

Vaccination Rates (Males)

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```
library(readxl); library(magrittr); library(dplyr); library(tidyr); library(reshape2); library(ggplot2)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

##
## Attaching package: 'tidyr'

## The following object is masked from 'package:magrittr':
##
##   extract

##
## Attaching package: 'reshape2'

## The following object is masked from 'package:tidyr':
##
##   smiths
```

Creating weights for each population type

```
## creating weights df
weights.df <- read_excel("Weights.xlsx", sheet = "HSU&ERP")

##HSU total weights
##using numbers
HSUn.df <- weights.df[-c(2:12),]
HSUn.df <- pivot_longer(HSUn.df, cols = 3:20, names_to = "AgeGroup", values_to = "Weights" ) #changing
HSUn.df <- HSUn.df[,c(3,4)] #only showing weights by age-groups
```

```

#HSU Māori weights
#using numbers
HSUMn.df <- weights.df[-c(1:2,4:12),]
HSUMn.df <- pivot_longer(HSUMn.df, cols = 3:20, names_to = "AgeGroup", values_to = "Weights" ) #changing
HSUMn.df <- HSUMn.df[,c(3,4)] #only showing weights by age-groups

#HSU NonMāori weights
#using numbers
HSUNMn.df <- weights.df[-c(1:4,6:12),]
HSUNMn.df <- pivot_longer(HSUNMn.df, cols = 3:20, names_to = "AgeGroup", values_to = "Weights" ) #changing
HSUNMn.df <- HSUNMn.df[,c(3,4)] #only showing weights by age-groups

#ERP total weights
#using numbers
ERPn.df <- weights.df[-c(1:6,8:12),]
ERPn.df <- pivot_longer(ERPn.df, cols = 3:20, names_to = "AgeGroup", values_to = "Weights" ) #changing
ERPn.df <- ERPn.df[,c(3,4)] #only showing weights by age-groups

#ERP Māori weights
#using numbers
ERPm.df <- weights.df[-c(1:8,10:12),]
ERPm.df <- pivot_longer(ERPm.df, cols = 3:20, names_to = "AgeGroup", values_to = "Weights" ) #changing
ERPm.df <- ERPm.df[,c(3,4)] #only showing weights by age-groups

#ERP NonMāori weights
#using numbers
ERPmNn.df <- weights.df[-c(1:10,12),]
ERPmNn.df <- pivot_longer(ERPmNn.df, cols = 3:20, names_to = "AgeGroup", values_to = "Weights" ) #changing
ERPmNn.df <- ERPmNn.df[,c(3,4)] #only showing weights by age-groups

```

Total Fully Vaccinated Rates

```

# Total fully vaccinated
TFVacc_SMnontotal.df <- read_excel("VaccinationDataR Updated HSU2021.xlsx", sheet = "TotalFullVacc")
TFVacc_SMnontotal.df <- subset(TFVacc_SMnontotal.df, Group!="Total" & Group!="Female" & DHB!="Total")

TFVacc_SMnontotal.df <- pivot_longer(TFVacc_SMnontotal.df, cols = 4:20, names_to = "AgeGroup", values_to = "Weights")
TFVacc_SMnontotal.df <- TFVacc_SMnontotal.df[,c(1,4,5,3)] #rearranging columns to match Daniel's example

# Using HSU Weights

## Join on the standard population weights (adds in a column called "Weights")
HSU_TFVacc_SMnontot.df <- left_join(TFVacc_SMnontotal.df, HSUn.df, by = "AgeGroup")

## Create a dataset for the total of each DHB (all age groups summed), doesn't include all DHB named 'Total'
HSU_TFVacc_SMt看ot.df <- HSU_TFVacc_SMnontot.df %>%
  group_by(DHB) %>%
  summarise(

```

```

    AgeGroup = "Total",
    Count = sum(Count), Total = sum(Weights) #sum weights as want to divide by total HSU population for
  )

## Calculate the age-specific rates for each age group in each year
alpha = 0.05 #added this in for 95% CI
HSU_TFVacc_SMnontot.df <- HSU_TFVacc_SMnontot.df %>%
  mutate(
    Rate      = Count / Weights, #dividing by age-band population for rate
    RateMult  = Rate * 100000,
    Variance  = Rate / Weights, ## Var(R) = Count / Weights^2

    Rate_KeyfitzLwr = (pmax(0, Rate - qnorm(1 - alpha / 2) * sqrt(Variance), na.rm = TRUE))*100000,
    Rate_KeyfitzUpr = (Rate + qnorm(1 - alpha / 2) * sqrt(Variance))*100000,

    Rate_Gamma1Lwr  = (0.5 * qchisq(alpha / 2, 2 * Count) / Weights)*100000,
    Rate_Gamma1Upr  = (0.5 * qchisq(1 - alpha / 2, 2 * (Count + 1)) / Weights)*100000
  )

# Using ERP Weights

## Join on the standard population weights (adds in a column called "Weights")
ERP_TFVacc_SMnontot.df <- left_join(TFVacc_SMnontotal.df, ERPn.df, by = "AgeGroup")

## Create a dataset for the total of each DHB (all age groups summed), doesn't include all DHB named 'T
ERP_TFVacc_SMt看df <- ERP_TFVacc_SMnontot.df %>%
  group_by(DHB) %>%
  summarise(
    AgeGroup = "Total",
    Count = sum(Count), Total = sum(Weights) #sum weights as want to divide by total HSU population for
  )

## Calculate the age-specific rates for each age group in each year
alpha = 0.05 #added this in for 95% CI
ERP_TFVacc_SMnontot.df <- ERP_TFVacc_SMnontot.df %>%
  mutate(
    Rate      = Count / Weights, #dividing by age-band population for rate
    RateMult  = Rate * 100000,
    Variance  = Rate / Weights, ## Var(R) = Count / Weights^2

    Rate_KeyfitzLwr = (pmax(0, Rate - qnorm(1 - alpha / 2) * sqrt(Variance), na.rm = TRUE))*100000,
    Rate_KeyfitzUpr = (Rate + qnorm(1 - alpha / 2) * sqrt(Variance))*100000,

    Rate_Gamma1Lwr  = (0.5 * qchisq(alpha / 2, 2 * Count) / Weights)*100000,
    Rate_Gamma1Upr  = (0.5 * qchisq(1 - alpha / 2, 2 * (Count + 1)) / Weights)*100000
  )

```

Māori Fully Vaccinated Rates

```

# Total fully vaccinated
MFVacc_SMnontotal.df <- read_excel("VaccinationDataR Updated HSU2021.xlsx", sheet = "MaoriFullVacc")

```

```

MFVacc_SMnontotal.df<- subset(MFVacc_SMnontotal.df, Group!="Total" & Group!="Female" & DHB!="Total")

MFVacc_SMnontotal.df <- pivot_longer(MFVacc_SMnontotal.df, cols = 4:20, names_to = "AgeGroup", values_to = "Count")
MFVacc_SMnontotal.df <- MFVacc_SMnontotal.df[,c(1,4,5,3)] #rearranging columns to match Daniel's example

# Using HSU Weights

## Join on the standard population weights (adds in a column called "Weights")
HSU_MFVacc_SMnontot.df <- left_join(MFVacc_SMnontotal.df, HSUMn.df, by = "AgeGroup")

## Create a dataset for the total of each DHB (all age groups summed), doesn't include all DHB named 'Total'
HSU_MFVacc_SMt看df <- HSU_MFVacc_SMnontot.df %>%
  group_by(DHB) %>%
  summarise(
    AgeGroup = "Total",
    Count = sum(Count), Total = sum(Weights) #sum weights as want to divide by total HSU population for each DHB
  )

## Calculate the age-specific rates for each age group in each year
alpha = 0.05 #added this in for 95% CI
HSU_MFVacc_SMnontot.df <- HSU_MFVacc_SMnontot.df %>%
  mutate(
    Rate = Count / Weights, #dividing by age-band population for rate
    RateMult = Rate * 100000,
    Variance = Rate / Weights, ## Var(R) = Count / Weights^2

    Rate_KeyfitzLwr = (pmax(0, Rate - qnorm(1 - alpha / 2) * sqrt(Variance), na.rm = TRUE))*100000,
    Rate_KeyfitzUpr = (Rate + qnorm(1 - alpha / 2) * sqrt(Variance))*100000,

    Rate_Gamma1Lwr = (0.5 * qchisq(alpha / 2, 2 * Count) / Weights)*100000,
    Rate_Gamma1Upr = (0.5 * qchisq(1 - alpha / 2, 2 * (Count + 1)) / Weights)*100000
  )

# Using ERP Weights

## Join on the standard population weights (adds in a column called "Weights")
ERP_MFVacc_SMnontot.df <- left_join(MFVacc_SMnontotal.df, ERPMn.df, by = "AgeGroup")

## Create a dataset for the total of each DHB (all age groups summed), doesn't include all DHB named 'Total'
ERP_MFVacc_SMt看df <- ERP_MFVacc_SMnontot.df %>%
  group_by(DHB) %>%
  summarise(
    AgeGroup = "Total",
    Count = sum(Count), Total = sum(Weights) #sum weights as want to divide by total HSU population for each DHB
  )

## Calculate the age-specific rates for each age group in each year
alpha = 0.05 #added this in for 95% CI
ERP_MFVacc_SMnontot.df <- ERP_MFVacc_SMnontot.df %>%
  mutate(

```

```

Rate      = Count / Weights, #dividing by age-band population for rate
RateMult  = Rate * 100000,
Variance  = Rate / Weights, ## Var(R) = Count / Weights^2

Rate_KeyfitzLwr = (pmax(0, Rate - qnorm(1 - alpha / 2) * sqrt(Variance), na.rm = TRUE))*100000,
Rate_KeyfitzUpr = (Rate + qnorm(1 - alpha / 2) * sqrt(Variance))*100000,

Rate_Gamma1Lwr  = (0.5 * qchisq(alpha / 2, 2 * Count) / Weights)*100000,
Rate_Gamma1Upr  = (0.5 * qchisq(1 - alpha / 2, 2 * (Count + 1)) / Weights)*100000
)

```

Rates of DHB Total by Age groups (Total pop)

```

# Total fully vaccinated
TFVacc_DHB_SMtotal.df <- read_excel("VaccinationDataR Updated HSU2021.xlsx", sheet = "TotalFullVacc")
TFVacc_DHB_SMtotal.df <- subset(TFVacc_DHB_SMtotal.df, Group!="Total" & Group!="Female" & DHB=="Total")

TFVacc_DHB_SMtotal.df <- pivot_longer(TFVacc_DHB_SMtotal.df, cols = 3, values_to = "Total" ) #changing
TFVacc_DHB_SMtotal.df <- pivot_longer(TFVacc_DHB_SMtotal.df, cols = 3:19, names_to = "AgeGroup", values_to = "Total")

TFVacc_DHB_SMtotal.df <- TFVacc_DHB_SMtotal.df[,c(1,5,6,4)] #rearranging columns to match Daniel's example

# Using HSU Weights

HSU_TFVacc_DHB_SMtot.df <- left_join(TFVacc_DHB_SMtotal.df, HSUn.df, by = "AgeGroup")

## Calculate the age-specific rates for each age group for total regions
alpha = 0.05 #added this in for 95% CI
HSU_TFVacc_DHB_SMtot.df <- HSU_TFVacc_DHB_SMtot.df %>%
  mutate(
    Rate      = Count / Weights,
    RateMult  = Rate * 100000,
    Variance  = Rate / Weights, ## Var(R) = Count / Total^2

    Rate_KeyfitzLwr = (pmax(0, Rate - qnorm(1 - alpha / 2) * sqrt(Variance), na.rm = TRUE))*100000,
    Rate_KeyfitzUpr = (Rate + qnorm(1 - alpha / 2) * sqrt(Variance))*100000,

    Rate_Gamma1Lwr  = (0.5 * qchisq(alpha / 2, 2 * Count) / Weights)*100000,
    Rate_Gamma1Upr  = (0.5 * qchisq(1 - alpha / 2, 2 * (Count + 1)) / Weights)*100000
  )

# Using ERP Weights

ERP_TFVacc_DHB_SMtot.df <- left_join(TFVacc_DHB_SMtotal.df, ERPn.df, by = "AgeGroup")

```

```
## Calculate the age-specific rates for each age group for total regions
alpha = 0.05 #added this in for 95% CI
ERP_TFVacc_DHB_SMtot.df <- ERP_TFVacc_DHB_SMtot.df %>%
  mutate(
    Rate      = Count / Weights,
    RateMult  = Rate * 100000,
    Variance  = Rate / Weights, ## Var(R) = Count / Total^2

    Rate_KeyfitzLwr = (pmax(0, Rate - qnorm(1 - alpha / 2) * sqrt(Variance), na.rm = TRUE))*100000,
    Rate_KeyfitzUpr = (Rate + qnorm(1 - alpha / 2) * sqrt(Variance))*100000,

    Rate_Gamma1Lwr  = (0.5 * qchisq(alpha / 2, 2 * Count) / Weights)*100000,
    Rate_Gamma1Upr  = (0.5 * qchisq(1 - alpha / 2, 2 * (Count + 1)) / Weights)*100000
  )
```

Rates of DHB Total by Age groups (Māori pop)

```
# Total fully vaccinated
MFVacc_DHB_SMtotal.df <- read_excel("VaccinationDataR Updated HSU2021.xlsx", sheet = "MaoriFullVacc")
MFVacc_DHB_SMtotal.df <- subset(MFVacc_DHB_SMtotal.df, Group!="Total" & Group!="Female" & DHB=="Total")

MFVacc_DHB_SMtotal.df <- pivot_longer(MFVacc_DHB_SMtotal.df, cols = 3, values_to = "Total" ) #changing
MFVacc_DHB_SMtotal.df <- pivot_longer(MFVacc_DHB_SMtotal.df, cols = 3:19, names_to = "AgeGroup", values_to = "Total")

MFVacc_DHB_SMtotal.df <- MFVacc_DHB_SMtotal.df[,c(1,5,6,4)] #rearranging columns to match Daniel's example

# Using HSU Weights

HSU_MFVacc_DHB_SMtot.df <- left_join(MFVacc_DHB_SMtotal.df, HSUMn.df, by = "AgeGroup")

## Calculate the age-specific rates for each age group for total regions
alpha = 0.05 #added this in for 95% CI
HSU_MFVacc_DHB_SMtot.df <- HSU_MFVacc_DHB_SMtot.df %>%
  mutate(
    Rate      = Count / Weights,
    RateMult  = Rate * 100000,
    Variance  = Rate / Weights, ## Var(R) = Count / Total^2

    Rate_KeyfitzLwr = (pmax(0, Rate - qnorm(1 - alpha / 2) * sqrt(Variance), na.rm = TRUE))*100000,
    Rate_KeyfitzUpr = (Rate + qnorm(1 - alpha / 2) * sqrt(Variance))*100000,

    Rate_Gamma1Lwr  = (0.5 * qchisq(alpha / 2, 2 * Count) / Weights)*100000,
    Rate_Gamma1Upr  = (0.5 * qchisq(1 - alpha / 2, 2 * (Count + 1)) / Weights)*100000
  )

# Using ERP Weights
```

```
ERP_MFVacc_DHB_SMt看df <- left_join(MFVacc_DHB_SMt看df, ERPMn.df, by = "AgeGroup")
```

```
## Calculate the age-specific rates for each age group for total regions
```

```
alpha = 0.05 #added this in for 95% CI
```

```
ERP_MFVacc_DHB_SMt看df <- ERP_MFVacc_DHB_SMt看df %>%
```

```
  mutate(
```

```
    Rate      = Count / Weights,
```

```
    RateMult = Rate * 100000,
```

```
    Variance = Rate / Weights, ## Var(R) = Count / Total^2
```

```
    Rate_KeyfitzLwr = (pmax(0, Rate - qnorm(1 - alpha / 2) * sqrt(Variance), na.rm = TRUE))*100000,
```

```
    Rate_KeyfitzUpr = (Rate + qnorm(1 - alpha / 2) * sqrt(Variance))*100000,
```

```
    Rate_Gamma1Lwr  = (0.5 * qchisq(alpha / 2, 2 * Count) / Weights)*100000,
```

```
    Rate_Gamma1Upr  = (0.5 * qchisq(1 - alpha / 2, 2 * (Count + 1)) / Weights)*100000
```

```
)
```

```
level_order <- c("5-11","12-17", "18-24", "25-29", "30-34", "35-39","40-44", "45-49", "50-54", "55-59",
```

```
HSUvsERP_TFVacc_DHB_SMt看df <- rbind(
```

```
  data.frame(HSU_TFVacc_DHB_SMt看df, population="HSU"),
```

```
  data.frame(ERP_TFVacc_DHB_SMt看df, population="ERP")
```

```
)
```

```
ggplot(subset(HSVsERP_TFVacc_DHB_SMt看df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, 
```

```
  geom_col(position = position_dodge()) +
```

```
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
```

```
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
```

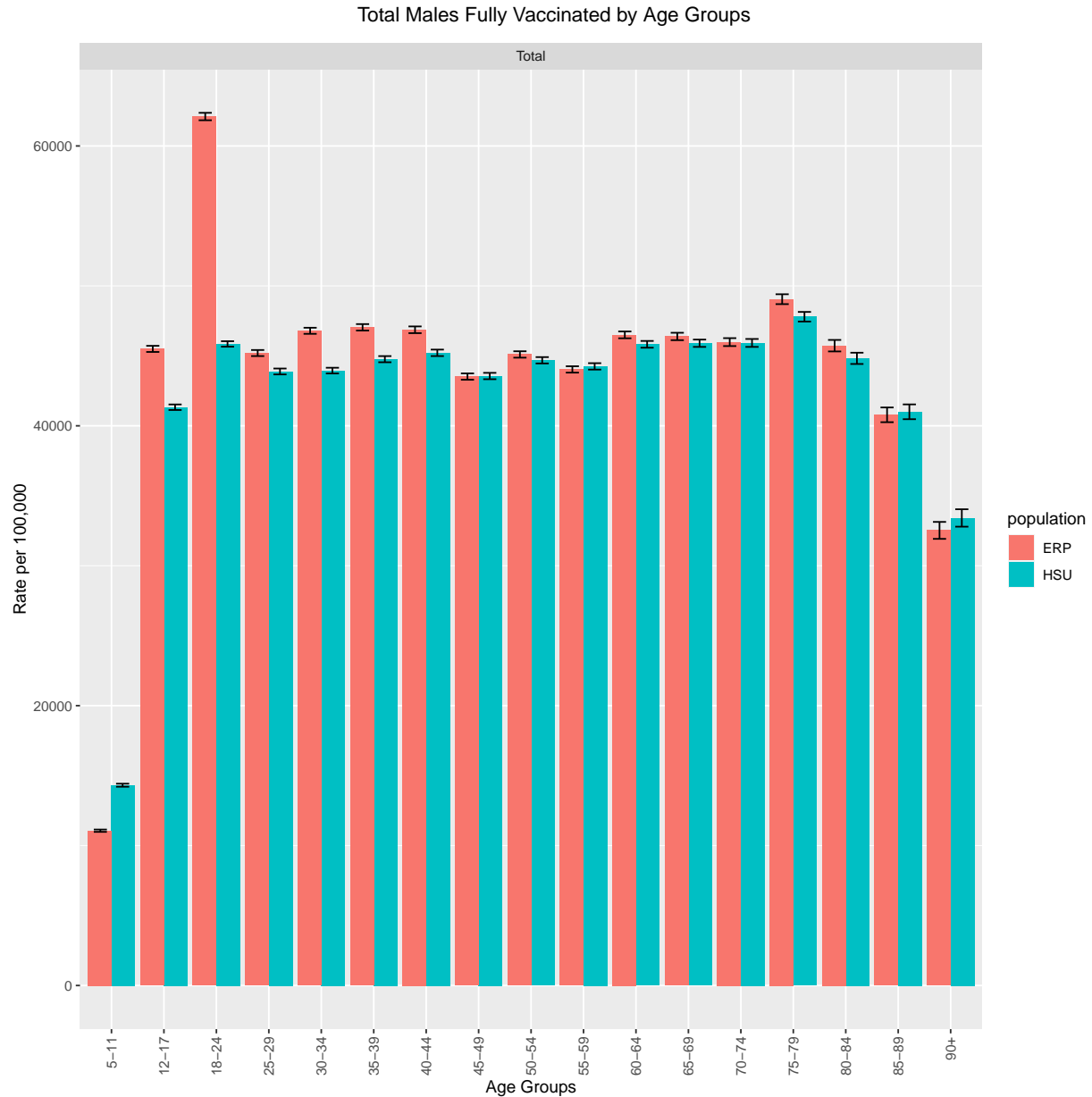
```
  facet_wrap(~DHB) +
```

```
  plot_annotation(title = "Total Males Fully Vaccinated by Age Groups") +
```

```
  labs(y= "Rate per 100,000",
```

```
    x= "Age Groups") &
```

```
  theme(plot.title = element_text(hjust = 0.5))
```



```
#pdf(file="Total Males Fully Vaccinated by Age Groups.pdf", width = 10, height = 10)
```

```
ggplot(subset(HSUvsERP_TFVacc_DHB_SMt0t.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult,
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Total Males Fully Vaccinated by Age Groups") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

```
dev.off()
```

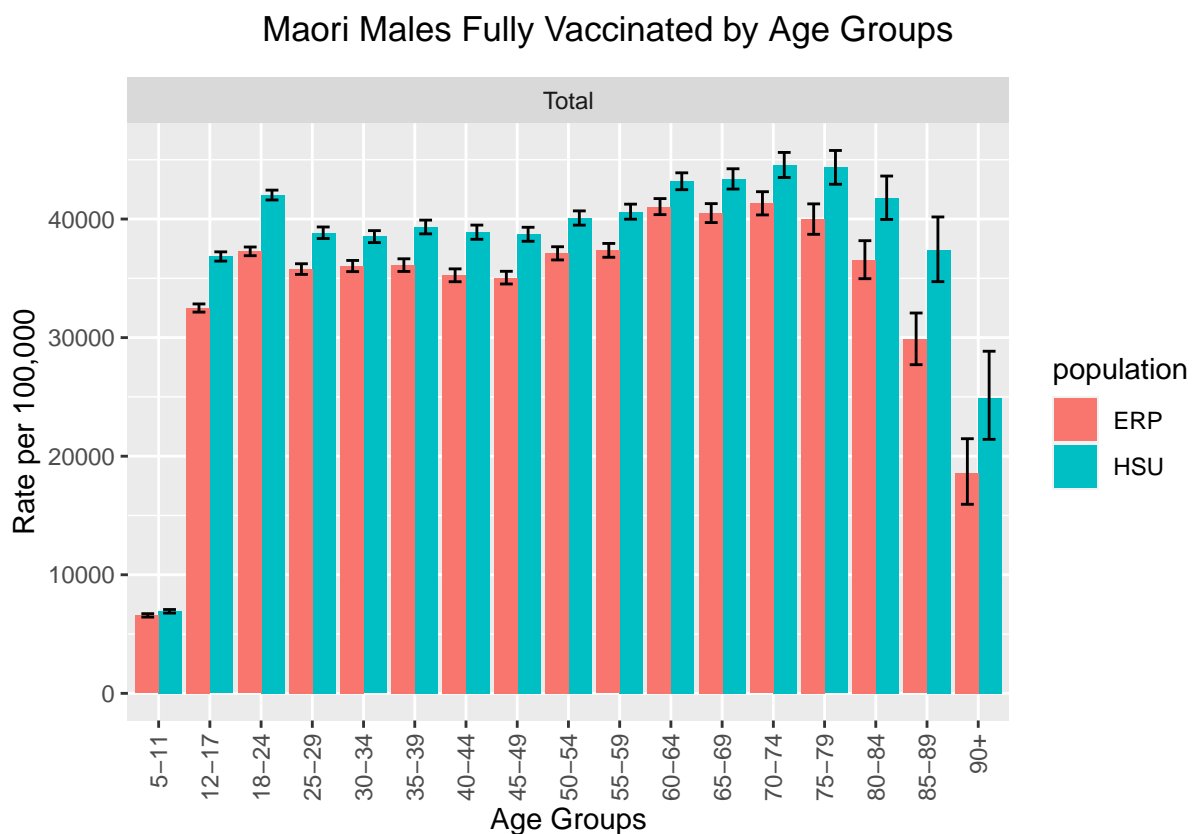


```

HSUvsERP_MFVacc_DHB_SMt看df <- rbind(
  data.frame(HSU_MFVacc_DHB_SMt看df, population="HSU"),
  data.frame(ERP_MFVacc_DHB_SMt看df, population="ERP")
)

ggplot(subset(HSUvsERP_MFVacc_DHB_SMt看df), aes(x=factor(AgeGroup, level= level_order), y = RateMult,
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Groups") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```



```

#pdf(file="Maori Males Fully Vaccinated by Age Groups.pdf", width = 10, height = 10)

```

```

ggplot(subset(HSUvsERP_MFVacc_DHB_SMt看df), aes(x=factor(AgeGroup, level= level_order), y = RateMult,
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Groups") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &

```

```

theme(plot.title = element_text(hjust = 0.5))

dev.off()

```

Total Vaccinations RR DHB total by agegroups

code for setting HSU as baseline for Total Vaccinations

```

HSU_TFVacc_SMBaseline.total <- HSU_TFVacc_DHB_SMt看df
ERP_TFVacc_SMpopulation.total <- ERP_TFVacc_DHB_SMt看df

## Rename variables so we can use them after joining to the other dataset (otherwise we get Rate.x and
HSU_TFVacc_SMBaseline.total <- HSU_TFVacc_SMBaseline.total %>%
  dplyr::rename(
    RateBaseline = Rate,
    VarianceBaseline = Variance,
    #W_meanBaseline = W_mean,
    RateBaselineLwr = Rate_KeyfitzLwr,
    RateBaselineUpr = Rate_KeyfitzUpr
  ) %>%
  dplyr::mutate(
    RRVarBaseline = ((Total - Count) / Total) / Count,
    ARVarBaseline = VarianceBaseline
  ) %>%
  dplyr::select(DHB, AgeGroup, RateBaseline, RRVarBaseline, ARVarBaseline, VarianceBaseline, RateBaselineLwr, RateBaselineUpr)

HSU_TFVacc_SMBaseline.other <- HSU_TFVacc_SMnontot.df
ERP_TFVacc_SMpopulation.other <- ERP_TFVacc_SMnontot.df

HSU_TFVacc_SMBaseline.other <- HSU_TFVacc_SMBaseline.other %>%
  dplyr::mutate(
    RateBaseline = Rate,
    RRVarBaseline = (1 / Count - 1 / Total),
    CountBaseline = Count,
    TotalBaseline = Total,

    RateBaselineLwr = Rate_KeyfitzLwr,
    RateBaselineUpr = Rate_KeyfitzUpr
  ) %>%
  dplyr::select(DHB, AgeGroup, RateBaseline, RRVarBaseline, CountBaseline, TotalBaseline, RateBaselineLwr, RateBaselineUpr)

## Join the baseline and other population datasets, calculating the RR and associated CI
ERP_TFVacc_SMpopulation.other <-ERP_TFVacc_SMpopulation.other %>%
  dplyr::left_join(HSU_TFVacc_SMBaseline.other, by = c("DHB", "AgeGroup")) %>%
  dplyr::mutate(
    RelativeRisk = Rate / RateBaseline,
    AttributableRisk = Rate - RateBaseline,
    # RRVar = (1 / Count) * ((Total - Count) / Total),

```

```

RRVar = (1 / Count - 1 / Total),
RelativeRiskLwr = exp(log(RelativeRisk) - 1.96 * sqrt(RRVar + RRVarBaseline)),
RelativeRiskUpr = exp(log(RelativeRisk) + 1.96 * sqrt(RRVar + RRVarBaseline)),
# ARVar = Rate * (1 - Rate) * (1 / Total + 1 / TotalBaseline),
ARVar = (Count + CountBaseline) / (Total + TotalBaseline) * (1 - (Count + CountBaseline) / (Total +
AttributableRiskLwr = AttributableRisk - 1.96 * sqrt(ARVar),
AttributableRiskUpr = AttributableRisk + 1.96 * sqrt(ARVar)
) %>%
dplyr::select(-RRVarBaseline, -RRVar, -ARVar, -CountBaseline, -TotalBaseline, -RateBaselineLwr, -RateBaselineUpr)

TFVacc_DHB_SMPopulation.df <- ERP_TFVacc_SMPopulation.total %>%
dplyr::left_join(HSU_TFVacc_SMBaseline.total, by = c("DHB", "AgeGroup")) %>%
dplyr::mutate(
  RelativeRisk = Rate / RateBaseline,
  RRVar = ((Total - Count) / Total) / Count,
  RelativeRiskLwr = exp(log(RelativeRisk) - 1.96 * sqrt(RRVar + RRVarBaseline)),
  RelativeRiskUpr = exp(log(RelativeRisk) + 1.96 * sqrt(RRVar + RRVarBaseline)),

  AttributableRisk = Rate - RateBaseline,
  ARVar = Variance,
  AttributableRiskLwr = AttributableRisk - 1.96 * sqrt(ARVar + ARVarBaseline),
  AttributableRiskUpr = AttributableRisk + 1.96 * sqrt(ARVar + ARVarBaseline)
) %>%
dplyr::select(-RRVarBaseline, -RRVar, -ARVarBaseline, -ARVar) %>%
dplyr::bind_rows(ERP_TFVacc_SMPopulation.other)

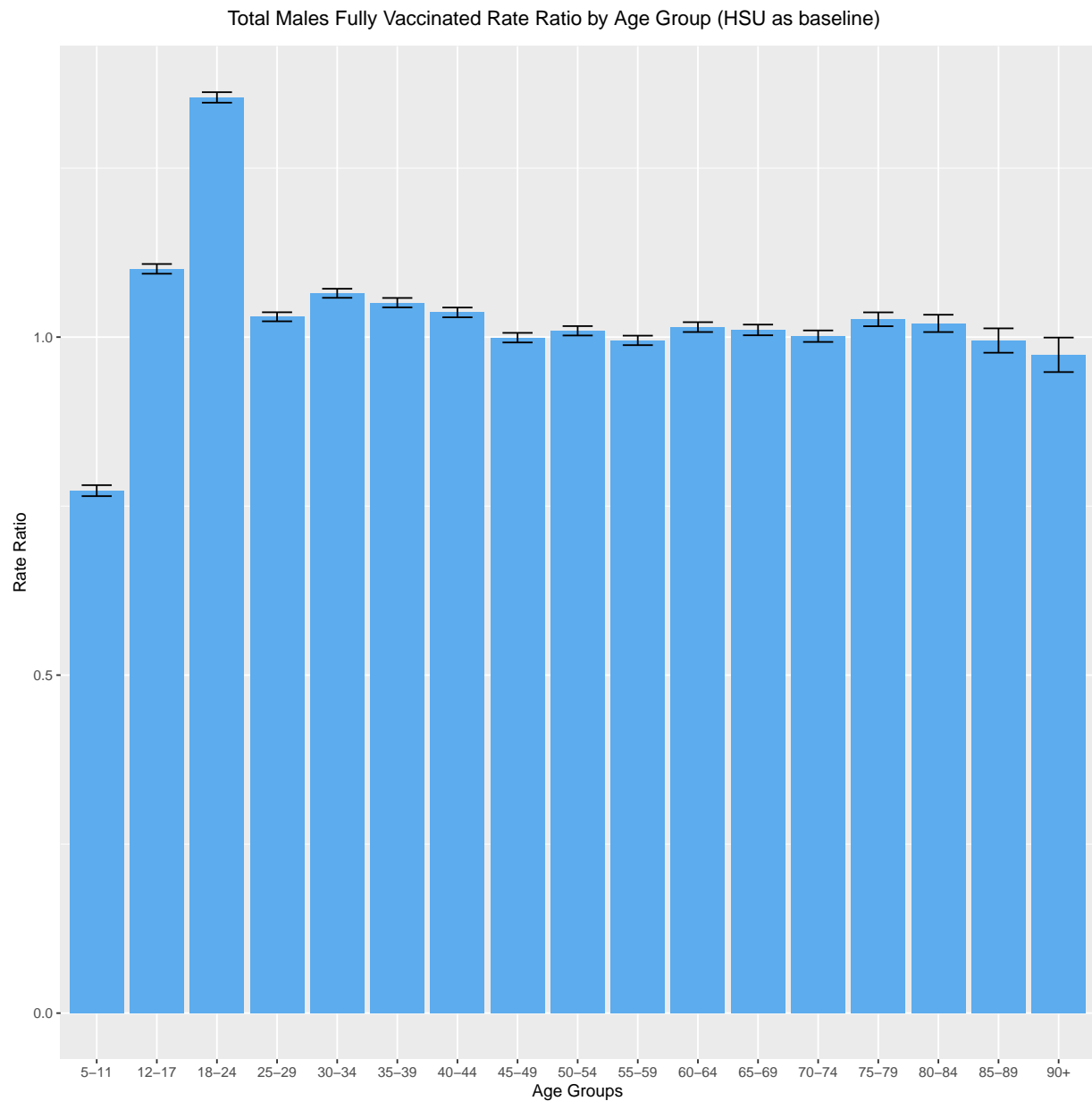
```

Rate ratio for Fully Vaccinated Rates by grouped DHB with 95% CI's

```

ggplot(subset(TFVacc_DHB_SMPopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, level= level_order), y=RateRatio,
  geom_col(fill = "Steel Blue 2")+
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUpr), width=0.5) +
  plot_annotation(title = "Total Males Fully Vaccinated Rate Ratio by Age Group (HSU as baseline)") +
  labs(y= "Rate Ratio",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```



```
#pdf(file="Total Males Fully Vaccinated Rate Ratio by Age Group (HSU as baseline).pdf", width = 10, height = 10)
```

```
ggplot(subset(TFVacc_DHB_SMPopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, level= level_order), y=RateRatio)) +
  geom_col(fill = "Steel Blue 2") +
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUpr), width=0.5) +
  plot_annotation(title = "Total Males Fully Vaccinated Rate Ratio by Age Group (HSU as baseline)") +
  labs(y= "Rate Ratio",
       x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

```
dev.off()
```

code for setting HSU as baseline for Māori Vaccinations

```
HSU_MFVacc_SMBaseline.total <- HSU_MFVacc_DHB_SMtot.df
ERP_MFVacc_SMpopulation.total <- ERP_MFVacc_DHB_SMtot.df

## Rename variables so we can use them after joining to the other dataset (otherwise we get Rate.x and L
HSU_MFVacc_SMBaseline.total <- HSU_MFVacc_SMBaseline.total %>%
  dplyr::rename(
    RateBaseline = Rate,
    VarianceBaseline = Variance,
    #W_meanBaseline = W_mean,
    RateBaselineLwr = Rate_KeyfitzLwr,
    RateBaselineUpr = Rate_KeyfitzUpr
  ) %>%
  dplyr::mutate(
    RRVarBaseline = ((Total - Count) / Total) / Count,
    ARVarBaseline = VarianceBaseline
  ) %>%
  dplyr::select(DHB, AgeGroup, RateBaseline, RRVarBaseline, ARVarBaseline, VarianceBaseline, RateBaselineLwr, RateBaselineUpr)

HSU_MFVacc_SMBaseline.other <- HSU_MFVacc_SMnontot.df
ERP_MFVacc_SMpopulation.other <- ERP_MFVacc_SMnontot.df

HSU_MFVacc_SMBaseline.other <- HSU_MFVacc_SMBaseline.other %>%
  dplyr::mutate(
    RateBaseline = Rate,
    RRVarBaseline = (1 / Count - 1 / Total),
    CountBaseline = Count,
    TotalBaseline = Total,

    RateBaselineLwr = Rate_KeyfitzLwr,
    RateBaselineUpr = Rate_KeyfitzUpr
  ) %>%
  dplyr::select(DHB, AgeGroup, RateBaseline, RRVarBaseline, CountBaseline, TotalBaseline, RateBaselineLwr, RateBaselineUpr)

## Join the baseline and other population datasets, calculating the RR and associated CI
ERP_MFVacc_SMpopulation.other <- ERP_MFVacc_SMpopulation.other %>%
  dplyr::left_join(HSU_MFVacc_SMBaseline.other, by = c("DHB", "AgeGroup")) %>%
  dplyr::mutate(
    RelativeRisk = Rate / RateBaseline,
    AttributableRisk = Rate - RateBaseline,
    # RRVar = (1 / Count) * ((Total - Count) / Total),
    RRVar = (1 / Count - 1 / Total),
    RelativeRiskLwr = exp(log(RelativeRisk) - 1.96 * sqrt(RRVar + RRVarBaseline)),
    RelativeRiskUpr = exp(log(RelativeRisk) + 1.96 * sqrt(RRVar + RRVarBaseline)),
    # ARVar = Rate * (1 - Rate) * (1 / Total + 1 / TotalBaseline),
    ARVar = (Count + CountBaseline) / (Total + TotalBaseline) * (1 - (Count + CountBaseline) / (Total + TotalBaseline)),
    AttributableRiskLwr = AttributableRisk - 1.96 * sqrt(ARVar),
    AttributableRiskUpr = AttributableRisk + 1.96 * sqrt(ARVar)
  ) %>%
```

```

dplyr::select(-RRVarBaseline, -RRVar, -ARVar, -CountBaseline, -TotalBaseline, -RateBaselineLwr, -RateBaselineUpr)

MFVacc_DHB_SMPopulation.df <- ERP_MFVacc_SMPopulation.total %>%
dplyr::left_join(HSU_MFVacc_SMBaseline.total, by = c("DHB", "AgeGroup")) %>%
dplyr::mutate(
  RelativeRisk      = Rate / RateBaseline,
  RRVar             = ((Total - Count) / Total) / Count,
  RelativeRiskLwr   = exp(log(RelativeRisk) - 1.96 * sqrt(RRVar + RRVarBaseline)),
  RelativeRiskUpr   = exp(log(RelativeRisk) + 1.96 * sqrt(RRVar + RRVarBaseline)),

  AttributableRisk  = Rate - RateBaseline,
  ARVar             = Variance,
  AttributableRiskLwr = AttributableRisk - 1.96 * sqrt(ARVar + ARVarBaseline),
  AttributableRiskUpr = AttributableRisk + 1.96 * sqrt(ARVar + ARVarBaseline)
) %>%
dplyr::select(-RRVarBaseline, -RRVar, -ARVarBaseline, -ARVar) %>%
dplyr::bind_rows(ERP_MFVacc_SMPopulation.other)

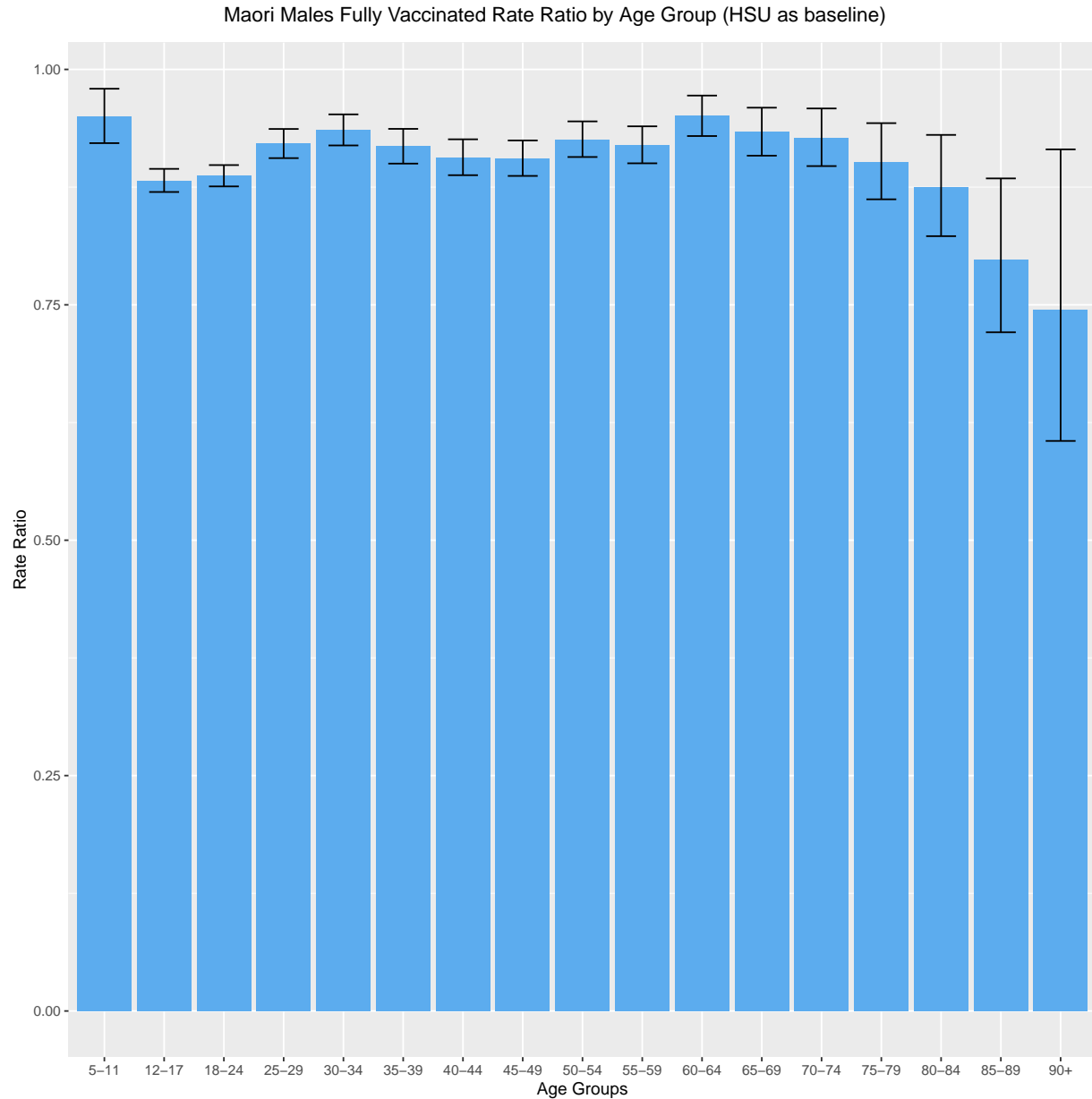
```

Rate ratio for Maori males Fully Vaccinated Rates by grouped DHB with 95% CI's

```

ggplot(subset(MFVacc_DHB_SMPopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, level= level_order), y=RateRatio,
  geom_col(fill = "Steel Blue 2")+
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUpr), width=0.5) +
  plot_annotation(title = "Maori Males Fully Vaccinated Rate Ratio by Age Group (HSU as baseline)" +
  labs(y= "Rate Ratio",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```



```
#pdf(file="Maori Males Fully Vaccinated Rate Ratio by Age Group (HSU as baseline).pdf", width = 10, height = 10)
```

```
ggplot(subset(MFVacc_DHB_SMPopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, level= level_order), y=RateRatio)) +
  geom_col(fill = "Steel Blue 2") +
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUp), width=0.5) +
  plot_annotation(title = "Maori Males Fully Vaccinated Rate Ratio by Age Group (HSU as baseline)") +
  labs(y= "Rate Ratio",
       x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

```
dev.off()
```

```

HSUvsERP_TFVacc_SMnontot.df <- rbind(
  data.frame(HSU_TFVacc_SMnontot.df, population="HSU"),
  data.frame(ERP_TFVacc_SMnontot.df, population="ERP")
)

ggplot(subset(HSUvsERP_TFVacc_SMnontot.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, f
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Total Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",
       x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

```

## Warning: Removed 4 rows containing missing values (geom_col).

```


Total Males Fully Vaccinated by Age Group & DHB



```
#pdf(file="Total Males Fully Vaccinated by Age Group & DHB Fullplot.pdf", width = 10, height = 10)

ggplot(subset(HSUvsERP_TFVacc_SMnontot.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, f
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Total Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",
       x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

dev.off()
```

```

HSU_MFVacc_nontot_high1.df <- HSU_MFVacc_SMnontot.df[HSU_MFVacc_SMnontot.df$DHB %in% c("Northland", "Waikato"), ]
HSU_MFVacc_nontot_high2.df <- HSU_MFVacc_SMnontot.df[HSU_MFVacc_SMnontot.df$DHB %in% c("Waitemata", "Lakes", "Bay of Plenty"), ]
HSU_MFVacc_nontot_mid1.df <- HSU_MFVacc_SMnontot.df[HSU_MFVacc_SMnontot.df$DHB %in% c("Canterbury", "South Island"), ]
HSU_MFVacc_nontot_mid2.df <- HSU_MFVacc_SMnontot.df[HSU_MFVacc_SMnontot.df$DHB %in% c("MidCentral", "Hawke's Bay"), ]

HSU_MFVacc_nontot_low.df <- HSU_MFVacc_SMnontot.df[HSU_MFVacc_SMnontot.df$DHB %in% c("South Canterbury", "Otago"), ]

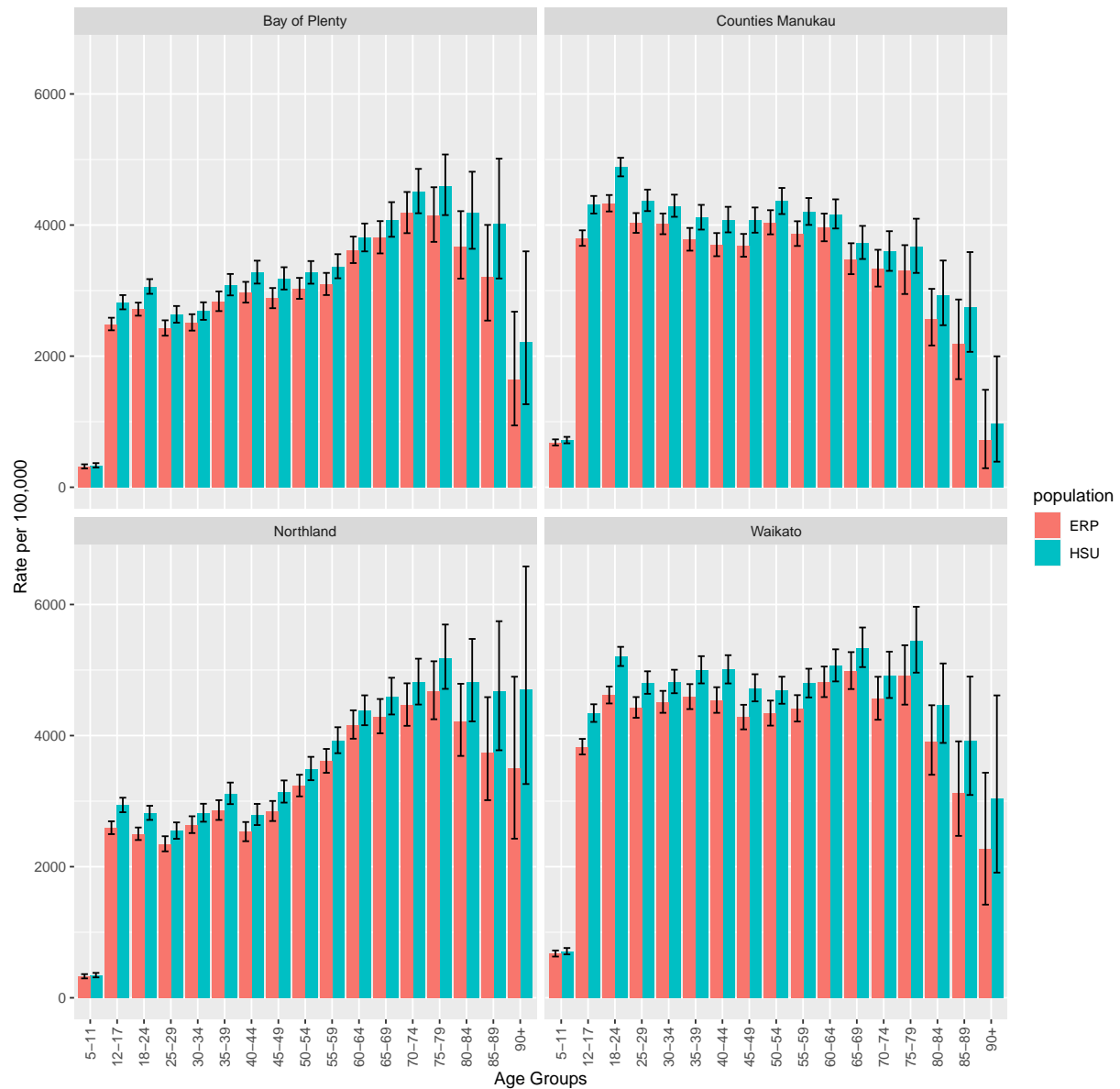
ERP_MFVacc_nontot_high1.df <- ERP_MFVacc_SMnontot.df[ERP_MFVacc_SMnontot.df$DHB %in% c("Northland", "Waikato"), ]
ERP_MFVacc_nontot_high2.df <- ERP_MFVacc_SMnontot.df[ERP_MFVacc_SMnontot.df$DHB %in% c("Waitemata", "Lakes", "Bay of Plenty"), ]
ERP_MFVacc_nontot_mid1.df <- ERP_MFVacc_SMnontot.df[ERP_MFVacc_SMnontot.df$DHB %in% c("Canterbury", "South Island"), ]
ERP_MFVacc_nontot_mid2.df <- ERP_MFVacc_SMnontot.df[ERP_MFVacc_SMnontot.df$DHB %in% c("MidCentral", "Hawke's Bay"), ]
ERP_MFVacc_nontot_low.df <- ERP_MFVacc_SMnontot.df[ERP_MFVacc_SMnontot.df$DHB %in% c("South Canterbury", "Otago"), ]

HSUvsERP_MFVacc_nontot_high1.df <- rbind(
  data.frame(HSU_MFVacc_nontot_high1.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_high1.df, population="ERP")
)

ggplot(subset(HSVsERP_MFVacc_nontot_high1.df), aes(x=factor(AgeGroup, level= level_order), y = RateMul,
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

Maori Males Fully Vaccinated by Age Group & DHB



```
#pdf(file="Maori Males Fully Vaccinated by Age Group & DHB high1.pdf", width = 10, height = 10)
```

```
ggplot(subset(HSUvsERP_MFVacc_nontot_high1.df), aes(x=factor(AgeGroup, level= level_order), y = RateMul)) +
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",
  x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

dev.off()
```

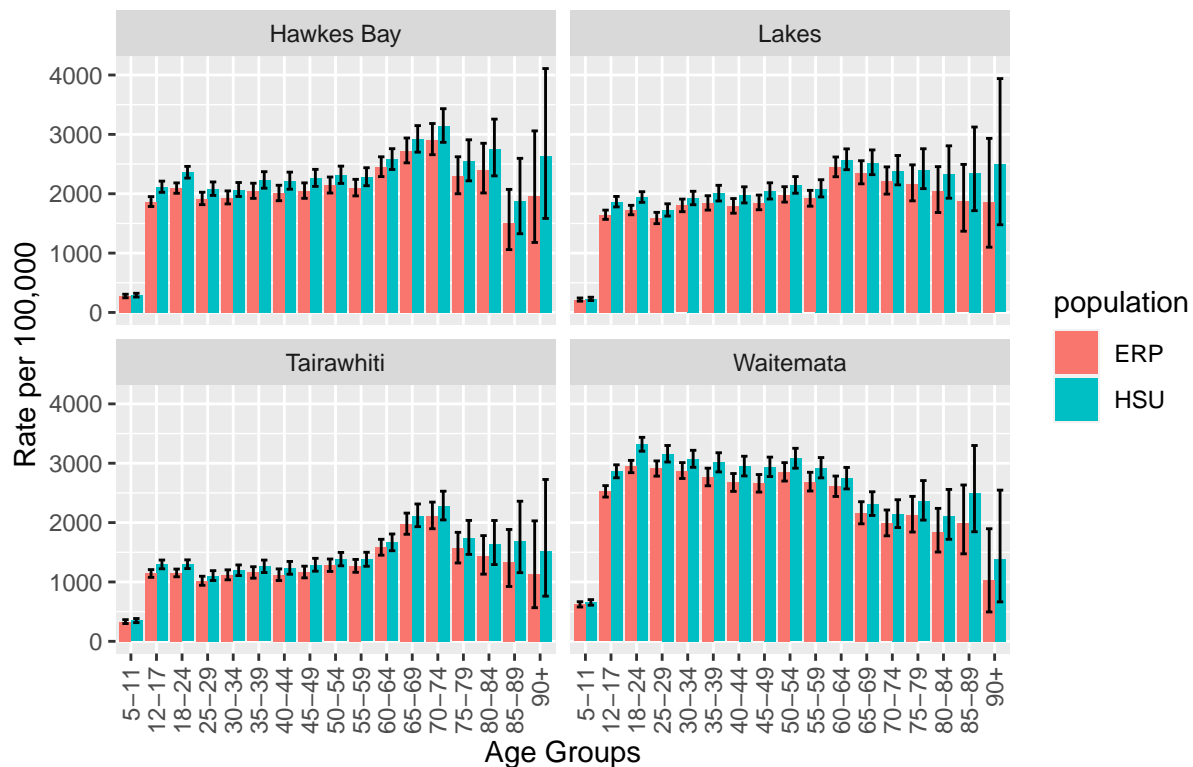
```

HSUvsERP_MFVacc_nontot_high2.df <- rbind(
  data.frame(HSU_MFVacc_nontot_high2.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_high2.df, population="ERP")
)

ggplot(subset(HSUvsERP_MFVacc_nontot_high2.df), aes(x=factor(AgeGroup, level= level_order), y = RateMul
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

Maori Males Fully Vaccinated by Age Group & DHB



```

#pdf(file="Maori Males Fully Vaccinated by Age Group & DHB high2.pdf", width = 10, height = 10)

```

```

ggplot(subset(HSUvsERP_MFVacc_nontot_high2.df), aes(x=factor(AgeGroup, level= level_order), y = RateMul
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",

```

```

    x= "Age Groups") &
    theme(plot.title = element_text(hjust = 0.5))

dev.off()

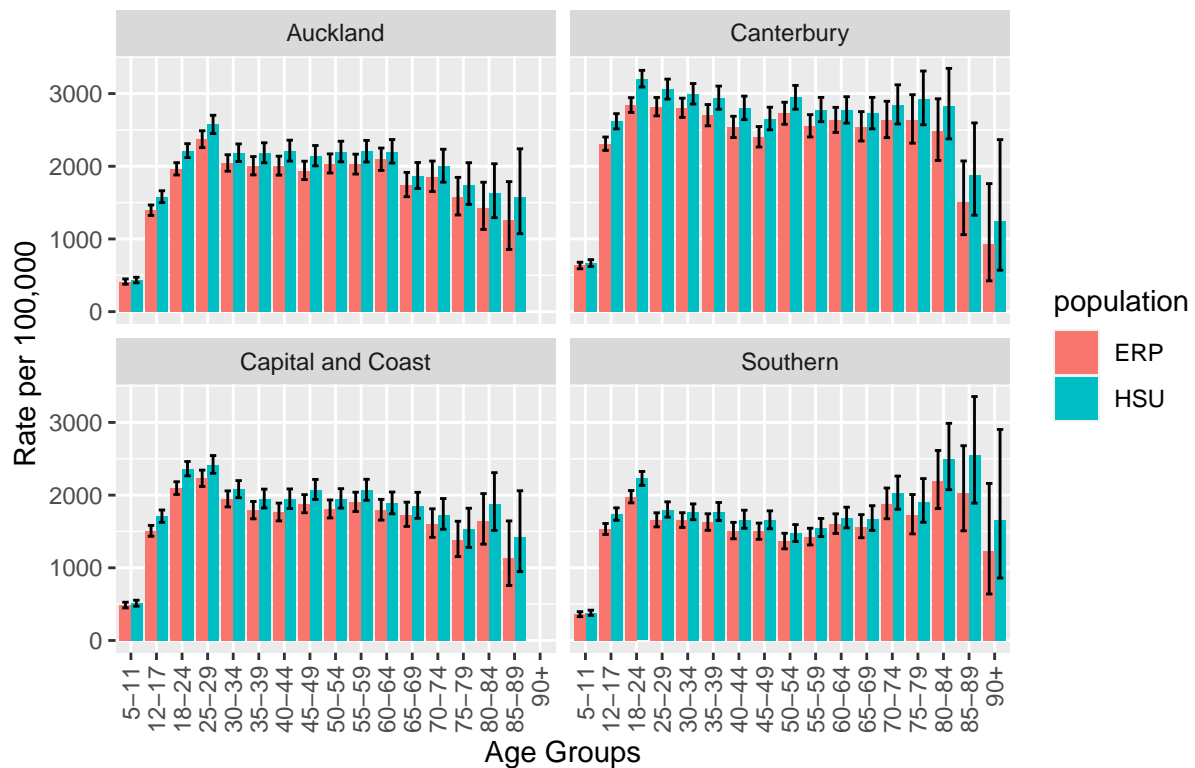
HSUvsERP_MFVacc_nontot_mid1.df <- rbind(
  data.frame(HSU_MFVacc_nontot_mid1.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_mid1.df, population="ERP")
)

ggplot(subset(HSVsERP_MFVacc_nontot_mid1.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

## Warning: Removed 4 rows containing missing values (geom_col).

```

Maori Males Fully Vaccinated by Age Group & DHB



```

#pdf(file="Maori Males Fully Vaccinated by Age Group & DHB mid1.pdf", width = 10, height = 10)

```

```

ggplot(subset(HSUvsERP_MFVacc_nontot_mid1.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

dev.off()

```

```

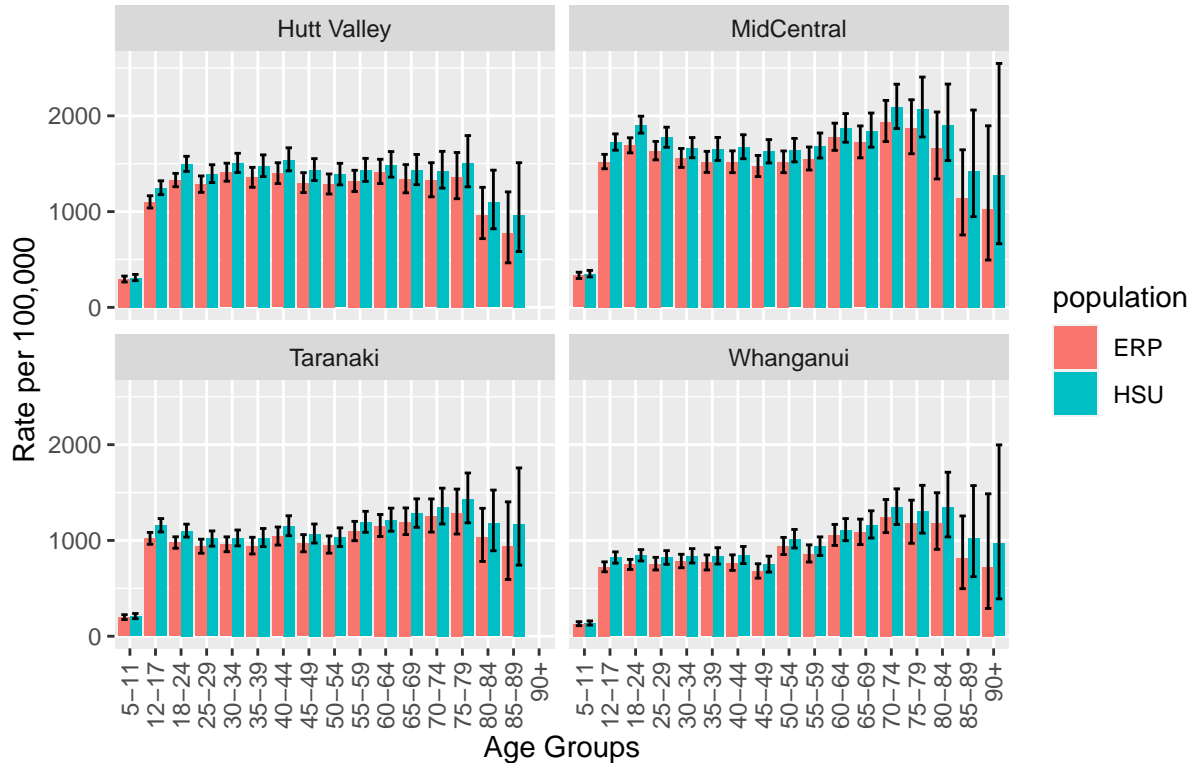
HSUvsERP_MFVacc_nontot_mid2.df <- rbind(
  data.frame(HSU_MFVacc_nontot_mid2.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_mid2.df, population="ERP")
)

ggplot(subset(HSUvsERP_MFVacc_nontot_mid2.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

```
## Warning: Removed 4 rows containing missing values (geom_col).
```

Maori Males Fully Vaccinated by Age Group & DHB



```
#pdf(file="Maori Males Fully Vaccinated by Age Group & DHB mid2.pdf", width = 10, height = 10)
```

```
ggplot(subset(HSUvsERP_MFVacc_nontot_mid2.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult,
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

```
dev.off()
```

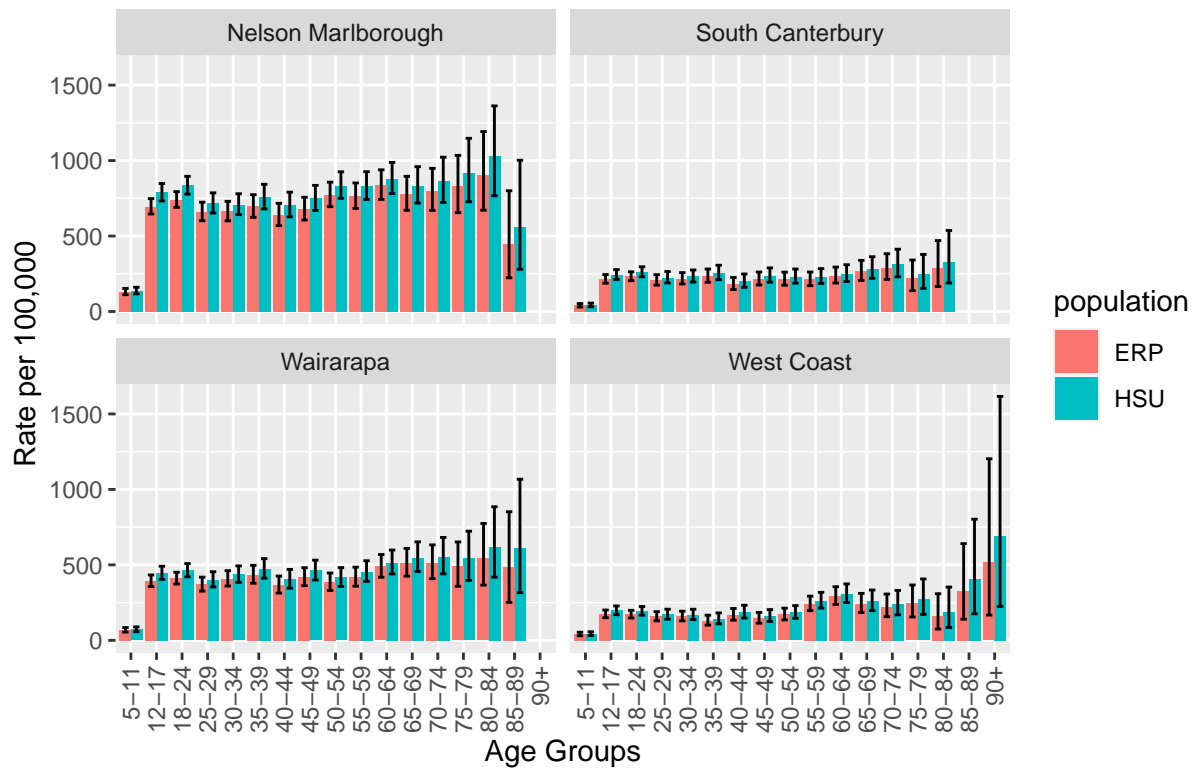
```
HSUvsERP_MFVacc_nontot_low.df <- rbind(
  data.frame(HSU_MFVacc_nontot_low.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_low.df, population="ERP")
)
```

```
ggplot(subset(HSUvsERP_MFVacc_nontot_low.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult,
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB") +
```

```
labs(y= "Rate per 100,000",
     x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))
```

```
## Warning: Removed 8 rows containing missing values (geom_col).
```

Maori Males Fully Vaccinated by Age Group & DHB



```
#pdf(file="Maori Males Fully Vaccinated by Age Group & DHB low.pdf", width = 10, height = 10)

ggplot(subset(HSUvsERP_MFVacc_nontot_low.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult,
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB") +
  labs(y= "Rate per 100,000",
       x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

dev.off()
```

presenting lowest vs. highest


```
# separated by rate levels
```

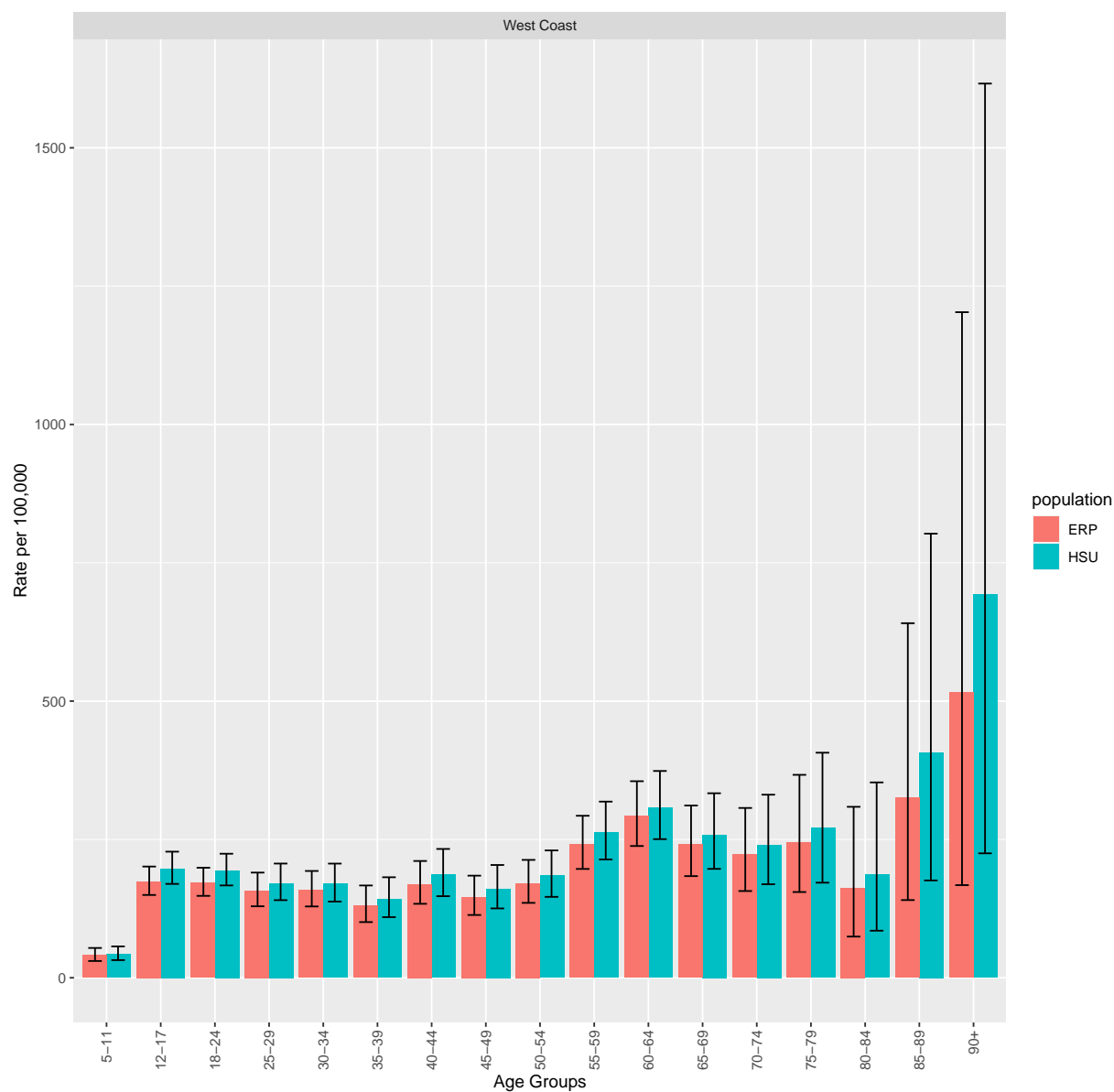
```
HSU_MFVacc_nontot_highest.df <- HSU_MFVacc_SMnontot.df[HSU_MFVacc_SMnontot.df$DHB %in% c("Northland"),]  
HSU_MFVacc_nontot_lowest.df <- HSU_MFVacc_SMnontot.df[HSU_MFVacc_SMnontot.df$DHB %in% c("West Coast"),]
```

```
ERP_MFVacc_nontot_highest.df <- ERP_MFVacc_SMnontot.df[ERP_MFVacc_SMnontot.df$DHB %in% c("Northland"),]  
ERP_MFVacc_nontot_lowest.df <- ERP_MFVacc_SMnontot.df[ERP_MFVacc_SMnontot.df$DHB %in% c("West Coast"),]
```

```
HSUvsERP_MFVacc_low.df <- rbind(  
  data.frame(HSU_MFVacc_nontot_lowest.df, population="HSU"),  
  data.frame(ERP_MFVacc_nontot_lowest.df, population="ERP")  
)
```

```
ggplot(subset(HSVsERP_MFVacc_low.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fill =  
  geom_col(position = position_dodge()) +  
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +  
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),  
  facet_wrap(~DHB) +  
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group for West Coast DHB (Lowest Rates p  
  labs(y= "Rate per 100,000",  
    x= "Age Groups") &  
  theme(plot.title = element_text(hjust = 0.5))
```

Maori Males Fully Vaccinated by Age Group for West Coast DHB (Lowest Rates per 100,000)



```
#pdf(file="Maori Males Fully Vaccinated by Age Group & lowest DHB.pdf", width = 10, height = 10)

ggplot(subset(HSUvsERP_MFVacc_low.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fill =
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Up), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group for West Coast DHB (Lowest Rates p
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

dev.off()
```

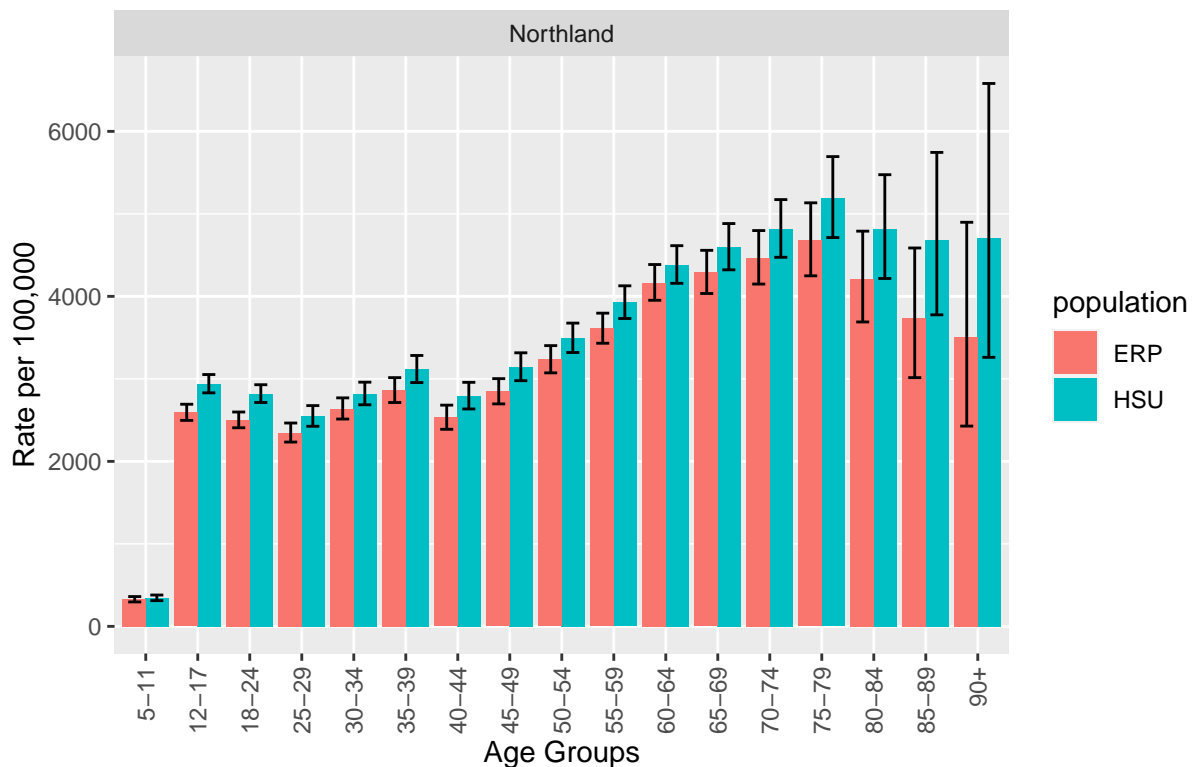
```

HSUvsERP_MFVacc_high.df <- rbind(
  data.frame(HSU_MFVacc_nontot_highest.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_highest.df, population="ERP")
)

ggplot(subset(HSUvsERP_MFVacc_high.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fill = population)) +
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group for Northland DHB (Highest Rates per 100,000)",
    labs(y= "Rate per 100,000",
      x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

i Males Fully Vaccinated by Age Group for Northland DHB (Highest Rates per 100



```

#pdf(file="Maori Males Fully Vaccinated by Age Group & highest DHB.pdf", width = 10, height = 10)

ggplot(subset(HSUvsERP_MFVacc_high.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fill = population)) +
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group for Northland DHB (Highest Rates per 100,000)",
    labs(y= "Rate per 100,000",
      x= "Age Groups") &

```

```

theme(plot.title = element_text(hjust = 0.5))

dev.off()

## collating plot into one for differences

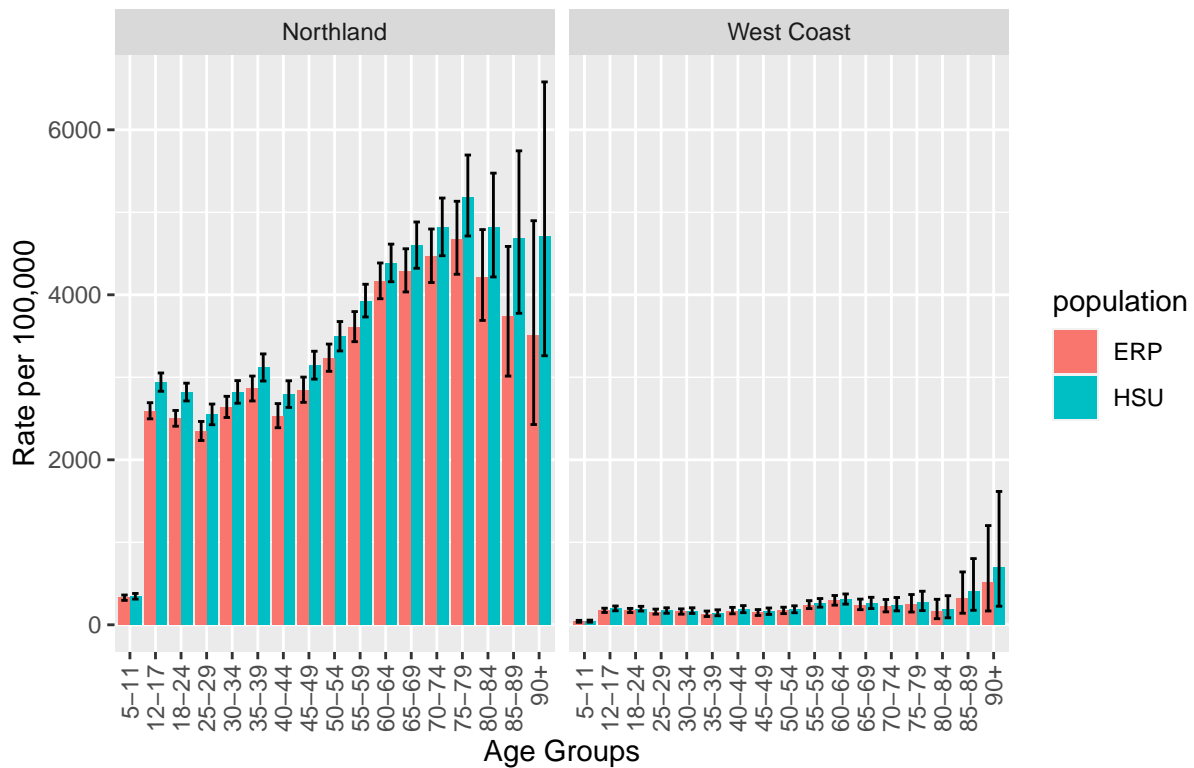
HSU_MFVacc_nontot_lowvshigh.df <- HSU_MFVacc_SMnontot.df[HSU_MFVacc_SMnontot.df$DHB %in% c("Northland",
ERP_MFVacc_nontot_lowvshigh.df <- ERP_MFVacc_SMnontot.df[ERP_MFVacc_SMnontot.df$DHB %in% c("Northland",

HSUvsERP_MFVacc_lowvshigh.df <- rbind(
  data.frame(HSU_MFVacc_nontot_lowvshigh.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_lowvshigh.df, population="ERP")
)

ggplot(subset(HSVsERP_MFVacc_lowvshigh.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult,
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB (Lowest vs. Highest rates per
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

ri Males Fully Vaccinated by Age Group & DHB (Lowest vs. Highest rates per 100,



```
#pdf(file="Maori Males Fully Vaccinated by Age Group & highest vs. lowest DHB.pdf", width = 10, height = 10)

ggplot(subset(HSUvsERP_MFVacc_lowvshigh.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult,
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group & DHB (Lowest vs. Highest rates per
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

dev.off()
```

presenting highest diff in comparison to Māori females

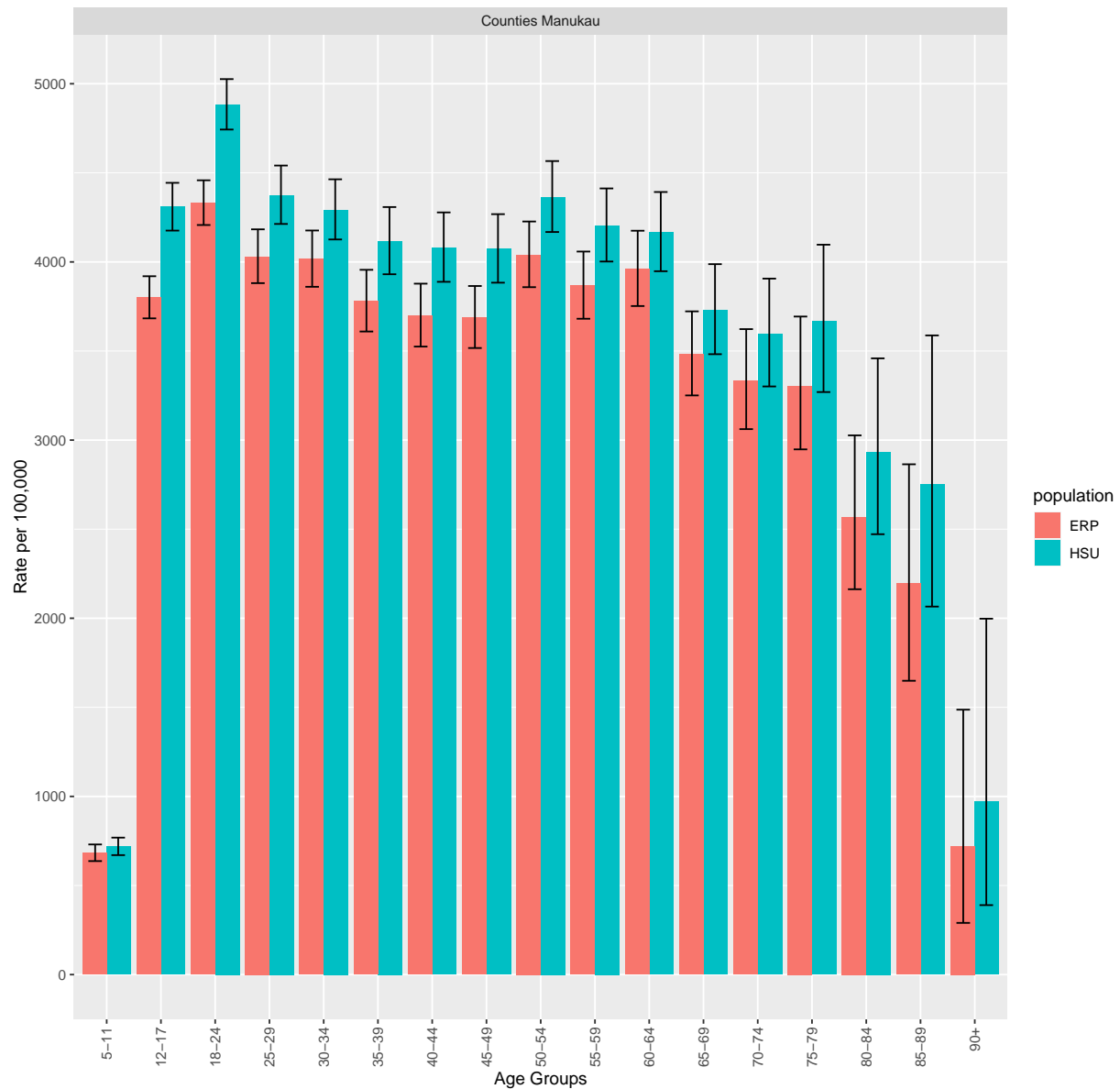
```
# separated by rate levels

HSU_MFVacc_nontot_highestdiff.df <- HSU_MFVacc_SMnontot.df[HSU_MFVacc_SMnontot.df$DHB %in% c("Counties Manukau", "DHB of Auckland"),]
ERP_MFVacc_nontot_highestdiff.df <- ERP_MFVacc_SMnontot.df[ERP_MFVacc_SMnontot.df$DHB %in% c("Counties Manukau", "DHB of Auckland"),]

HSUvsERP_MFVacc_highestdiff.df <- rbind(
  data.frame(HSU_MFVacc_nontot_highestdiff.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_highestdiff.df, population="ERP")
)

ggplot(subset(HSUvsERP_MFVacc_highestdiff.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult,
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group for Counties Manukau DHB (Rates per
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

Maori Males Fully Vaccinated by Age Group for Counties Manukau DHB (Rates per 100,000)



```
#pdf(file="Maori Males Fully Vaccinated by Age Group & highest diff DHB.pdf", width = 10, height = 10)

ggplot(subset(HSUvsERP_MFVacc_highestdiff.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Males Fully Vaccinated by Age Group for Counties Manukau DHB (Rates per
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

dev.off()
```