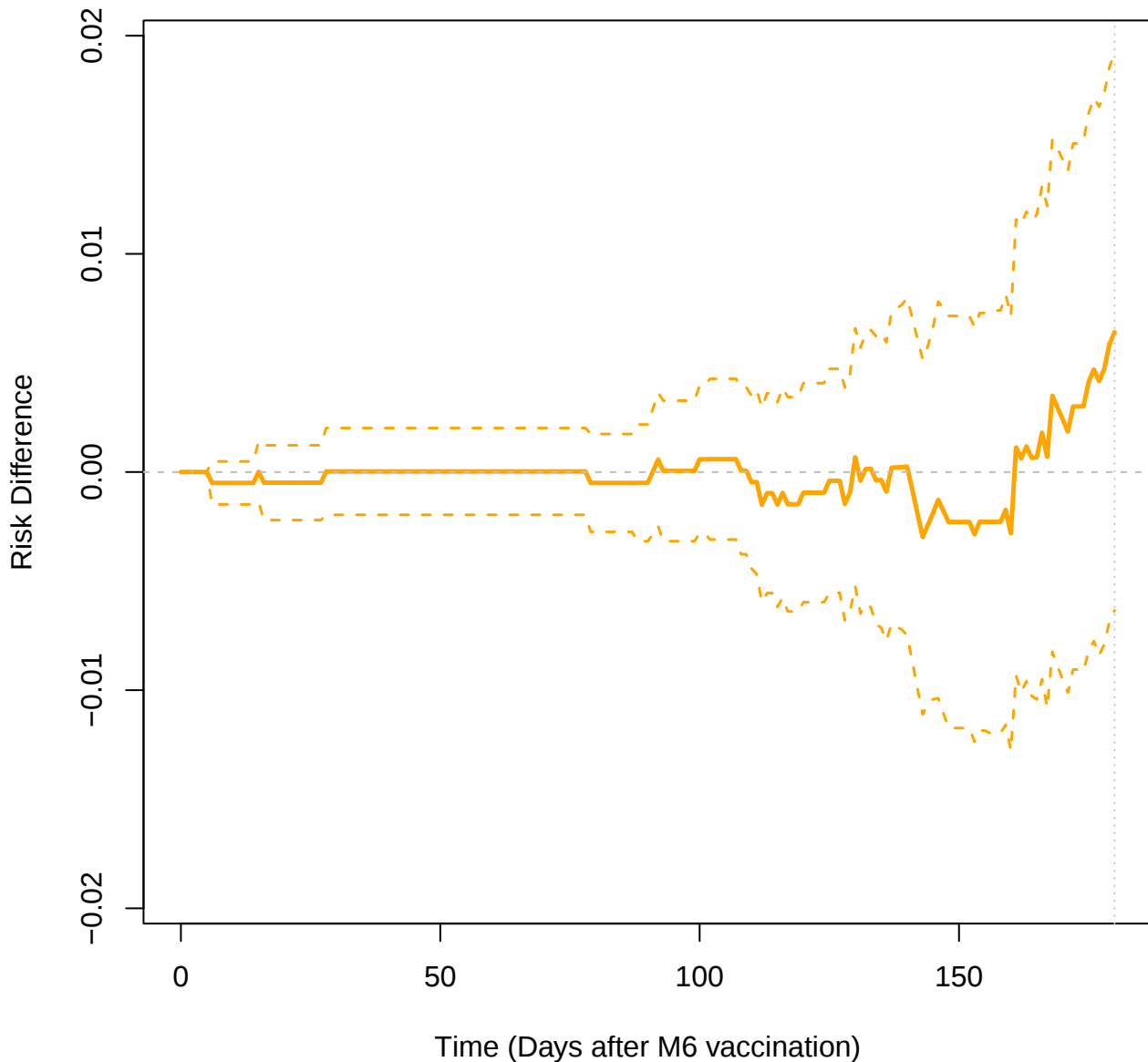
MBoost vs BBoost, FPP, CDC14M18, Sensitivity (PLWH)



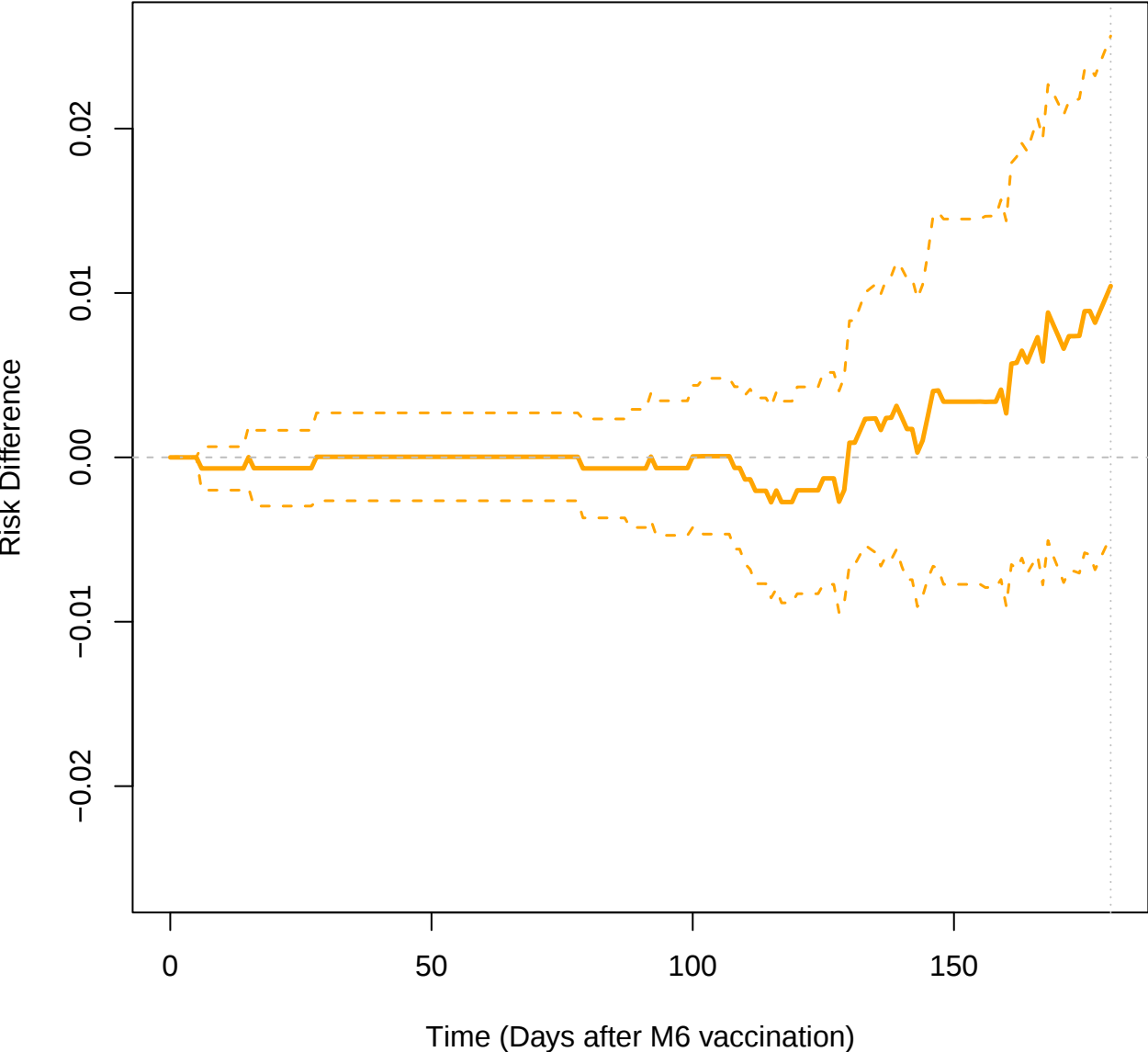
MBoost vs BBoost, FPP, CDC14M18, Sensitivity (PLWoH)



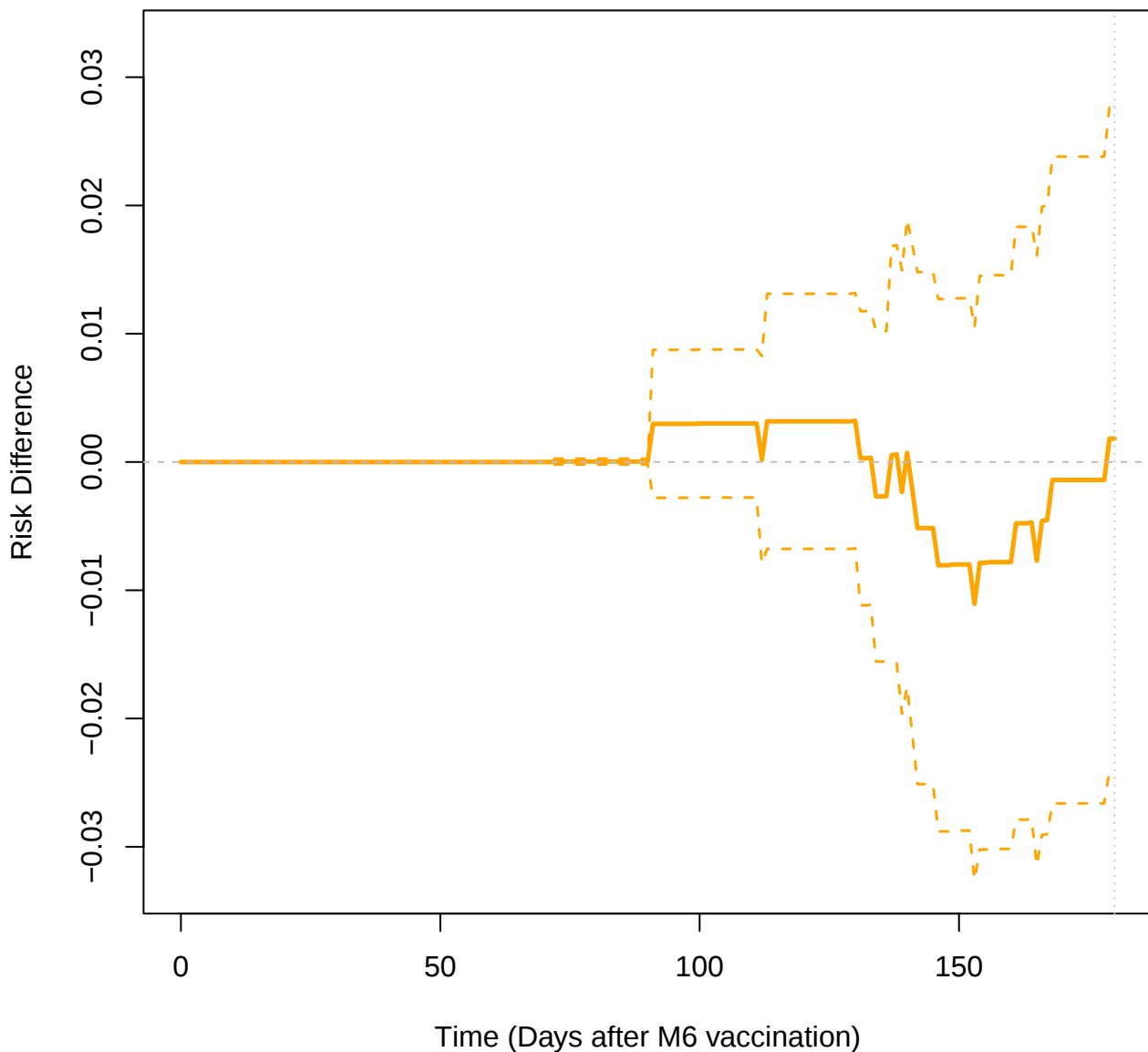
MBoost vs BBoost, RM6, ANYINF, Primary



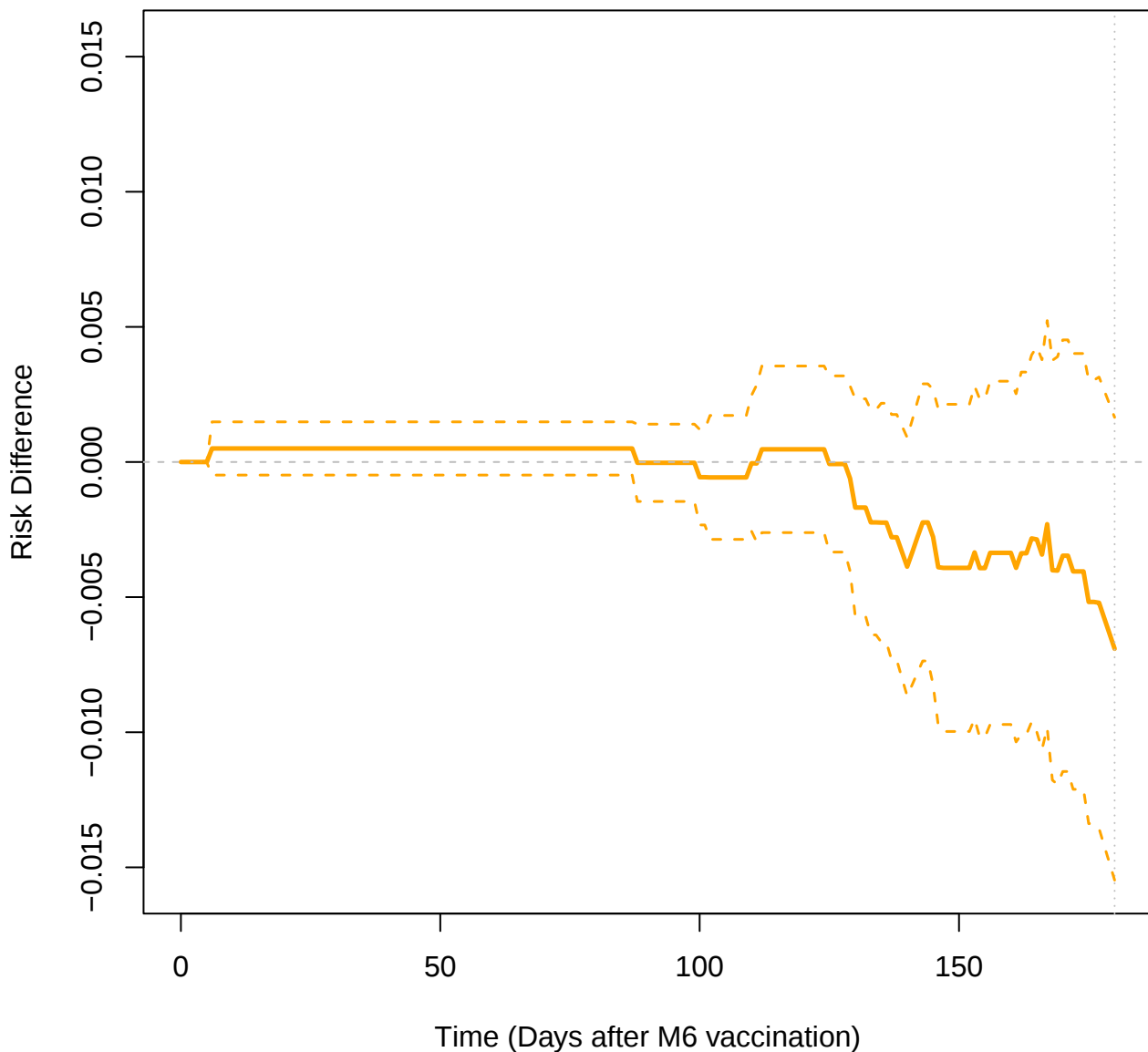
MBoost vs BBoost, RM6, ANYINF, Primary, Hybrid Immunity



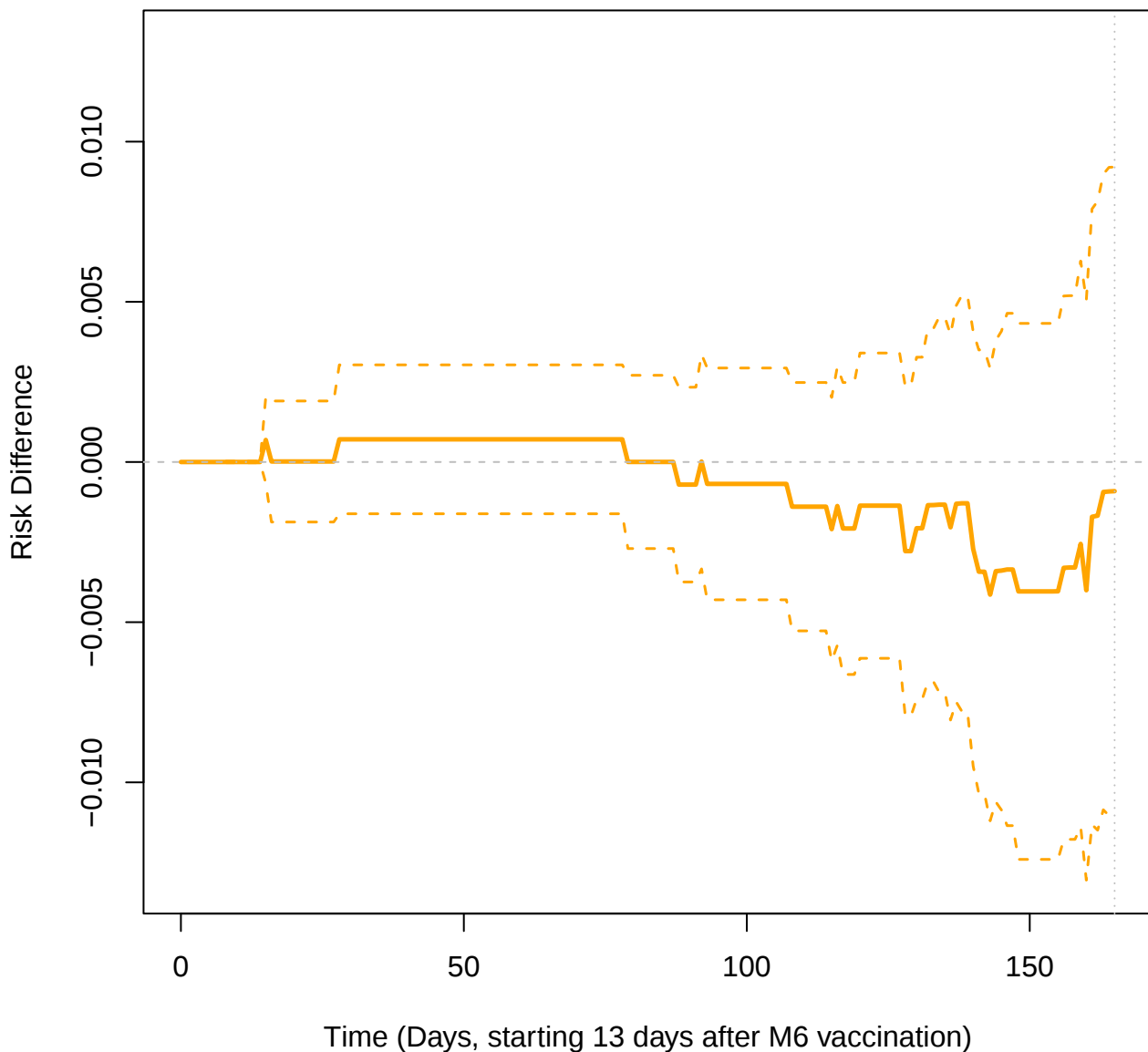
MBoost vs BBoost, RM6, ANYINF, Primary, Vaccine Immunity



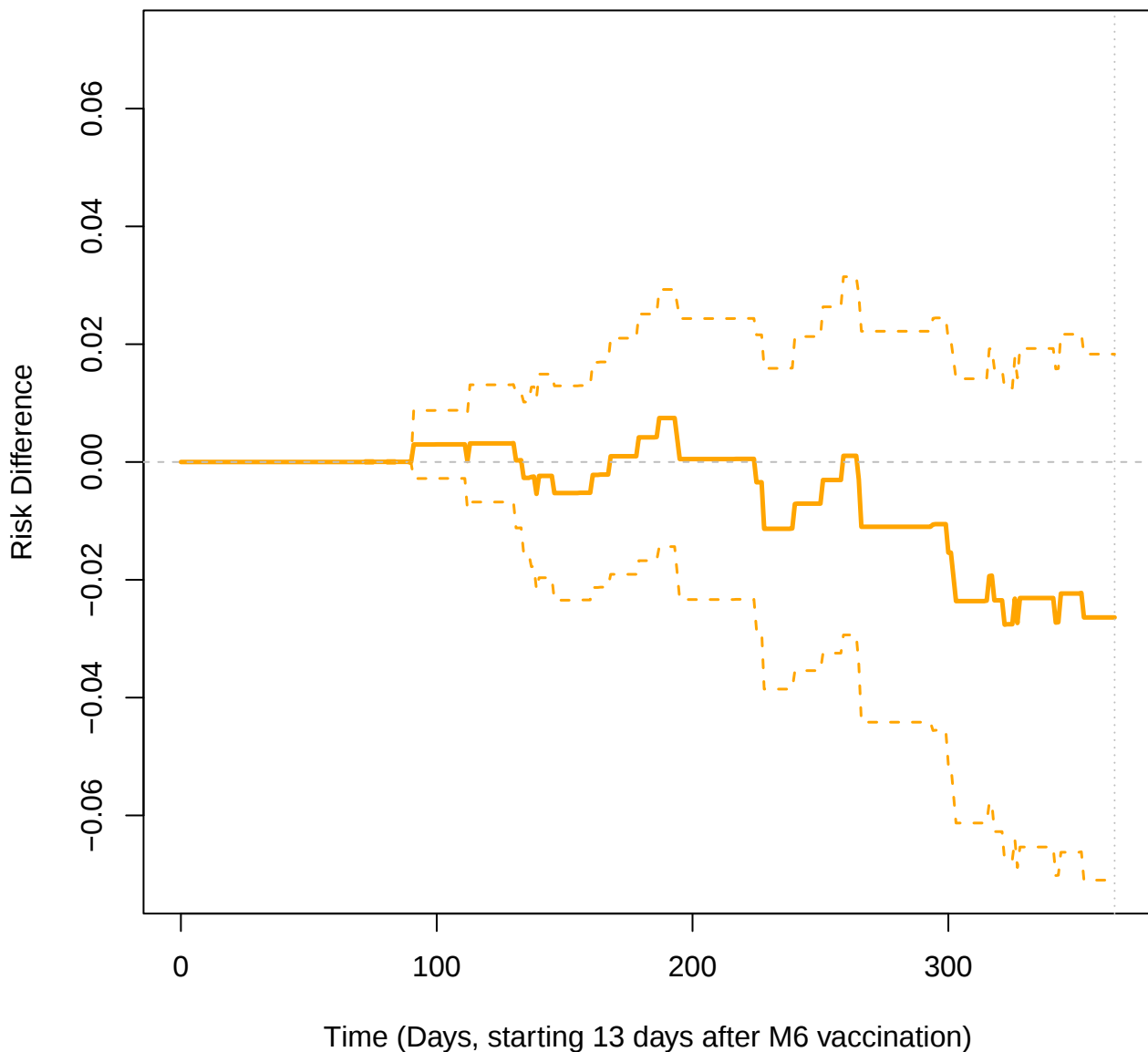
MBoost vs BBoost, RM6, ASYMINF, Primary



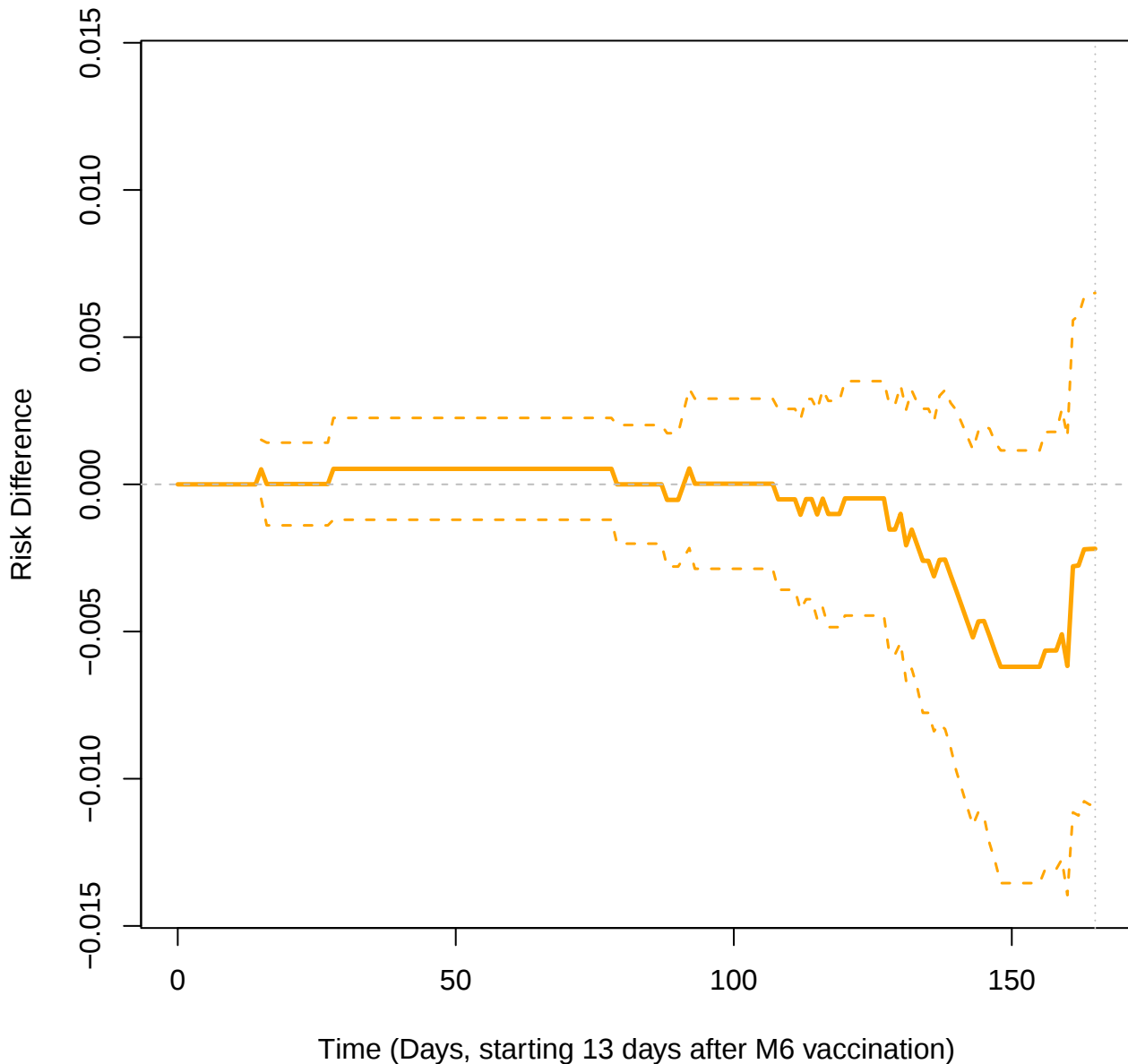
MBoost vs BBoost, RM6, CD14M18, Primary, Hybrid Immunity



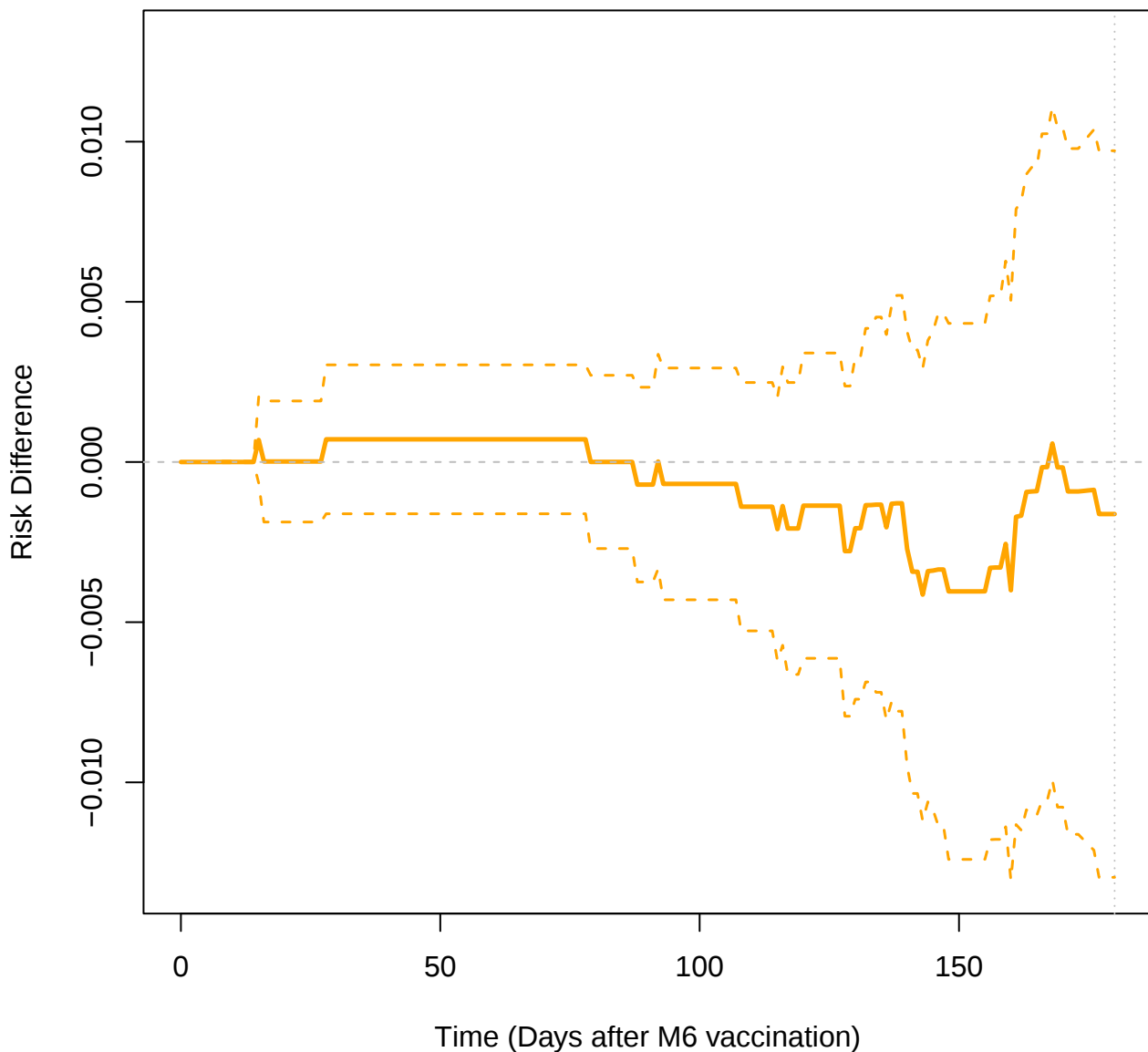
MBoost vs BBoost, RM6, CD14M18, Primary, Vaccine Immunity



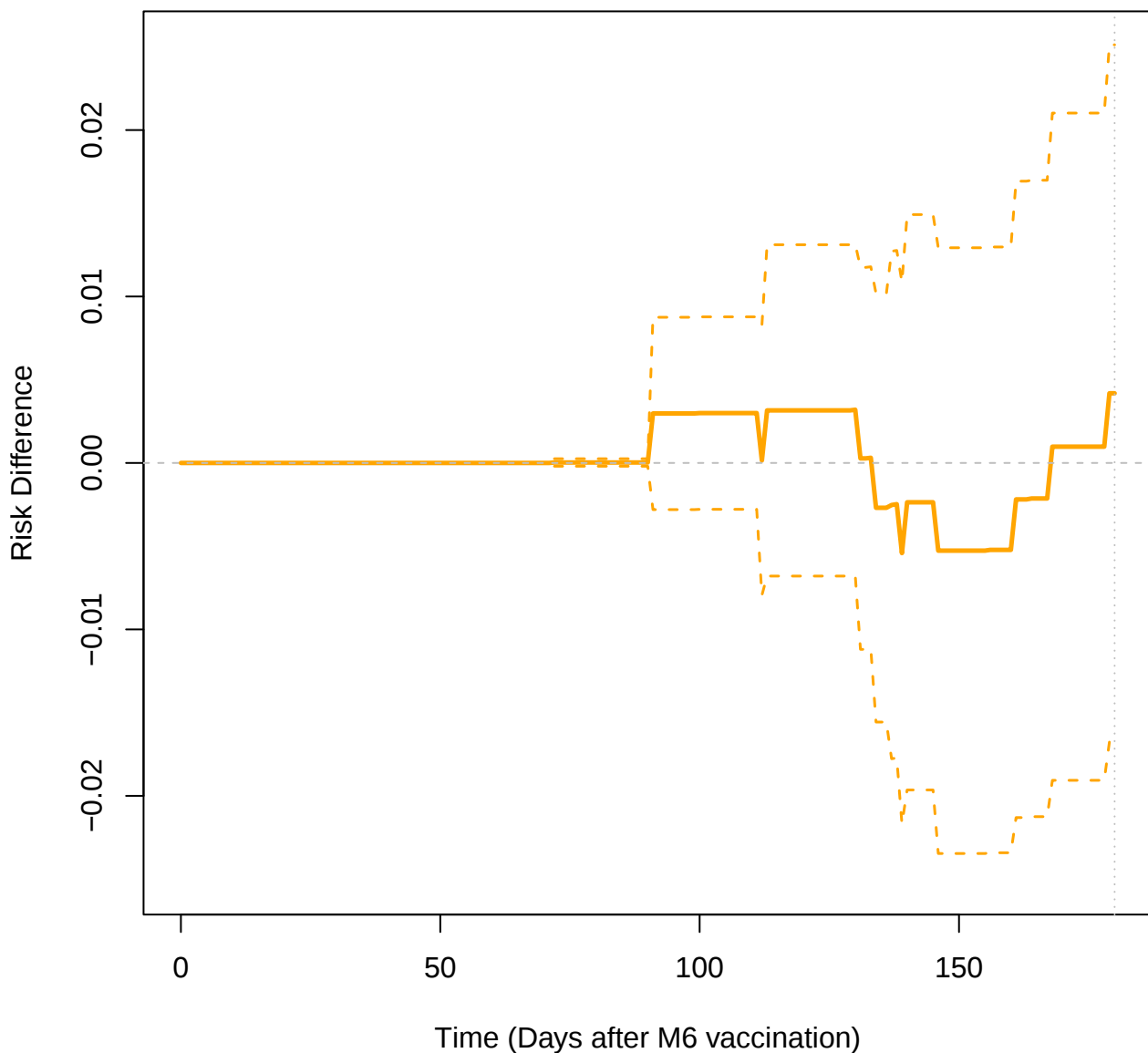
MBoost vs BBoost, RM6, CD14M18, Primary



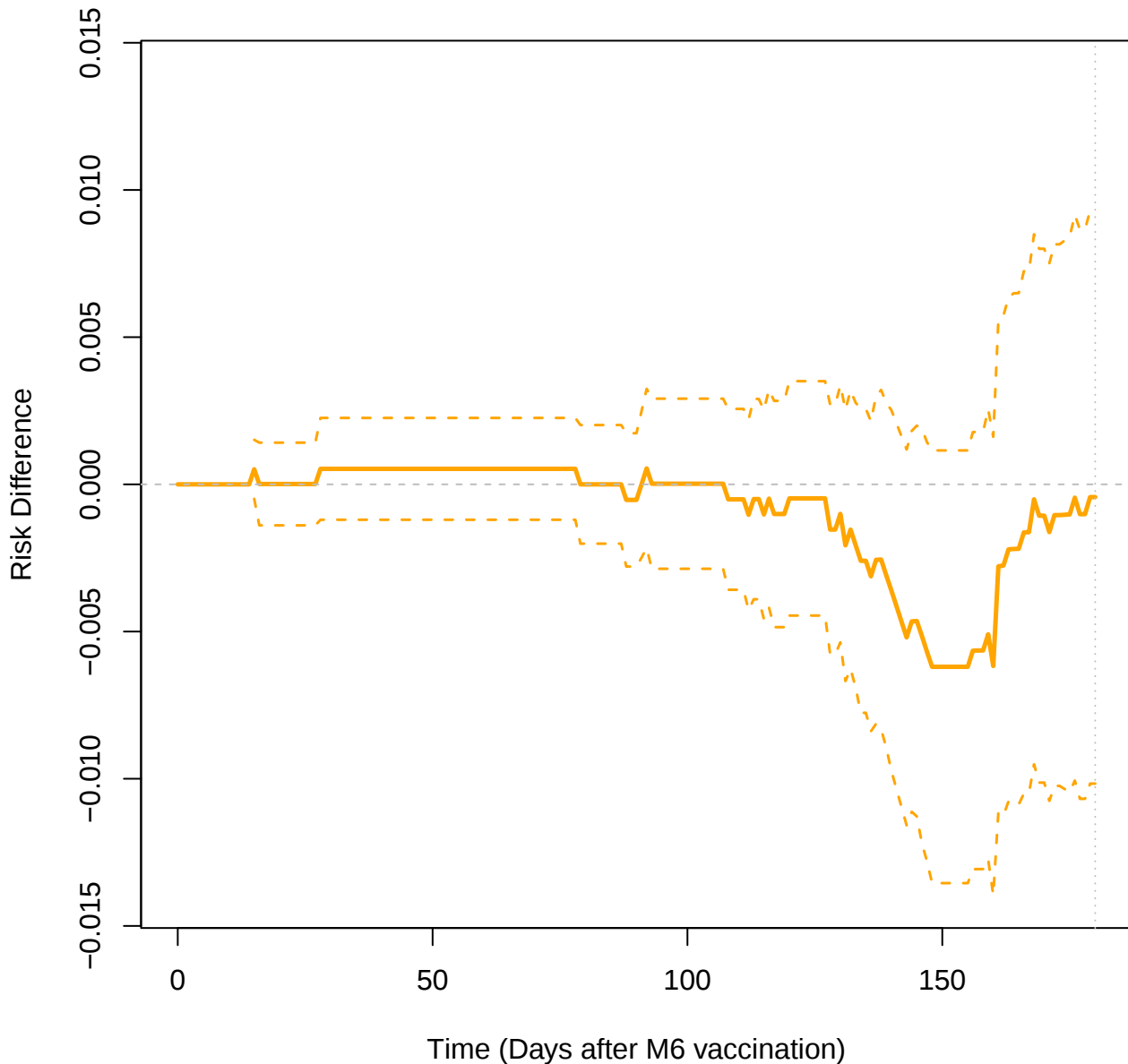
MBoost vs BBoost, RM6, CD1M18, Primary, Hybrid Immunity



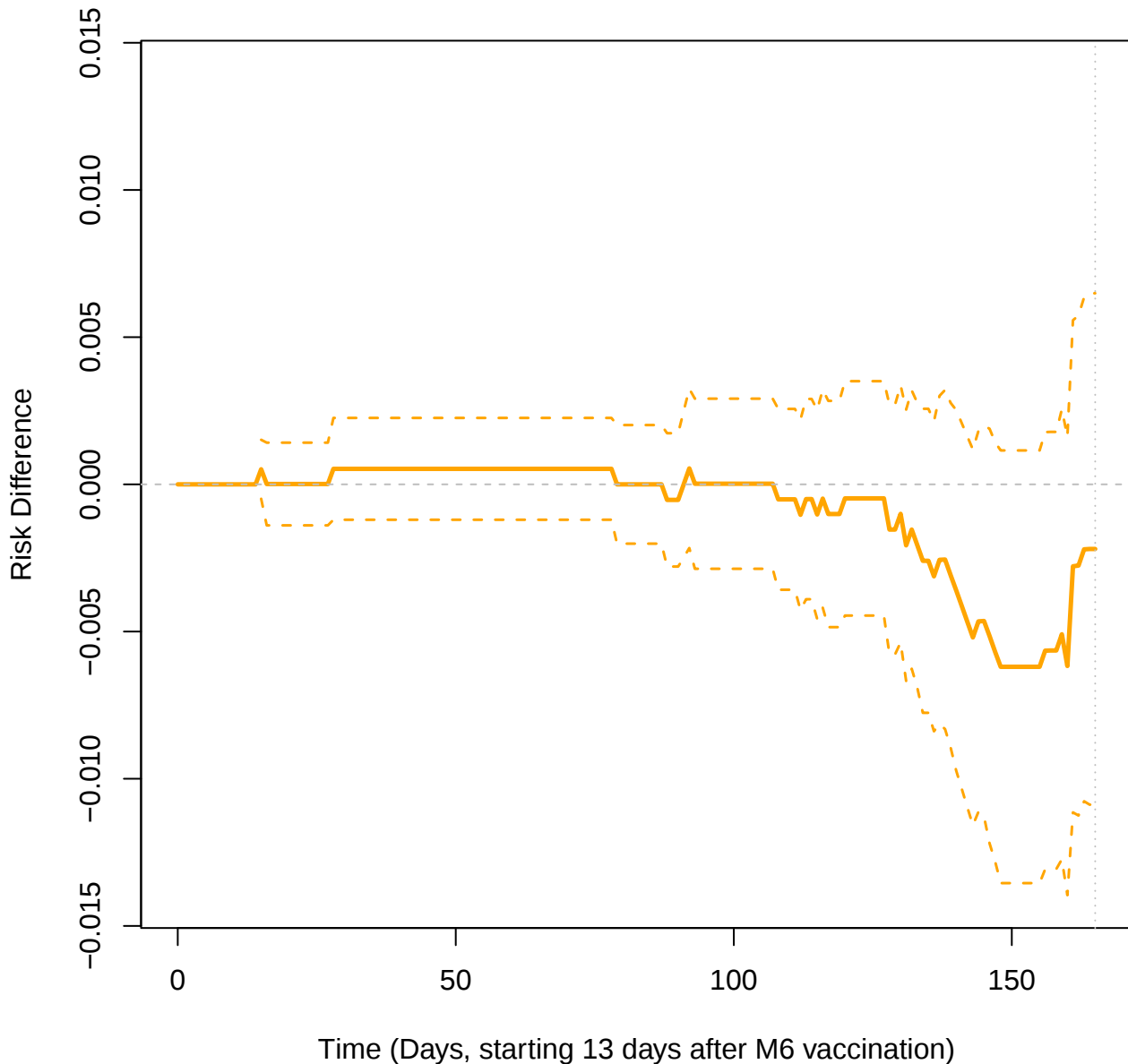
MBoost vs BBoost, RM6, CD1M18, Primary, Vaccine Immunity



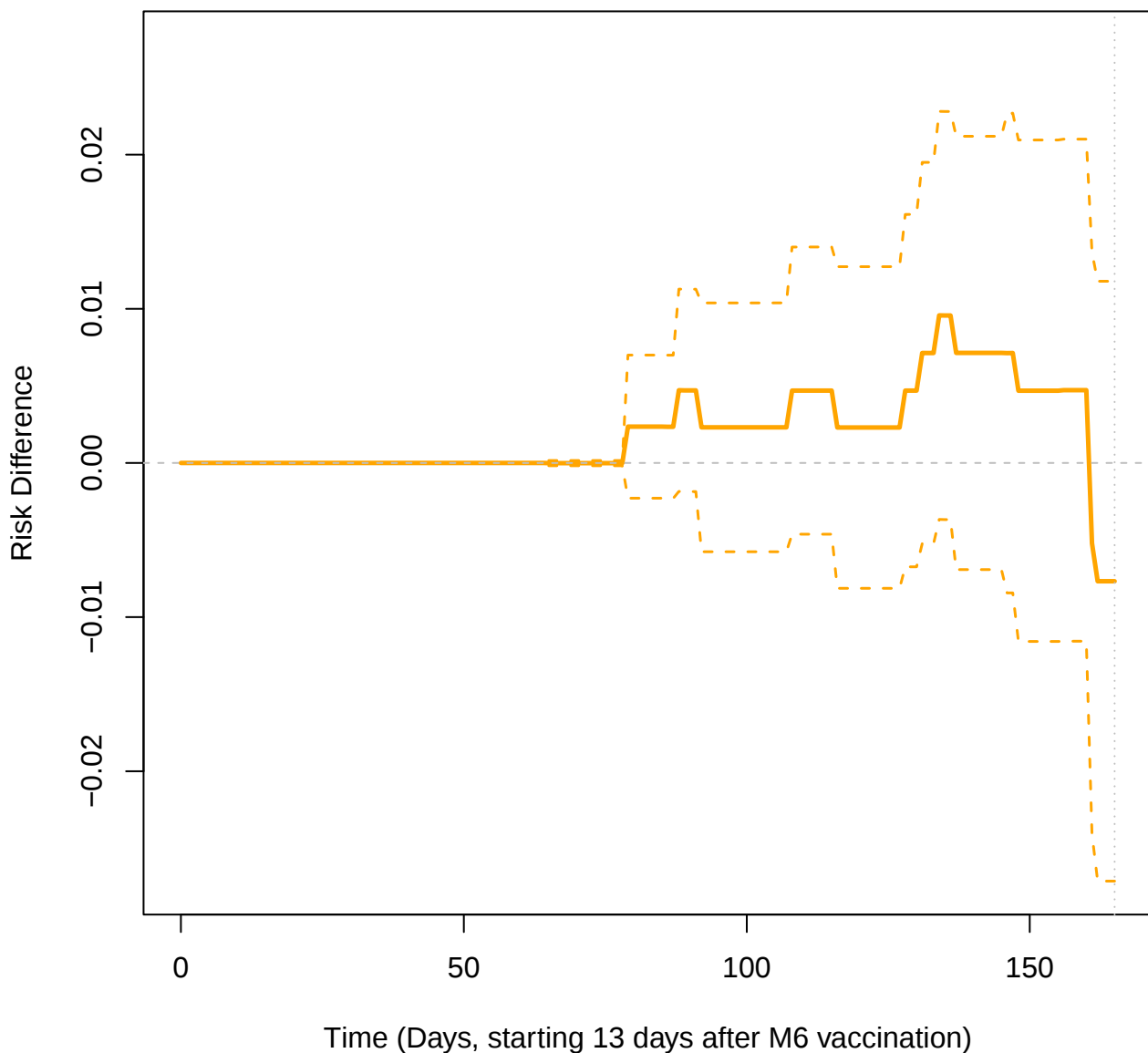
MBoost vs BBoost, RM6, CD1M18, Primary



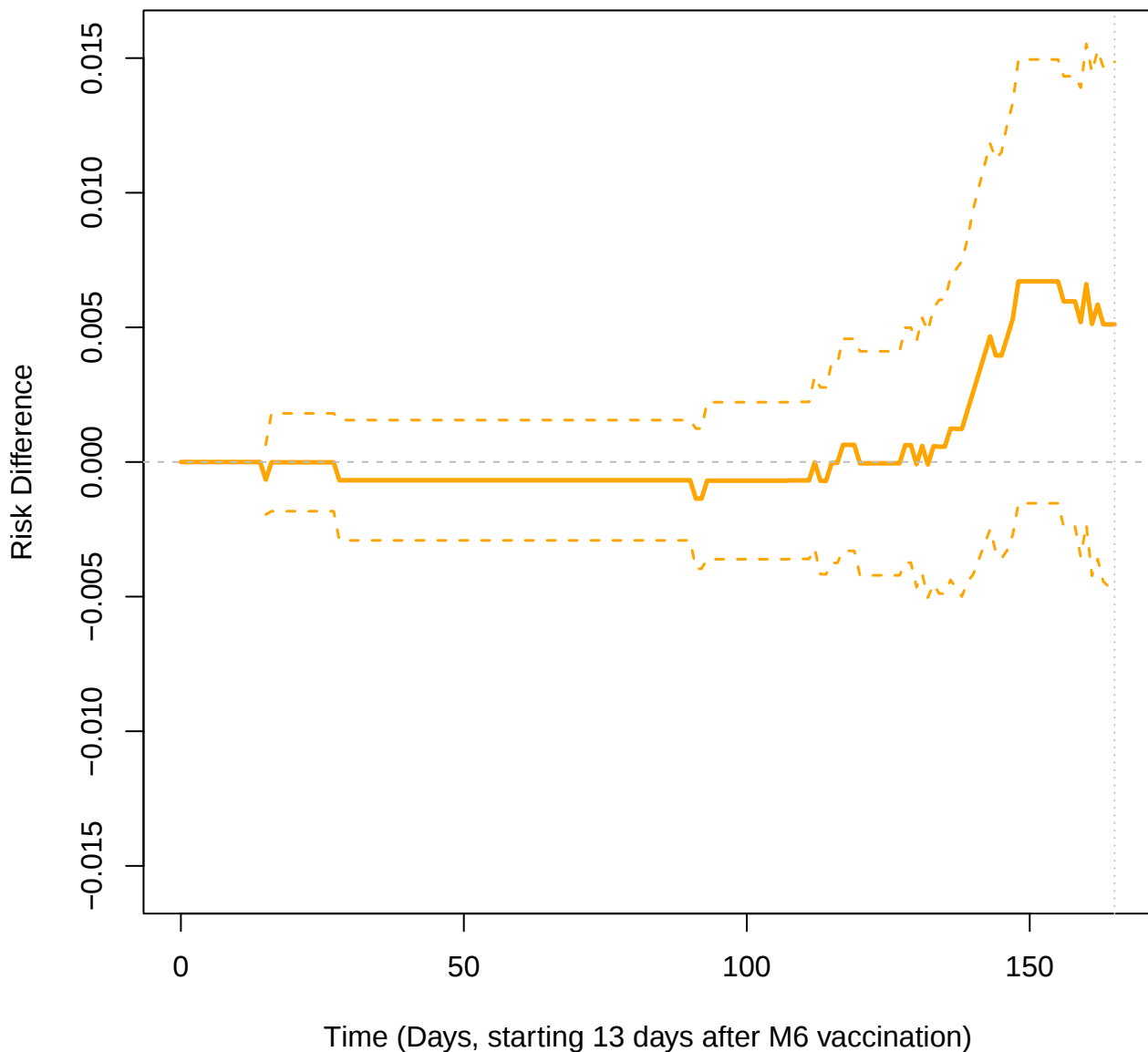
MBoost vs BBoost, RM6, CDC14M12, Primary



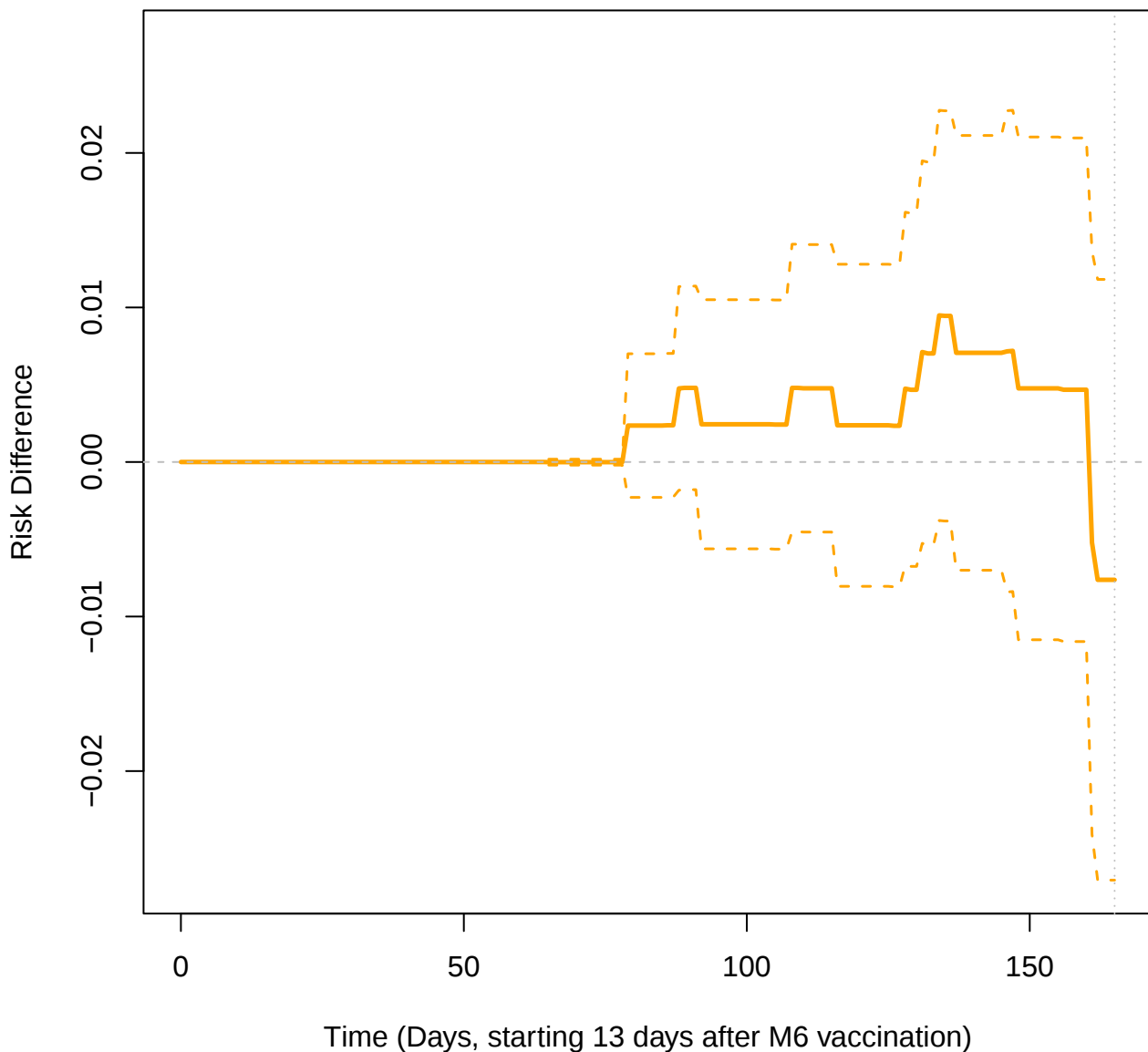
MBoost vs BBoost, RM6, CDC14M12, Primary (PLWoH)



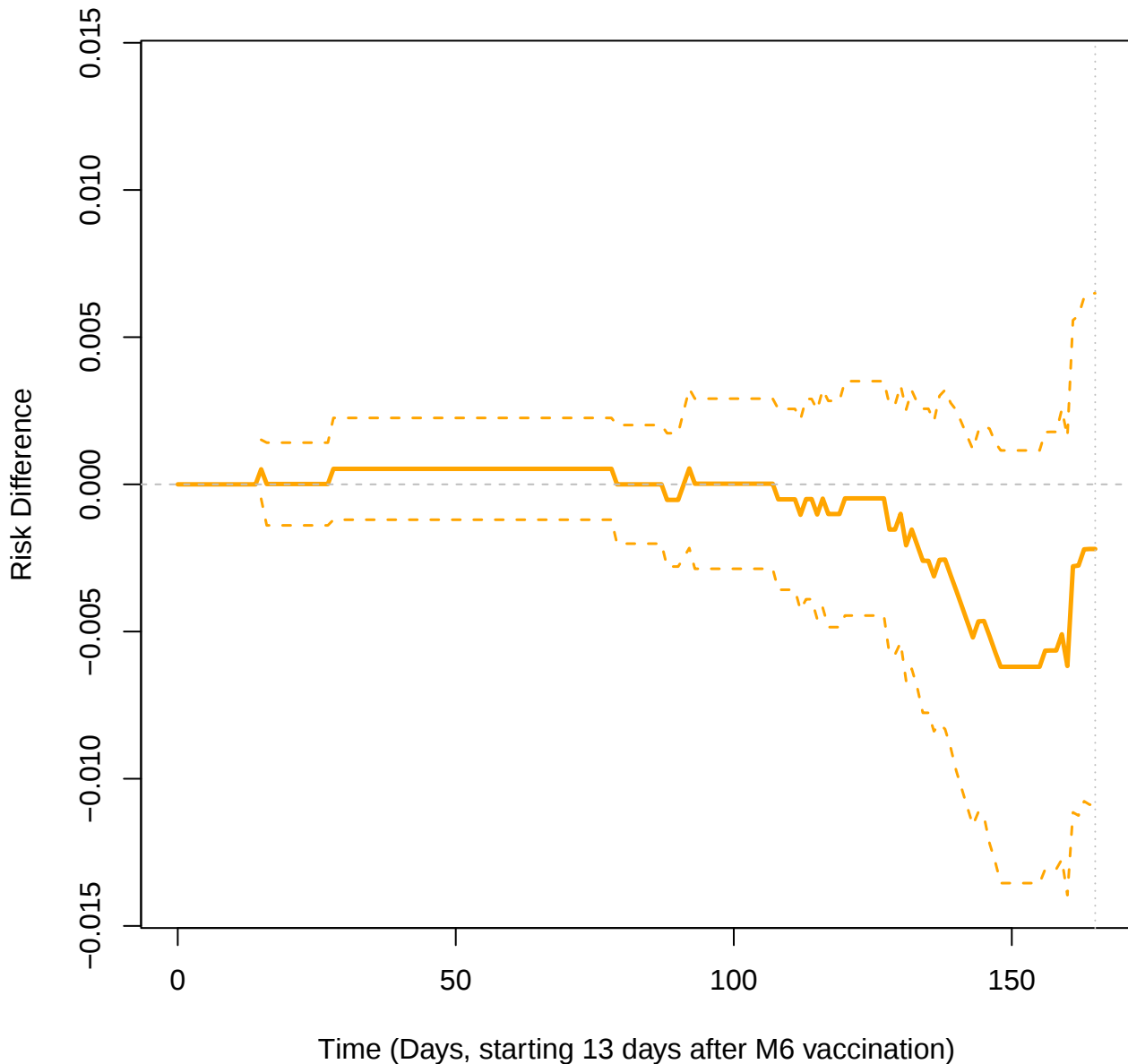
MBoost vs BBoost, RM6, CDC14M12, Sensitivity (PLWH)



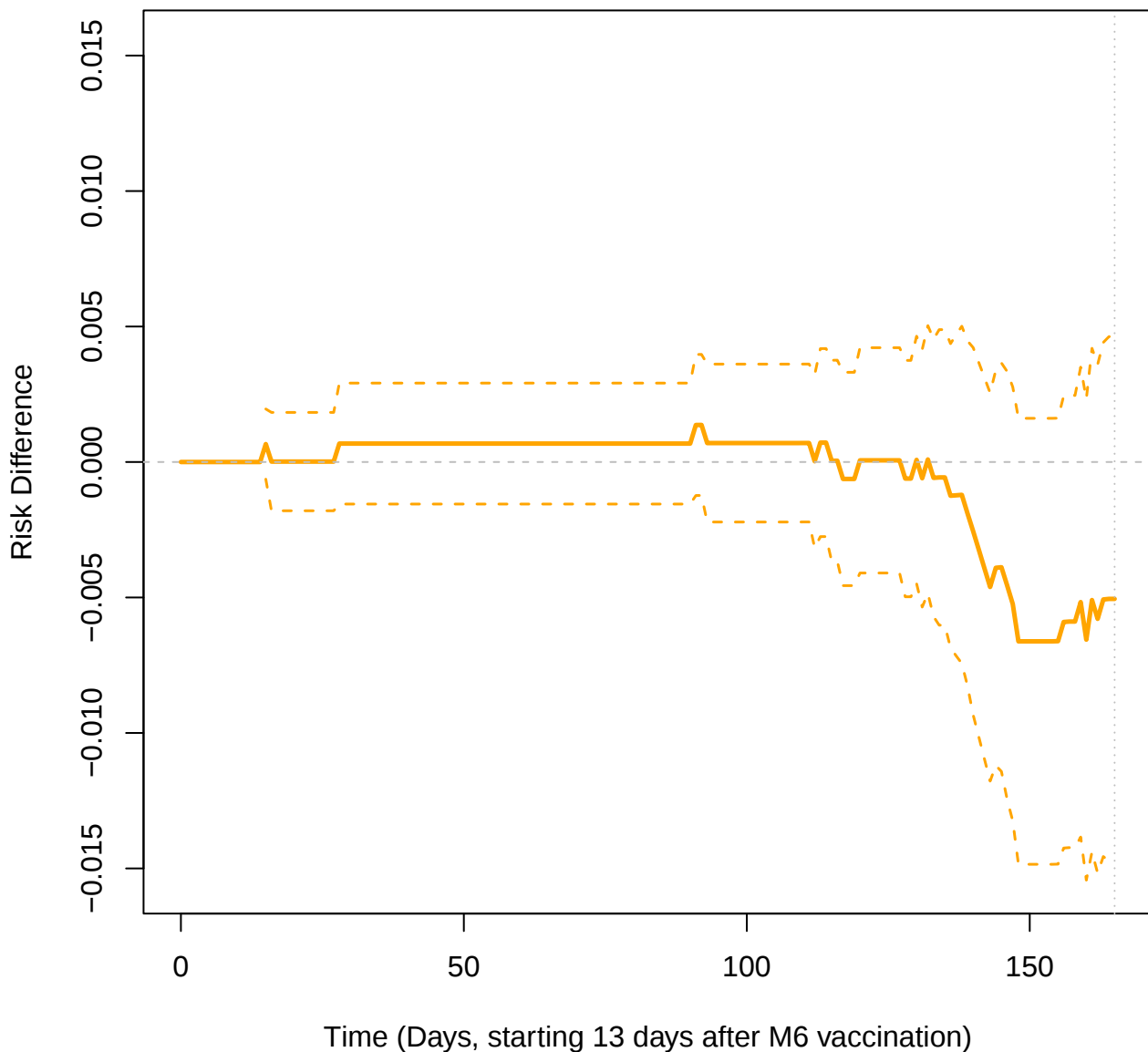
MBoost vs BBoost, RM6, CDC14M12, Sensitivity (PLWoH)



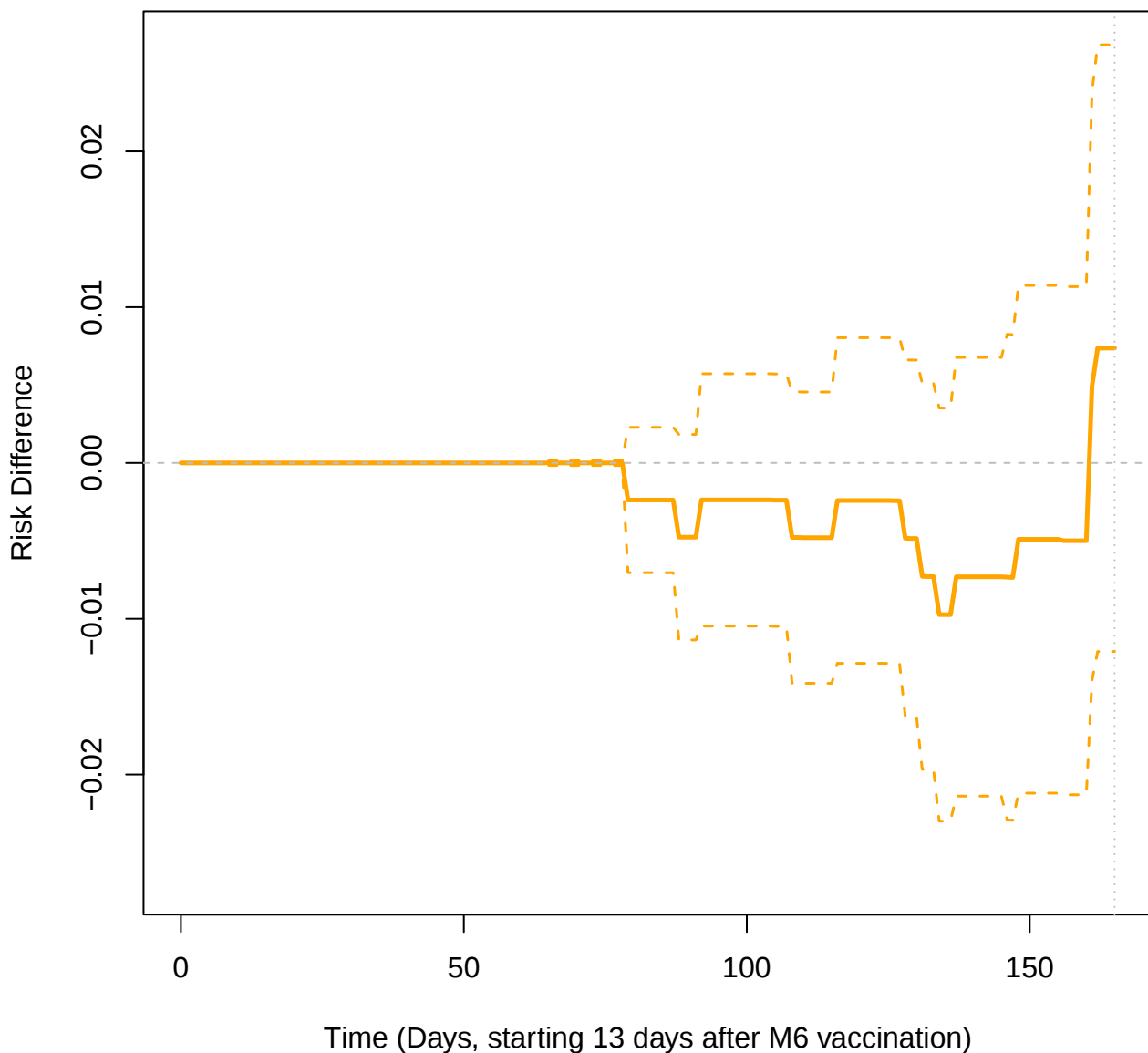
MBoost vs BBoost, RM6, CDC14M18, Primary



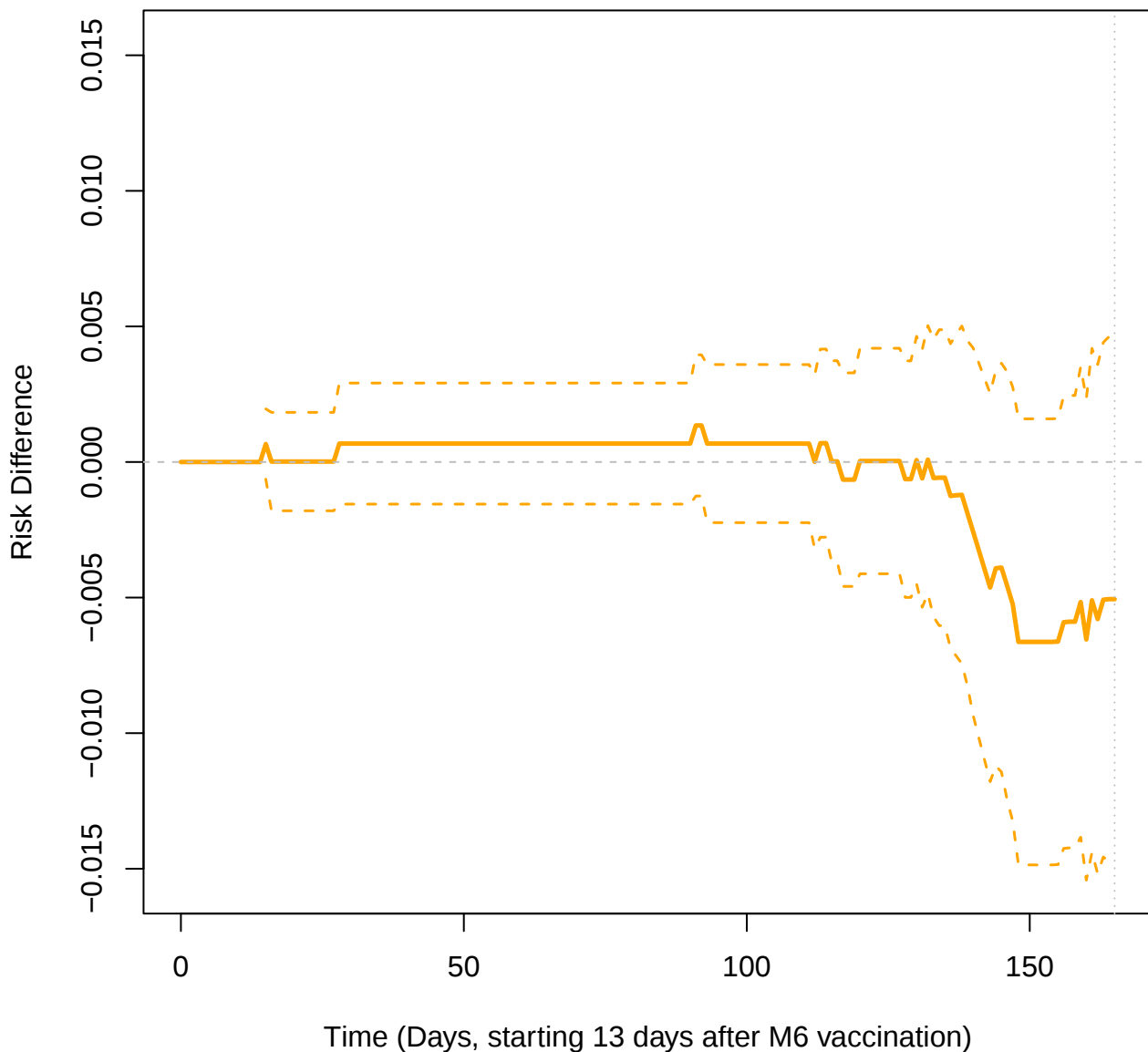
MBoost vs BBoost, RM6, CDC14M18, Primary (PLWH)



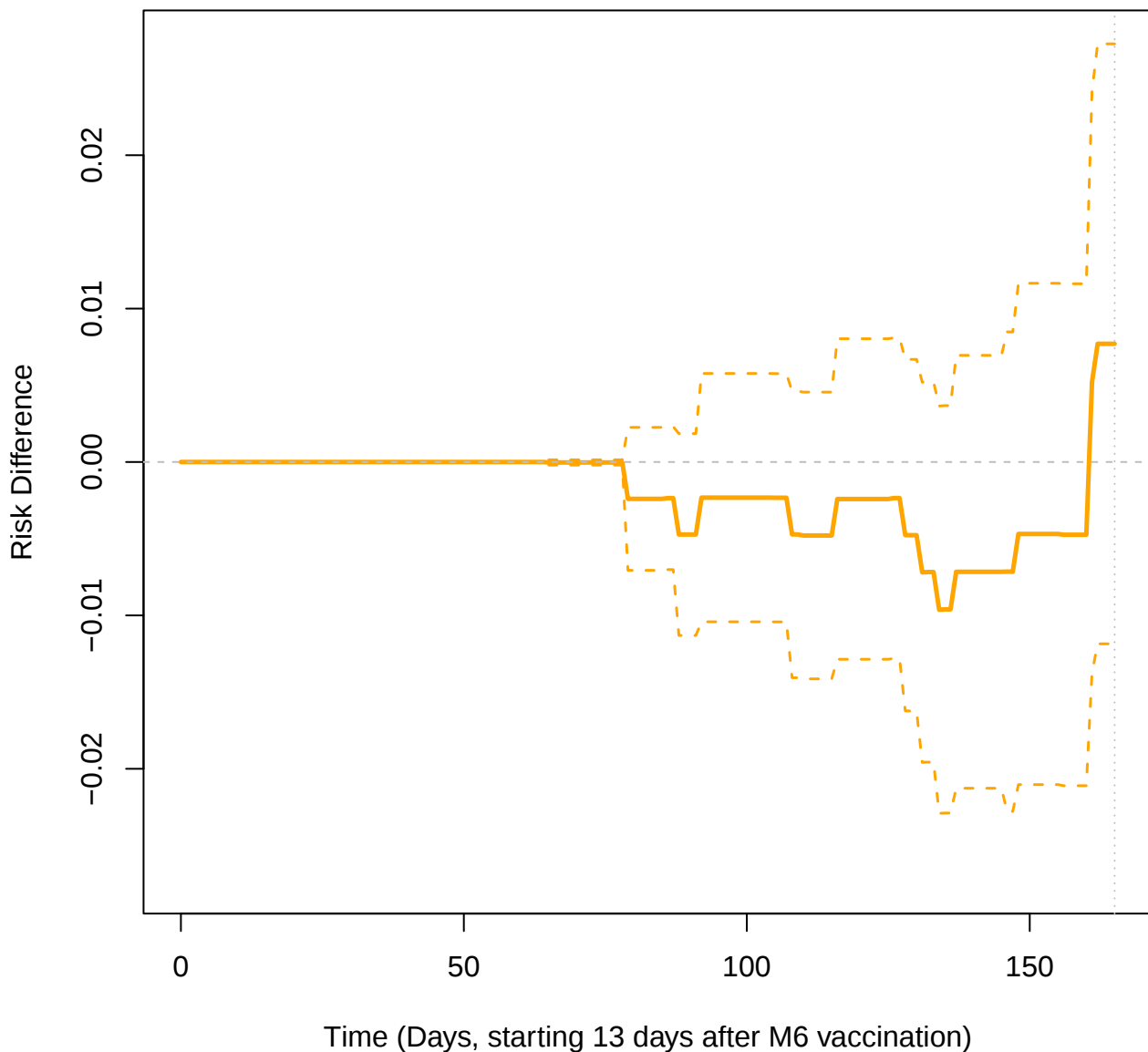
MBoost vs BBoost, RM6, CDC14M18, Primary (PLWoH)



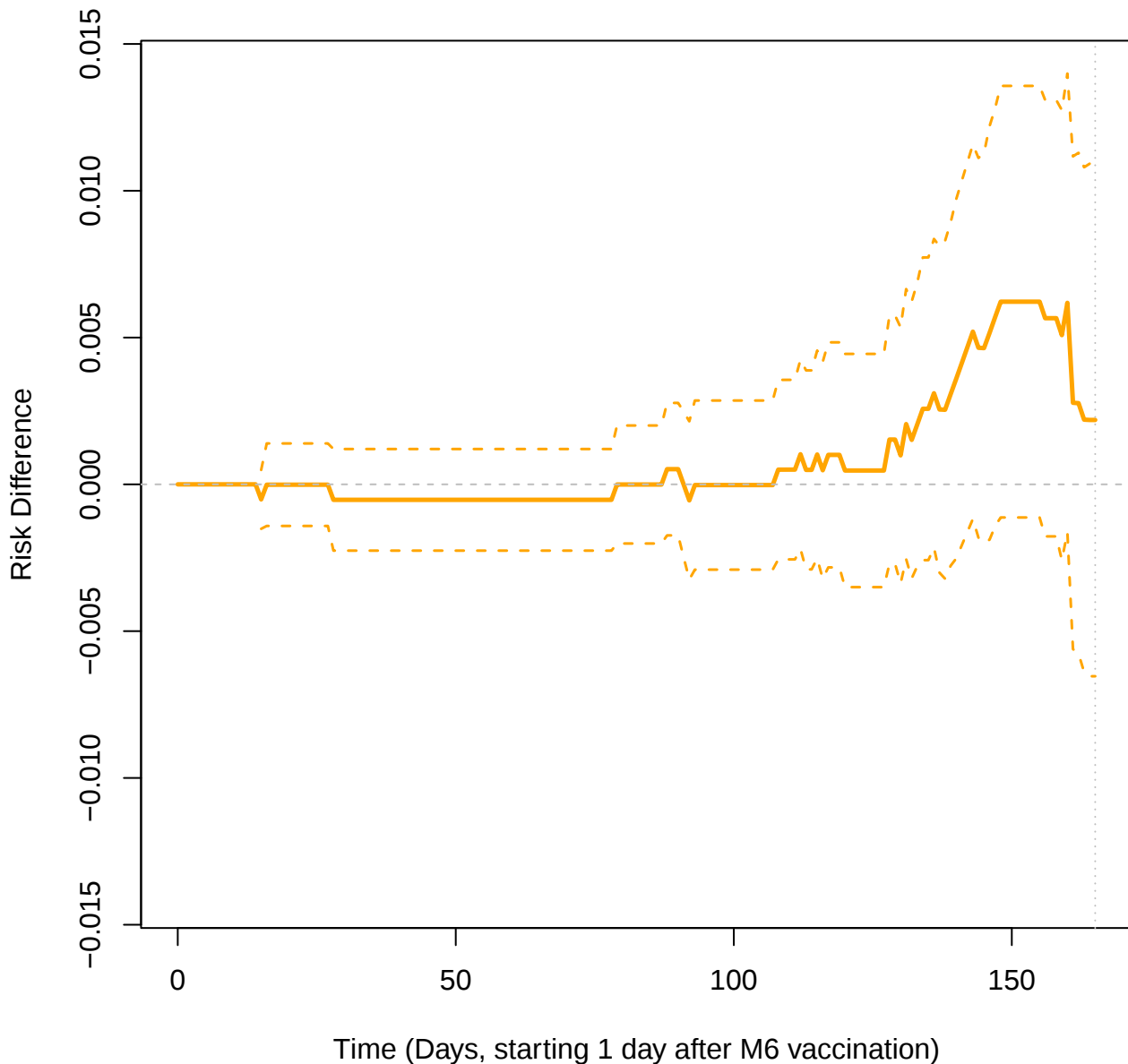
MBoost vs BBoost, RM6, CDC14M18, Sensitivity (PLWH)



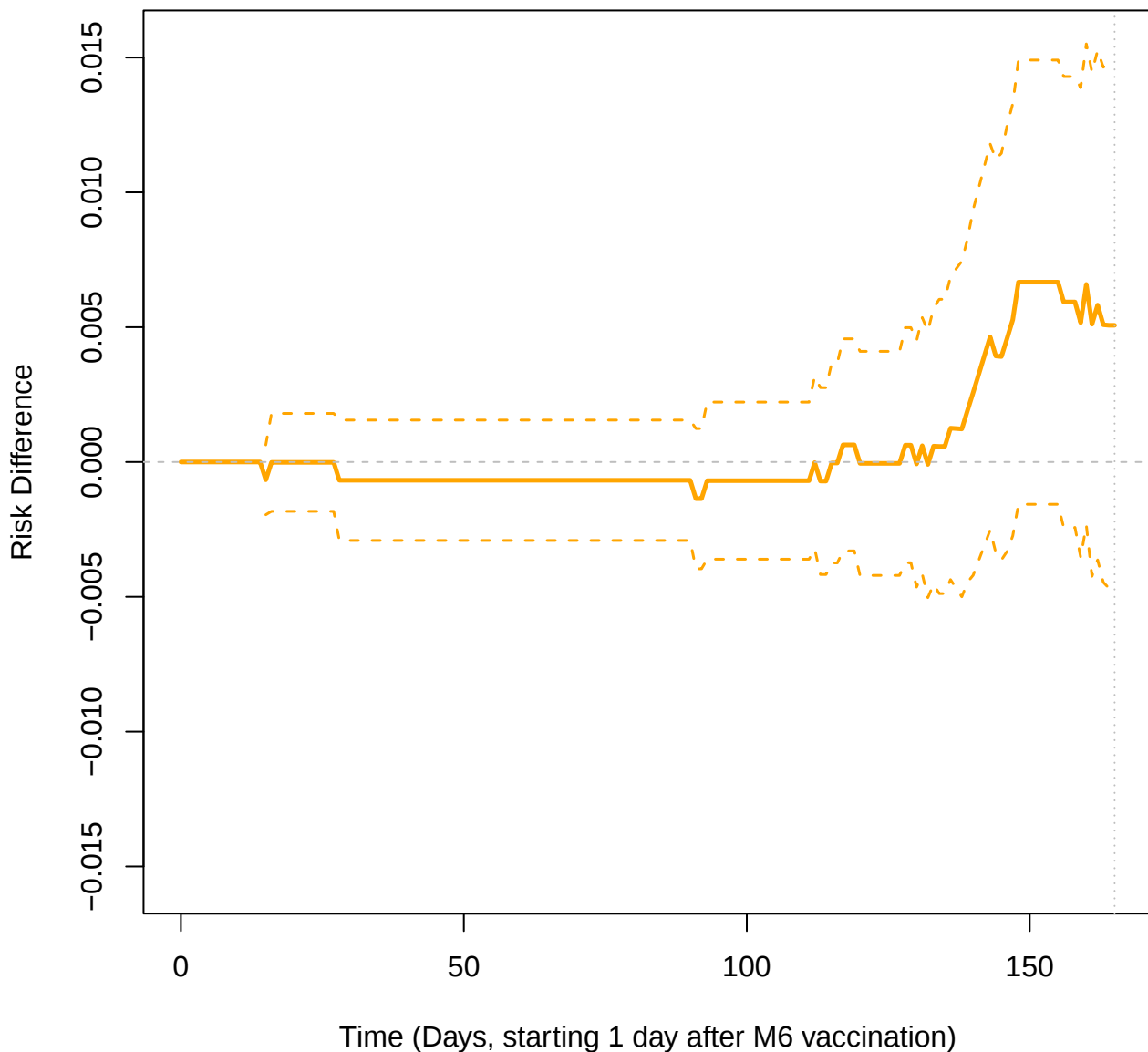
MBoost vs BBoost, RM6, CDC14M18, Sensitivity (PLWoH)



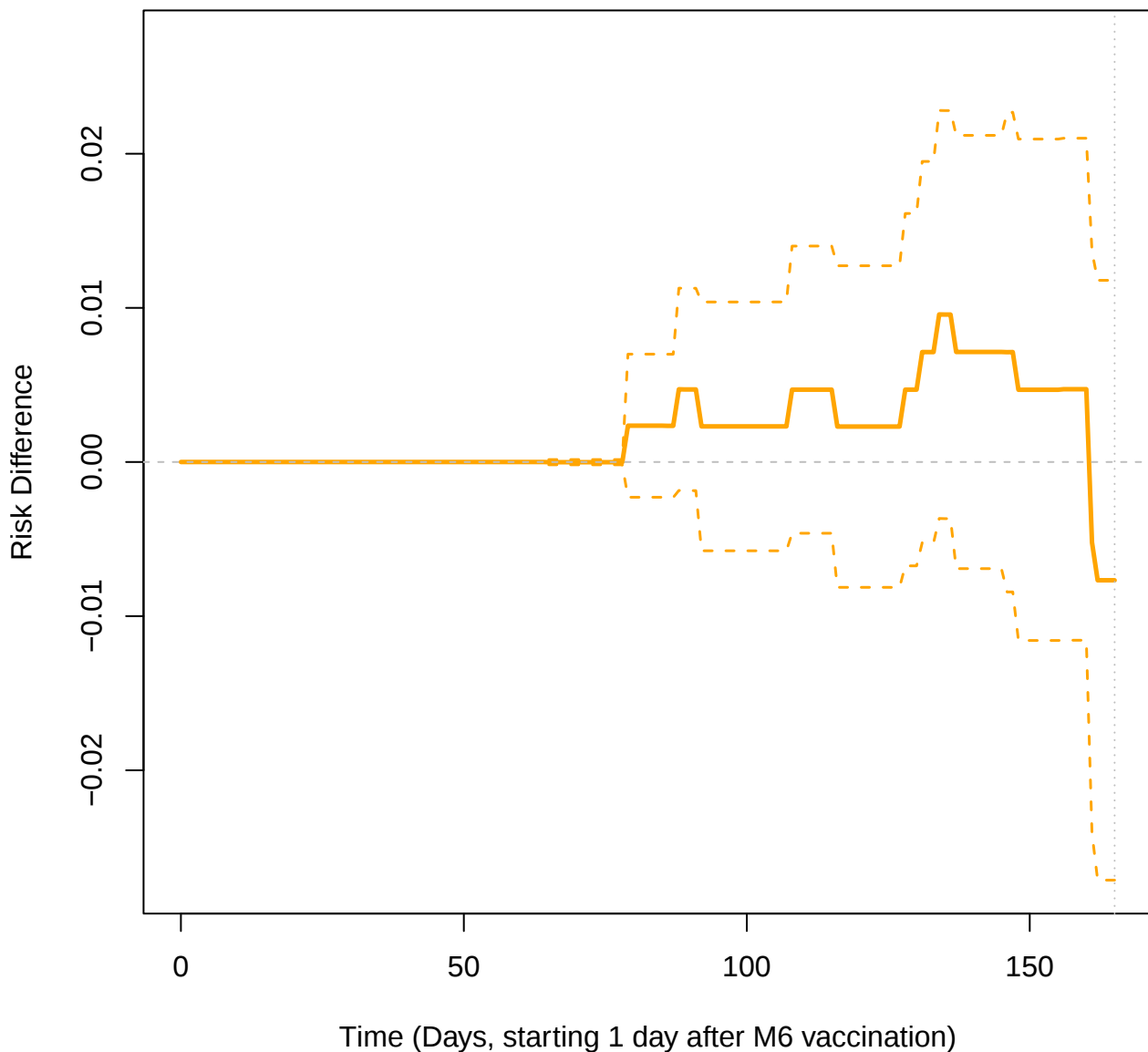
MBoost vs BBoost, RM6, CDC1M12, Primary



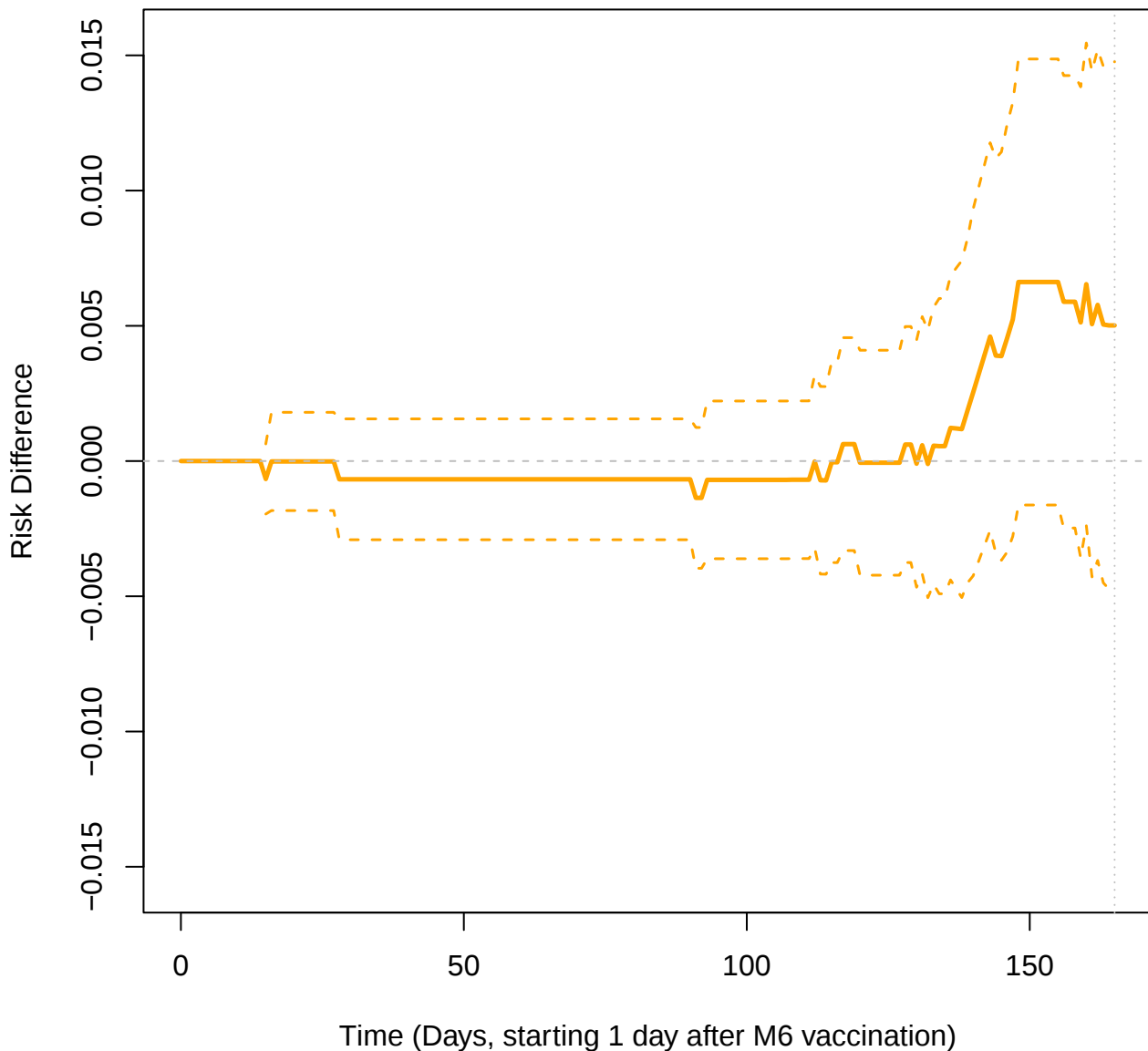
MBoost vs BBoost, RM6, CDC1M12, Primary (PLWH)



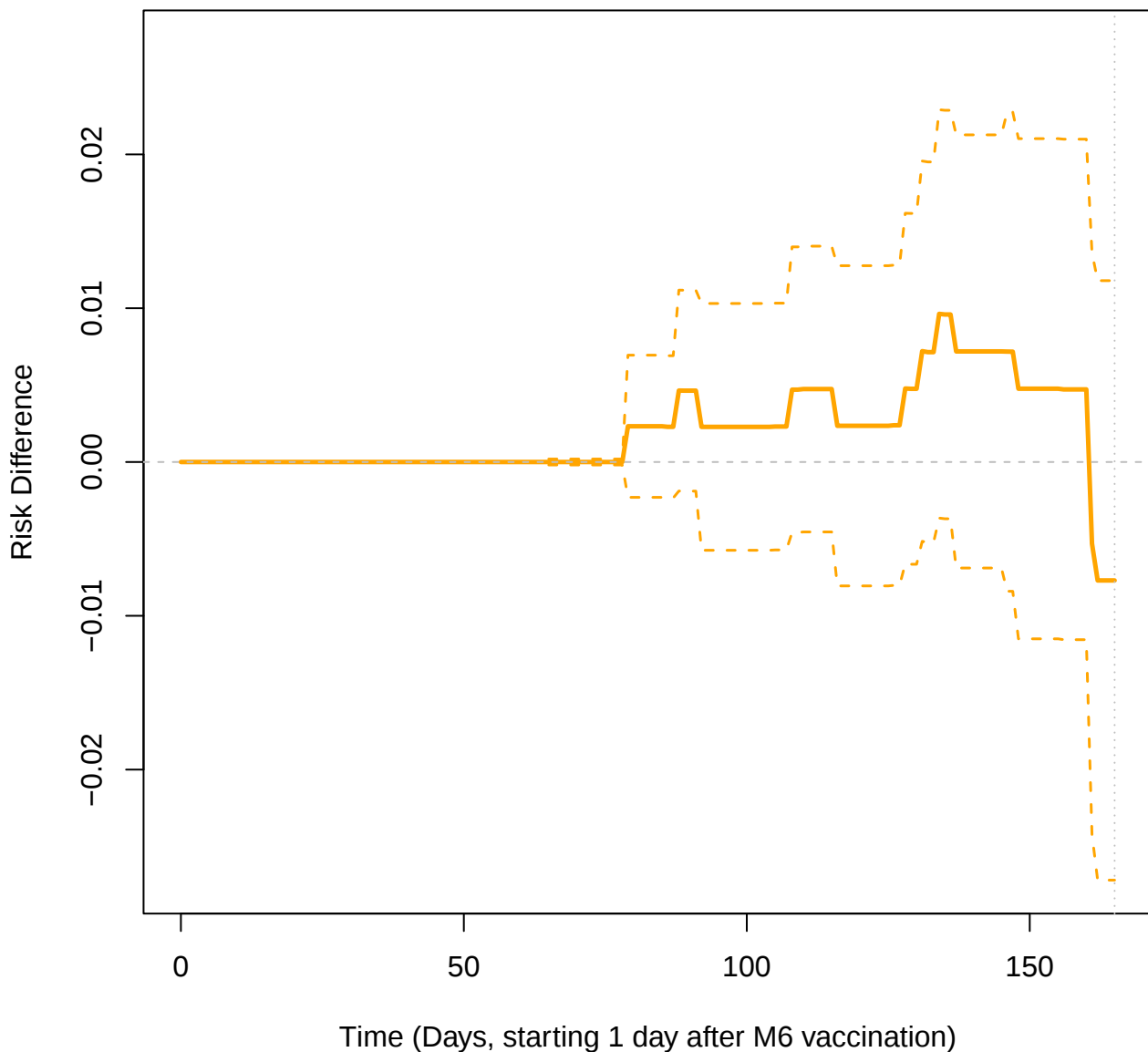
MBoost vs BBoost, RM6, CDC1M12, Primary (PLWoH)



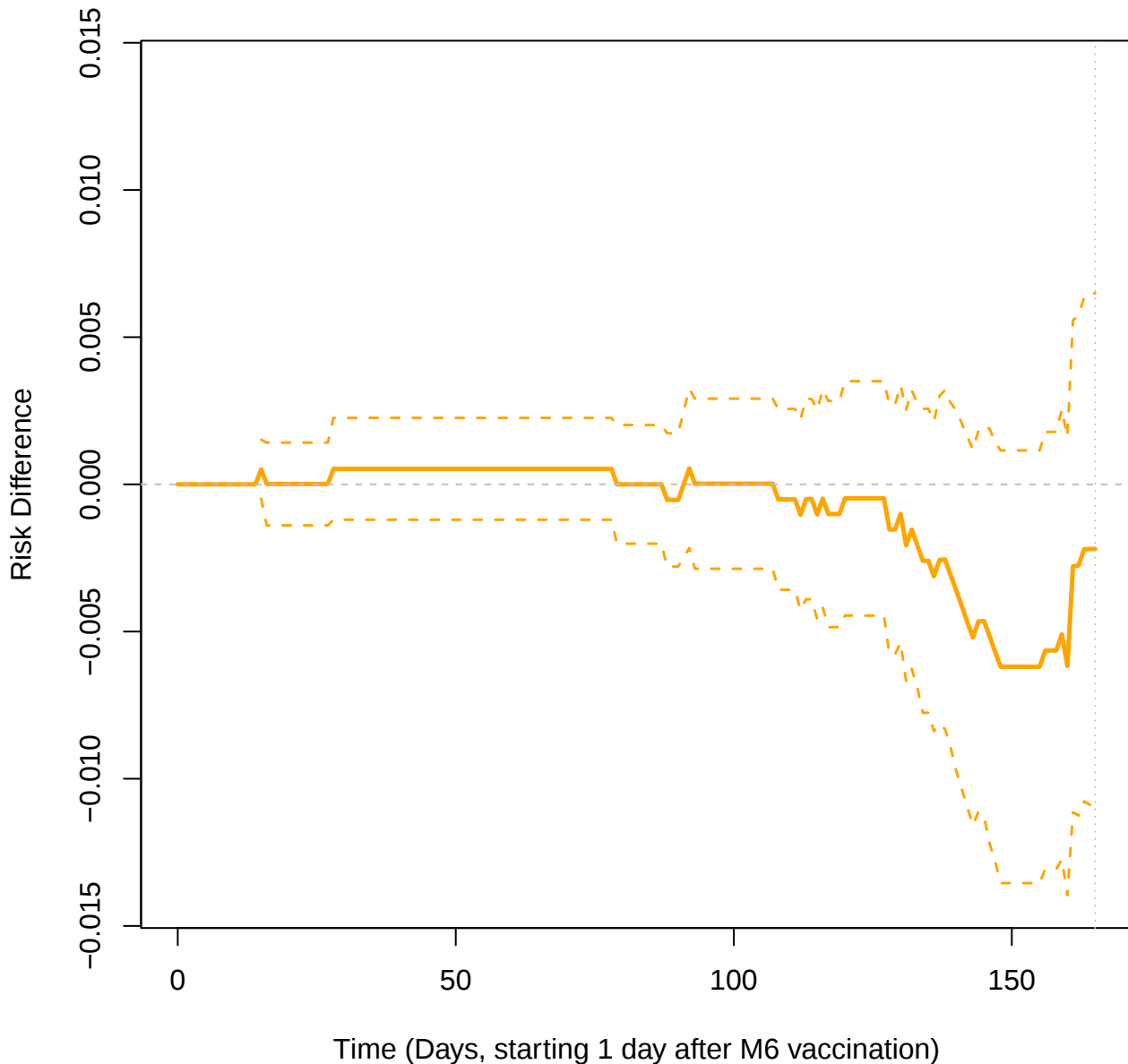
MBoost vs BBoost, RM6, CDC1M12, Sensitivity (PLWH)



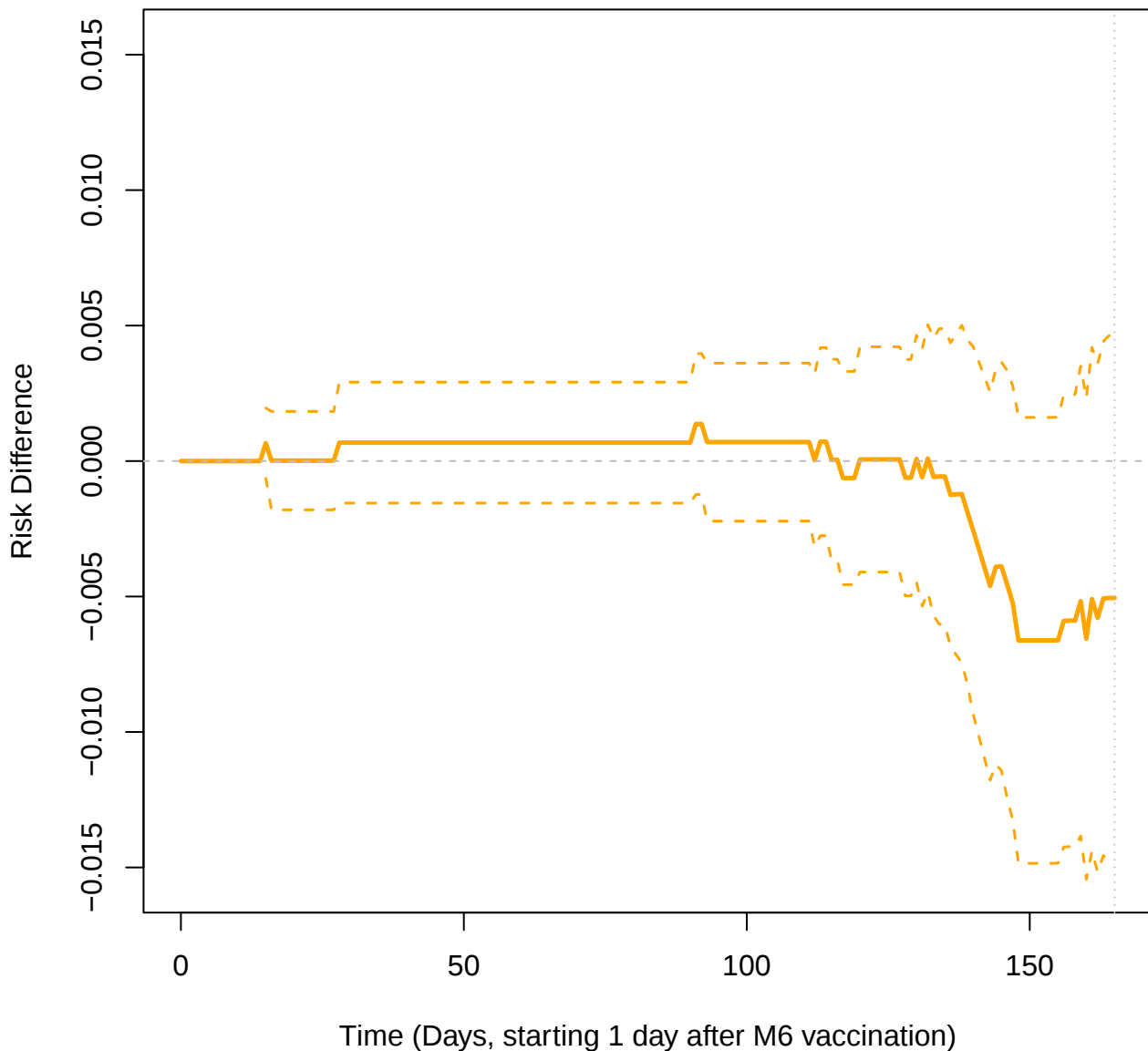
MBoost vs BBoost, RM6, CDC1M12, Sensitivity (PLWoH)



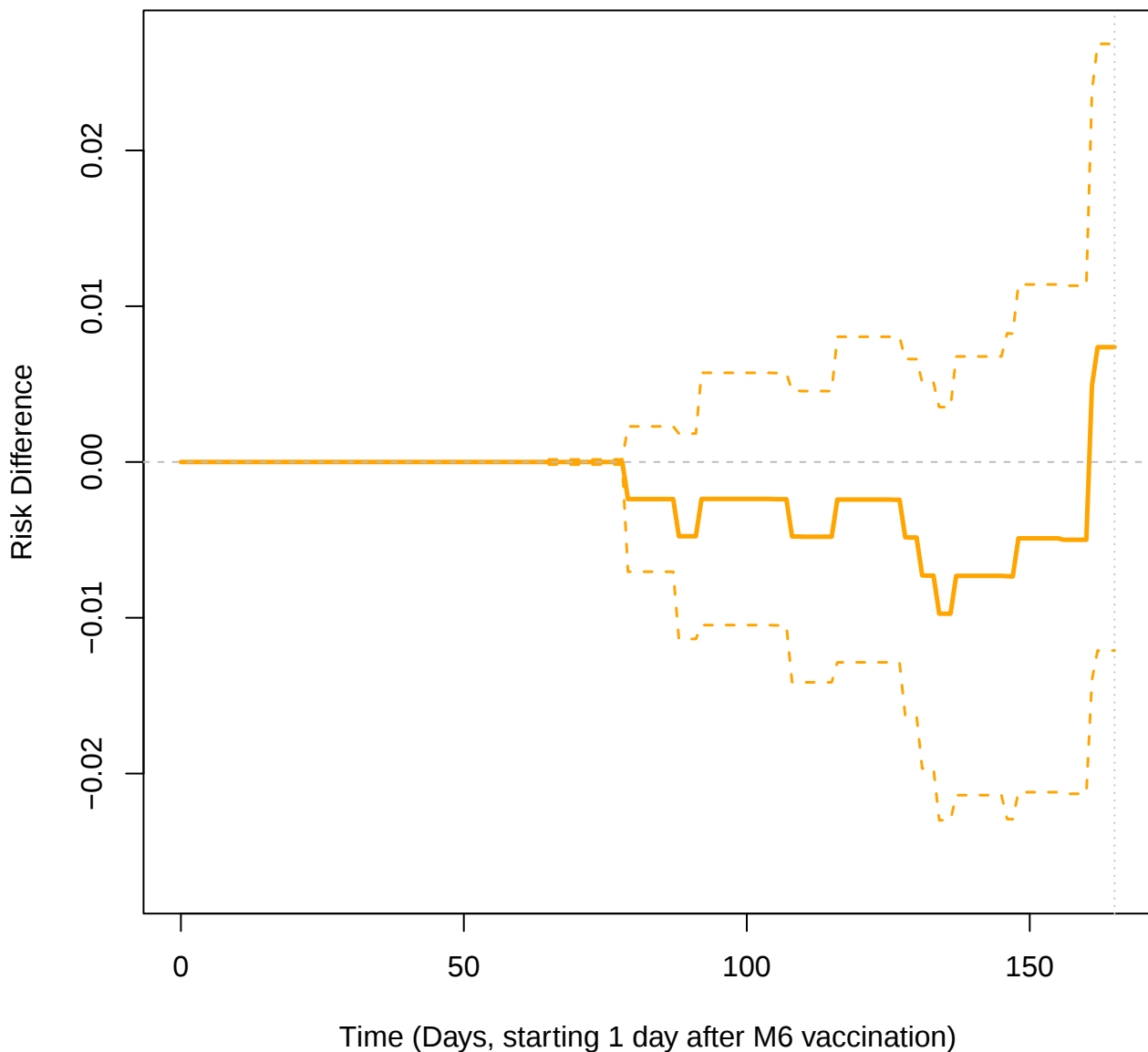
MBoost vs BBoost, RM6, CDC1M18, Primary



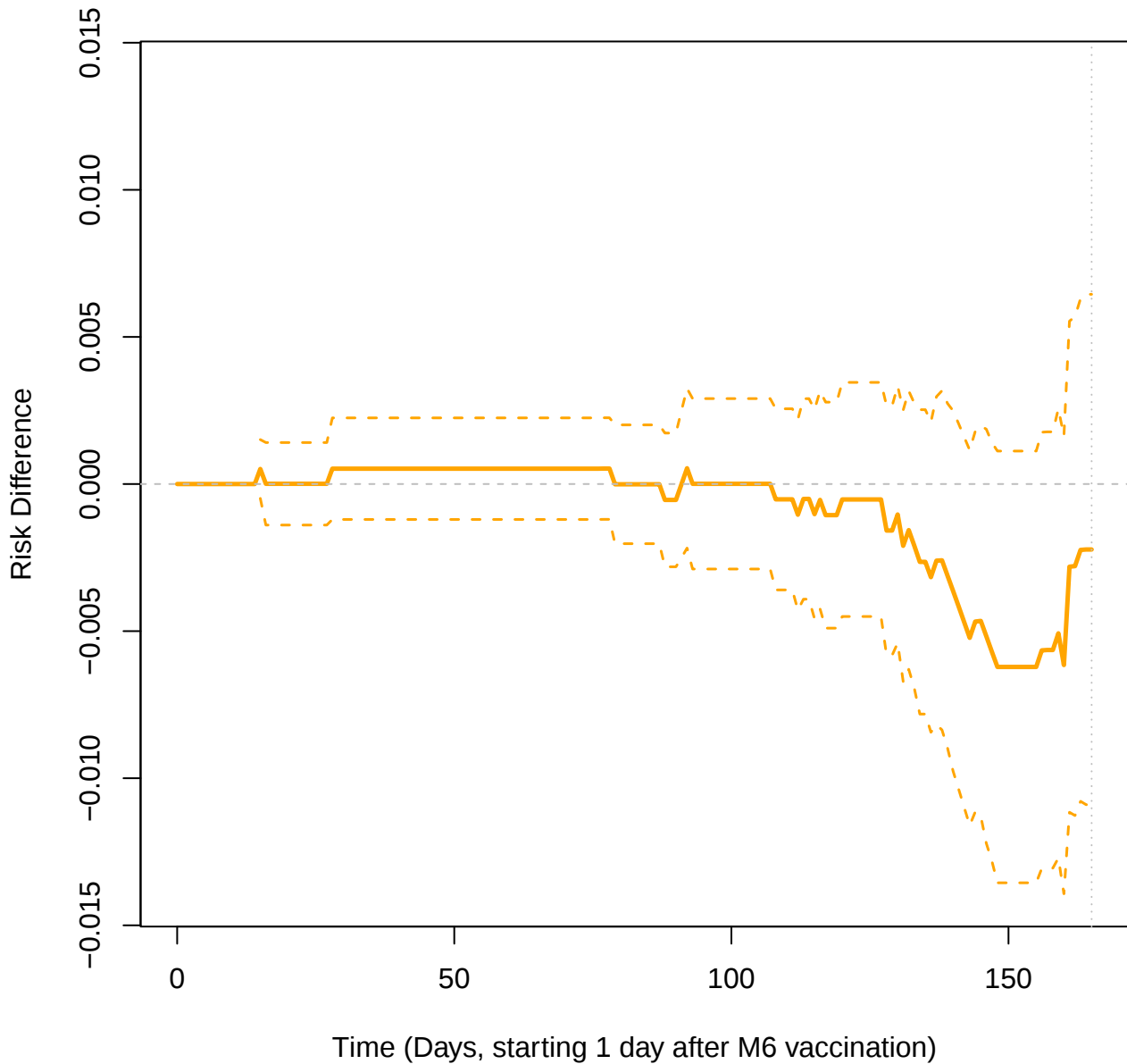
MBoost vs BBoost, RM6, CDC1M18, Primary (PLWH)



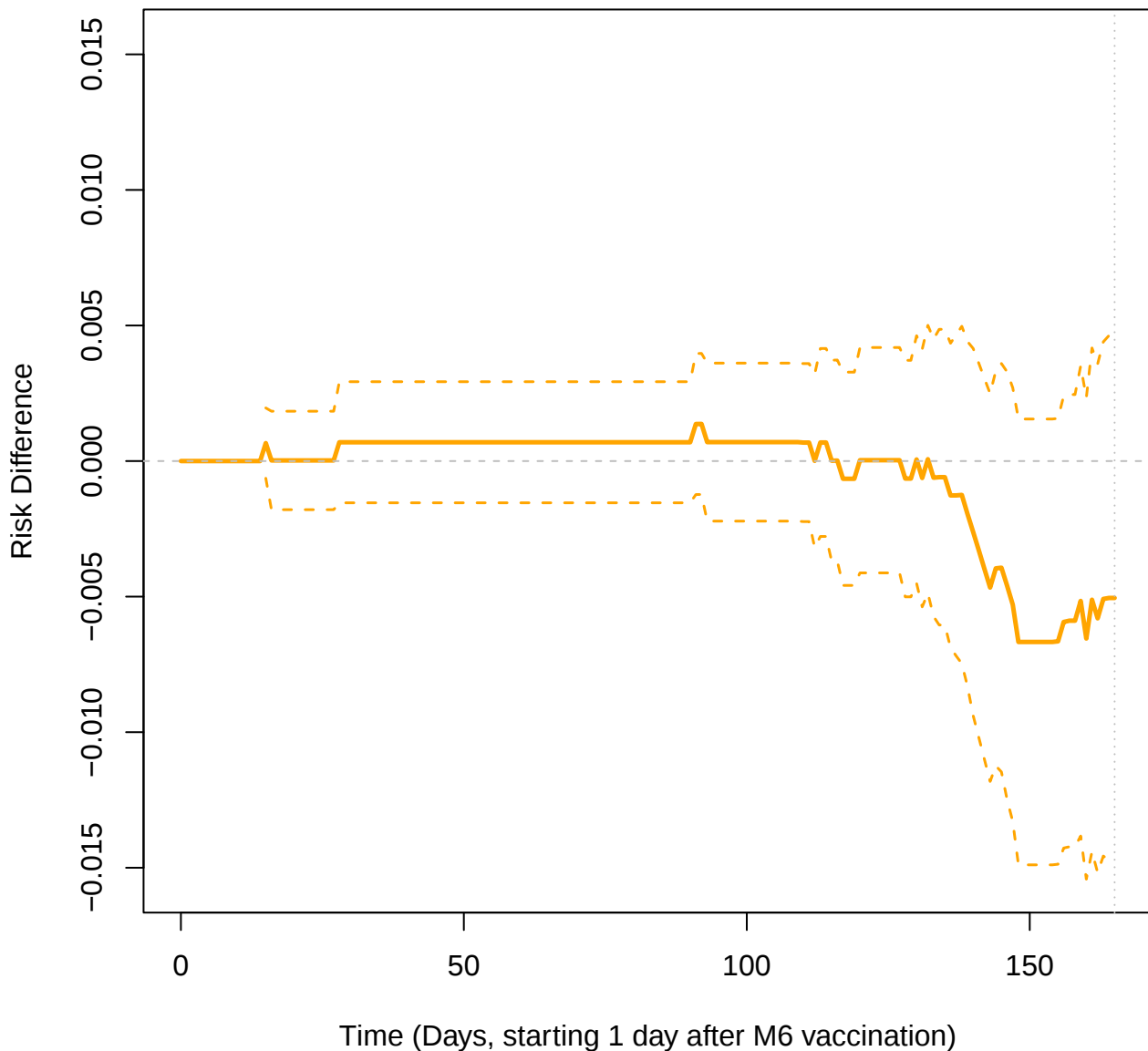
MBoost vs BBoost, RM6, CDC1M18, Primary (PLWoH)



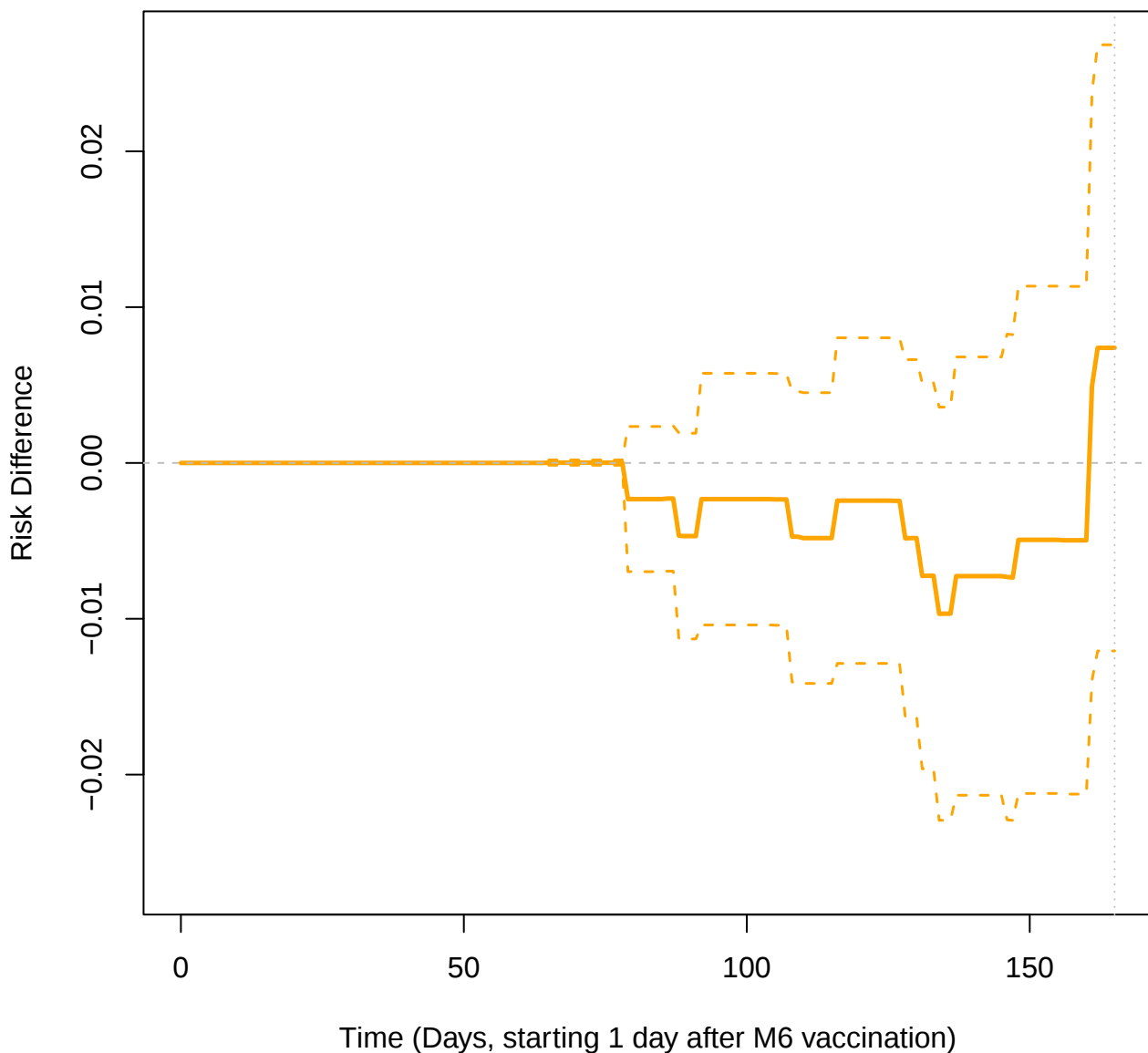
MBoost vs BBoost, RM6, CDC1M18, Sensitivity



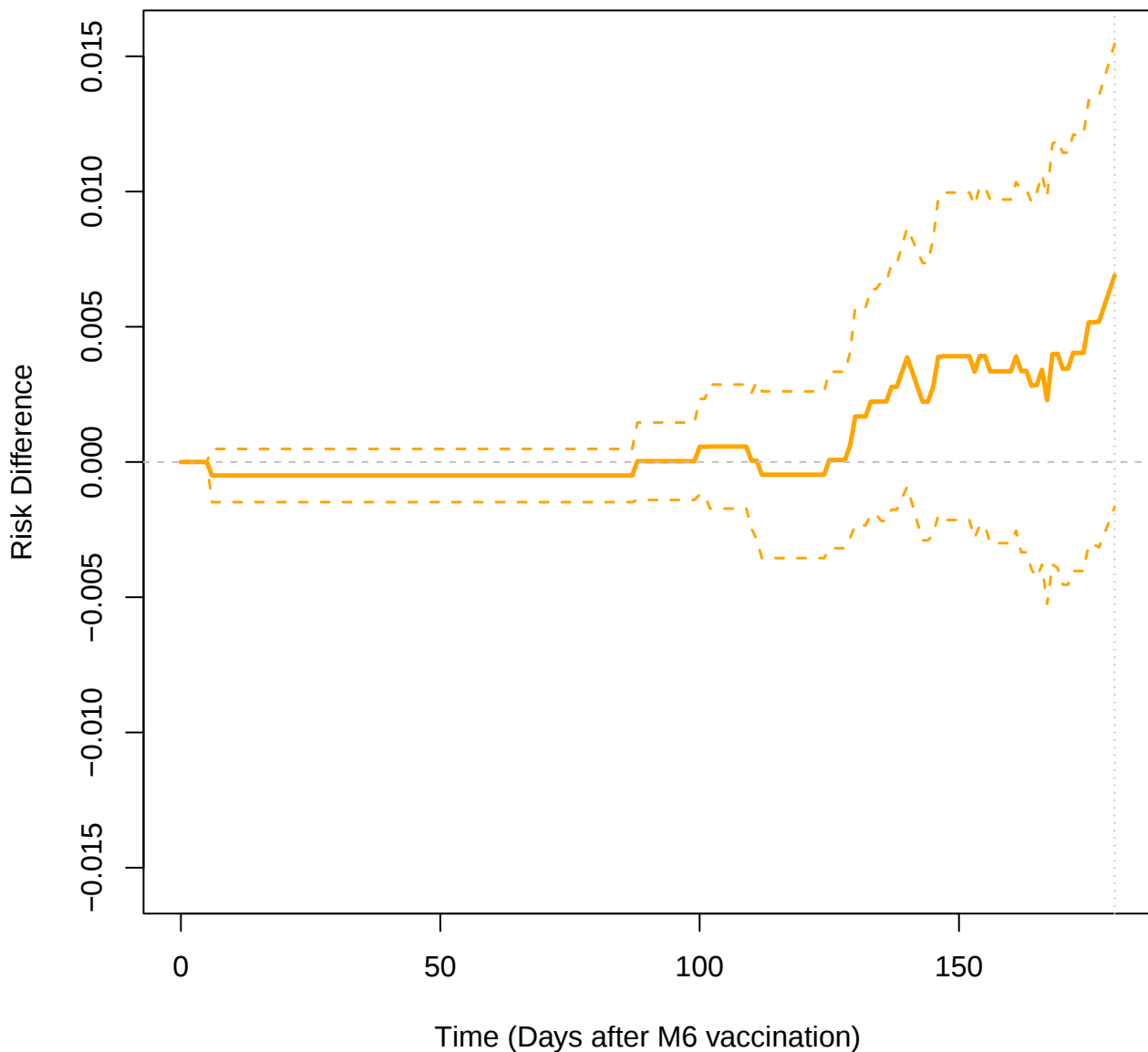
MBoost vs BBoost, RM6, CDC1M18, Sensitivity (PLWH)



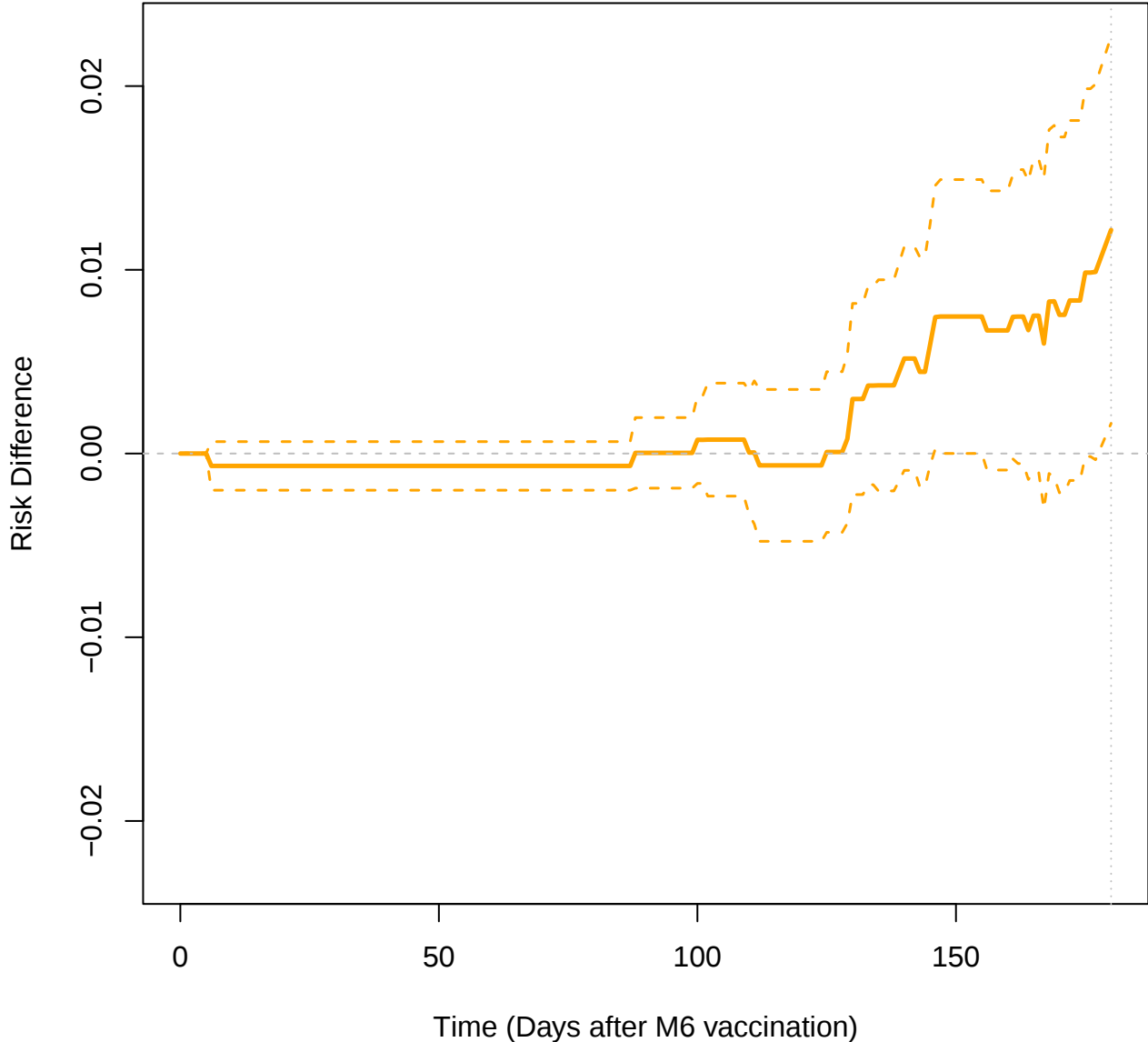
MBoost vs BBoost, RM6, CDC1M18, Sensitivity (PLWoH)



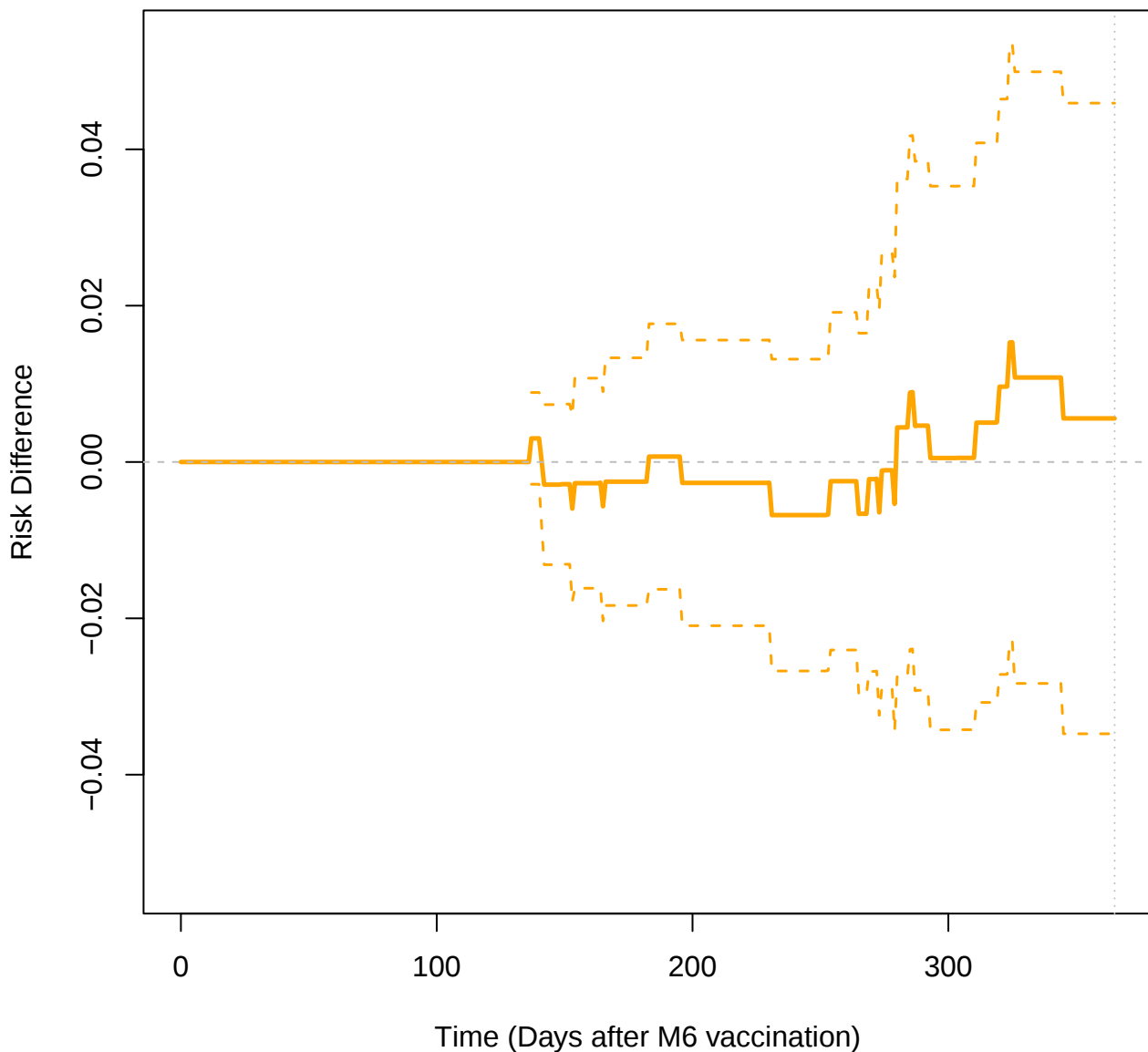
MBoost vs BBoost, RM6, SUBCINF, Primary



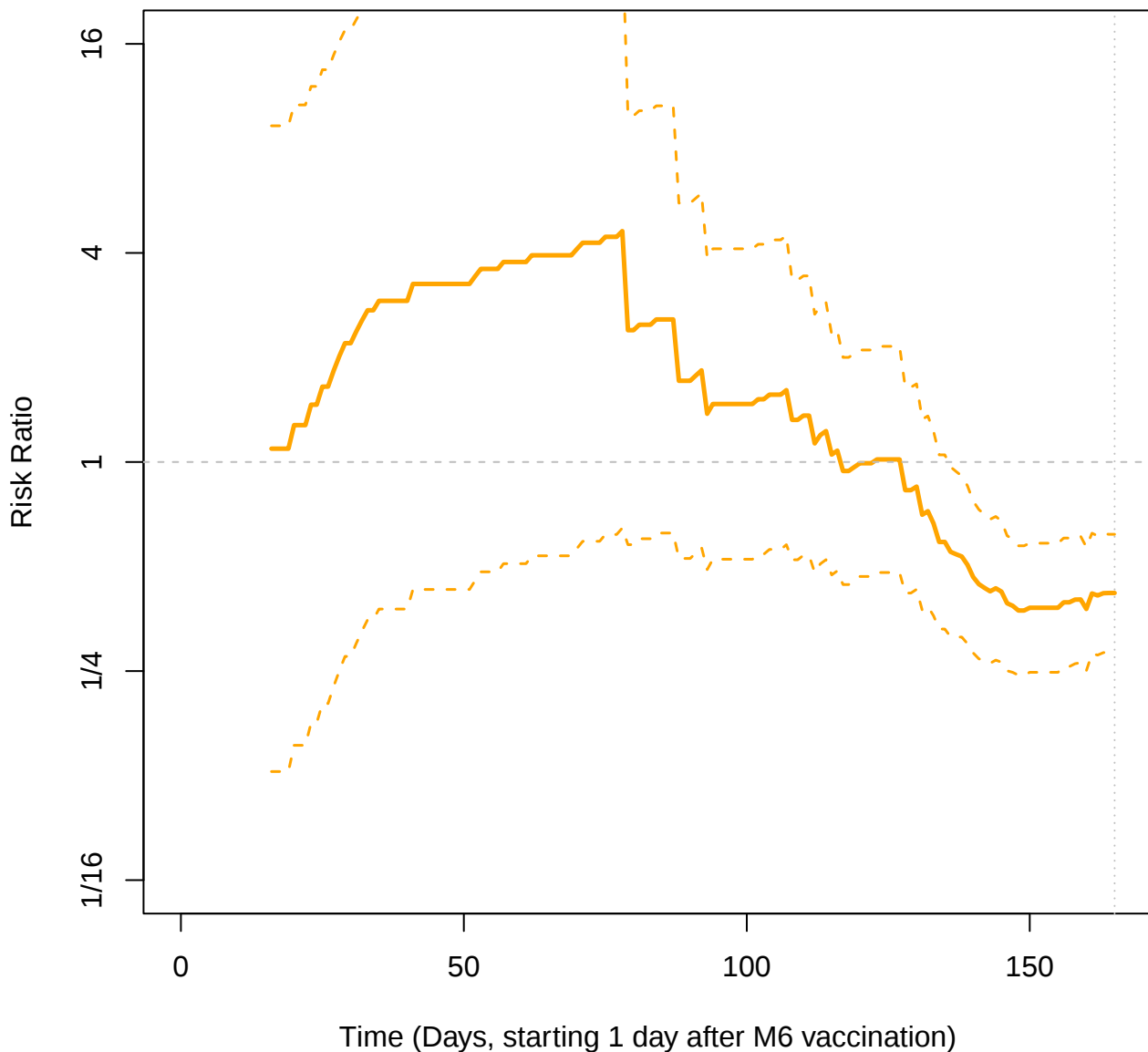
MBoost vs BBoost, RM6, SUBCINF, Primary, Hybrid Immunity



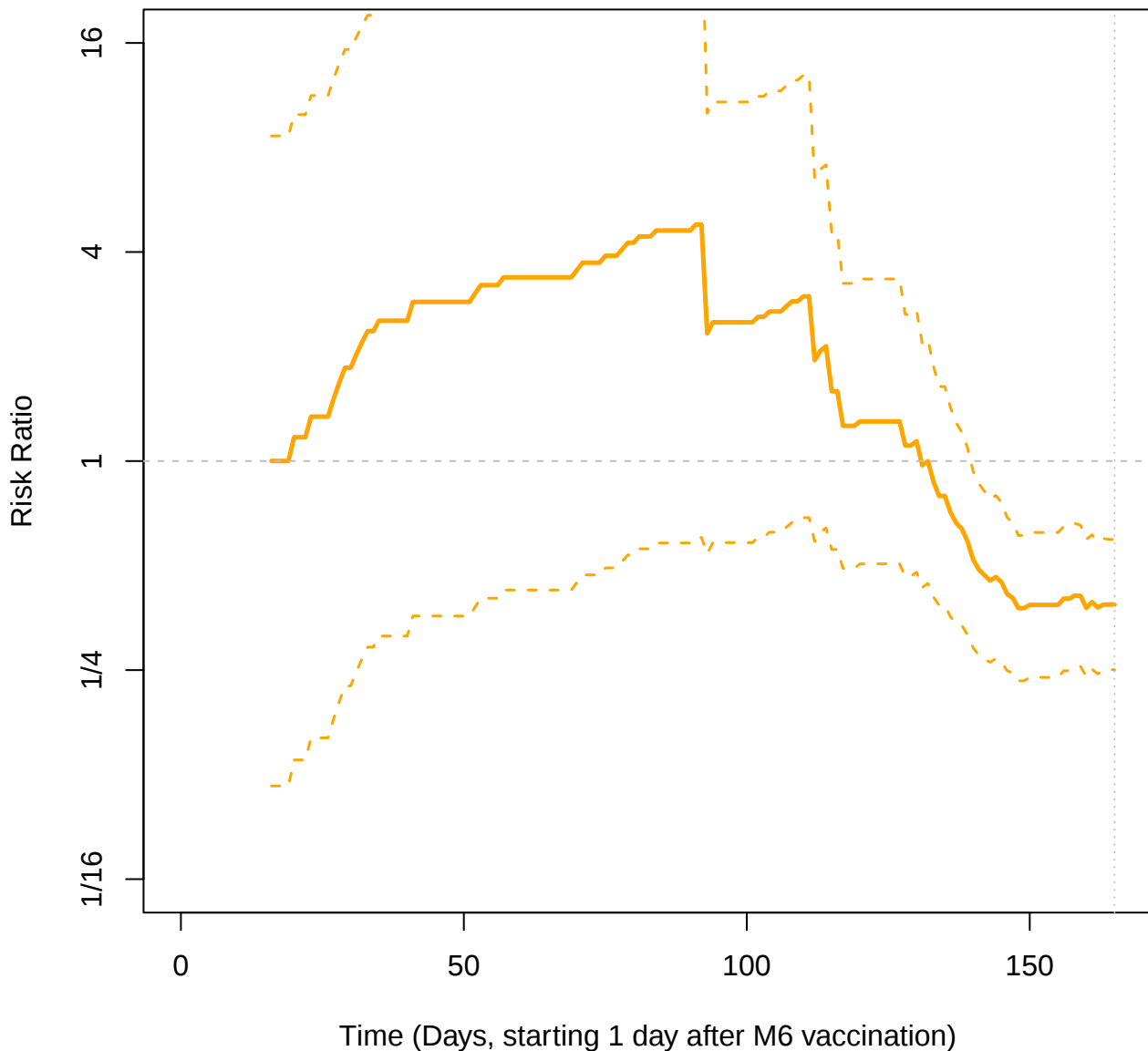
MBoost vs BBoost, RM6, SUBCINF, Primary, Vaccine Immunity



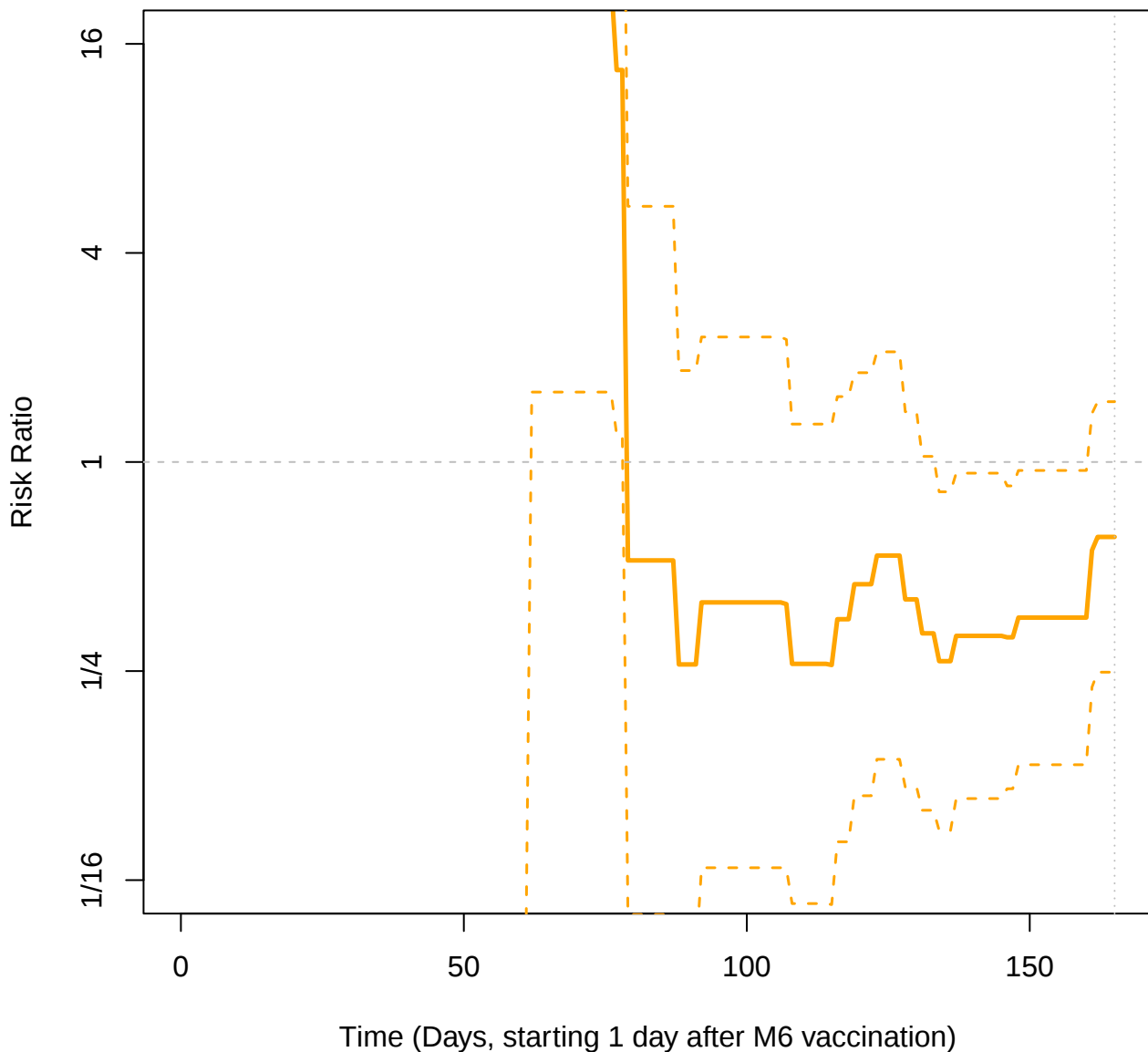
MBoost vs BBoost, FM6, CDC1M18, Primary



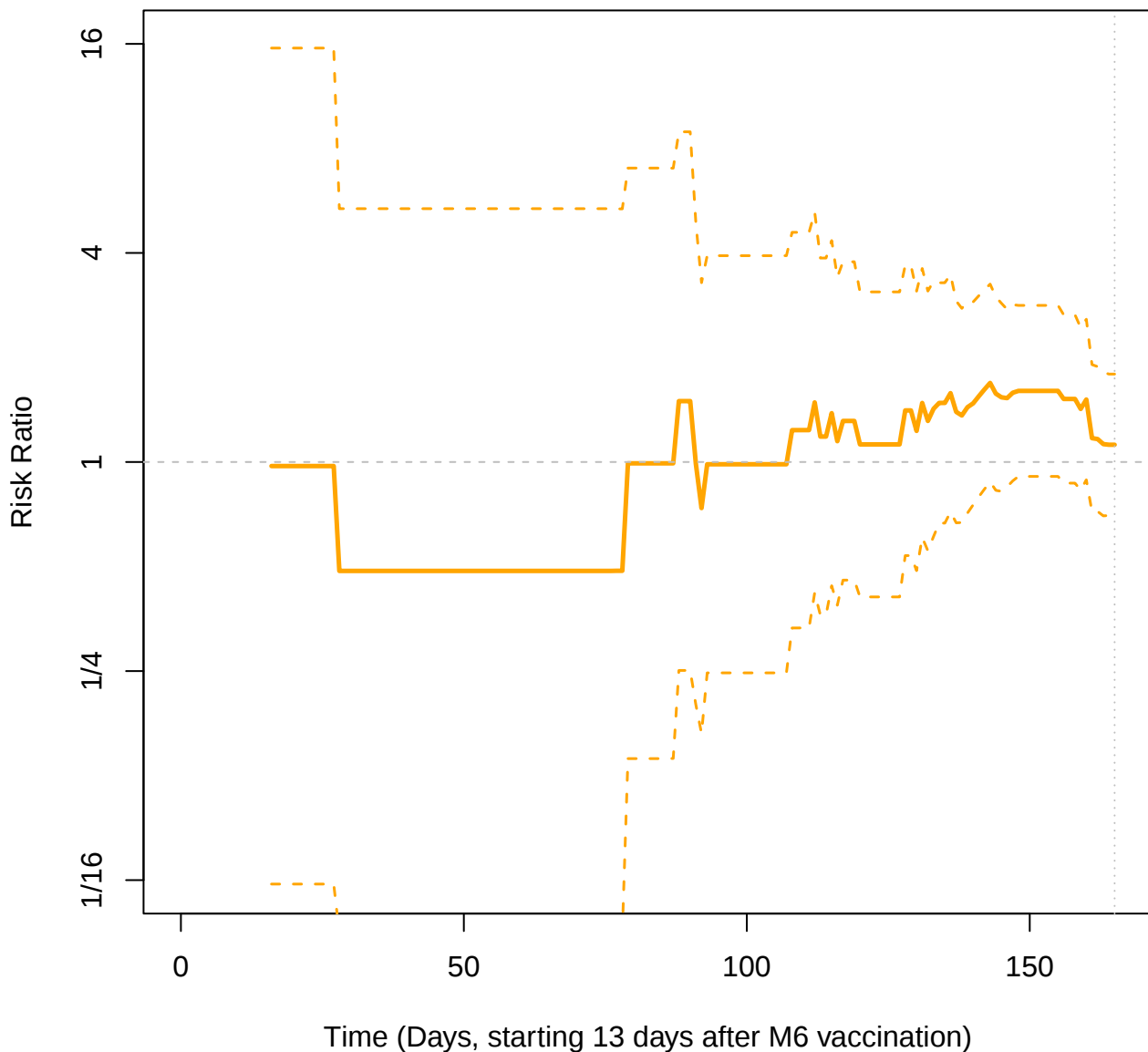
MBoost vs BBoost, FM6, CDC1M18, Primary (PLWH)



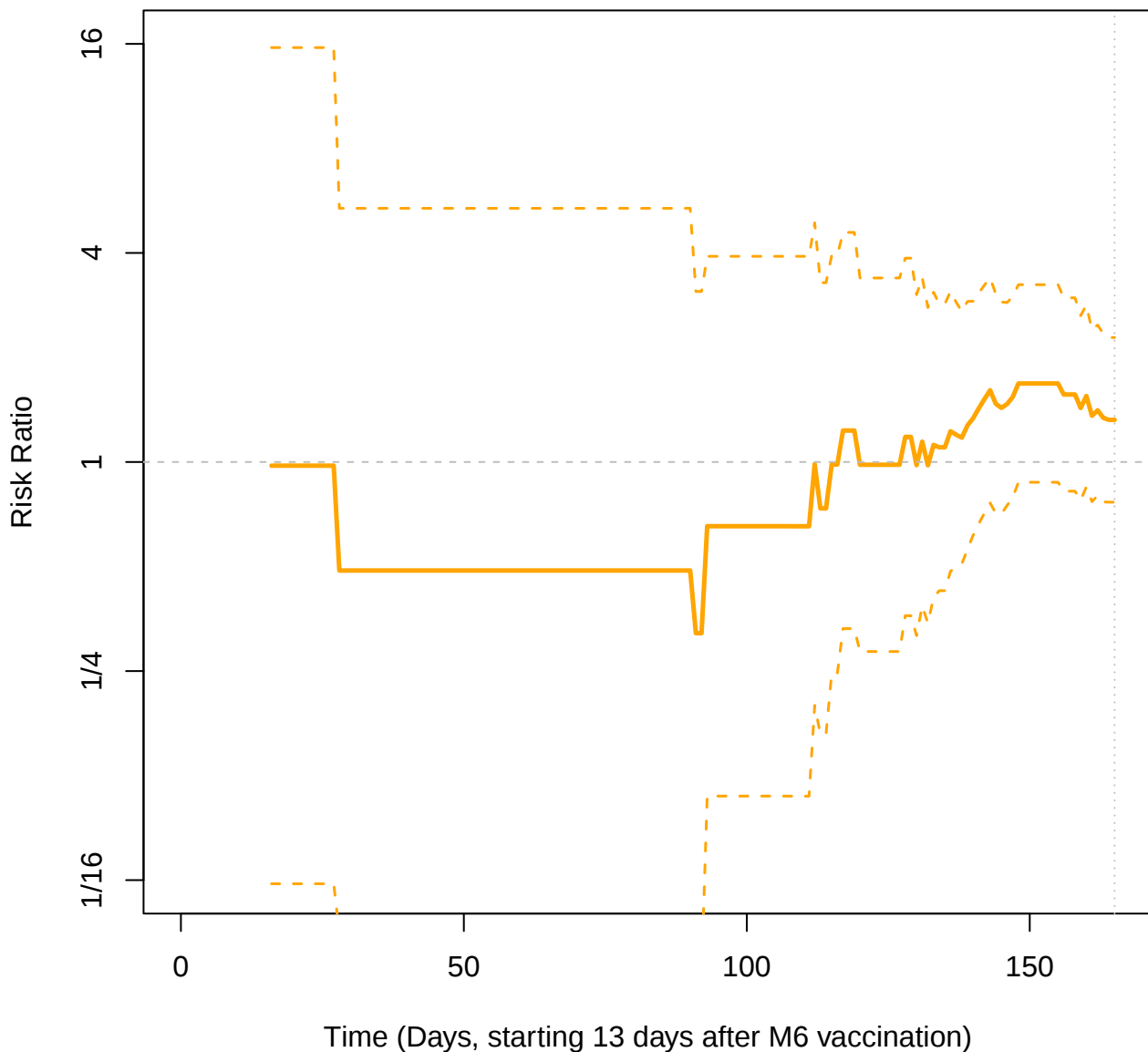
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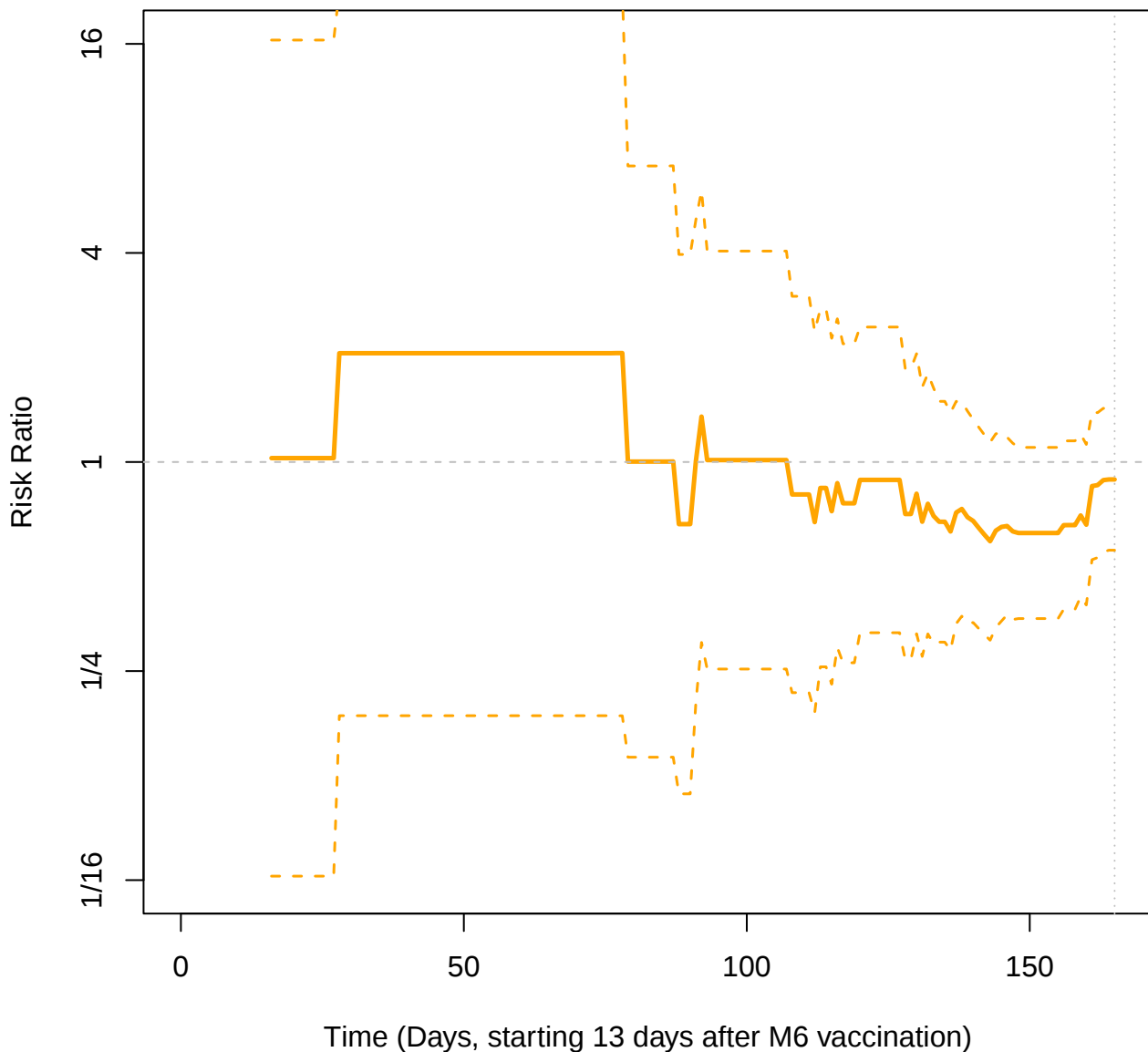
MBoost vs BBoost, FPP, CDC14M12, Primary



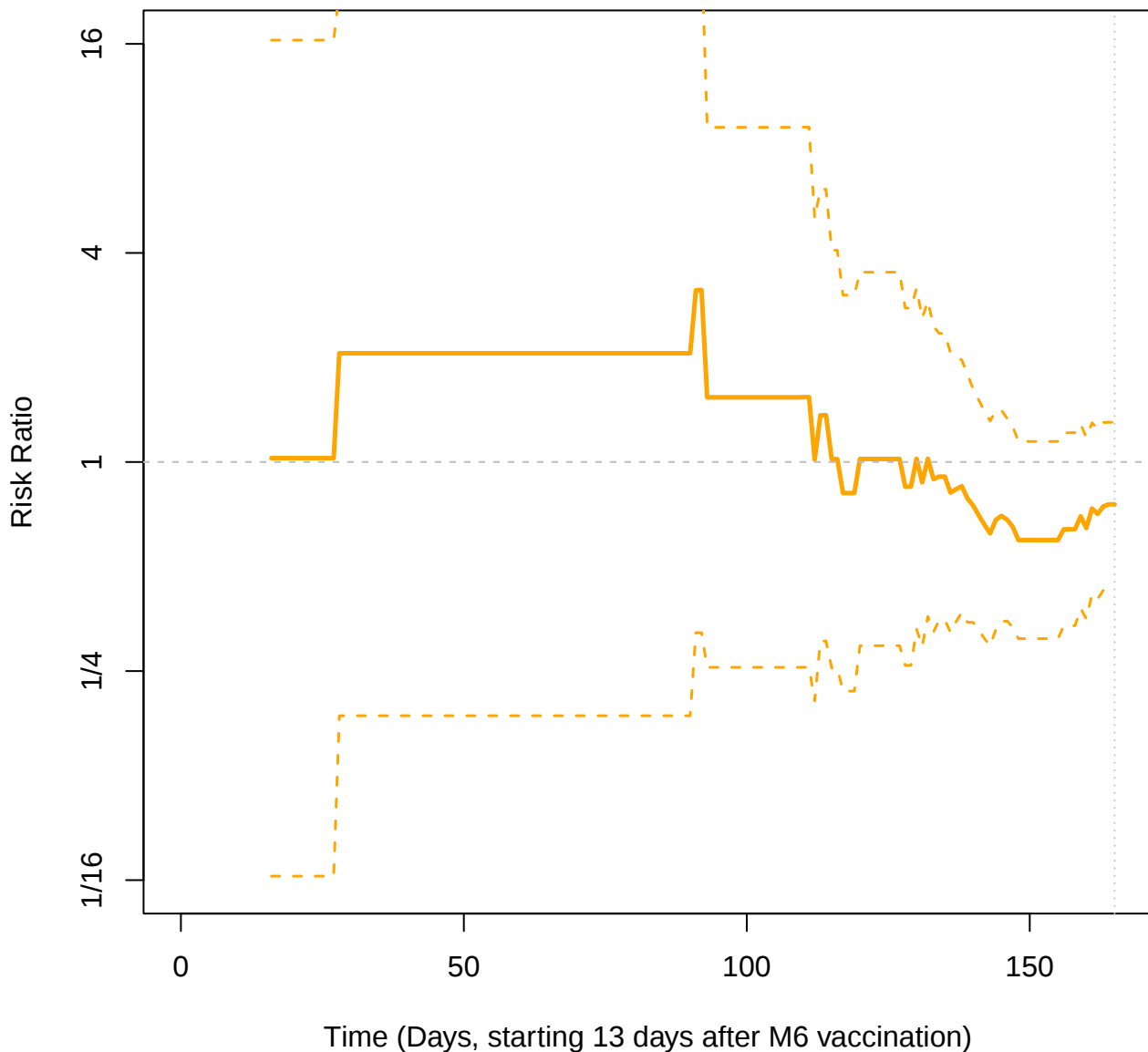
MBoost vs BBoost, FPP, CDC14M12, Primary (PLWH)



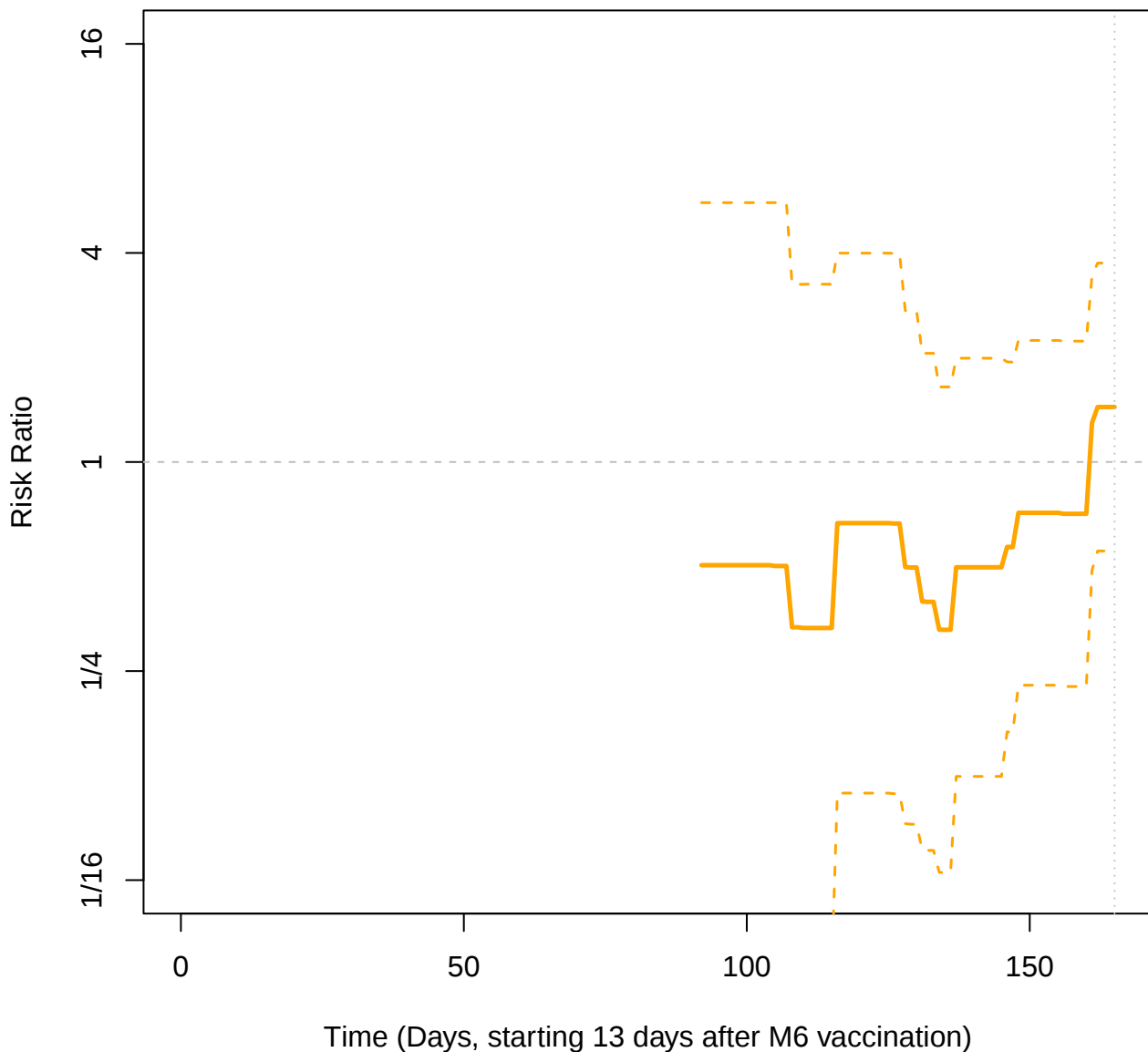
MBoost vs BBoost, FPP, CDC14M18, Primary



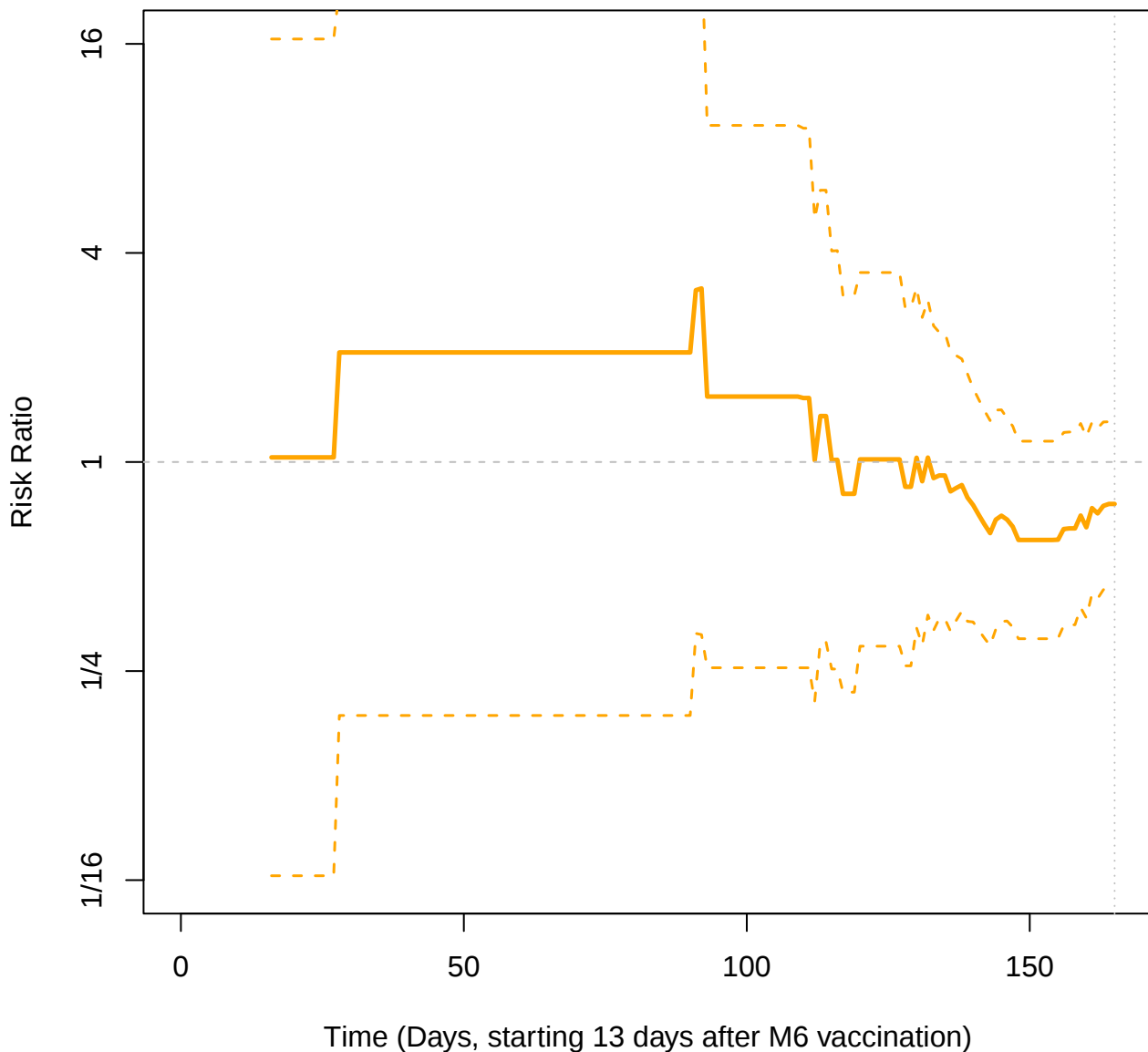
MBoost vs BBoost, FPP, CDC14M18, Primary (PLWH)



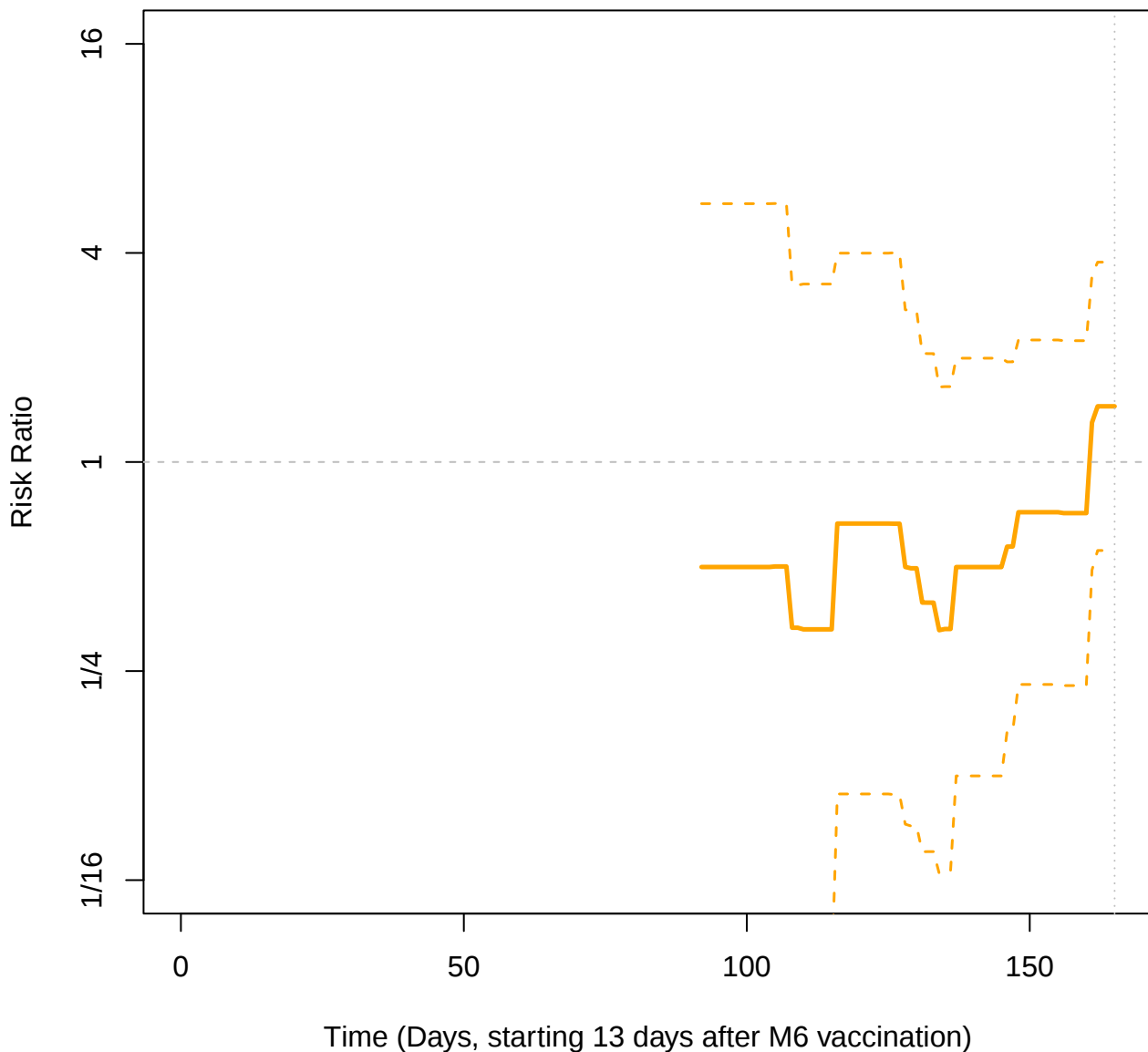
MBoost vs BBoost, FPP, CDC14M18, Primary (PLWoH)



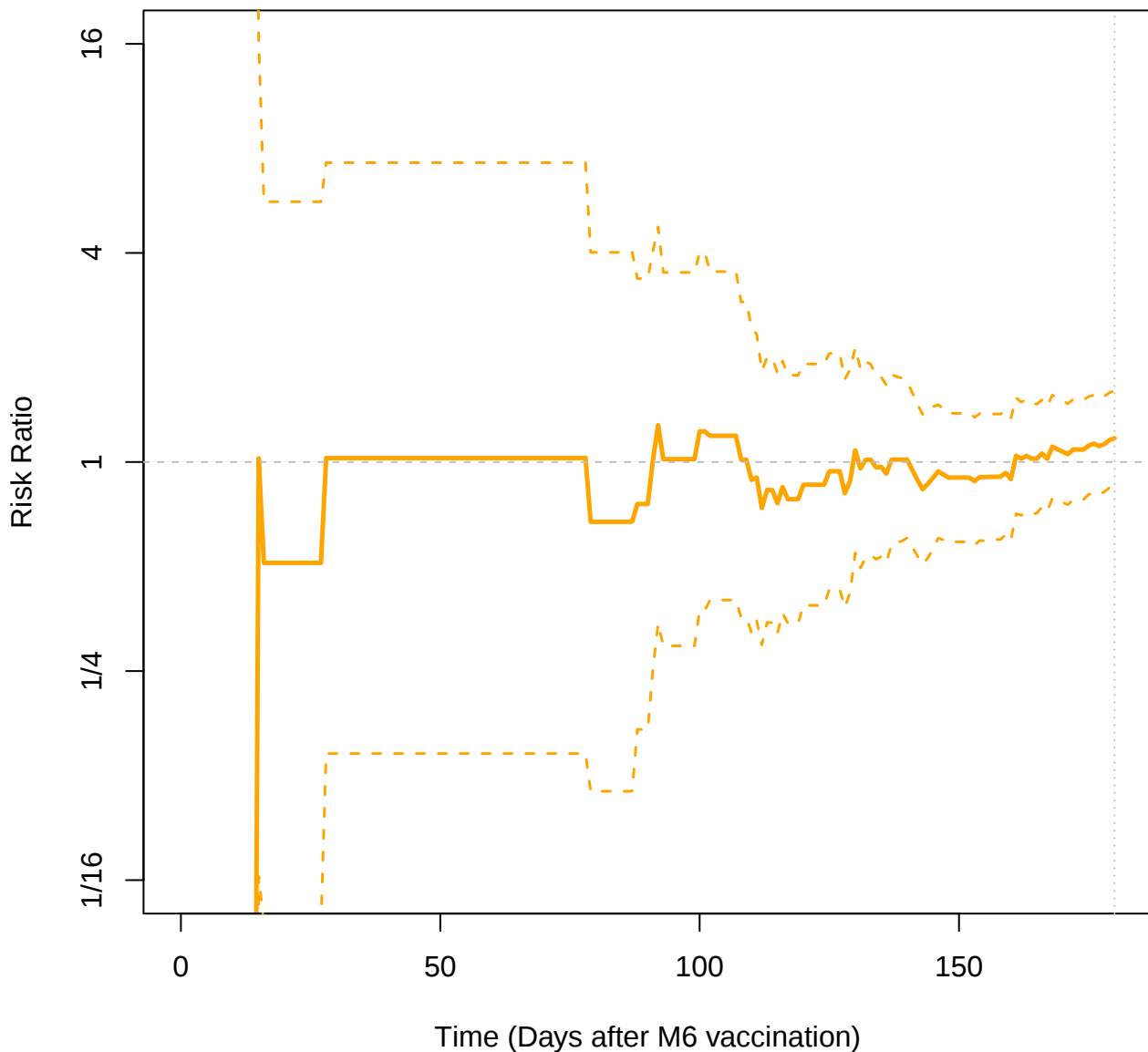
MBoost vs BBoost, FPP, CDC14M18, Sensitivity (PLWH)



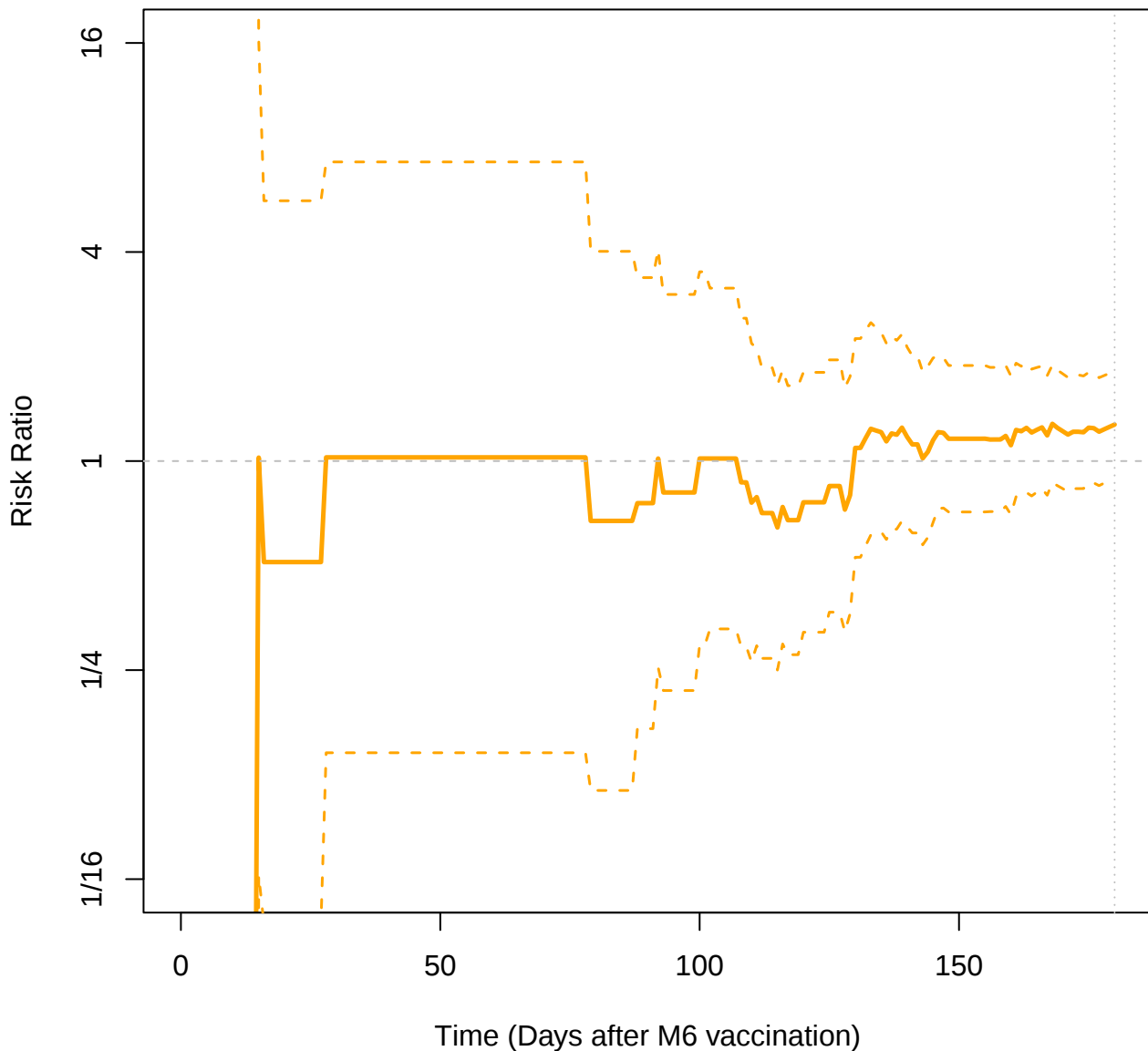
MBoost vs BBoost, FPP, CDC14M18, Sensitivity (PLWoH)



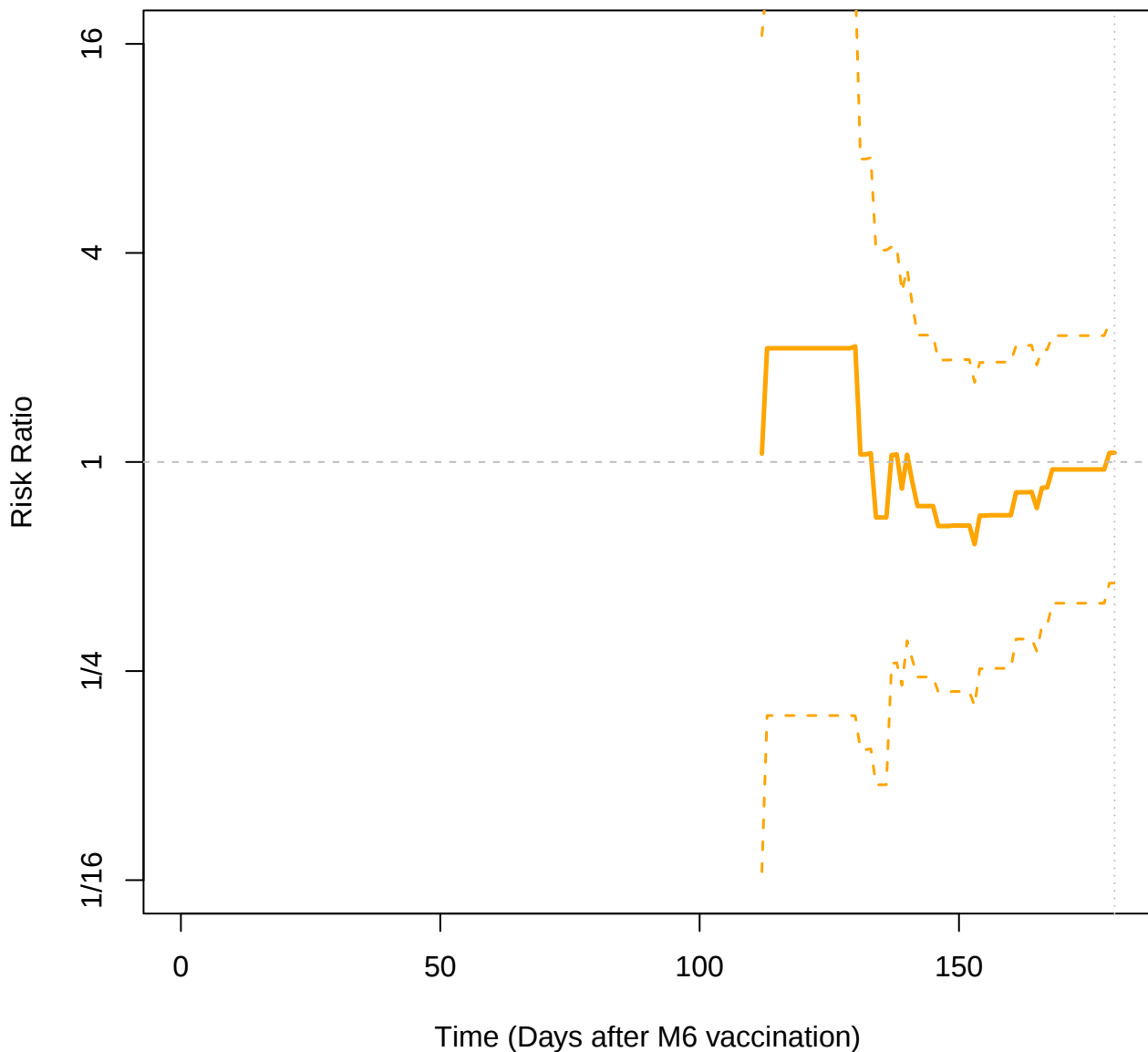
MBoost vs BBoost, RM6, ANYINF, Primary



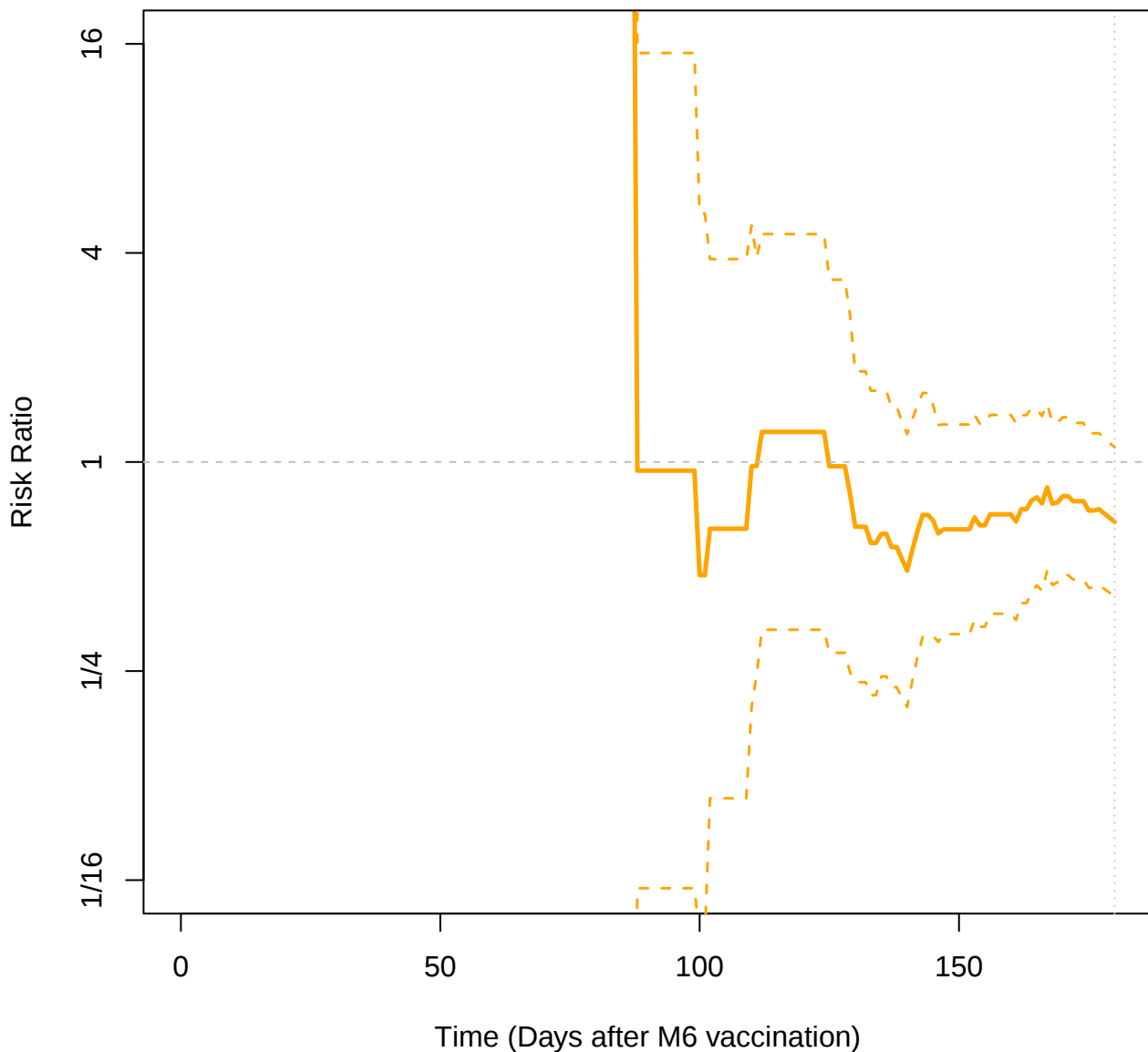
MBoost vs BBoost, RM6, ANYINF, Primary, Hybrid Immunity



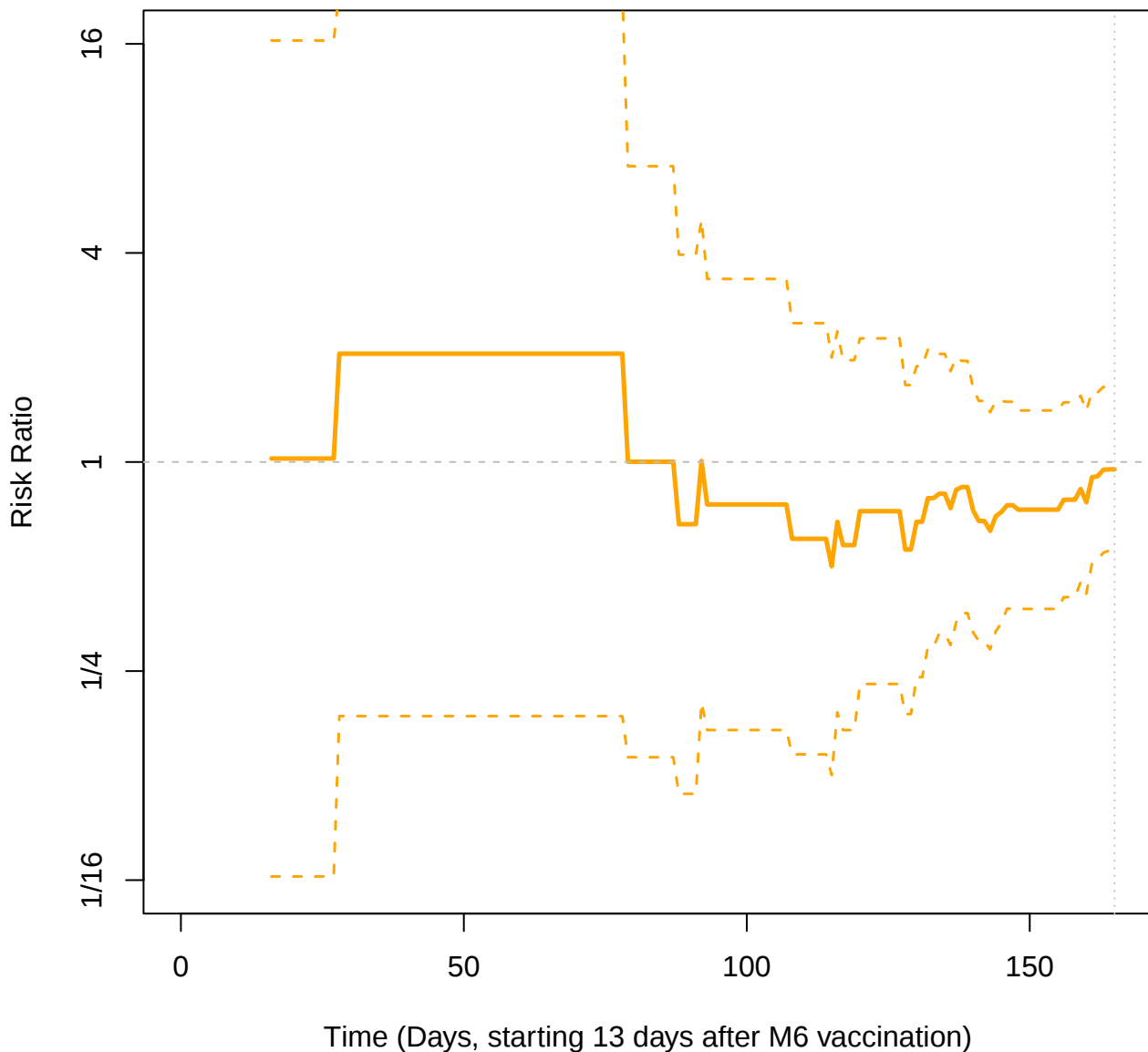
MBoost vs BBoost, RM6, ANYINF, Primary, Vaccine Immunity



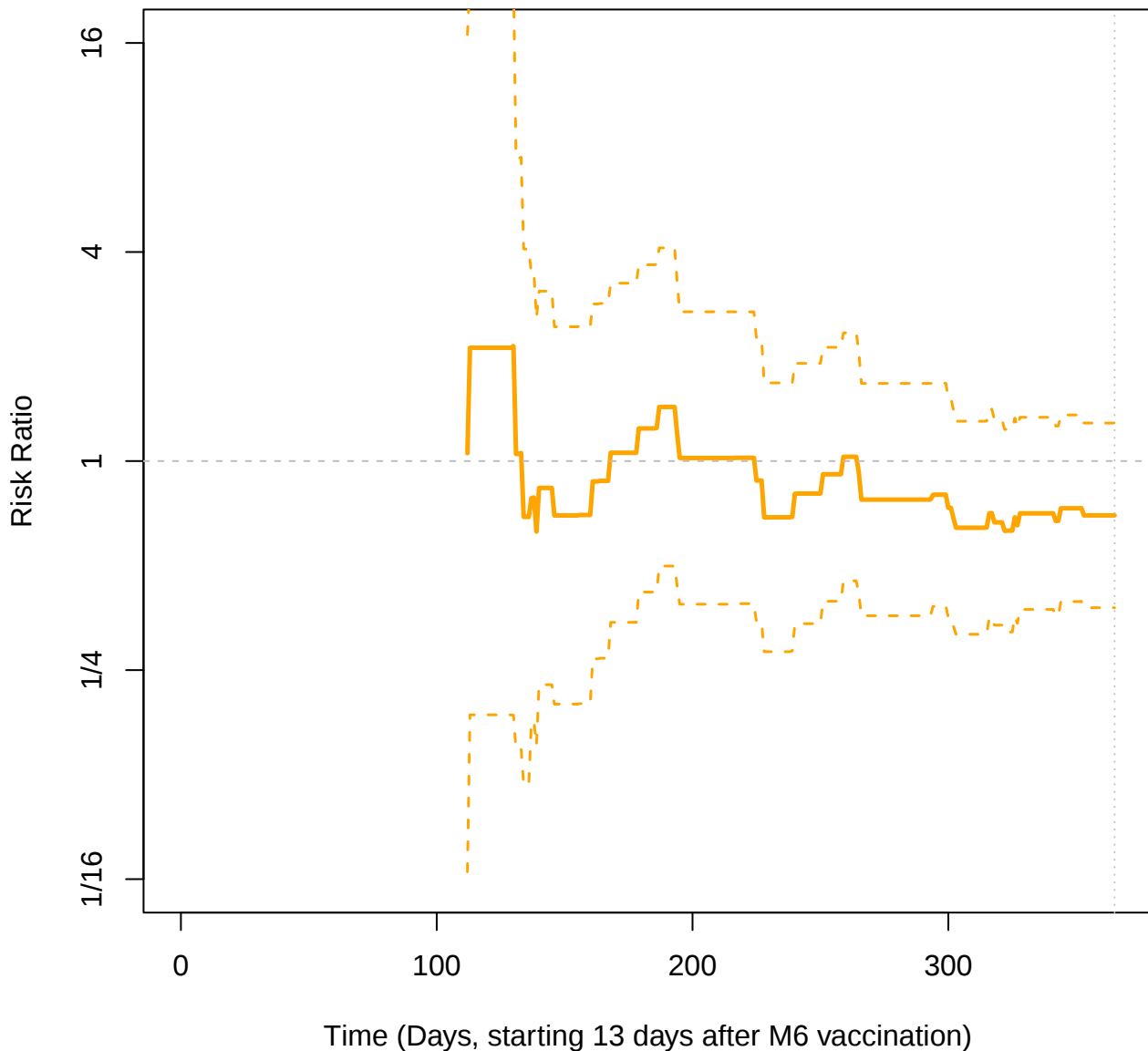
MBoost vs BBoost, RM6, ASYMINF, Primary



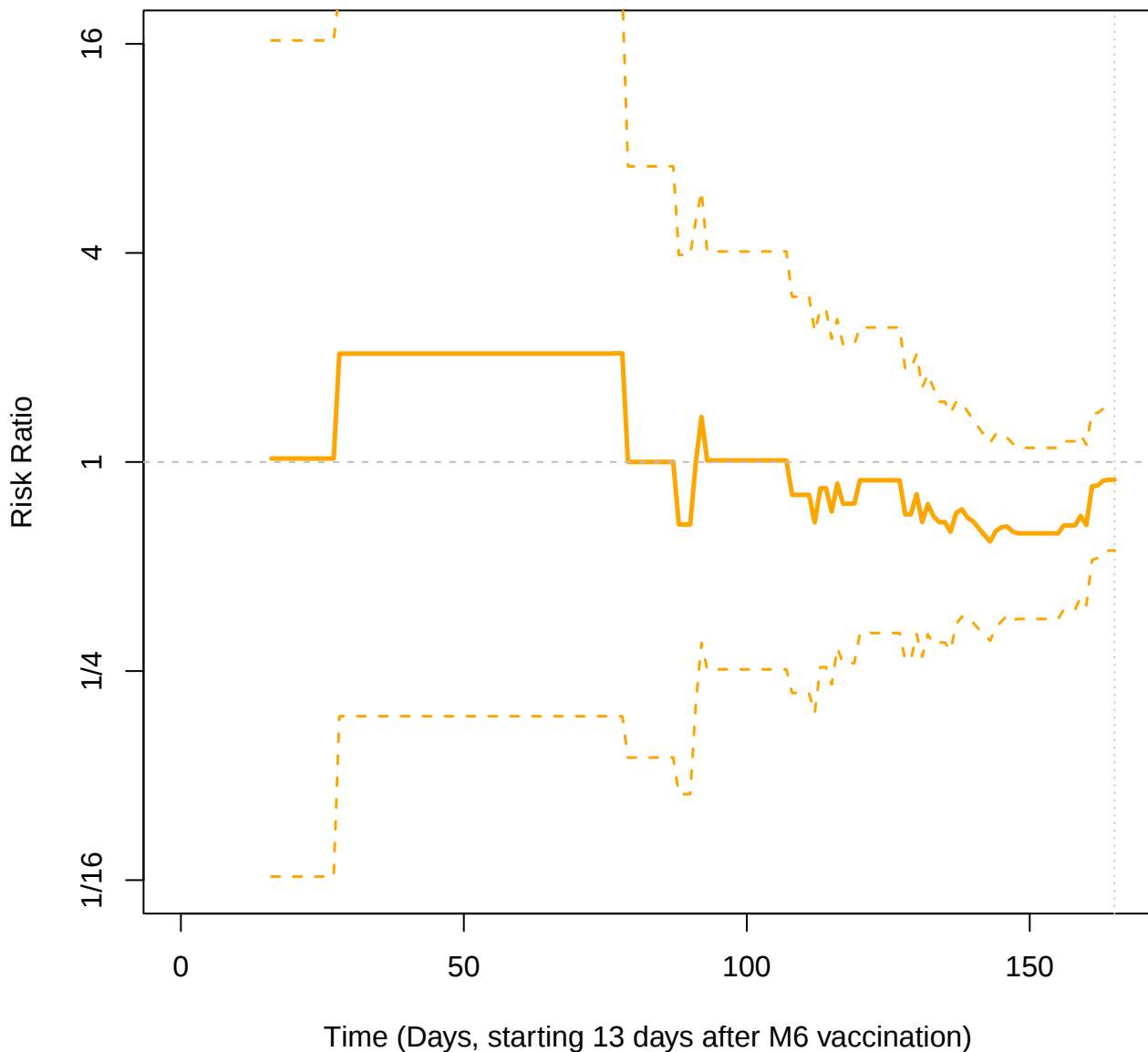
MBoost vs BBoost, RM6, CD14M18, Primary, Hybrid Immunity



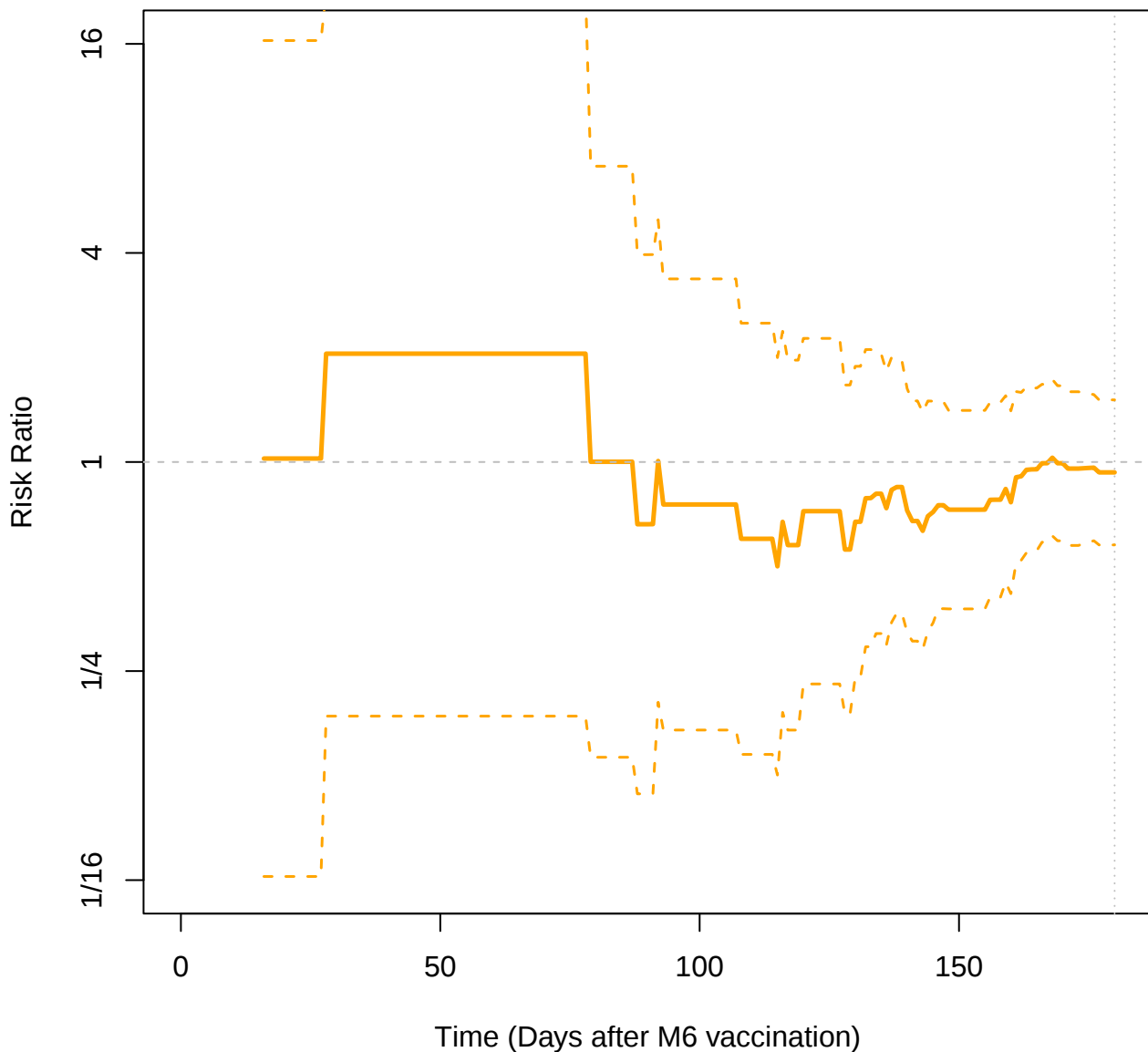
MBoost vs BBoost, RM6, CD14M18, Primary, Vaccine Immunity



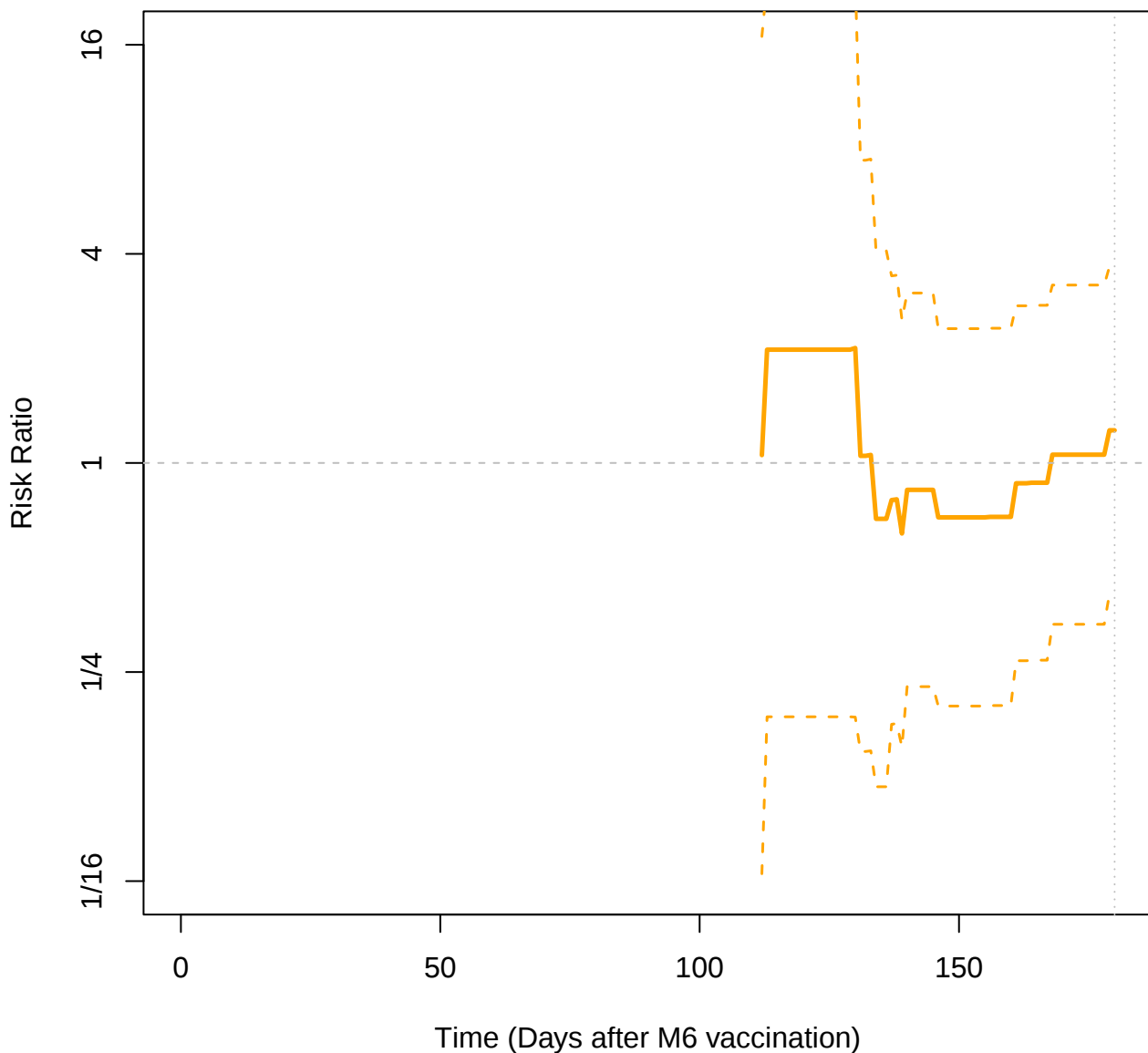
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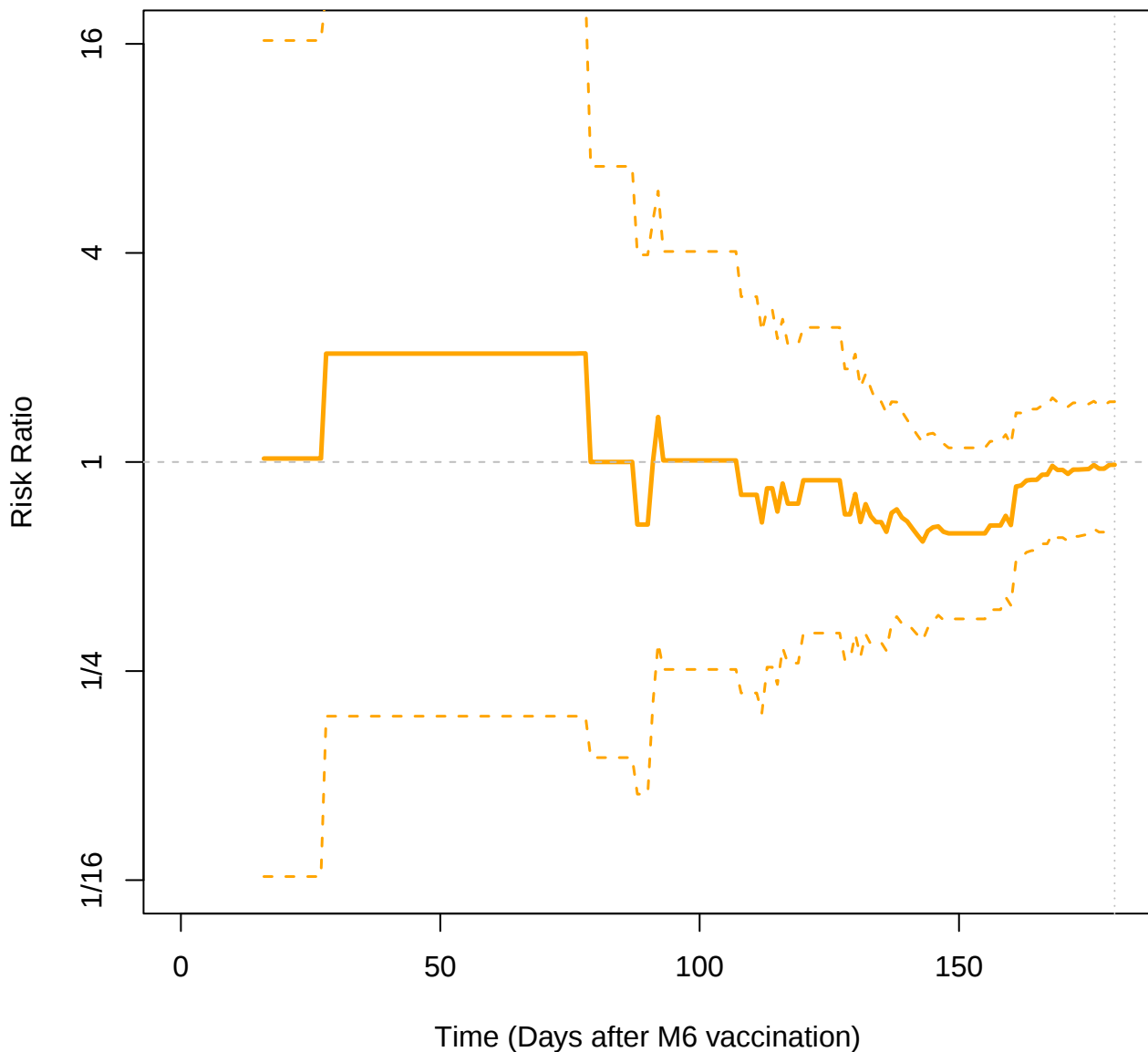
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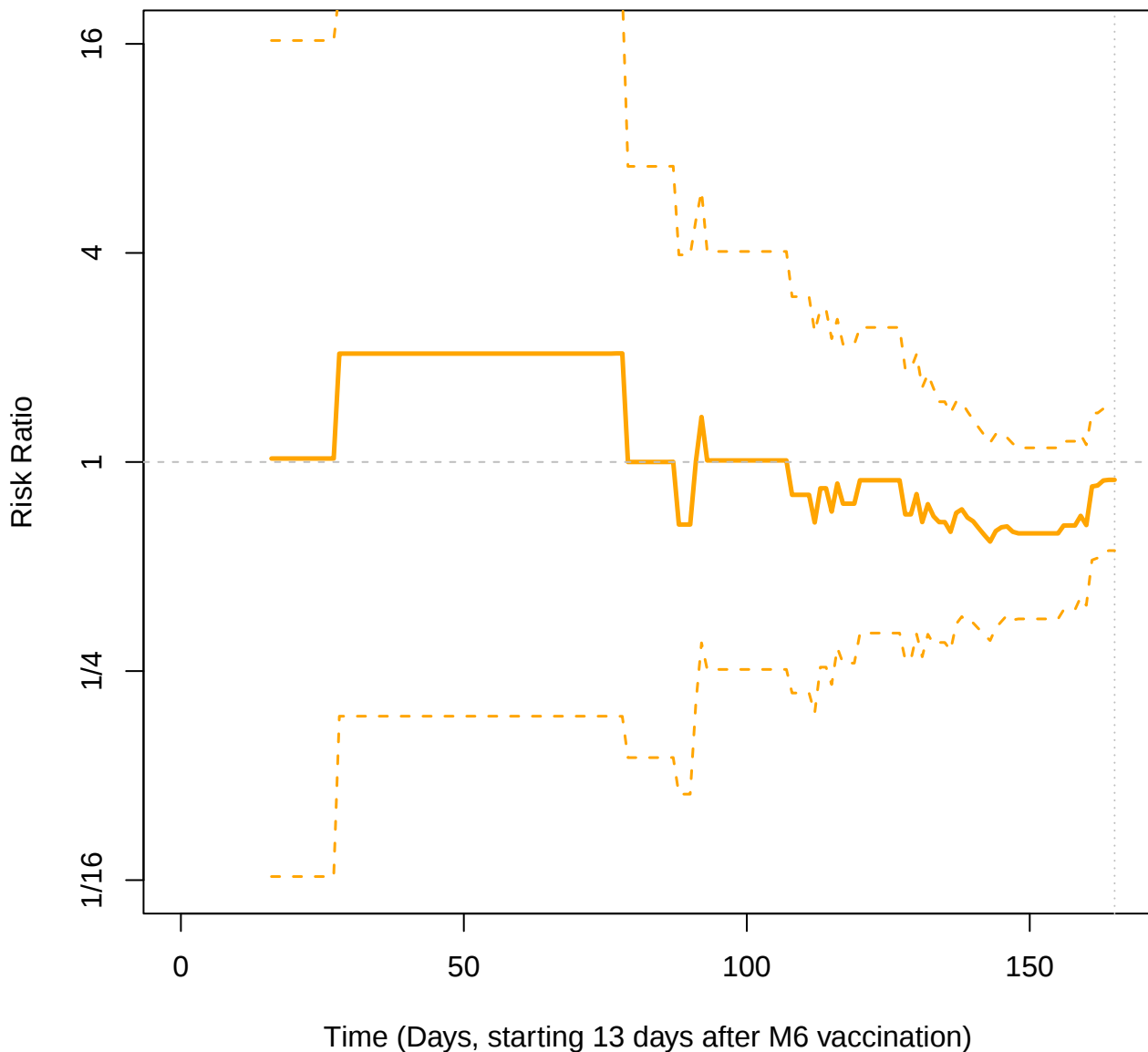
MBoost vs BBoost, RM6, CD1M18, Primary, Vaccine Immunity



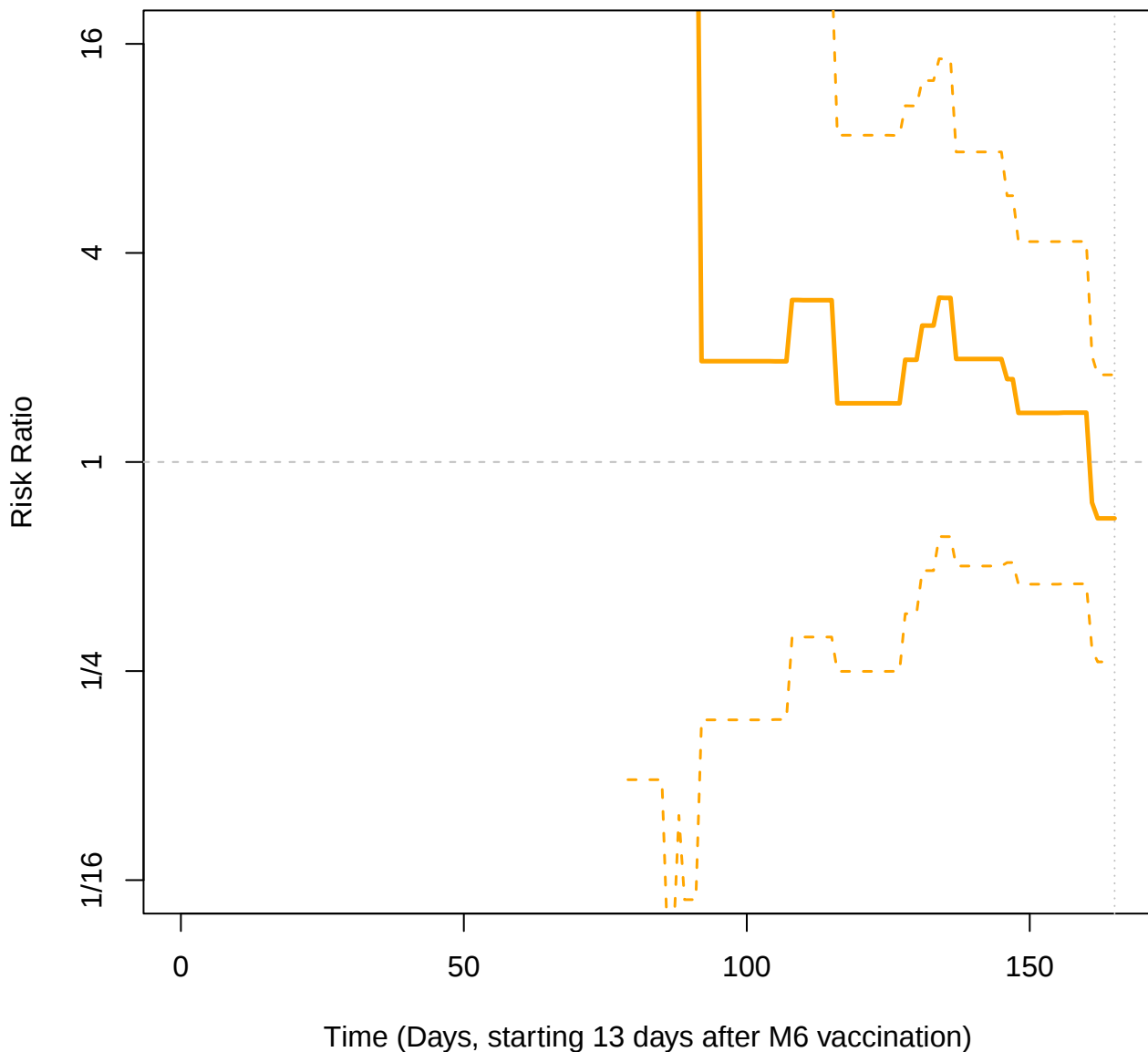
MBoost vs BBoost, RM6, CD1M18, Primary



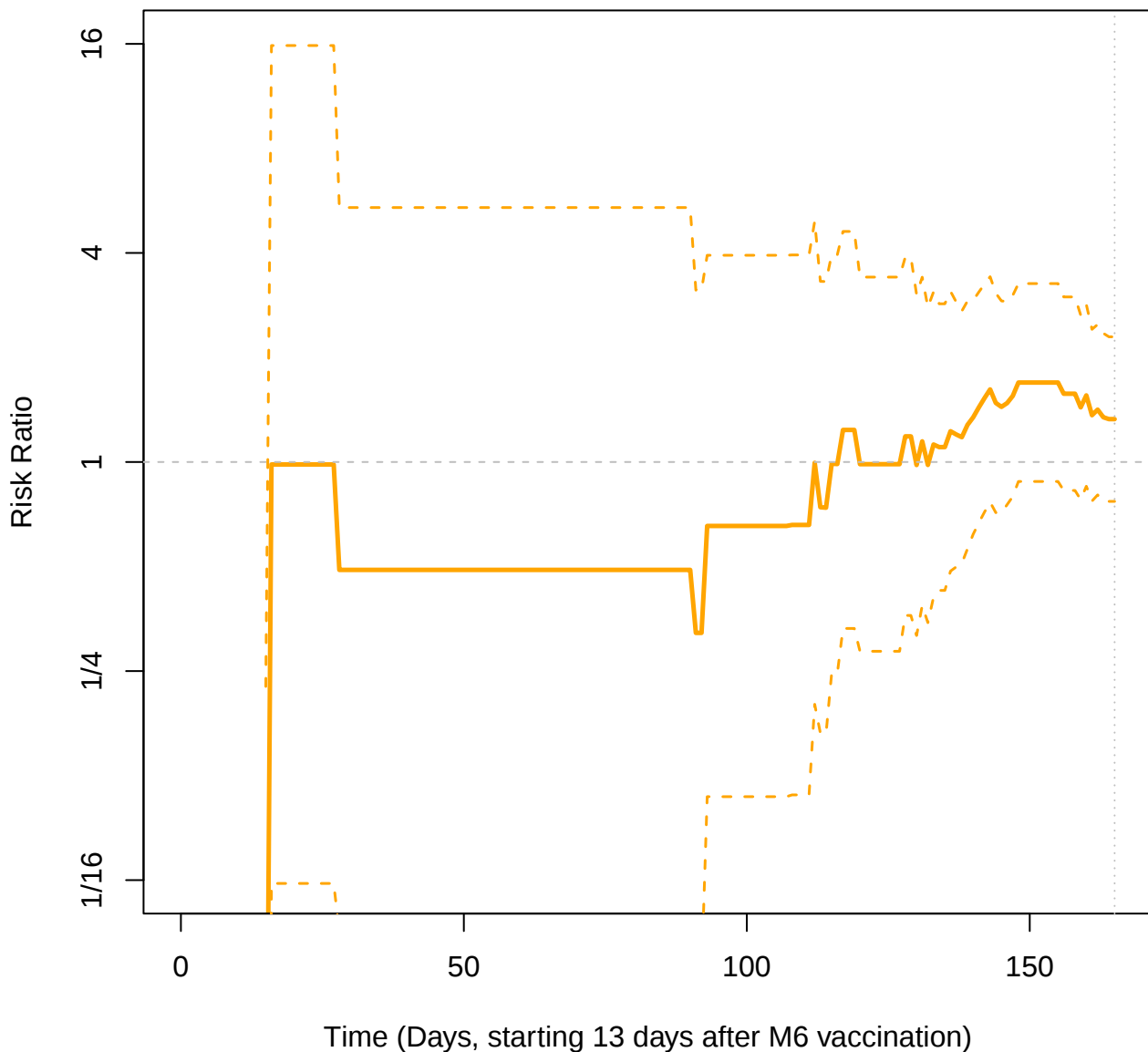
MBoost vs BBoost, RM6, CDC14M12, Primary



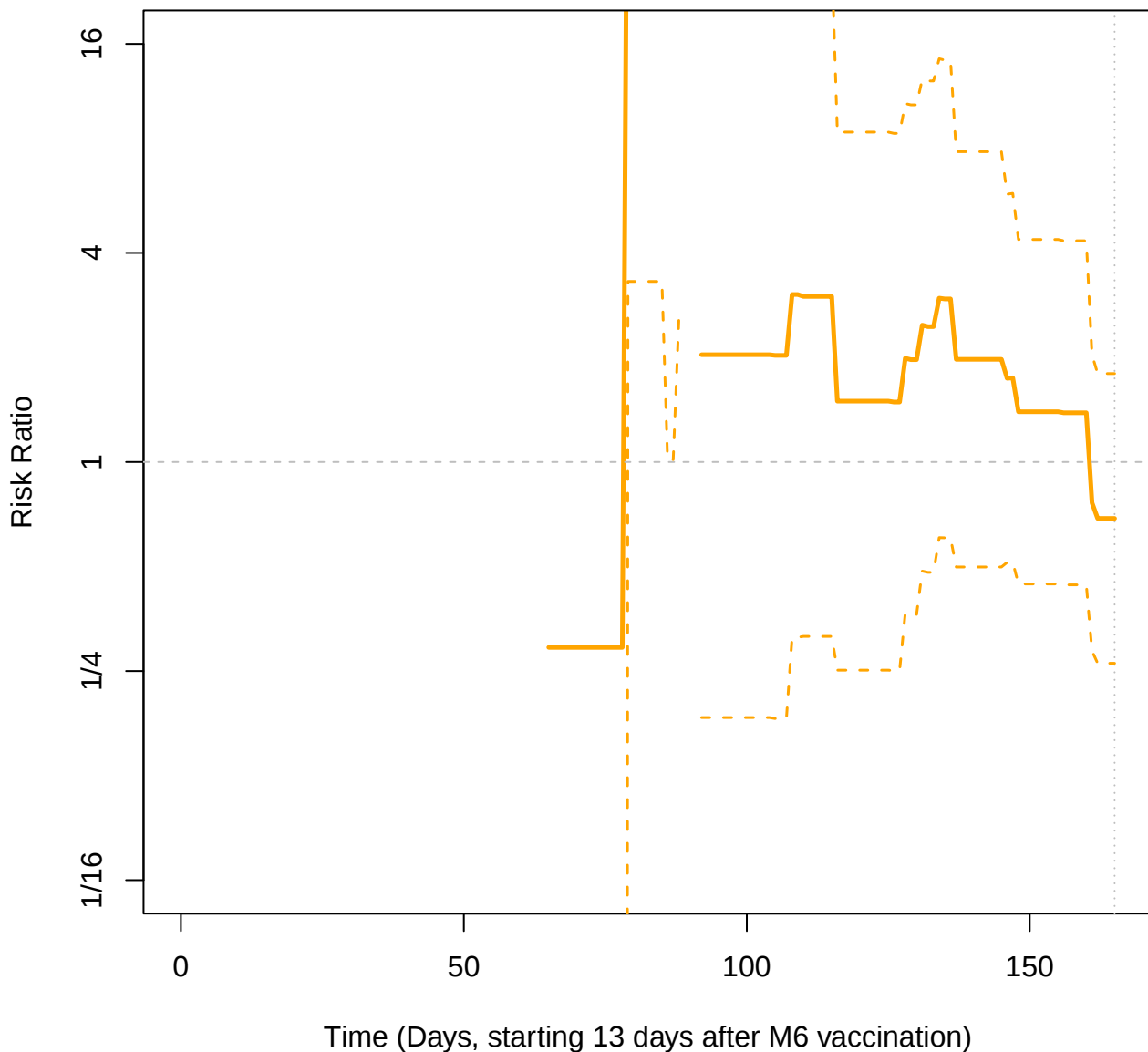
MBoost vs BBoost, RM6, CDC14M12, Primary (PLWoH)



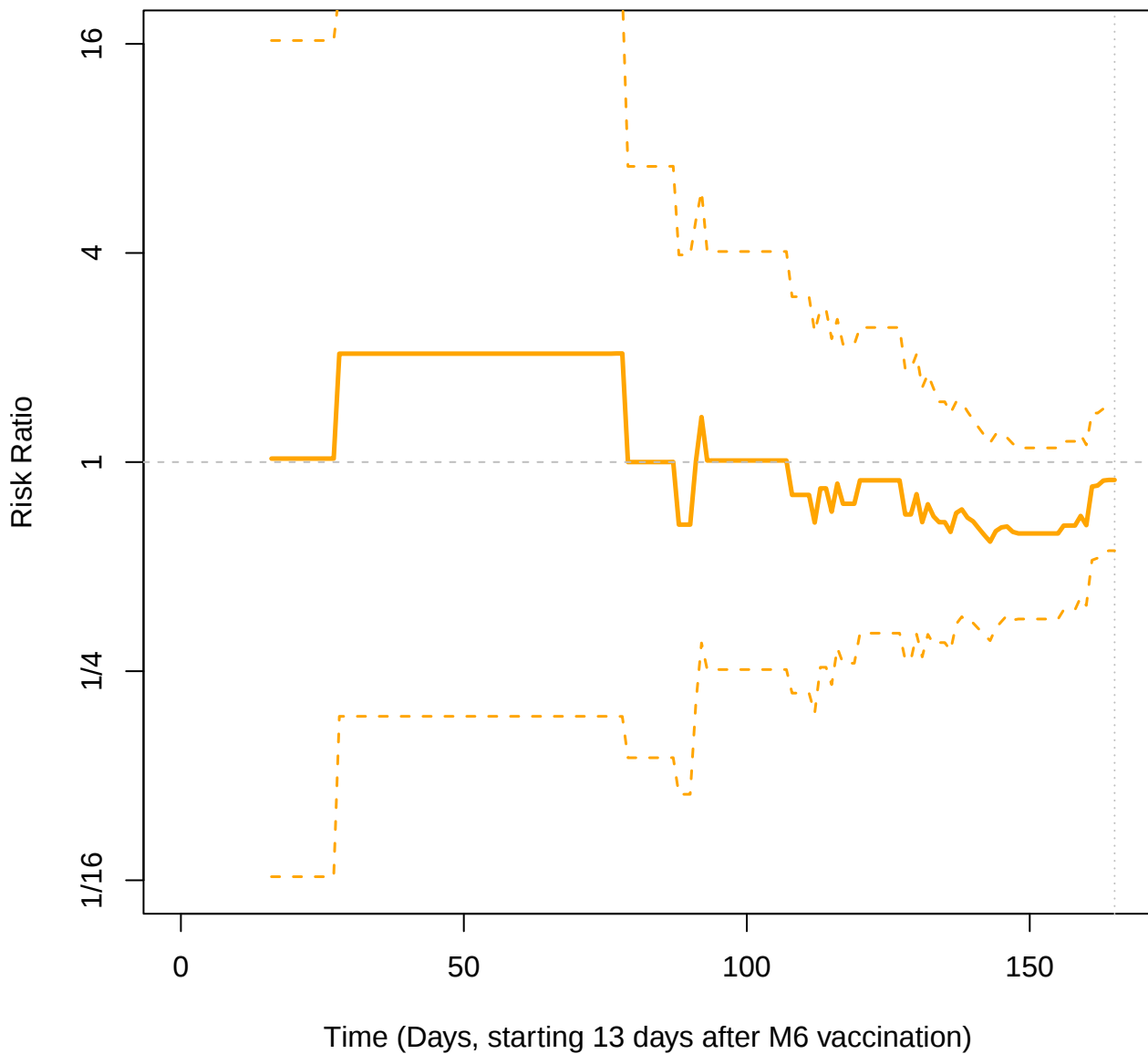
MBoost vs BBoost, RM6, CDC14M12, Sensitivity (PLWH)



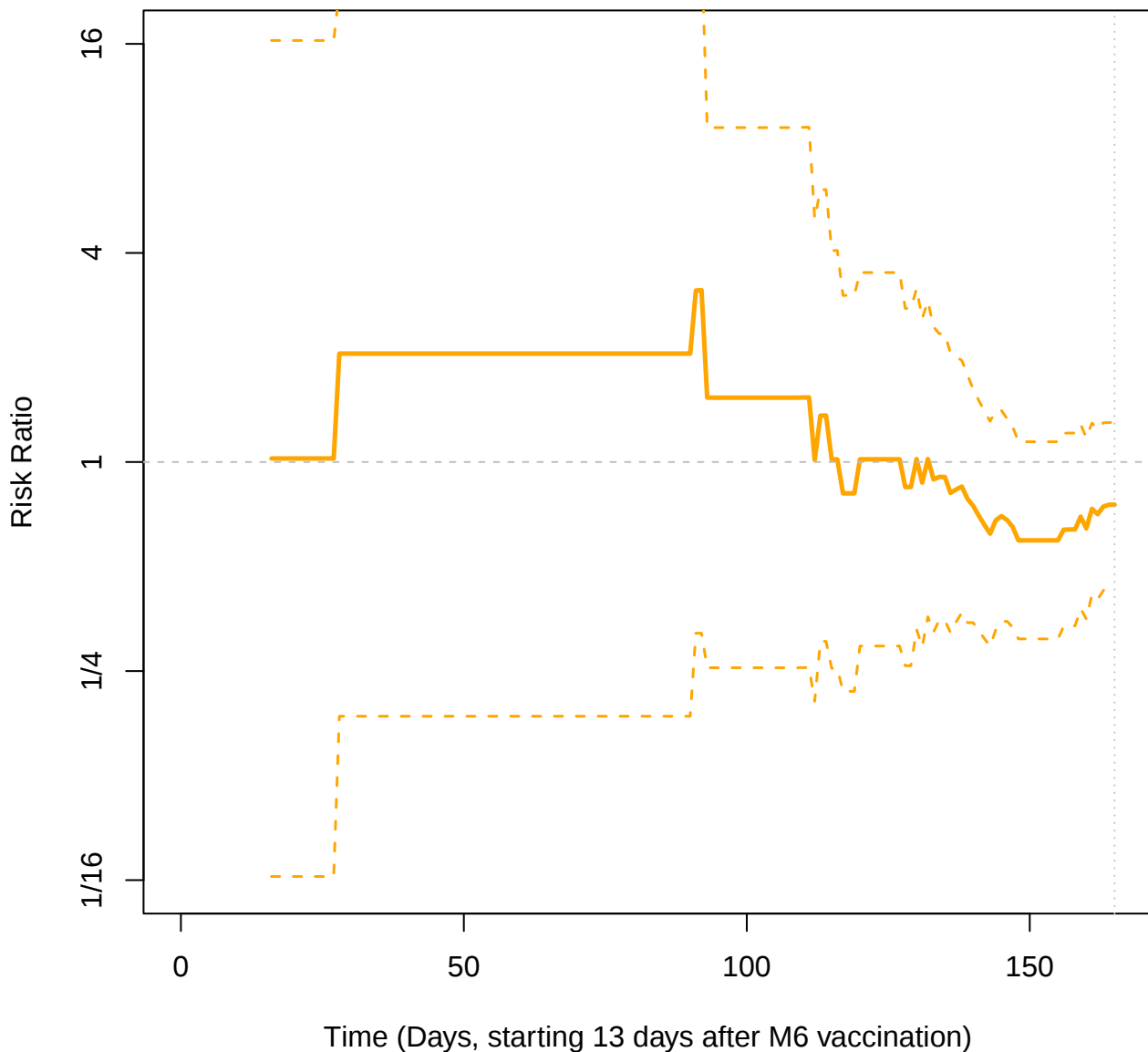
MBoost vs BBoost, RM6, CDC14M12, Sensitivity (PLWoH)



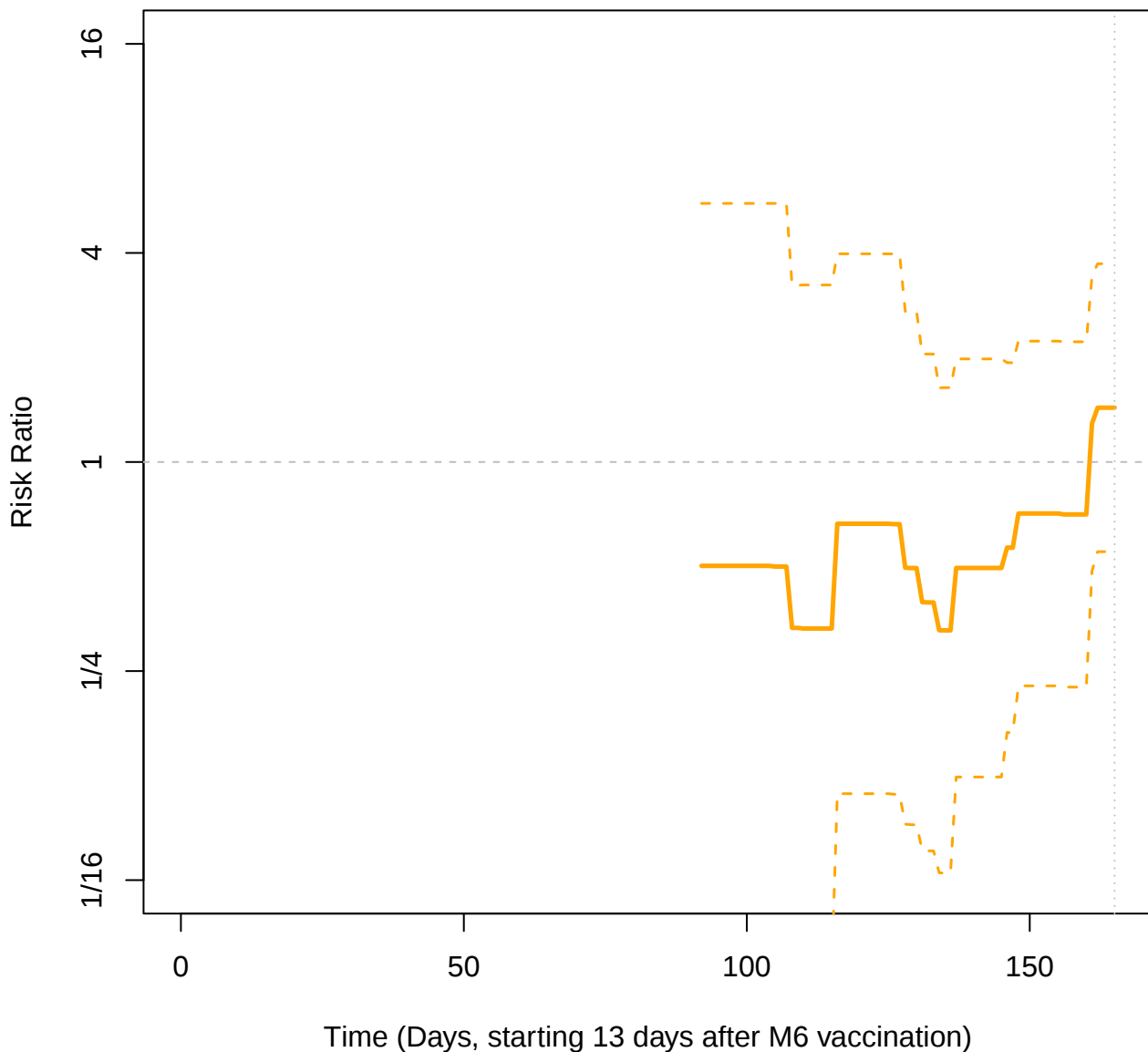
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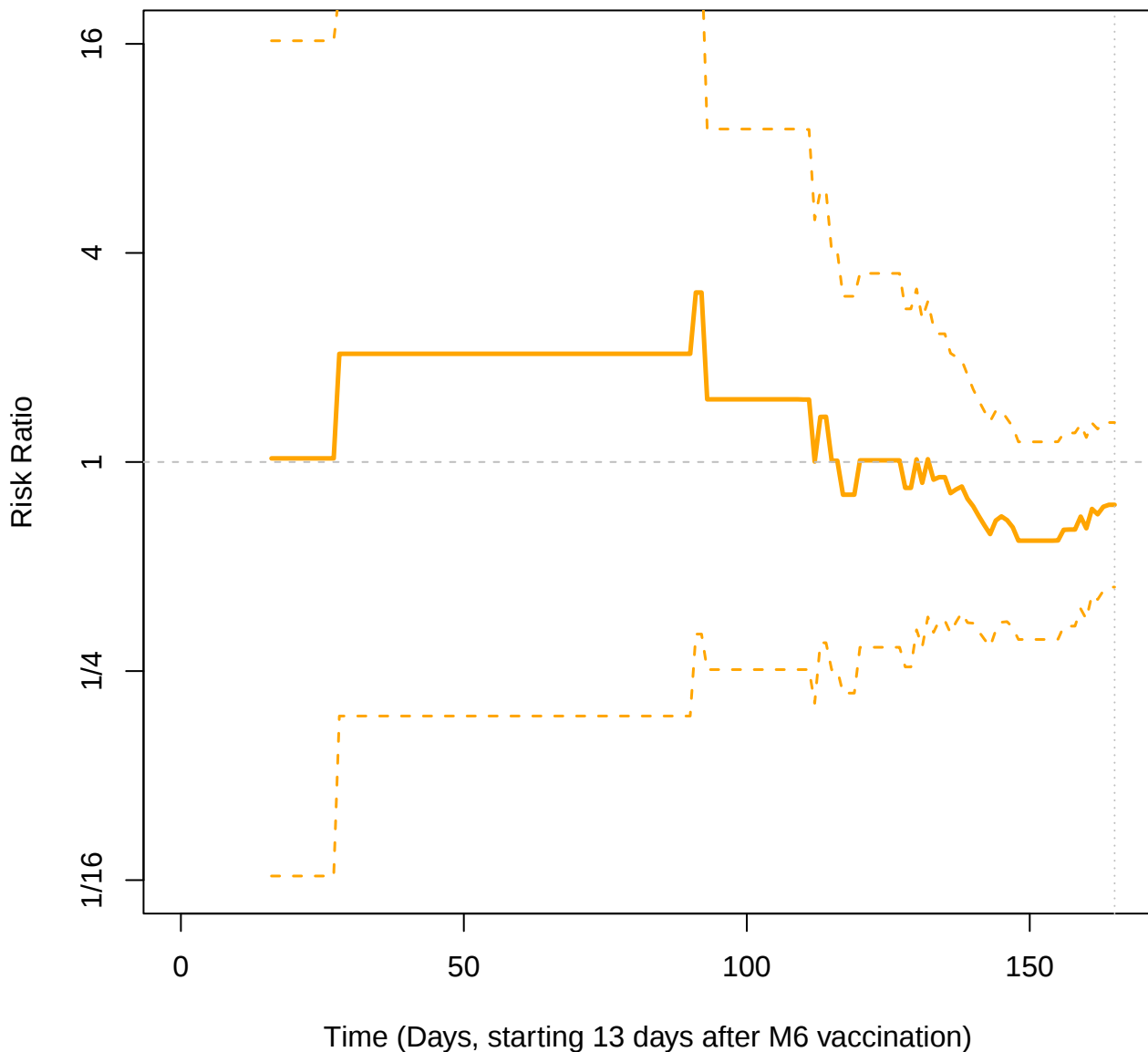
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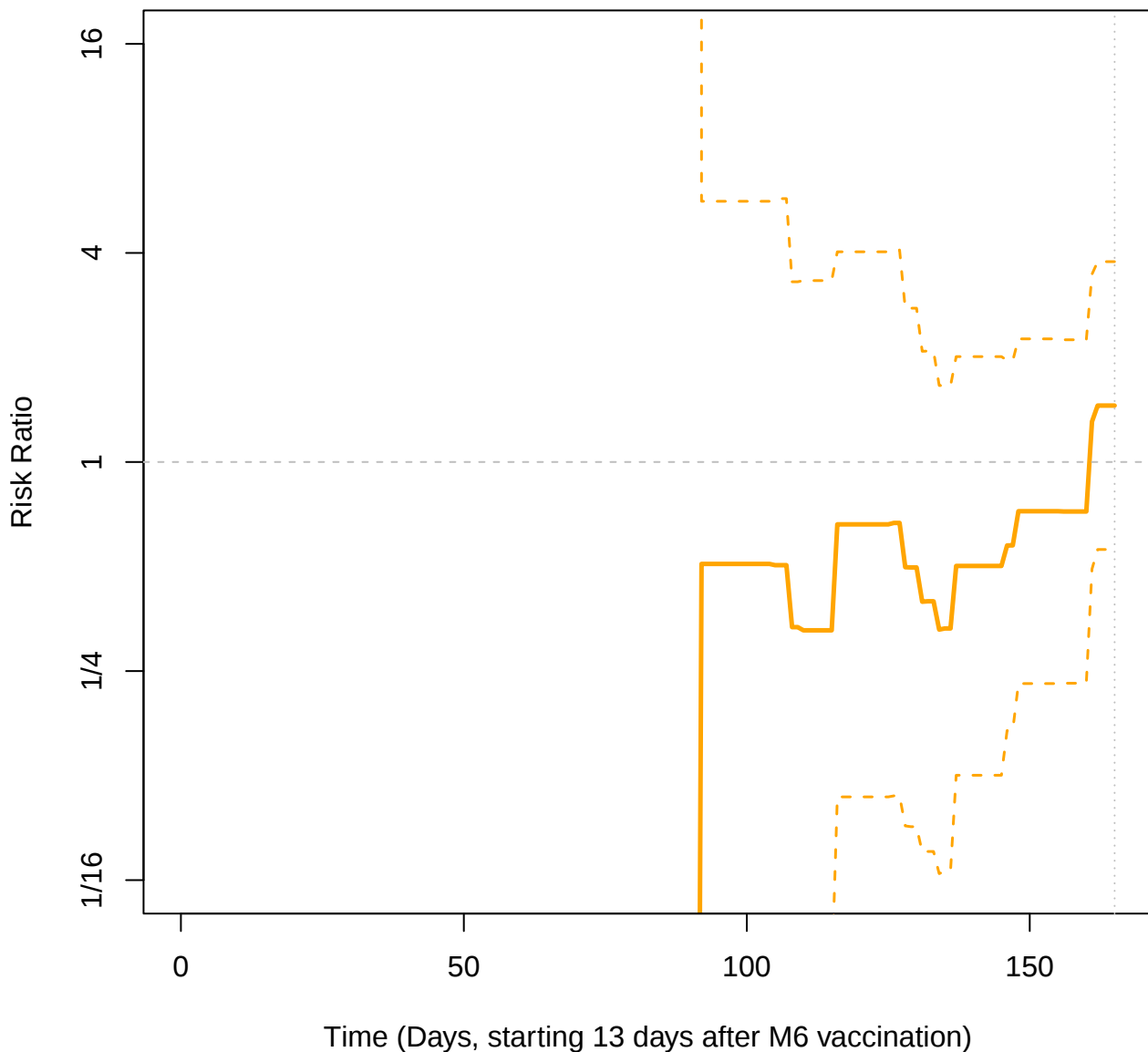
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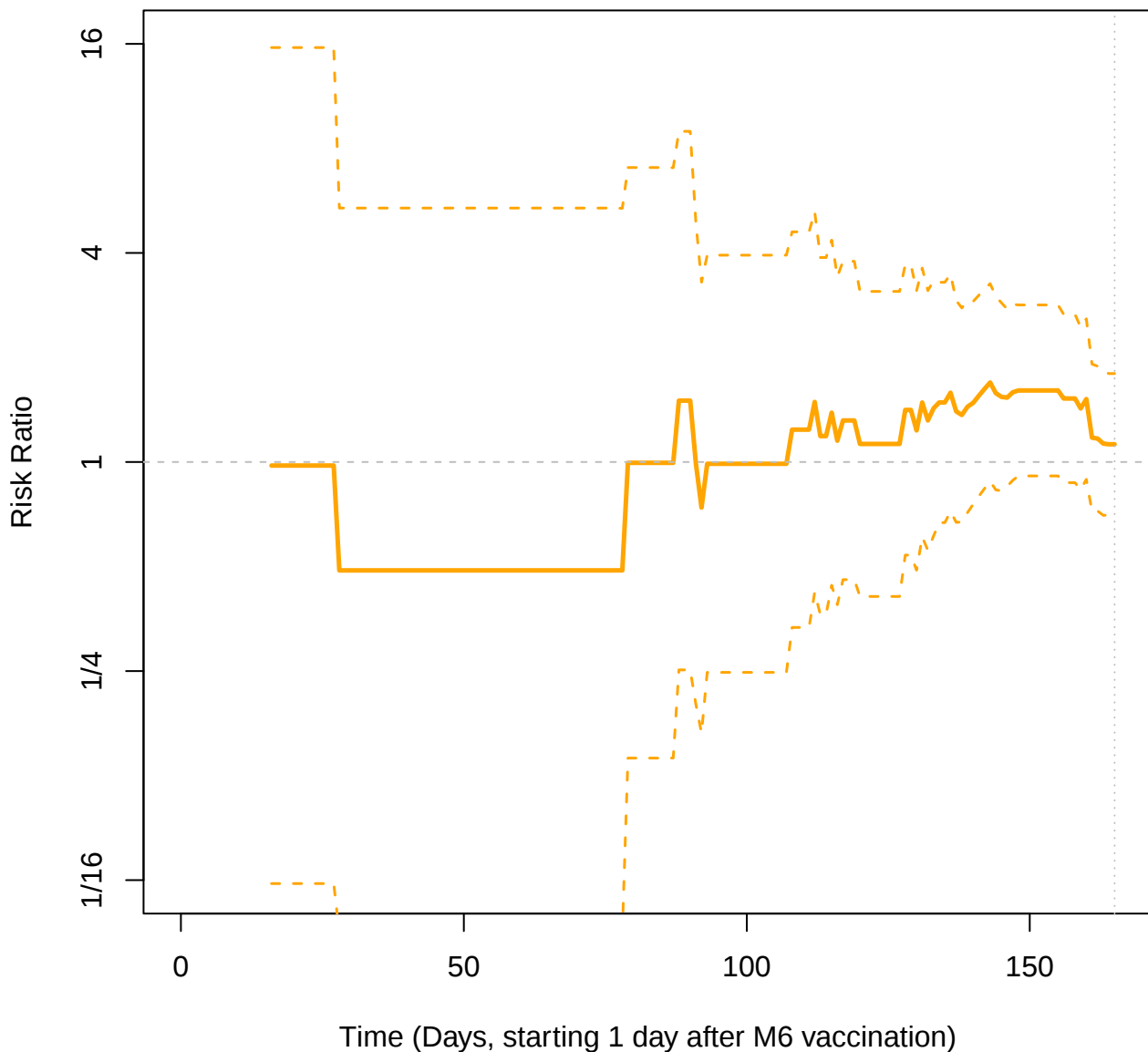
MBoost vs BBoost, RM6, CDC14M18, Sensitivity (PLWH)



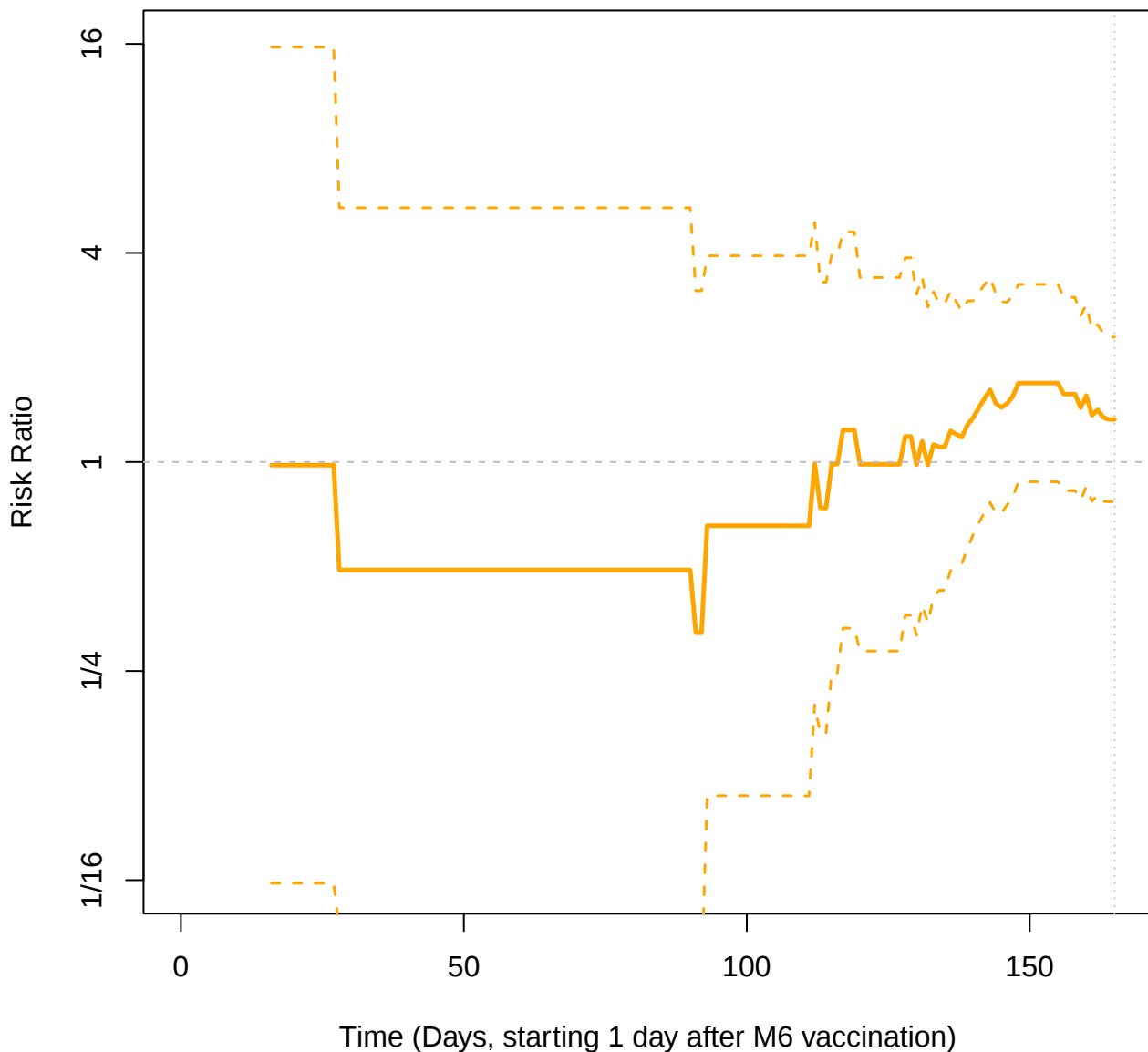
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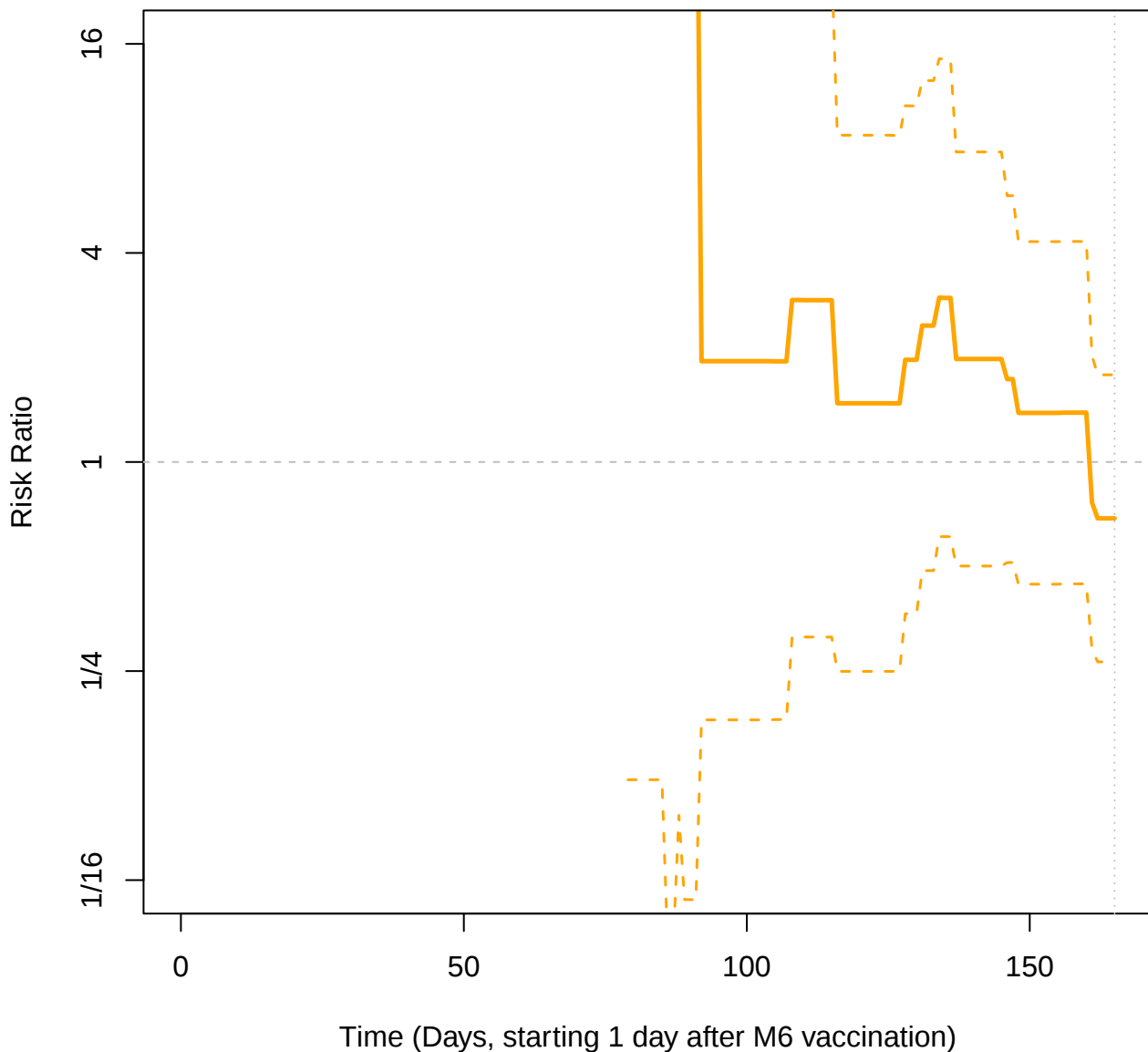
MBoost vs BBoost, RM6, CDC1M12, Primary



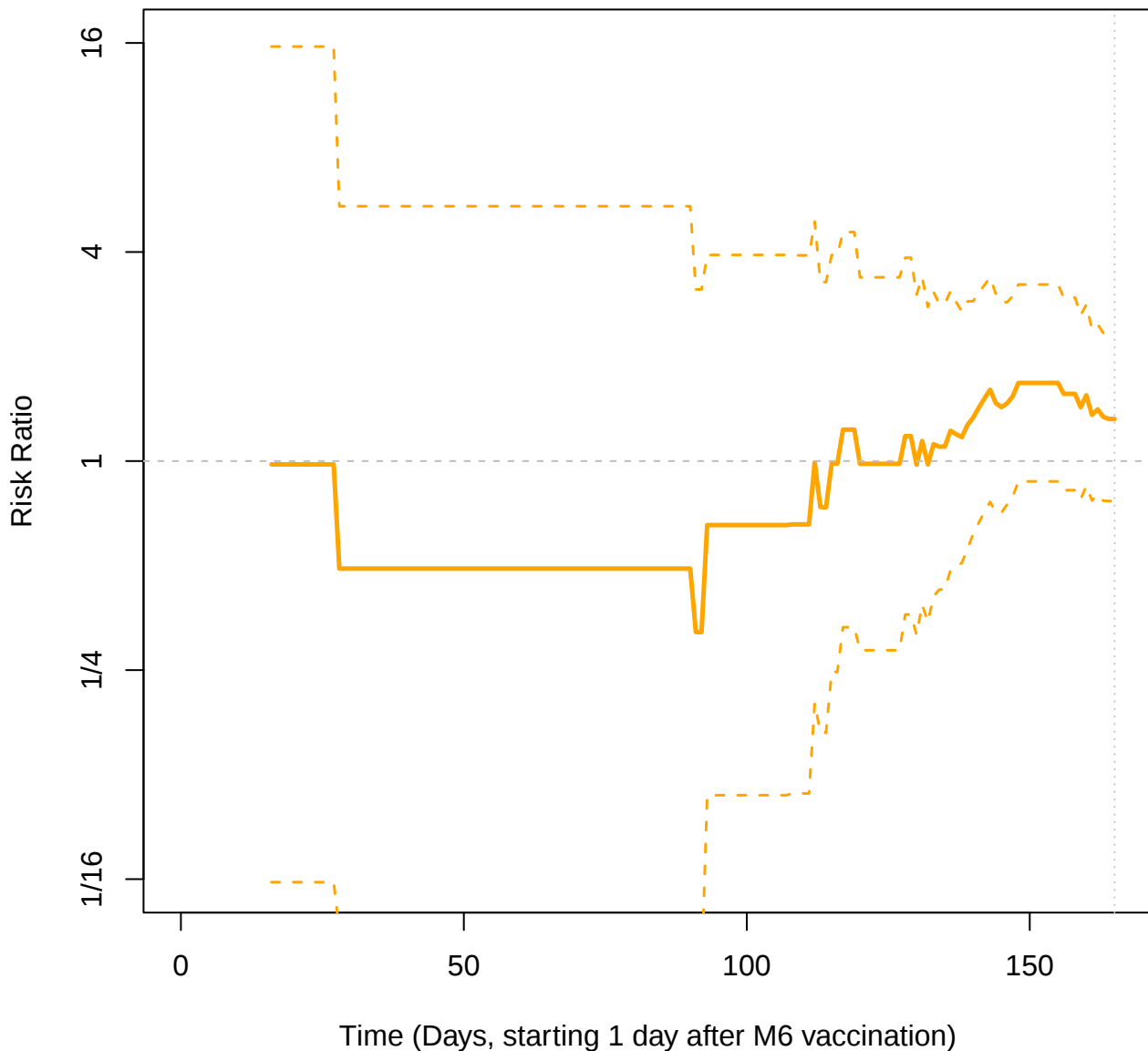
MBoost vs BBoost, RM6, CDC1M12, Primary (PLWH)



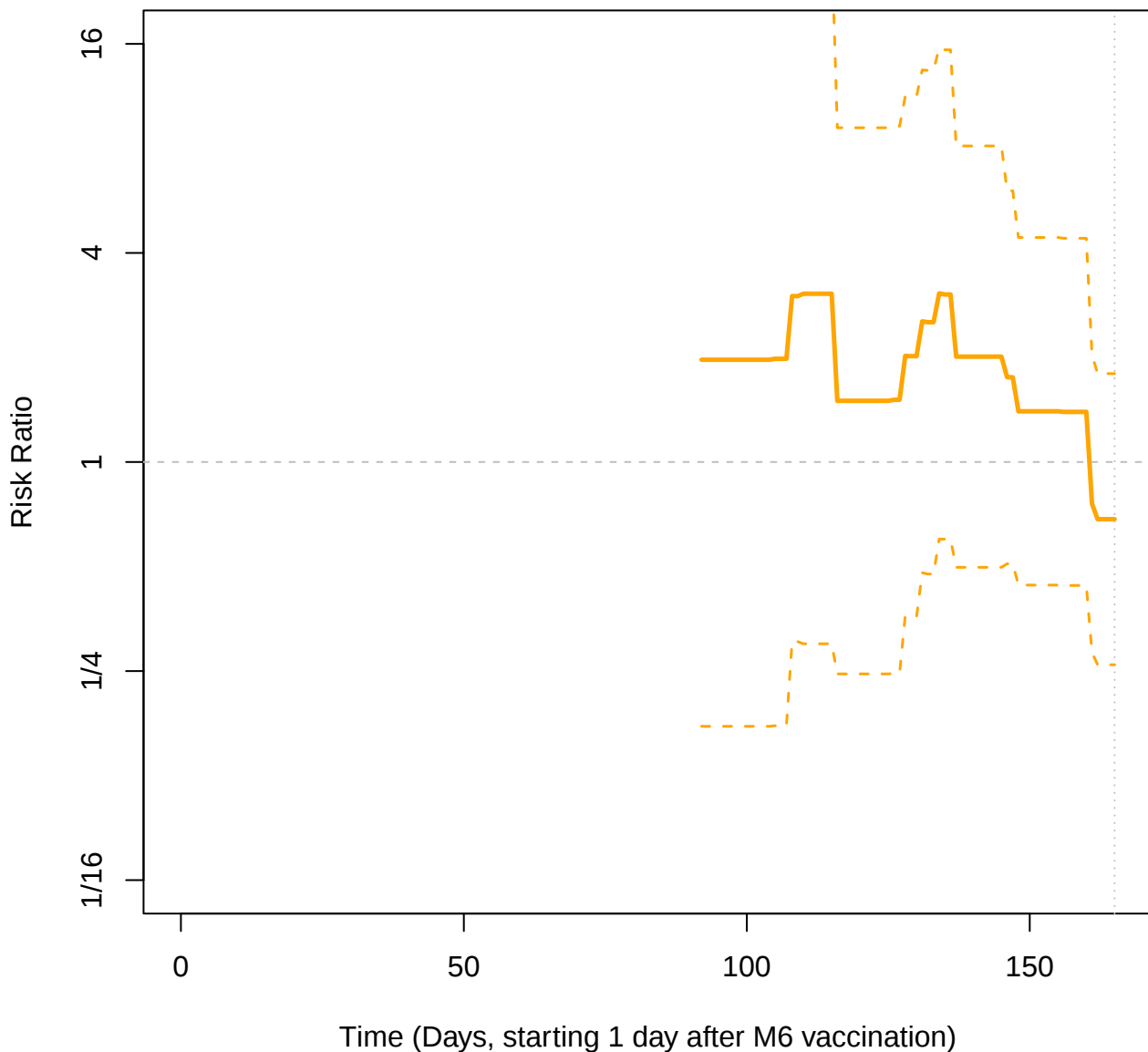
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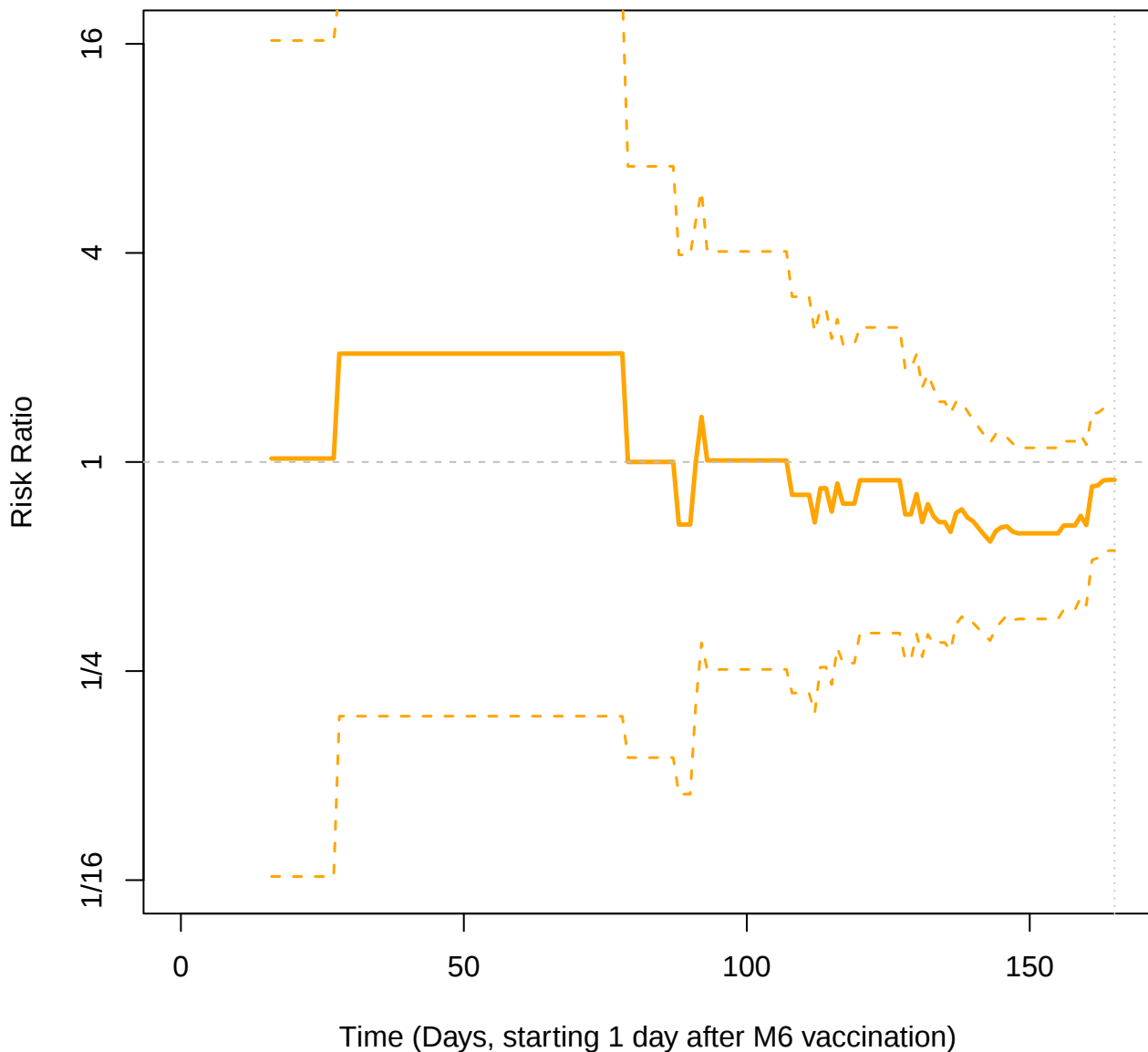
MBoost vs BBoost, RM6, CDC1M12, Sensitivity (PLWH)



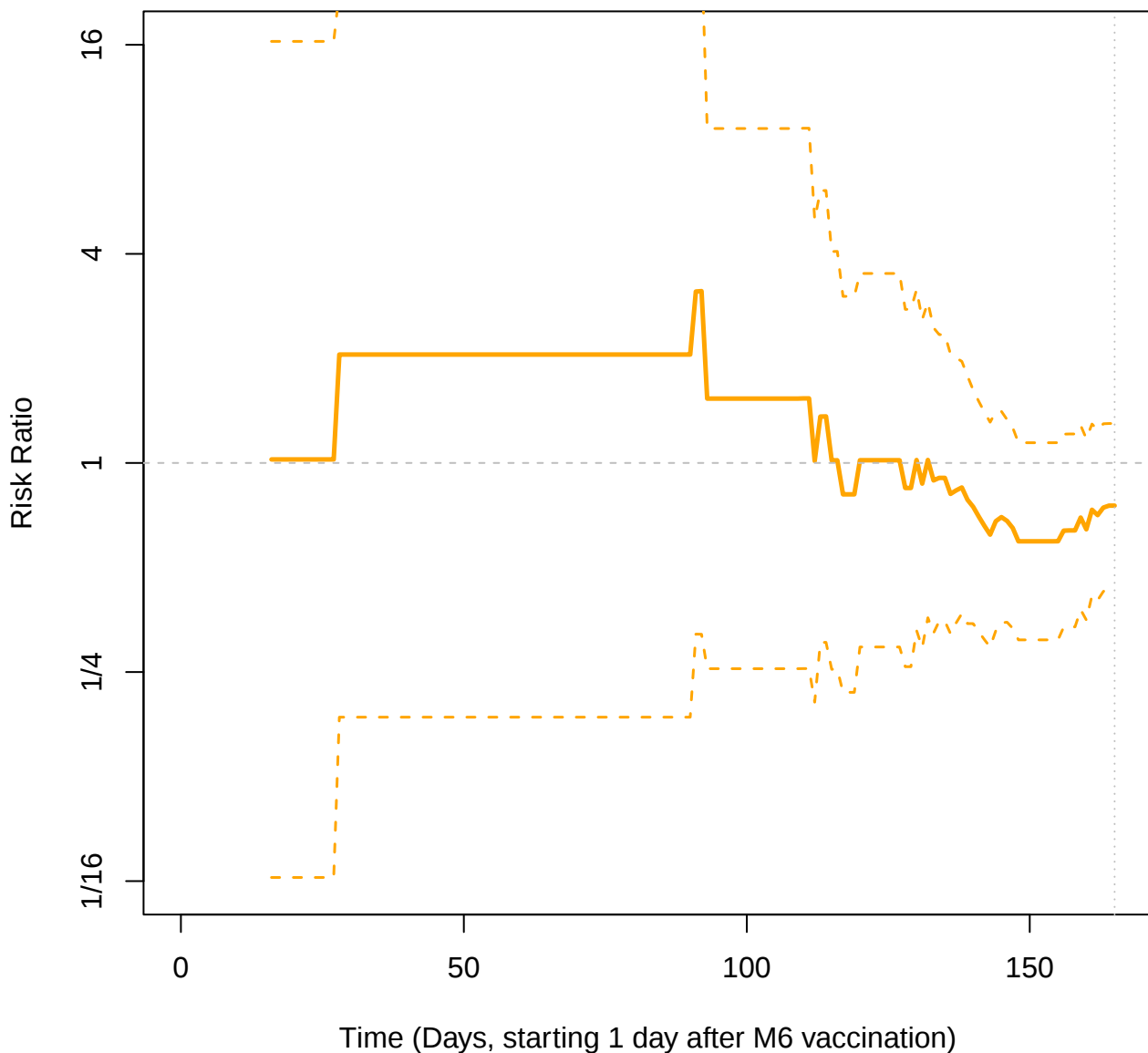
MBoost vs BBoost, RM6, CDC1M12, Sensitivity (PLWoH)



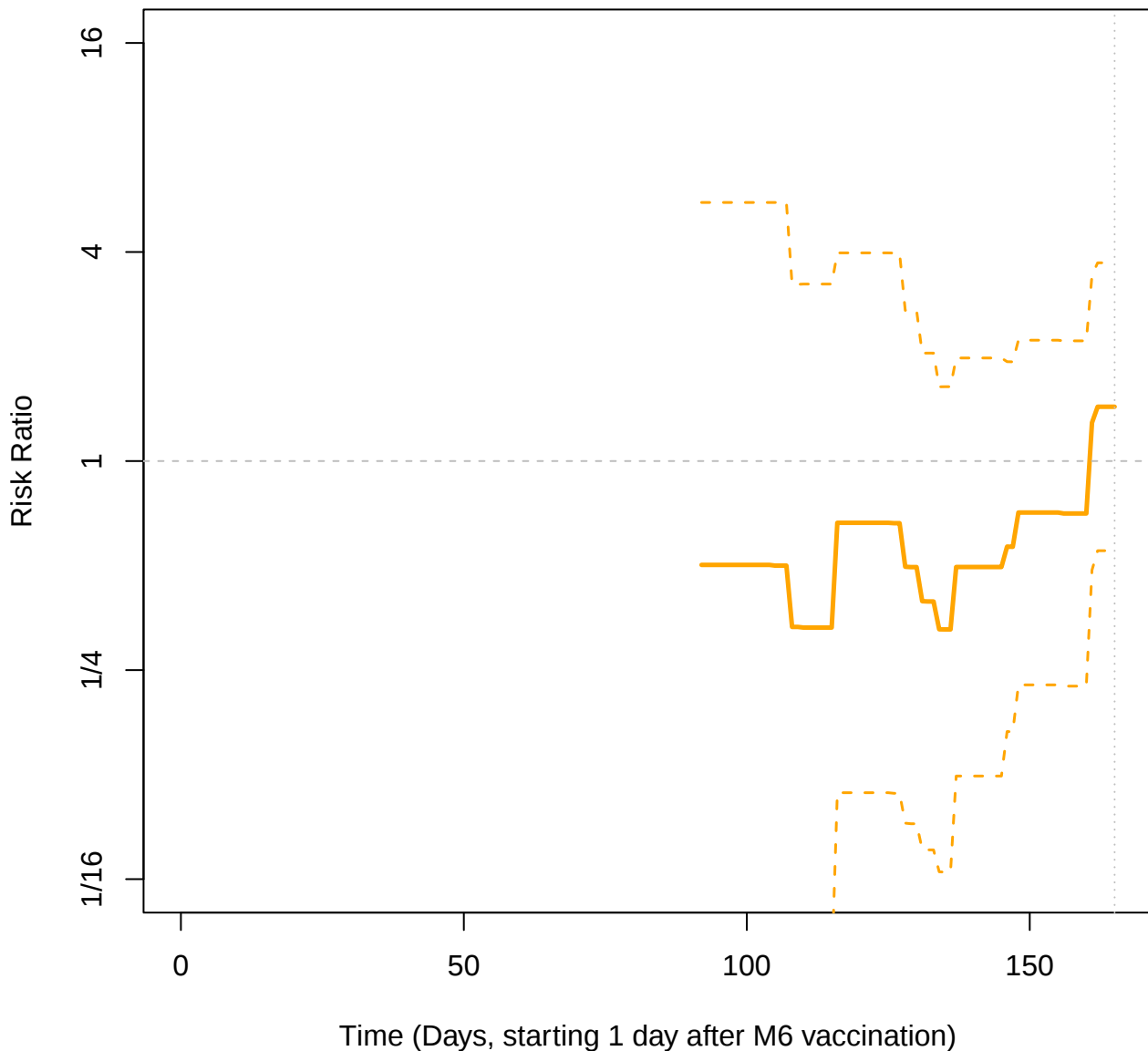
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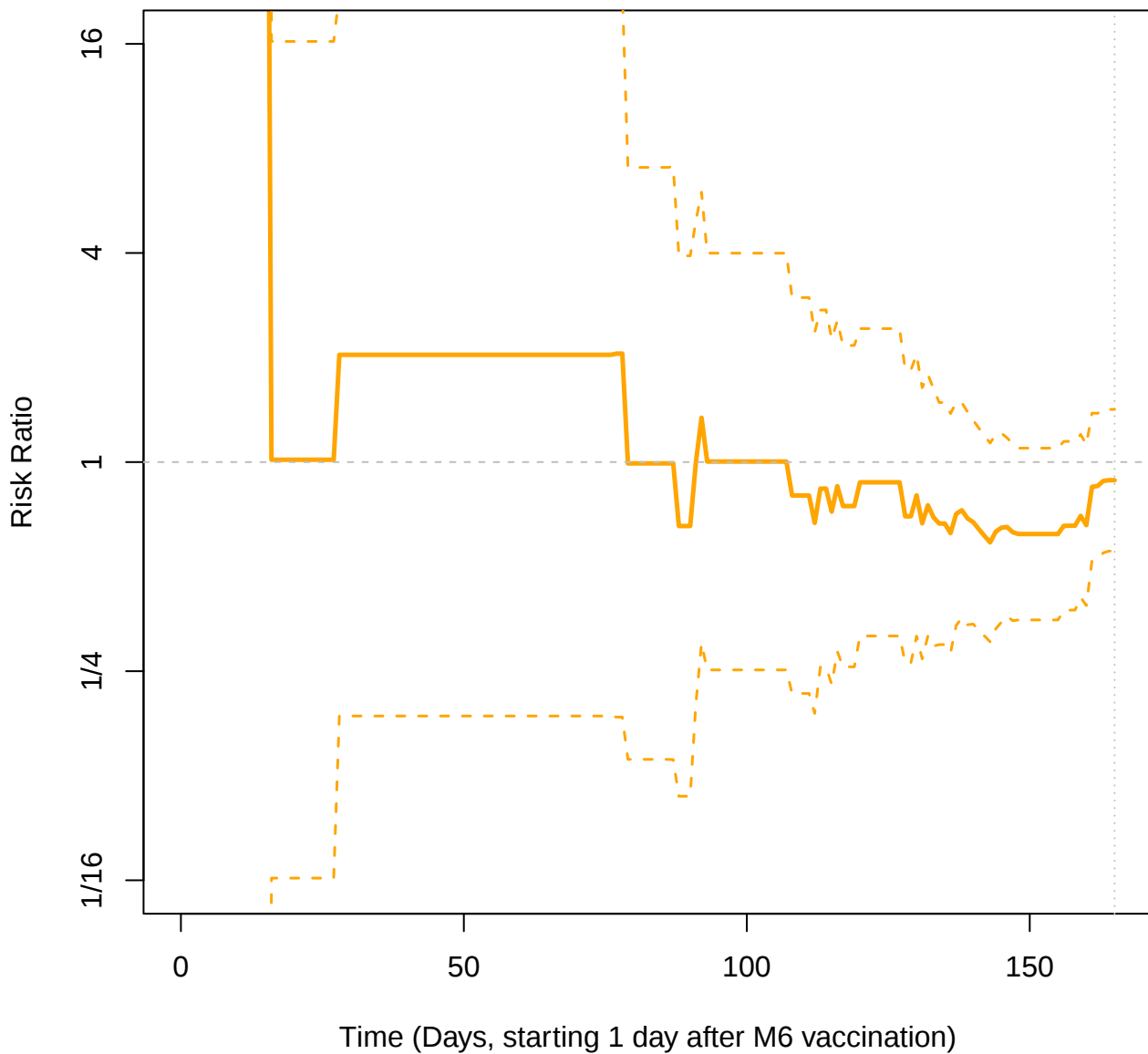
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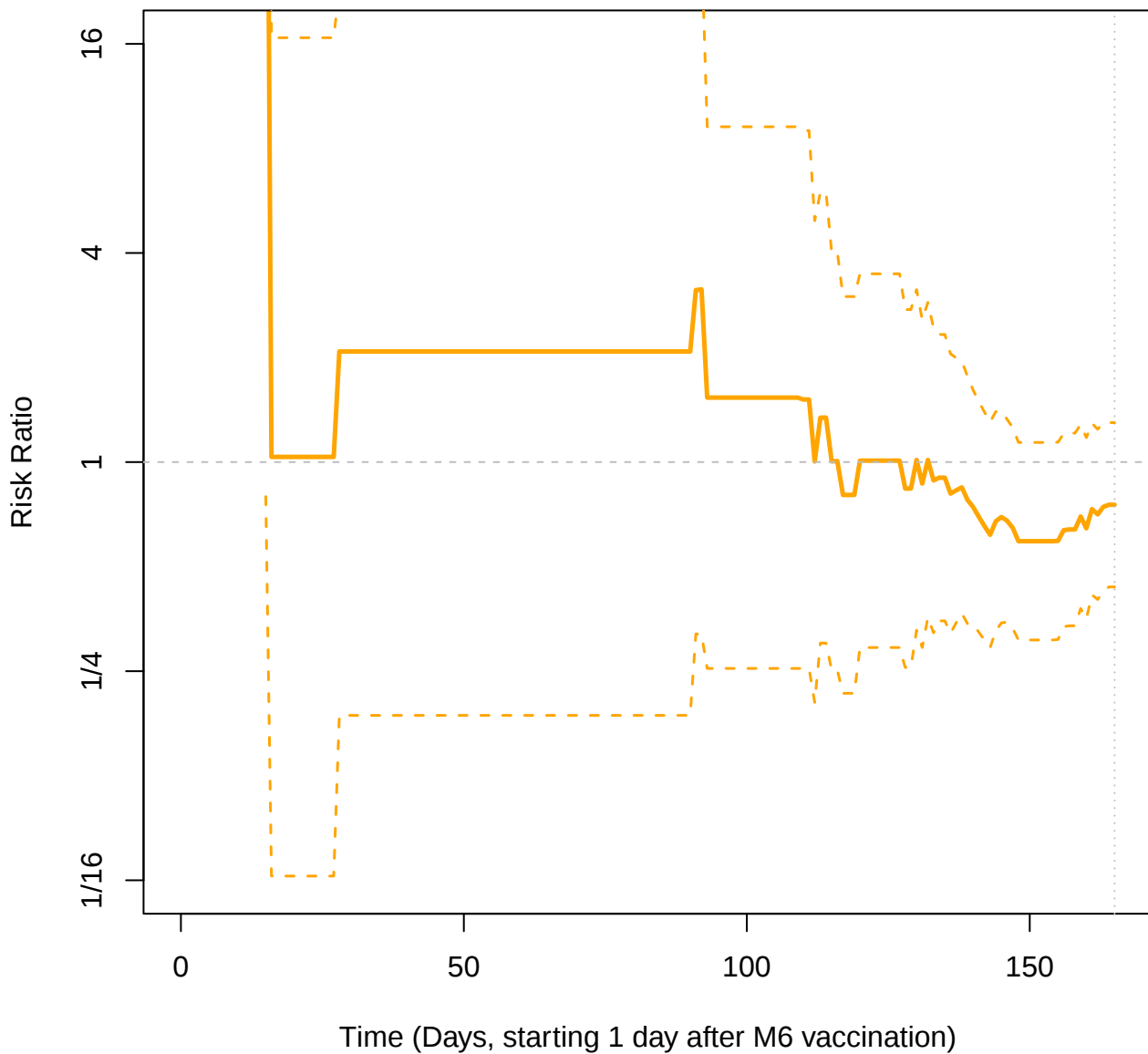
MBoost vs BBoost, RM6, CDC1M18, Primary (PLWoH)



MBoost vs BBoost, RM6, CDC1M18, Sensitivity



MBoost vs BBoost, RM6, CDC1M18, Sensitivity (PLWH)



MBoost vs BBoost, RM6, CDC1M18, Sensitivity (PLWoH)

