

Vaccination Rates V2

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

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

```

Total Fully Vaccinated Rates

```

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

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

# Using HSU Weights

## Join on the standard population weights (adds in a column called "Weights")
HSU_TFVacc_nontot.df <- left_join(TFVacc_nontotal.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_tot.df <- HSU_TFVacc_nontot.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_nontot.df <- HSU_TFVacc_nontot.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_nontot.df <- left_join(TFVacc_nontotal.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_tot.df <- ERP_TFVacc_nontot.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_nontot.df <- ERP_TFVacc_nontot.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_nontotal.df <- read_excel("VaccinationDataR Updated HSU2021.xlsx", sheet = "MaoriFullVacc")

```

```

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

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

# Using HSU Weights

## Join on the standard population weights (adds in a column called "Weights")
HSU_MFVacc_nontot.df <- left_join(MFVacc_nontotal.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_tot.df <- HSU_MFVacc_nontot.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 DHB
alpha = 0.05 #added this in for 95% CI
HSU_MFVacc_nontot.df <- HSU_MFVacc_nontot.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_nontot.df <- left_join(MFVacc_nontotal.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_tot.df <- ERP_MFVacc_nontot.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 DHB
alpha = 0.05 #added this in for 95% CI
ERP_MFVacc_nontot.df <- ERP_MFVacc_nontot.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
)

```

Non-Māori Fully Vaccinated Rates

```

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

NMFVacc_nontotal.df <- pivot_longer(NMFVacc_nontotal.df, cols = 4:20, names_to = "AgeGroup", values_to = "Count")
NMFVacc_nontotal.df <- NMFVacc_nontotal.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_NMFVacc_nontot.df <- left_join(NMFVacc_nontotal.df, HSUNMn.df, by = "AgeGroup")

## Create a dataset for the total of each DHB (all age groups summed), doesn't include all DHB named 'Total'
HSU_NMFVacc_tot.df <- HSU_NMFVacc_nontot.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 DHB
alpha = 0.05 #added this in for 95% CI
HSU_NMFVacc_nontot.df <- HSU_NMFVacc_nontot.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_NMFVacc_nontot.df <- left_join(NMFVacc_nontotal.df, ERPNMn.df, by = "AgeGroup")

## Create a dataset for the total of each DHB (all age groups summed), doesn't include all DHB named 'T
ERP_NMFVacc_tot.df <- ERP_NMFVacc_nontot.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 DHB
alpha = 0.05 #added this in for 95% CI
ERP_NMFVacc_nontot.df <- ERP_NMFVacc_nontot.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_DHBtotal.df <- read_excel("VaccinationDataR Updated HSU2021.xlsx", sheet = "TotalFullVacc")
TFVacc_DHBtotal.df <- subset(TFVacc_DHBtotal.df, Group!="Male" & Group!="Female" & DHB=="Total")

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

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

# Using HSU Weights

HSU_TFVacc_DHBtot.df <- left_join(TFVacc_DHBtotal.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_DHBtot.df <- HSU_TFVacc_DHBtot.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_DHBtot.df <- left_join(TFVacc_DHBtotal.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_DHBtot.df <- ERP_TFVacc_DHBtot.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_DHBtotal.df <- read_excel("VaccinationDataR Updated HSU2021.xlsx", sheet = "MaoriFullVacc")
MFVacc_DHBtotal.df <- subset(MFVacc_DHBtotal.df, Group!="Male" & Group!="Female" & DHB=="Total")

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

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

# Using HSU Weights

HSU_MFVacc_DHBtot.df <- left_join(MFVacc_DHBtotal.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_DHBtot.df <- HSU_MFVacc_DHBtot.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_DHBtot.df <- left_join(MFVacc_DHBtotal.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_DHBtot.df <- ERP_MFVacc_DHBtot.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 (Non-Māori pop)

```

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

NMFVacc_DHBtotal.df <- pivot_longer(NMFVacc_DHBtotal.df, cols = 3, values_to = "Total" ) #changing from wide to long
NMFVacc_DHBtotal.df <- pivot_longer(NMFVacc_DHBtotal.df, cols = 3:19, names_to = "AgeGroup", values_to = "Total")

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

# Using HSU Weights

HSU_NMFVacc_DHBtot.df <- left_join(NMFVacc_DHBtotal.df, HSUNMn.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_NMFVacc_DHBtot.df <- HSU_NMFVacc_DHBtot.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_NMFVacc_DHBtot.df <- left_join(NMFVacc_DHBtotal.df, ERPNMn.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_NMFVacc_DHBtot.df <- ERP_NMFVacc_DHBtot.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
  )

```

Plots

Total Fully Vaccinated rates using HSU and ERP, by national total (DHB=total)

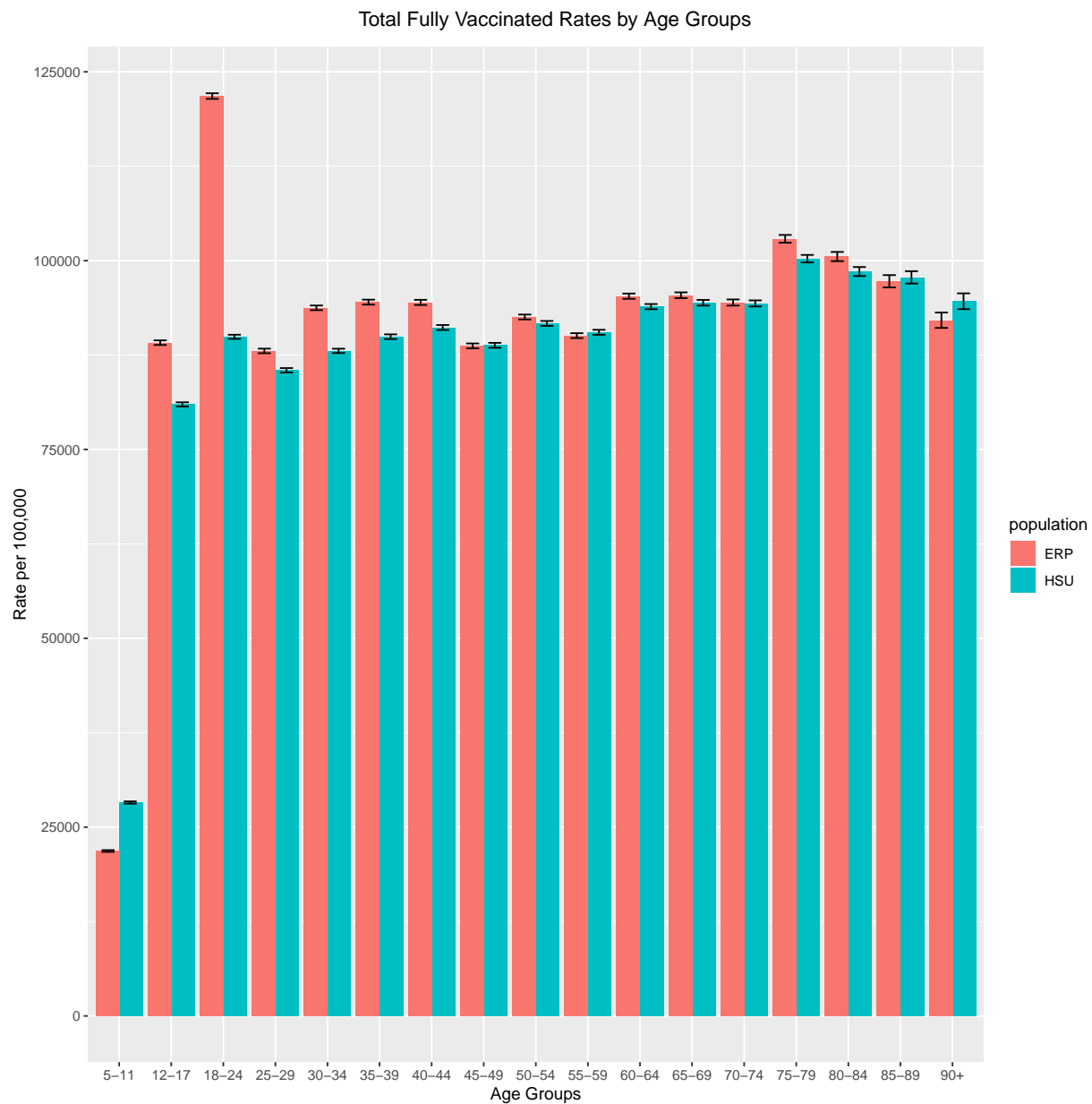
```

level_order <- c("5-11", "12-17", "18-24", "25-29", "30-34", "35-39", "40-44", "45-49", "50-54", "55-59",
# use this to create HSU and ERP on one plot

HSUvsERP_TFVacc_DHB.df <- rbind(
  data.frame(HSU_TFVacc_DHBtot.df, population="HSU"),
  data.frame(ERP_TFVacc_DHBtot.df, population="ERP")
)

```

```
ggplot(subset(HSUvsERP_TFVacc_DHB.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fill =
  geom_col(position = position_dodge()) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr),position = position_dodge(width = 0.85),
  #guides(fill = 'none') +
  plot_annotation(title = "Total Fully Vaccinated Rates by Age Groups") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```



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

ggplot(subset(HSUvsERP_TFVacc_DHB.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fill =
  geom_col(position = position_dodge()) +
```

```

geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr),position = position_dodge(width = 0.85),
#guides(fill = 'none') +
plot_annotation(title = "Total Fully Vaccinated Rates by Age Groups") +
labs(y= "Rate per 100,000",
      x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))

dev.off()

```

Māori Fully Vaccinated rates using HSU and ERP, by national total (DHB=total)

```

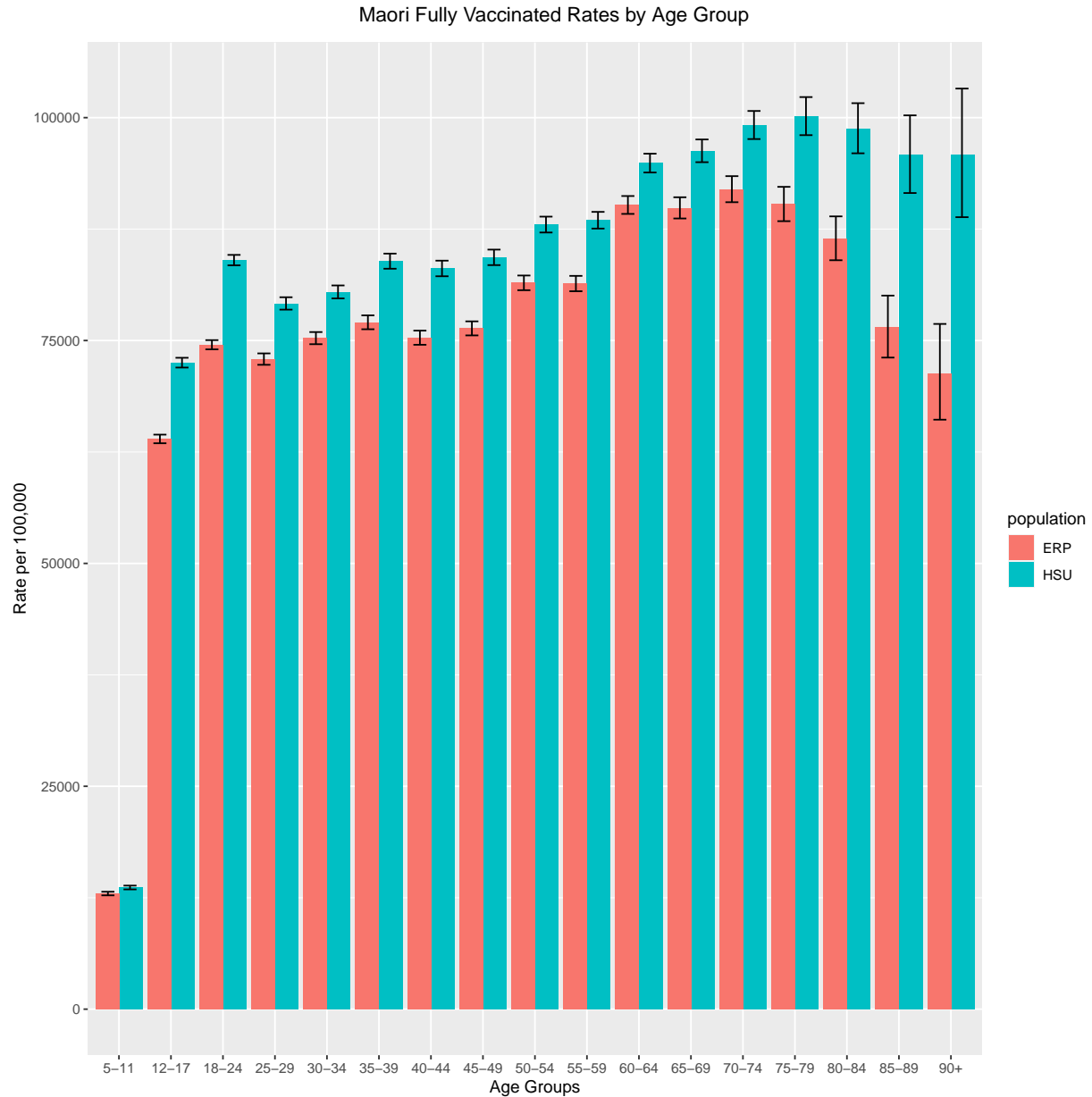
level_order <- c("5-11","12-17", "18-24", "25-29", "30-34", "35-39","40-44", "45-49", "50-54", "55-59",

# use this to create HSU and ERP on one plot

HSUvsERP_MFVacc_DHB.df <- rbind(
  data.frame(HSU_MFVacc_DHBtot.df, population="HSU"),
  data.frame(ERP_MFVacc_DHBtot.df, population="ERP")
)

ggplot(subset(HSVsERP_MFVacc_DHB.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fill =
  geom_col(position = position_dodge()) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr),position = position_dodge(width = 0.85),
#guides(fill = 'none') +
plot_annotation(title = "Maori Fully Vaccinated Rates by Age Group") +
labs(y= "Rate per 100,000",
      x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))

```



```
#pdf(file="Maori Fully Vaccinated Rates by Age Group.pdf", width = 10, height = 10)
```

```
ggplot(subset(HSUvsERP_MFVacc_DHB.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fill =
  geom_col(position = position_dodge()) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr),position = position_dodge(width = 0.85), v
  #guides(fill = 'none') +
  plot_annotation(title = "Maori Fully Vaccinated Rates by Age Group") +
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

```
dev.off()
```

Rate-Ratios

Total Vaccinations RR DHB total by agegroups

code for setting HSU as baseline for Total Vaccinations

```
HSU_TFVacc_baseline.total <- HSU_TFVacc_DHBtot.df
ERP_TFVacc_population.total <- ERP_TFVacc_DHBtot.df

## Rename variables so we can use them after joining to the other dataset (otherwise we get Rate.x and L
HSU_TFVacc_baseline.total <- HSU_TFVacc_baseline.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_baseline.other <- HSU_TFVacc_nontot.df
ERP_TFVacc_population.other <- ERP_TFVacc_nontot.df

HSU_TFVacc_baseline.other$AgeGroup <- as.character(HSU_TFVacc_baseline.other$AgeGroup)
ERP_TFVacc_population.other$AgeGroup <- as.character(ERP_TFVacc_population.other$AgeGroup)

HSU_TFVacc_baseline.other <- HSU_TFVacc_baseline.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_population.other <- ERP_TFVacc_population.other %>%
  dplyr::left_join(HSU_TFVacc_baseline.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_DHBpopulation.df <- ERP_TFVacc_population.total %>%
dplyr::left_join(HSU_TFVacc_baseline.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_population.other)

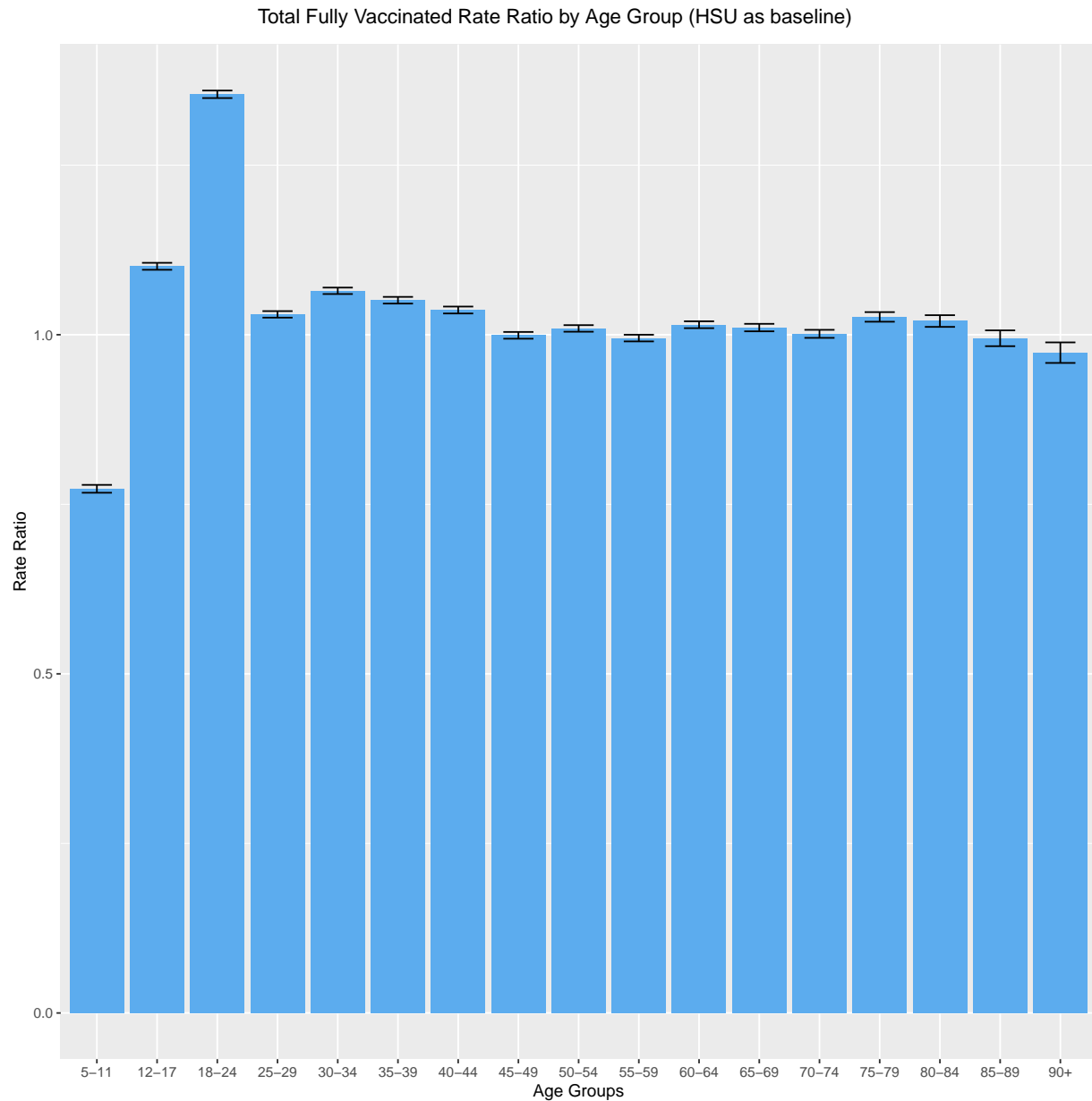
```

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

```

ggplot(subset(TFVacc_DHBpopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, level= level_order), y =
  geom_col(fill = "Steel Blue 2")+
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUpr), width=0.5) +
  plot_annotation(title = "Total 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 Fully Vaccinated Rate Ratio by Age Group (HSU as baseline).pdf", width = 10, height = 10)
```

```
ggplot(subset(TFVacc_DHBpopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, level= level_order), y =
  geom_col(fill = "Steel Blue 2")+
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUpr), width=0.5) +
  plot_annotation(title = "Total 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()
```

Total Māori Vaccinations RR

code for setting ERP as baseline for Māori Vaccinations

```
HSU_MFVacc_baseline.total <- HSU_MFVacc_DHBtot.df
ERP_MFVacc_population.total <- ERP_MFVacc_DHBtot.df

## Rename variables so we can use them after joining to the other dataset (otherwise we get Rate.x and I
HSU_MFVacc_baseline.total <- HSU_MFVacc_baseline.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_baseline.other <- HSU_MFVacc_nontot.df
ERP_MFVacc_population.other <- ERP_MFVacc_nontot.df

HSU_MFVacc_baseline.other$AgeGroup <- as.character(HSU_MFVacc_baseline.other$AgeGroup)
ERP_MFVacc_population.other$AgeGroup <- as.character(ERP_MFVacc_population.other$AgeGroup)

HSU_MFVacc_baseline.other <- HSU_MFVacc_baseline.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_population.other <- ERP_MFVacc_population.other %>%
  dplyr::left_join(HSU_MFVacc_baseline.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, -RateUpr)

MFVacc_DHBpopulation.df <- ERP_MFVacc_population.total %>%
  dplyr::left_join(HSU_MFVacc_baseline.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_population.other)

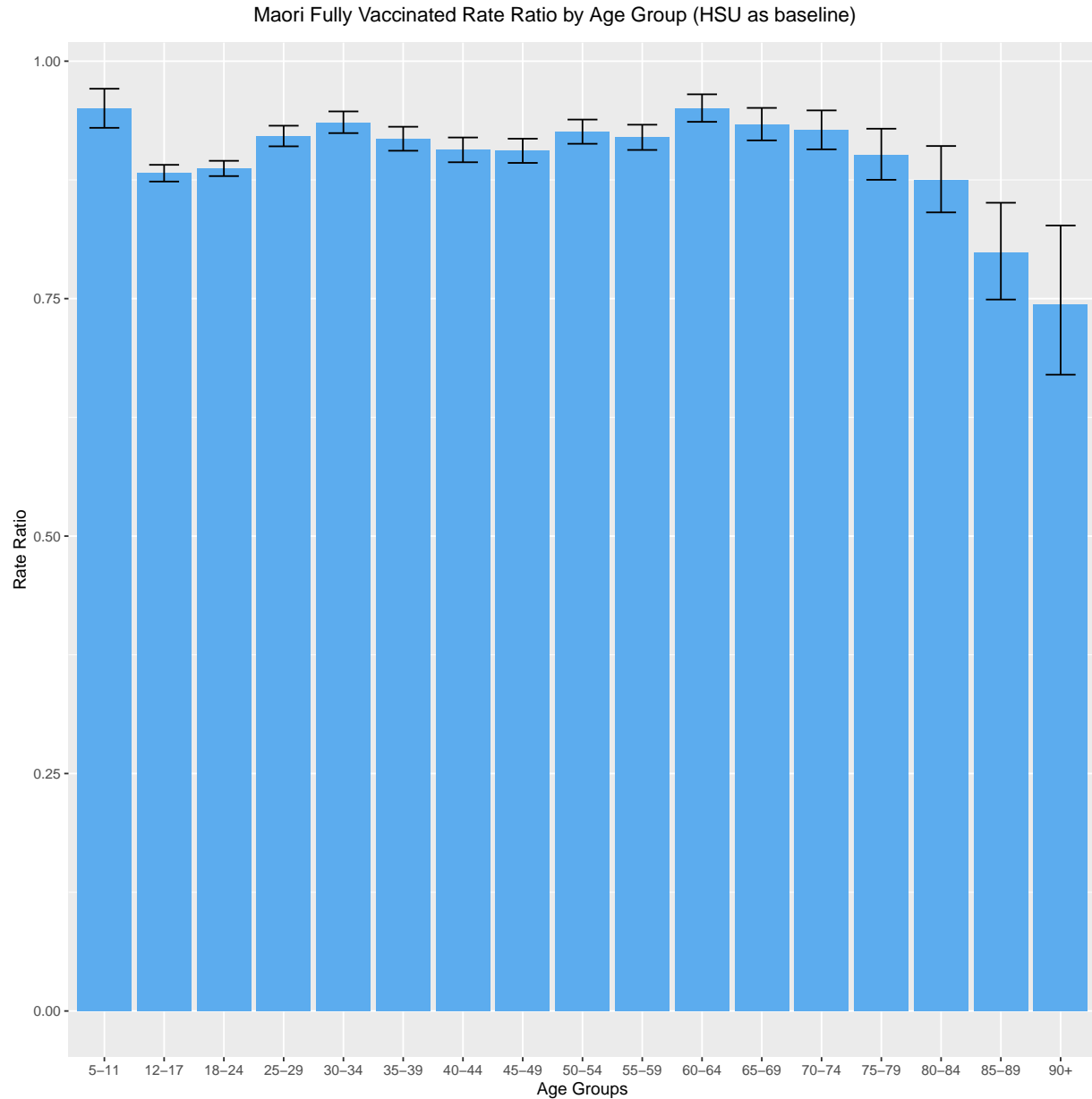
```

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

```

ggplot(subset(MFVacc_DHBpopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, level= level_order), y =
  geom_col(fill = "Steel Blue 2")+
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUpr), width=0.5) +
  plot_annotation(title = "Maori 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 Fully Vaccinated Rate Ratio by Age Group (HSU as baseline).pdf", width = 10, height = 10)

ggplot(subset(MFVacc_DHBpopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, level= level_order), y =
  geom_col(fill = "Steel Blue 2")+
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUp), width=0.5) +
  plot_annotation(title = "Maori 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()
```

Total Non-Māori Vaccinations RR

code for setting ERP as baseline for Non-Māori Vaccinations

```
HSU_NMFVacc_baseline.total <- HSU_NMFVacc_DHBtot.df
ERP_NMFVacc_population.total <- ERP_NMFVacc_DHBtot.df

## Rename variables so we can use them after joining to the other dataset (otherwise we get Rate.x and I
HSU_NMFVacc_baseline.total <- HSU_NMFVacc_baseline.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_NMFVacc_baseline.other <- HSU_NMFVacc_nontot.df
ERP_NMFVacc_population.other <- ERP_NMFVacc_nontot.df

HSU_NMFVacc_baseline.other$AgeGroup <- as.character(HSU_NMFVacc_baseline.other$AgeGroup)
ERP_NMFVacc_population.other$AgeGroup <- as.character(ERP_NMFVacc_population.other$AgeGroup)

HSU_NMFVacc_baseline.other <- HSU_NMFVacc_baseline.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_NMFVacc_population.other <- ERP_NMFVacc_population.other %>%
  dplyr::left_join(HSU_NMFVacc_baseline.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)

NMFVacc_DHBpopulation.df <- ERP_NMFVacc_population.total %>%
  dplyr::left_join(HSU_NMFVacc_baseline.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_NMFVacc_population.other)

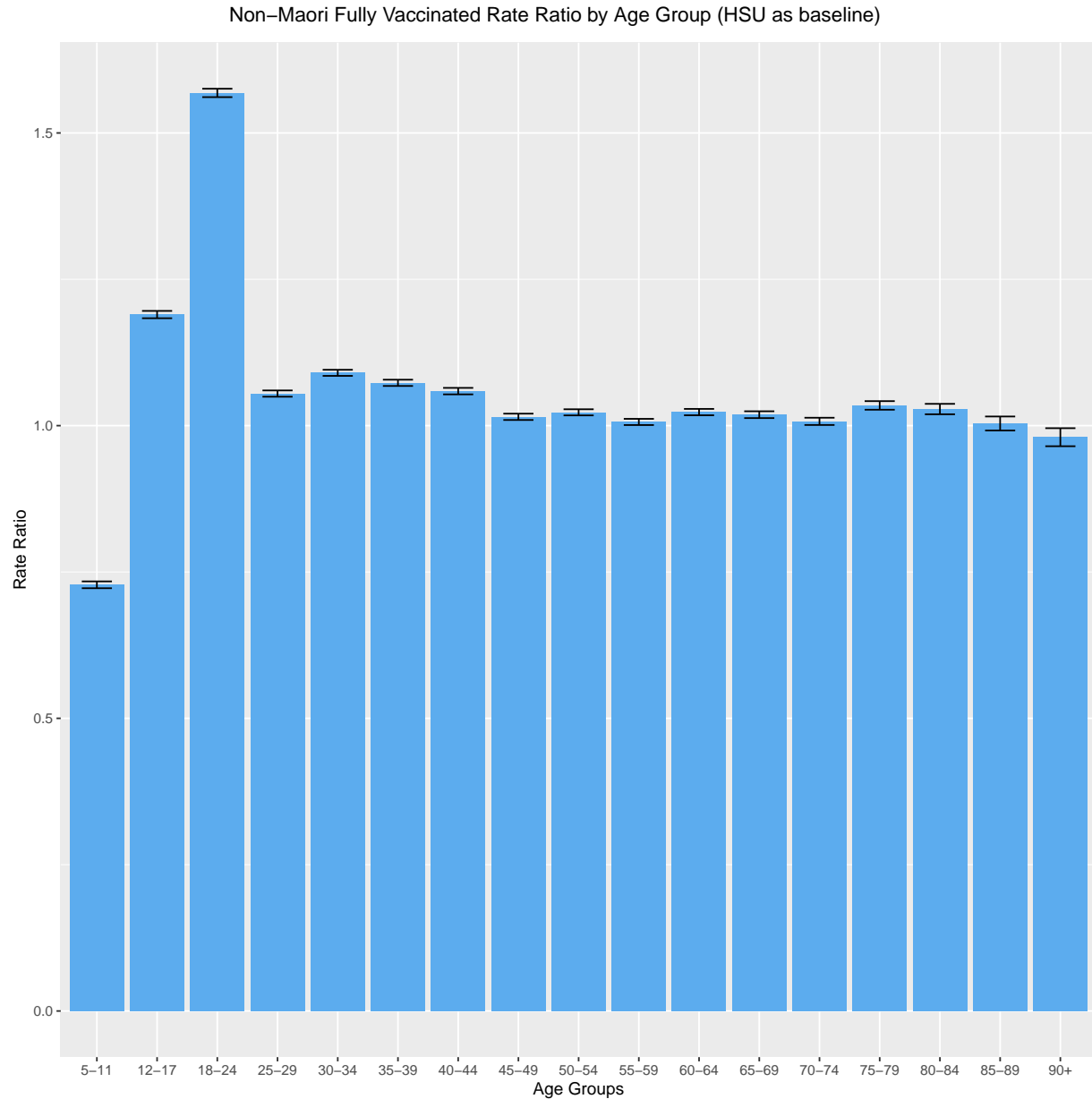
```

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

```

ggplot(subset(NMFVacc_DHBpopulation.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 = "Non-Maori 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="Non-Maori Fully Vaccinated Rate Ratio by Age Group (HSU as baseline).pdf", width = 10, height = 10)

ggplot(subset(NMFVacc_DHBpopulation.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 = "Non-Maori 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()
```

Rate ratio for Fully Vaccinated Rates by national total (DHB=total) with 95% CI's

```
TVacc_RR_DHB.plot <-ggplot(subset(TFVacc_DHBpopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, levels=c("0-4", "5-14", "15-24", "25-34", "35-44", "45-54", "55-64", "65-74", "75-84", "85-94")),
  geom_col()+
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUpr), width=0.5)

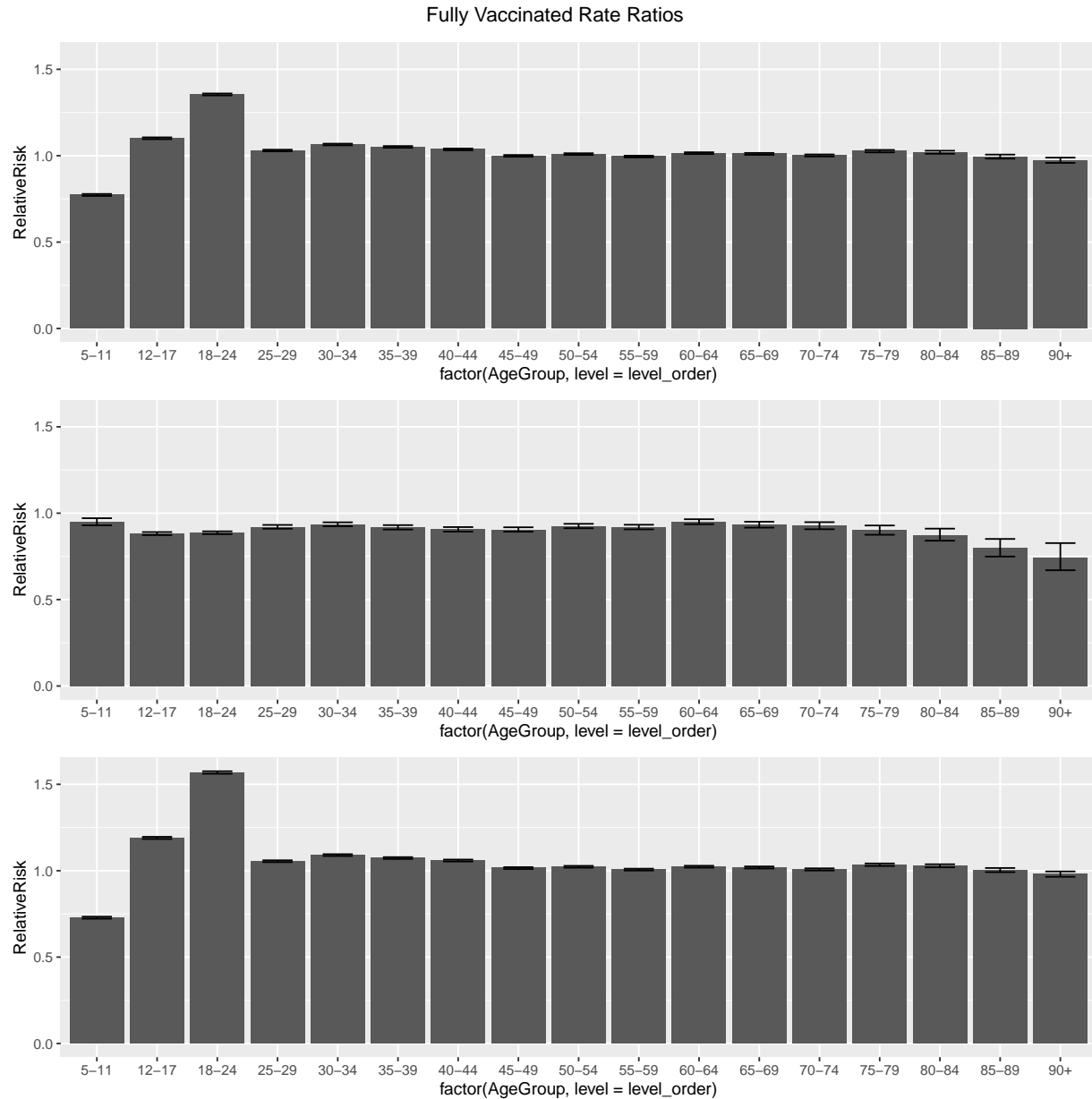
MVacc_RR_DHB.plot <-ggplot(subset(MFVacc_DHBpopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, levels=c("0-4", "5-14", "15-24", "25-34", "35-44", "45-54", "55-64", "65-74", "75-84", "85-94")),
  geom_col()+
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUpr), width=0.5)

NMVacc_RR_DHB.plot <-ggplot(subset(NMFVacc_DHBpopulation.df, DHB == "Total"), aes(x=factor(AgeGroup, levels=c("0-4", "5-14", "15-24", "25-34", "35-44", "45-54", "55-64", "65-74", "75-84", "85-94")),
  geom_col()+
  geom_errorbar(aes(min=RelativeRiskLwr, ymax=RelativeRiskUpr), width=0.5)

FVaccRR_DHBtot.plot <- (TVacc_RR_DHB.plot / MVacc_RR_DHB.plot / NMVacc_RR_DHB.plot) +
  plot_annotation(title = "Fully Vaccinated Rate Ratios") &
  theme(plot.title = element_text(hjust = 0.5))

# fixing the y axes to keep consistent scale
p_ranges_y <- c(ggplot_build(FVaccRR_DHBtot.plot[[1]])$layout$panel_scales_y[[1]]$range$range,
  ggplot_build(FVaccRR_DHBtot.plot[[2]])$layout$panel_scales_y[[1]]$range$range,
  ggplot_build(FVaccRR_DHBtot.plot[[3]])$layout$panel_scales_y[[1]]$range$range)

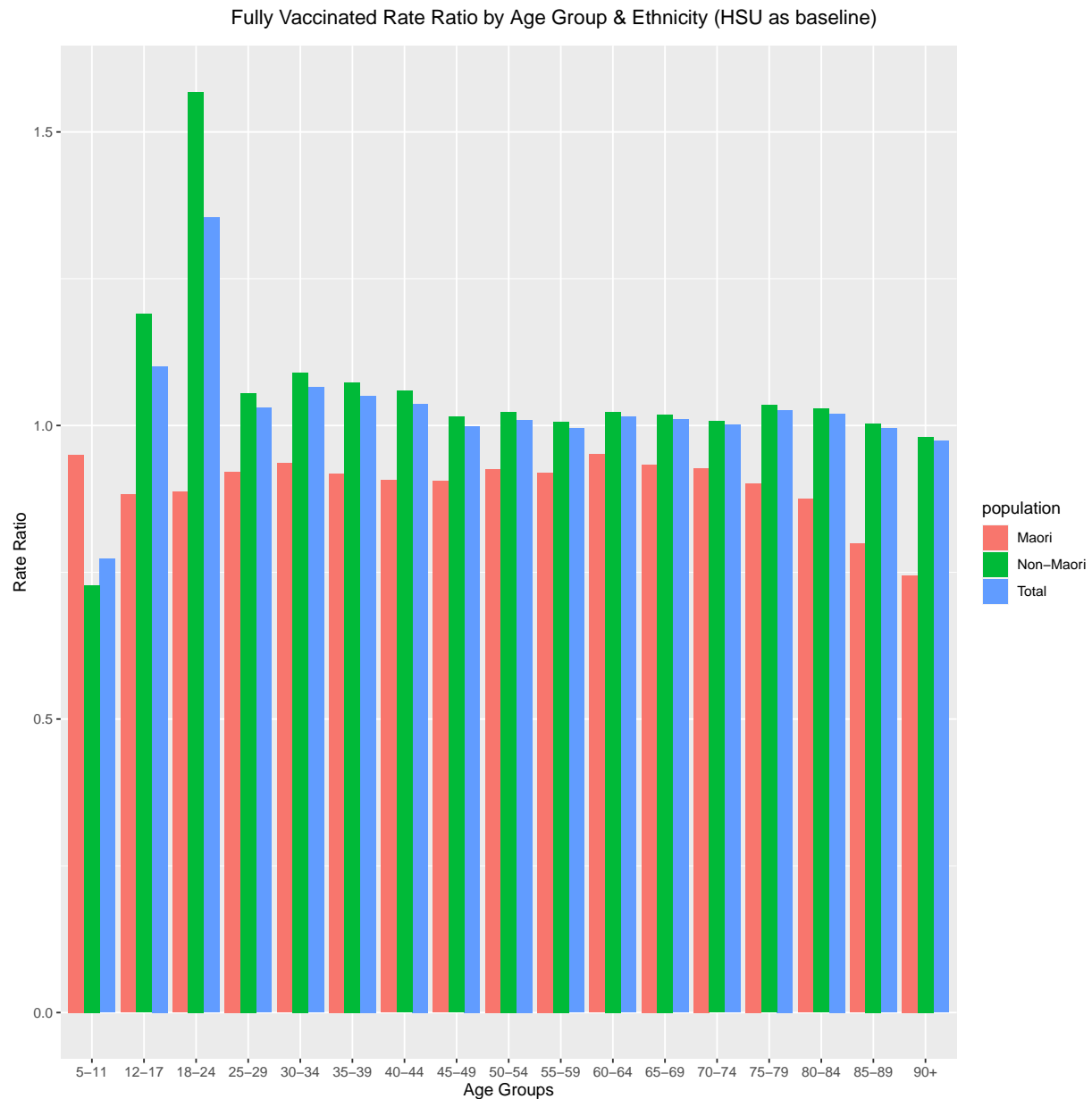
FVaccRR_DHBtot.plot &
  ylim(min(p_ranges_y), max(p_ranges_y))
```



```
AllFVacc_DHBpopulation.df <- rbind(
  data.frame(TFVacc_DHBpopulation.df, population="Total"),
  data.frame(MFVacc_DHBpopulation.df, population="Maori"),
  data.frame(NMFVacc_DHBpopulation.df, population="Non-Maori")
)

ggplot(subset(AllFVacc_DHBpopulation.df), aes(x=factor(AgeGroup, level= level_order), y = RelativeRisk
  geom_col(position = "dodge") +
  #geom_errorbar(aes(ymin=RelativeRiskLwr, ymax=RelativeRiskUpr),position = position_dodge(width = 0.85)
  #guides(fill = 'none') +
  plot_annotation(title = "Fully Vaccinated Rate Ratio by Age Group & Ethnicity (HSU as baseline)") +
  labs(y= "Rate Ratio",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

```
## Warning: Removed 6 rows containing missing values (geom_col).
```



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

ggplot(subset(AllFVacc_DHBpopulation.df), aes(x=factor(AgeGroup, level= level_order), y = RelativeRisk,
  geom_col(position = position_dodge()) +
  #geom_errorbar(aes(ymin=RelativeRiskLwr, ymax=RelativeRiskUpr),position = position_dodge(width = 0.85))
  #guides(fill = 'none') +
  plot_annotation(title = "Fully Vaccinated Rate Ratio by Age Group & Ethnicity (HSU as baseline)") +
  labs(y= "Rate Ratio",
    x= "Age Groups") &
```



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

dev.off()
```

Total Fully Vaccinated Rates by DHB

separated DHB's by rate levels

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

# separated by rate levels

HSU_TFVacc_nontot_high15000.df <- HSU_TFVacc_nontot.df[HSU_TFVacc_nontot.df$DHB %in% c("Auckland", "Waikato", "Bay of Plenty", "Northland", "Midland", "Lakes", "Taranaki", "West Coast", "Taieriaki")]
HSU_TFVacc_nontot_mid10000.df <- HSU_TFVacc_nontot.df[HSU_TFVacc_nontot.df$DHB %in% c("Auckland", "Waikato", "Bay of Plenty", "Northland", "Midland", "Lakes", "Taranaki", "West Coast", "Taieriaki")]
HSU_TFVacc_nontot_mid5000.df <- HSU_TFVacc_nontot.df[HSU_TFVacc_nontot.df$DHB %in% c("Auckland", "Waikato", "Bay of Plenty", "Northland", "Midland", "Lakes", "Taranaki", "West Coast", "Taieriaki")]
HSU_TFVacc_nontot_mid3500.df <- HSU_TFVacc_nontot.df[HSU_TFVacc_nontot.df$DHB %in% c("Auckland", "Waikato", "Bay of Plenty", "Northland", "Midland", "Lakes", "Taranaki", "West Coast", "Taieriaki")]
HSU_TFVacc_nontot_low2000.df <- HSU_TFVacc_nontot.df[HSU_TFVacc_nontot.df$DHB %in% c("Auckland", "Waikato", "Bay of Plenty", "Northland", "Midland", "Lakes", "Taranaki", "West Coast", "Taieriaki")]

ERP_TFVacc_nontot_high15000.df <- ERP_TFVacc_nontot.df[ERP_TFVacc_nontot.df$DHB %in% c("Auckland", "Waikato", "Bay of Plenty", "Northland", "Midland", "Lakes", "Taranaki", "West Coast", "Taieriaki")]
ERP_TFVacc_nontot_mid10000.df <- ERP_TFVacc_nontot.df[ERP_TFVacc_nontot.df$DHB %in% c("Auckland", "Waikato", "Bay of Plenty", "Northland", "Midland", "Lakes", "Taranaki", "West Coast", "Taieriaki")]
ERP_TFVacc_nontot_mid5000.df <- ERP_TFVacc_nontot.df[ERP_TFVacc_nontot.df$DHB %in% c("Auckland", "Waikato", "Bay of Plenty", "Northland", "Midland", "Lakes", "Taranaki", "West Coast", "Taieriaki")]
ERP_TFVacc_nontot_mid3500.df <- ERP_TFVacc_nontot.df[ERP_TFVacc_nontot.df$DHB %in% c("Auckland", "Waikato", "Bay of Plenty", "Northland", "Midland", "Lakes", "Taranaki", "West Coast", "Taieriaki")]
ERP_TFVacc_nontot_low2000.df <- ERP_TFVacc_nontot.df[ERP_TFVacc_nontot.df$DHB %in% c("Auckland", "Waikato", "Bay of Plenty", "Northland", "Midland", "Lakes", "Taranaki", "West Coast", "Taieriaki")]

# plots for high range(approx 15,000)

HSUvsERP_TFVacc_high15000.df <- rbind(
  data.frame(HSU_TFVacc_nontot_high15000.df, population="HSU"),
  data.frame(ERP_TFVacc_nontot_high15000.df, population="ERP")
)

ggplot(subset(HSUvsERP_TFVacc_high15000.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 Fully Vaccinated by Age Group & DHB (Rates approx <15,000 per 100,000)",
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

Total Fully Vaccinated by Age Group & DHB (Rates approx <15,000 per 100,000)



#pdf(file="Total Fully Vaccinated by Age Group & DHB (Rates approx <15,000 per 100,000).pdf", width = 1

```
ggplot(subset(HSUvsERP_TFVacc_high15000.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 Fully Vaccinated by Age Group & DHB (Rates approx <15,000 per 100,000)",
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

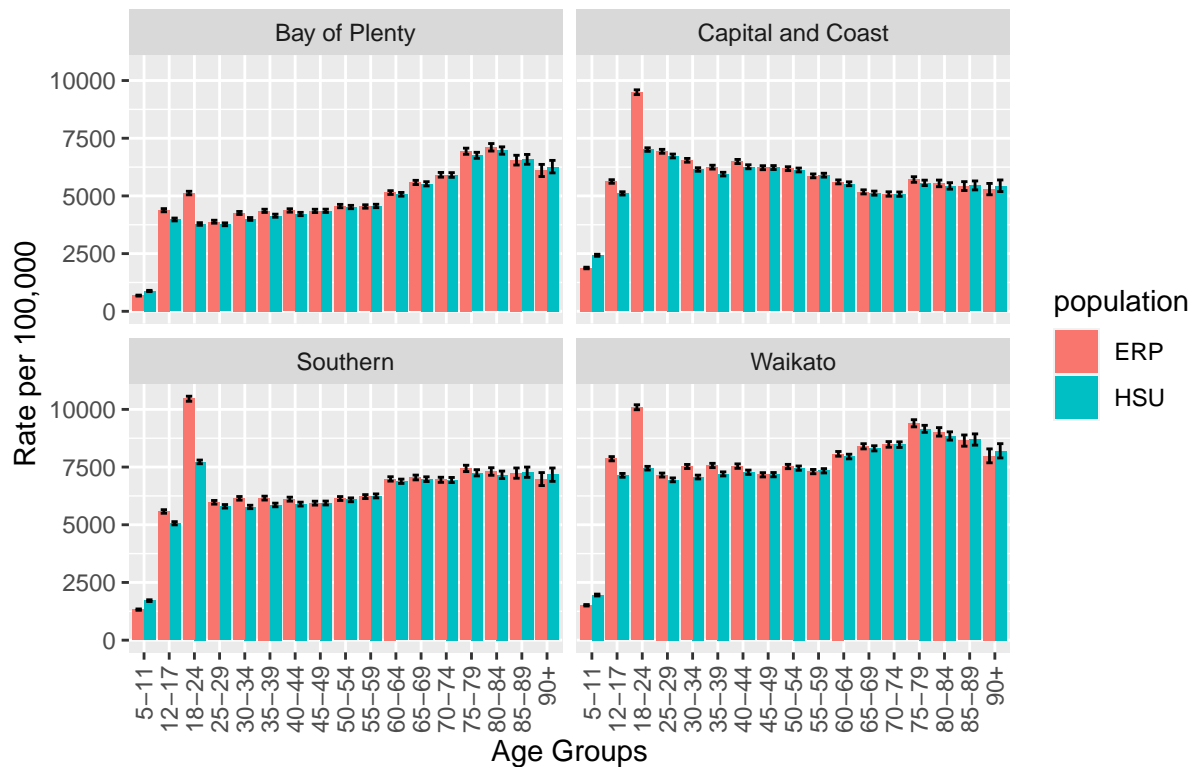
```
dev.off()
```

```
# plots for mid range(less than 10,000)
```

```
HSUvsERP_TFVacc_mid10000.df <- rbind(
  data.frame(HSU_TFVacc_nontot_mid10000.df, population="HSU"),
  data.frame(ERP_TFVacc_nontot_mid10000.df, population="ERP")
)
```

```
ggplot(subset(HSUvsERP_TFVacc_mid10000.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 Fully Vaccinated by Age Group & DHB (Rates approx <10,000 per 100,000)
  labs(y= "Rate per 100,000",
        x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

Total Fully Vaccinated by Age Group & DHB (Rates approx <10,000 per 100,000)



```
#pdf(file="Total Fully Vaccinated by Age Group & DHB (Rates approx <10,000 per 100,000).pdf", width = 1
```

```
ggplot(subset(HSUvsERP_TFVacc_mid10000.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 Fully Vaccinated by Age Group & DHB (Rates approx <10,000 per 100,000)",
labs(y= "Rate per 100,000",
x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))

dev.off()

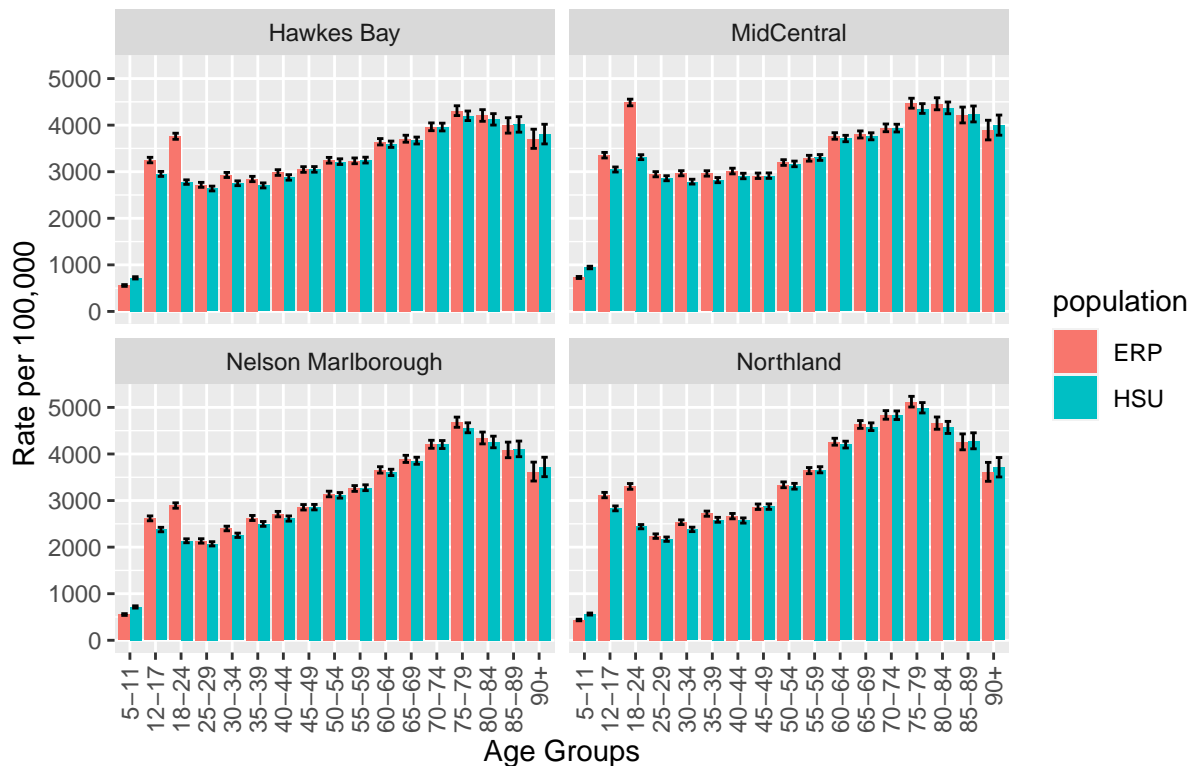
# plots for mid range (less than 5,000)

HSUvsERP_TFVacc_mid5000.df <- rbind(
  data.frame(HSU_TFVacc_nontot_mid5000.df, population="HSU"),
  data.frame(ERP_TFVacc_nontot_mid5000.df, population="ERP")
)

ggplot(subset(HSUvsERP_TFVacc_mid5000.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_Gamma1Up), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Total Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)",
labs(y= "Rate per 100,000",
x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))

```

Total Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)



```
#pdf(file="Total Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000).pdf", width = 10)

ggplot(subset(HSUvsERP_TFVacc_mid5000.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fi
  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 Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)",
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

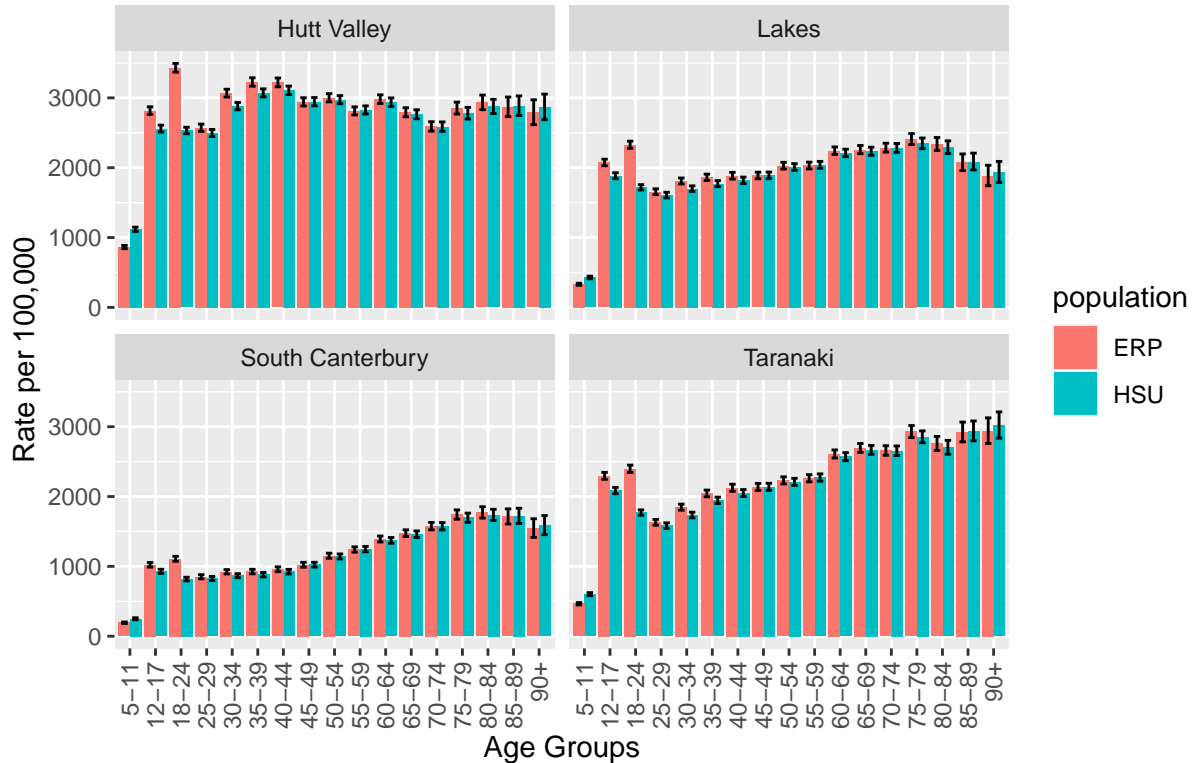
dev.off()
```

```
# plots for mid range(less than 3500)

HSUvsERP_TFVacc_mid3500.df <- rbind(
  data.frame(HSU_TFVacc_nontot_mid3500.df, population="HSU"),
  data.frame(ERP_TFVacc_nontot_mid3500.df, population="ERP")
)

ggplot(subset(HSUvsERP_TFVacc_mid3500.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fi
  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 Fully Vaccinated by Age Group & DHB (Rates approx <3,500 per 100,000)",
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

Total Fully Vaccinated by Age Group & DHB (Rates approx <3,500 per 100,000)



```
#pdf(file="Total Fully Vaccinated by Age Group & DHB (Rates approx <3,500 per 100,000).pdf", width = 10
```

```
ggplot(subset(HSUvsERP_TFVacc_mid3500.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fi
  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 Fully Vaccinated by Age Group & DHB (Rates approx <3,500 per 100,000)",
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

```
dev.off()
```

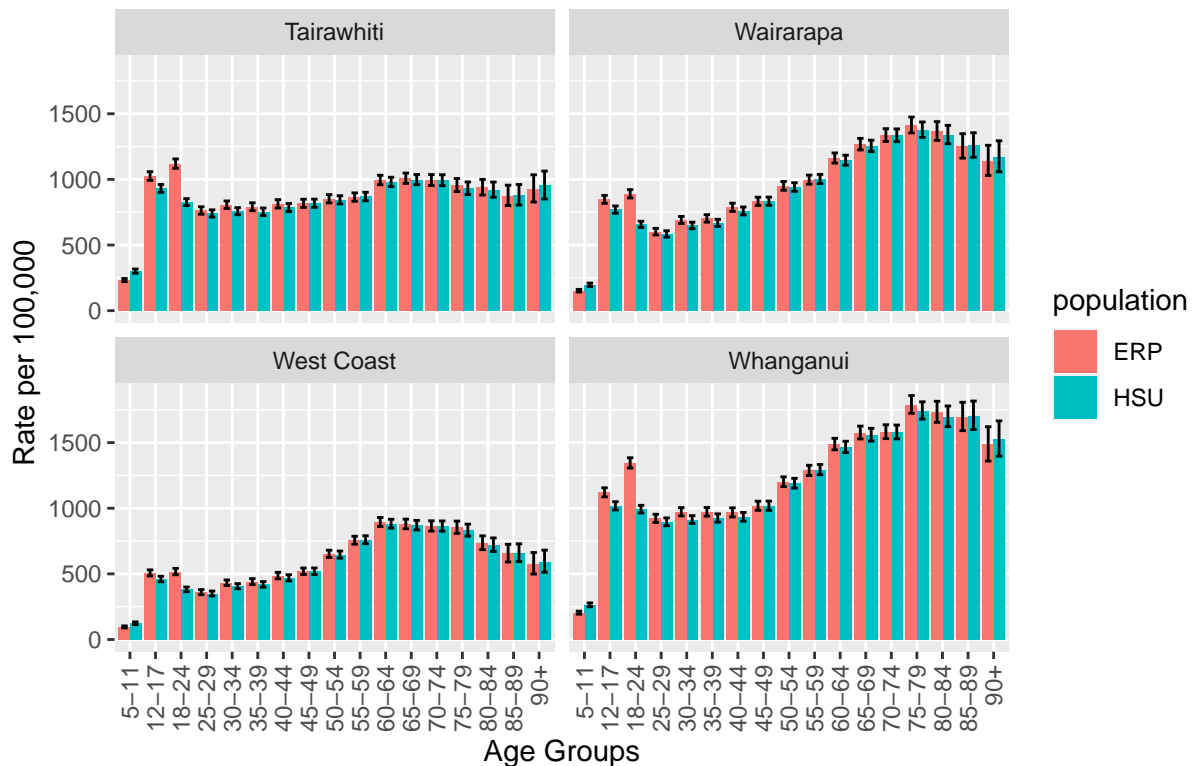
```
# plots for low range(less than 2500)
```

```
HSUvsERP_TFVacc_low2000.df <- rbind(
  data.frame(HSU_TFVacc_nontot_low2000.df, population="HSU"),
  data.frame(ERP_TFVacc_nontot_low2000.df, population="ERP")
)
```

```
ggplot(subset(HSUvsERP_TFVacc_low2000.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fi
  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 Fully Vaccinated by Age Group & DHB (Rates approx <2,000 per 100,000)",
labs(y= "Rate per 100,000",
x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))
```

Total Fully Vaccinated by Age Group & DHB (Rates approx <2,000 per 100,000)



```
#pdf(file="Total Fully Vaccinated by Age Group & DHB (Rates approx <2,000 per 100,000).pdf", width = 10
ggplot(subset(HSUvsERP_TFVacc_low2000.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fi
  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 Fully Vaccinated by Age Group & DHB (Rates approx <2,000 per 100,000)",
  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
```

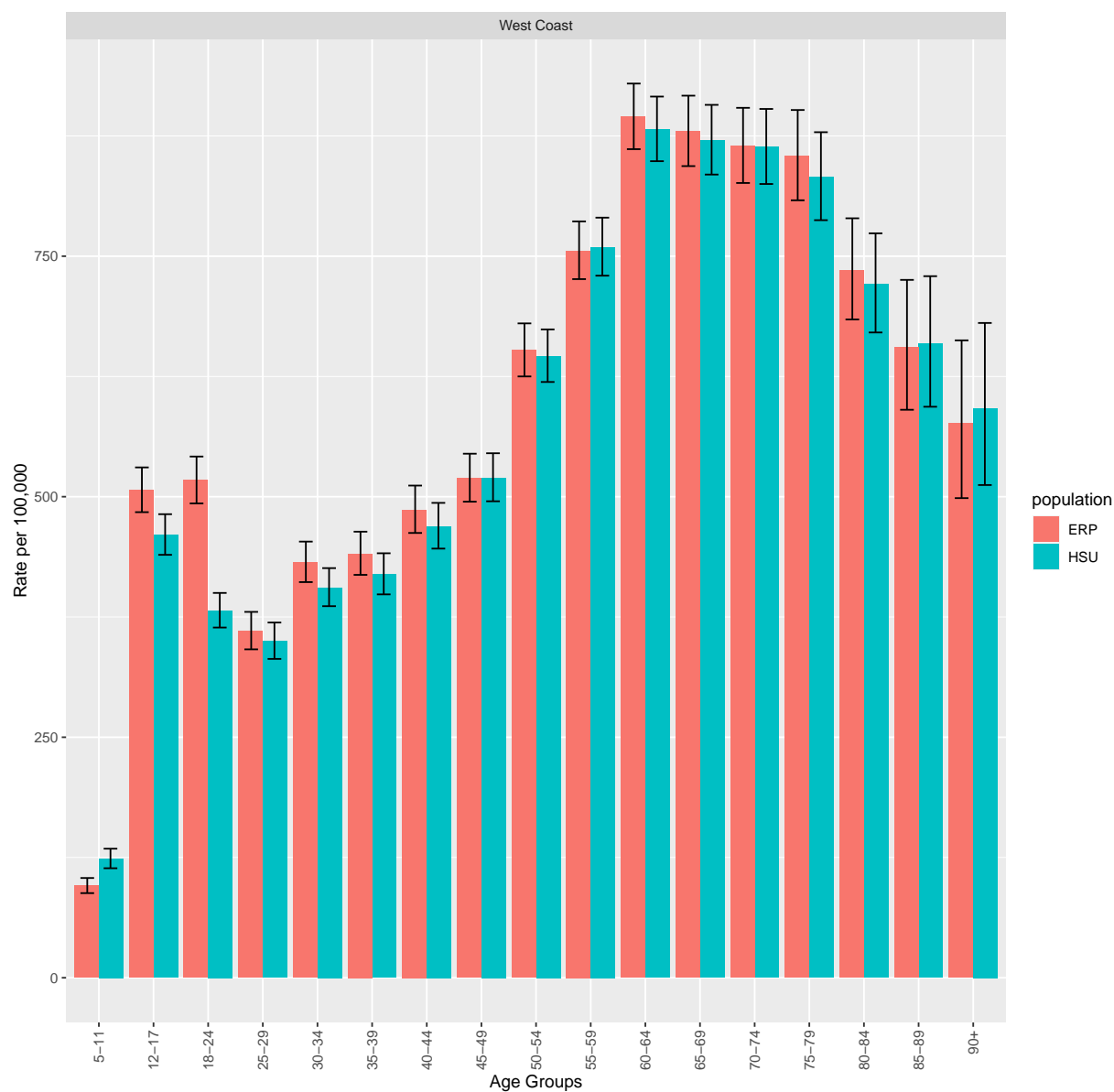
```
HSU_TFVacc_nontot_highest.df <- HSU_TFVacc_nontot.df[HSU_TFVacc_nontot.df$DHB %in% c("Counties Manukau",  
HSU_TFVacc_nontot_lowest.df <- HSU_TFVacc_nontot.df[HSU_TFVacc_nontot.df$DHB %in% c("West Coast"),]
```

```
ERP_TFVacc_nontot_highest.df <- ERP_TFVacc_nontot.df[ERP_TFVacc_nontot.df$DHB %in% c("Counties Manukau",  
ERP_TFVacc_nontot_lowest.df <- ERP_TFVacc_nontot.df[ERP_TFVacc_nontot.df$DHB %in% c("West Coast"),]
```

```
HSUvsERP_TFVacc_low.df <- rbind(  
  data.frame(HSU_TFVacc_nontot_lowest.df, population="HSU"),  
  data.frame(ERP_TFVacc_nontot_lowest.df, population="ERP")  
)
```

```
ggplot(subset(HSUvsERP_TFVacc_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 = "Total Fully Vaccinated by Age Group for West Coast DHB (Lowest Rates per 100  
  labs(y= "Rate per 100,000",  
    x= "Age Groups") &  
  theme(plot.title = element_text(hjust = 0.5))
```


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



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

```
ggplot(subset(HSUvsERP_TFVacc_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 = "Total Fully Vaccinated by Age Group for West Coast DHB (Lowest Rates per 100
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

```
dev.off()
```

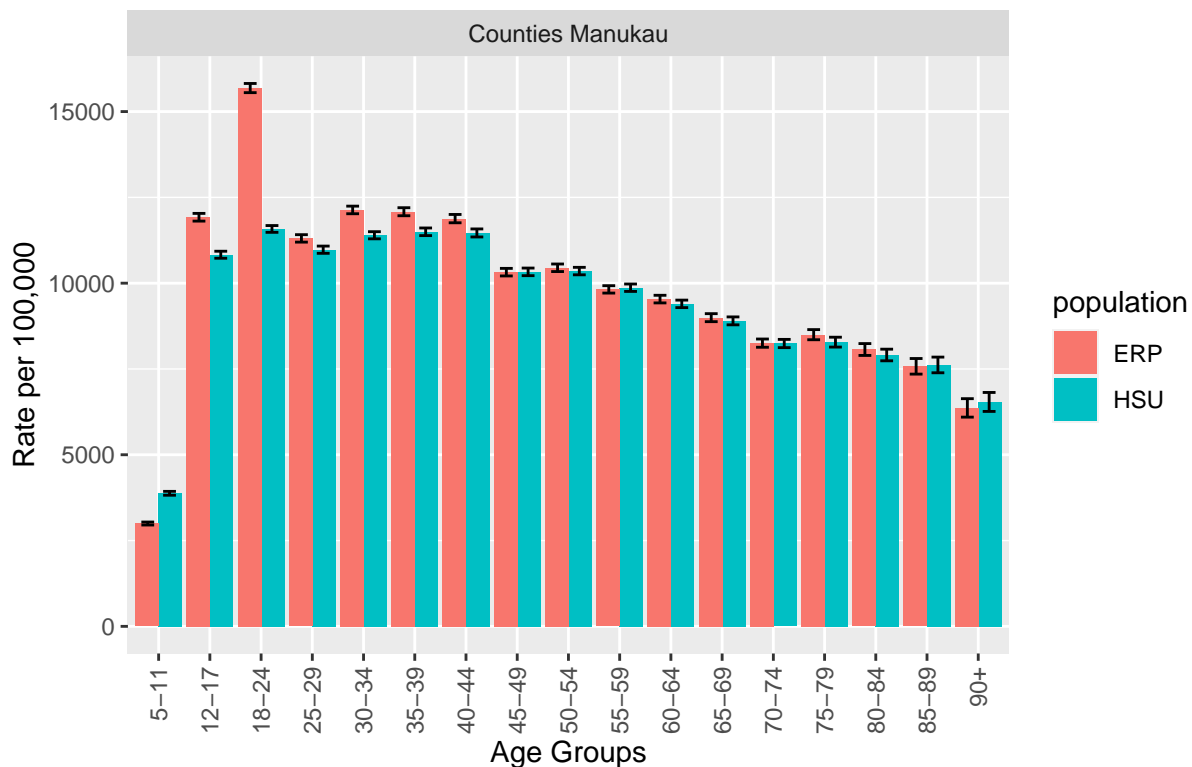
```

HSUvsERP_TFVacc_high.df <- rbind(
  data.frame(HSU_TFVacc_nontot_highest.df, population="HSU"),
  data.frame(ERP_TFVacc_nontot_highest.df, population="ERP")
)

ggplot(subset(HSUvsERP_TFVacc_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 = "Total Fully Vaccinated by Age Group for Counties Manukau DHB (Highest Rates per 100,000)",
  labs(y= "Rate per 100,000",
  x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

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



```

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

ggplot(subset(HSUvsERP_TFVacc_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 = "Total Fully Vaccinated by Age Group for Counties Manukau 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

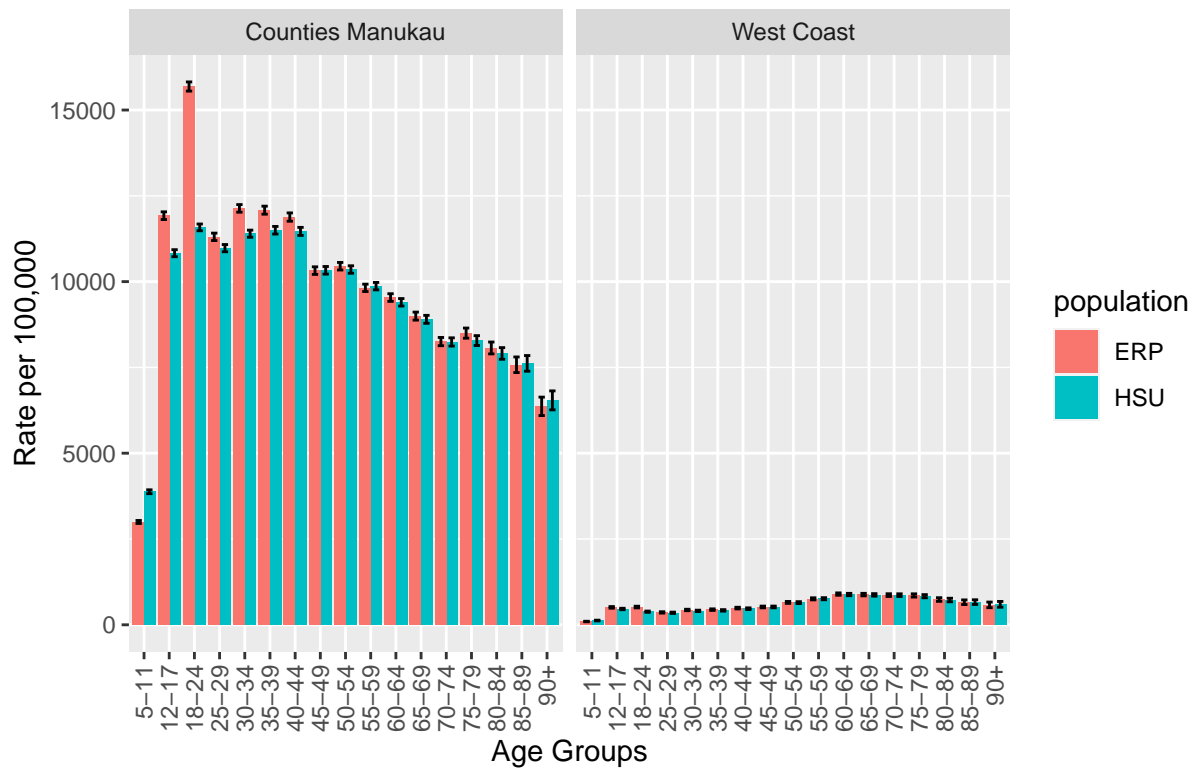
HSU_TFVacc_nontot_lowvshigh.df <- HSU_TFVacc_nontot.df[HSU_TFVacc_nontot.df$DHB %in% c("Counties Manukau", "West Coast"),]
ERP_TFVacc_nontot_lowvshigh.df <- ERP_TFVacc_nontot.df[ERP_TFVacc_nontot.df$DHB %in% c("Counties Manukau", "West Coast"),]

HSUvsERP_TFVacc_lowvshigh.df <- rbind(
  data.frame(HSU_TFVacc_nontot_lowvshigh.df, population="HSU"),
  data.frame(ERP_TFVacc_nontot_lowvshigh.df, population="ERP")
)

ggplot(subset(HSVsERP_TFVacc_lowvshigh.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, population = 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), width = 0.2) +
  facet_wrap(~DHB) +
  plot_annotation(title = "Total Fully Vaccinated by Age Group & DHB (Lowest vs. Highest rates per 100,000)",
    labs(y= "Rate per 100,000",
      x= "Age Groups") &
    theme(plot.title = element_text(hjust = 0.5))

```

Total Fully Vaccinated by Age Group & DHB (Lowest vs. Highest rates per 100,000)



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

ggplot(subset(HSUvsERP_TFVacc_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 = "Total Fully Vaccinated by Age Group & DHB (Lowest vs. Highest rates per 100,000)",
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

dev.off()
```

#separating by DHB for Māori

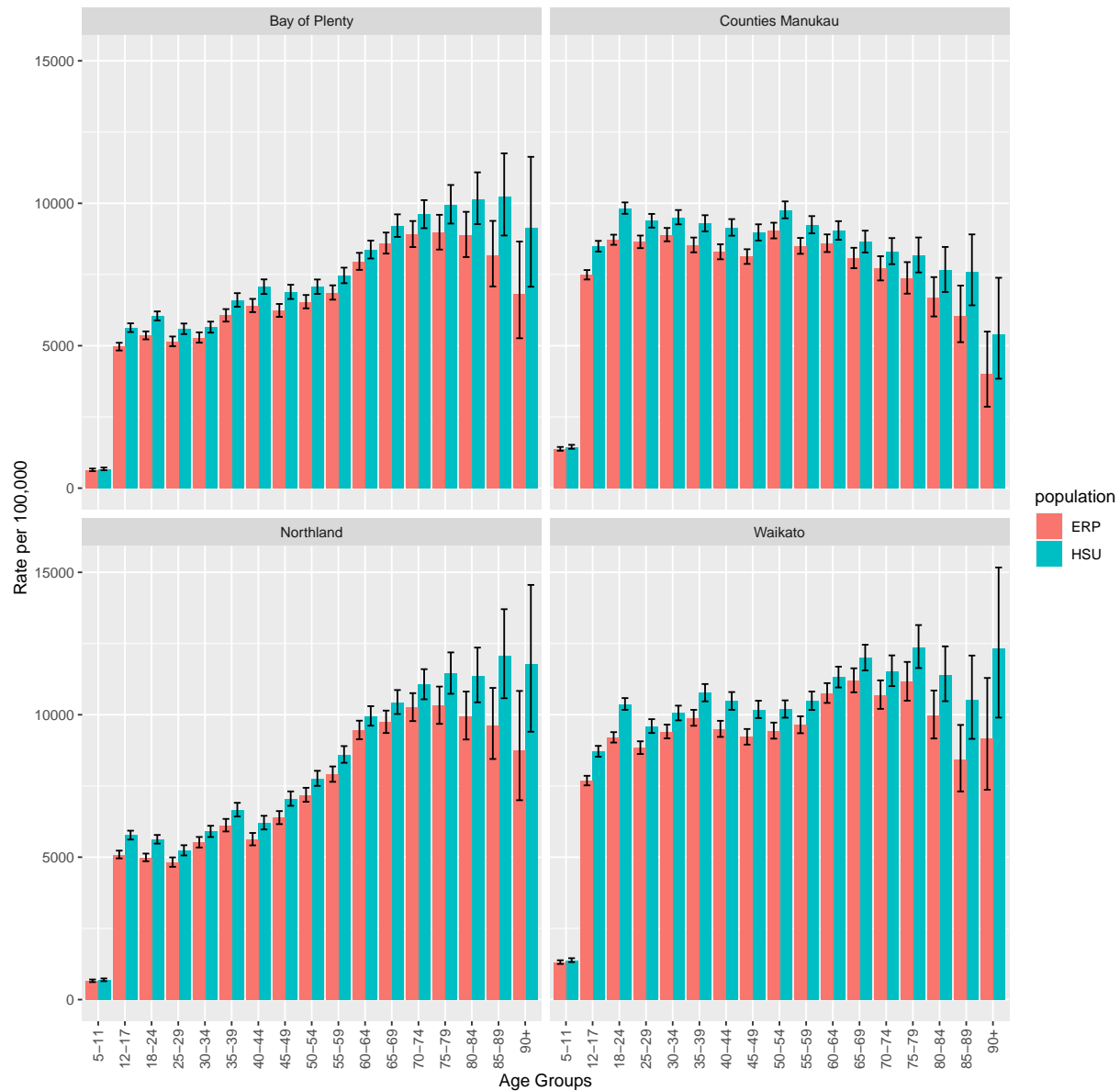
```
HSU_MFVacc_nontot_high15000.df <- HSU_MFVacc_nontot.df[HSU_MFVacc_nontot.df$DHB %in% c("Northland", "Waikato", "Bay of Plenty", "Auckland", "Hawke's Bay", "Manawatu", "Wellington", "Tairāhema", "Otago", "Southland")]
HSU_MFVacc_nontot_mid10000.df <- HSU_MFVacc_nontot.df[HSU_MFVacc_nontot.df$DHB %in% c("Waitemata", "Lakes", "Tairāhema", "Otago", "Southland")]
HSU_MFVacc_nontot_mid1.df <- HSU_MFVacc_nontot.df[HSU_MFVacc_nontot.df$DHB %in% c("Canterbury", "South Canterbury", "Wellington", "Hawke's Bay", "Manawatu", "Bay of Plenty", "Auckland", "Northland", "Waikato")]
HSU_MFVacc_nontot_mid2.df <- HSU_MFVacc_nontot.df[HSU_MFVacc_nontot.df$DHB %in% c("MidCentral", "Hutt Valley", "Wellington", "Hawke's Bay", "Manawatu", "Bay of Plenty", "Auckland", "Northland", "Waikato")]
HSU_MFVacc_nontot_low.df <- HSU_MFVacc_nontot.df[HSU_MFVacc_nontot.df$DHB %in% c("South Canterbury", "Wellington", "Hawke's Bay", "Manawatu", "Bay of Plenty", "Auckland", "Northland", "Waikato")]

ERP_MFVacc_nontot_high15000.df <- ERP_MFVacc_nontot.df[ERP_MFVacc_nontot.df$DHB %in% c("Northland", "Waikato", "Bay of Plenty", "Auckland", "Hawke's Bay", "Manawatu", "Wellington", "Tairāhema", "Otago", "Southland")]
ERP_MFVacc_nontot_mid10000.df <- ERP_MFVacc_nontot.df[ERP_MFVacc_nontot.df$DHB %in% c("Waitemata", "Lakes", "Tairāhema", "Otago", "Southland")]
ERP_MFVacc_nontot_mid1.df <- ERP_MFVacc_nontot.df[ERP_MFVacc_nontot.df$DHB %in% c("Canterbury", "South Canterbury", "Wellington", "Hawke's Bay", "Manawatu", "Bay of Plenty", "Auckland", "Northland", "Waikato")]
ERP_MFVacc_nontot_mid2.df <- ERP_MFVacc_nontot.df[ERP_MFVacc_nontot.df$DHB %in% c("MidCentral", "Hutt Valley", "Wellington", "Hawke's Bay", "Manawatu", "Bay of Plenty", "Auckland", "Northland", "Waikato")]
ERP_MFVacc_nontot_low.df <- ERP_MFVacc_nontot.df[ERP_MFVacc_nontot.df$DHB %in% c("South Canterbury", "Wellington", "Hawke's Bay", "Manawatu", "Bay of Plenty", "Auckland", "Northland", "Waikato")]

# plots for high range(approx 15000)
HSUvsERP_MFVacc_high15000.df <- rbind(
  data.frame(HSU_MFVacc_nontot_high15000.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_high15000.df, population="ERP")
)

ggplot(subset(HSUvsERP_MFVacc_high15000.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 Fully Vaccinated by Age Group & DHB (Rates approx <15,000 per 100,000)",
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

Maori Fully Vaccinated by Age Group & DHB (Rates approx <15,000 per 100,000)



```
#pdf(file="Maori Fully Vaccinated by Age Group & DHB (Rates approx <15,000 per 100,000).pdf", width = 1
```

```
ggplot(subset(HSUvsERP_MFVacc_high15000.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 Fully Vaccinated by Age Group & DHB (Rates approx <15,000 per 100,000)",
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

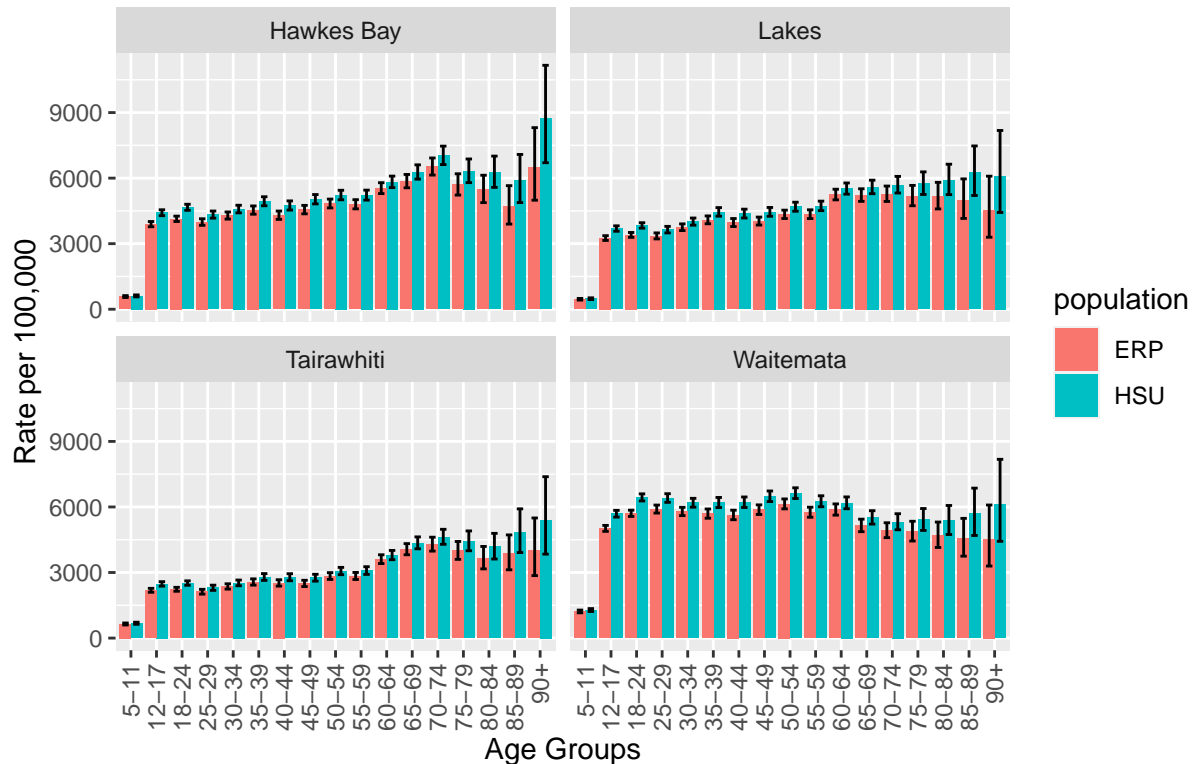
```
dev.off()
```

```
# plots for mid range(approx 10,000)
```

```
HSUvsERP_MFVacc_mid10000.df <- rbind(
  data.frame(HSU_MFVacc_nontot_mid10000.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_mid10000.df, population="ERP")
)
```

```
ggplot(subset(HSUvsERP_MFVacc_mid10000.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 = "Maori Fully Vaccinated by Age Group & DHB (Rates approx <7,500 per 100,000)",
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

Maori Fully Vaccinated by Age Group & DHB (Rates approx <7,500 per 100,000)



```
#pdf(file="Maori Fully Vaccinated by Age Group & DHB (Rates approx <7,500 per 100,000)1.pdf", width = 1
```

```
ggplot(subset(HSUvsERP_MFVacc_mid10000.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 = "Maori Fully Vaccinated by Age Group & DHB (Rates approx <7,500 per 100,000)",
```

```

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

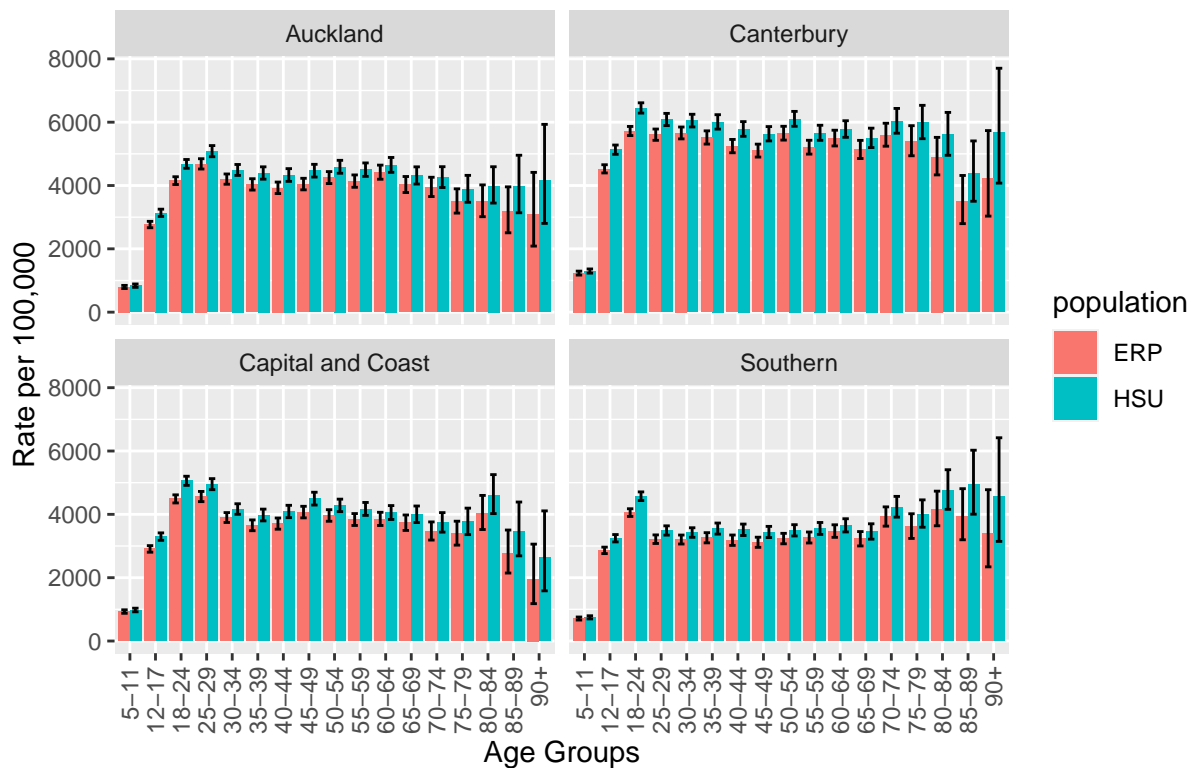
dev.off()

# mid range
HSUvsERP_MFVacc_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_mid1.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 Fully Vaccinated by Age Group & DHB (Rates approx <7,500 per 100,000)",
  labs(y= "Rate per 100,000",
       x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

Maori Fully Vaccinated by Age Group & DHB (Rates approx <7,500 per 100,000)



```

#pdf(file="Maori Fully Vaccinated by Age Group & DHB (Rates approx <7,500 per 100,000)2.pdf", width = 10, height = 10)

ggplot(subset(HSVsERP_MFVacc_mid1.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 Fully Vaccinated by Age Group & DHB (Rates approx <7,500 per 100,000)",
labs(y= "Rate per 100,000",
x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))

dev.off()

```

```

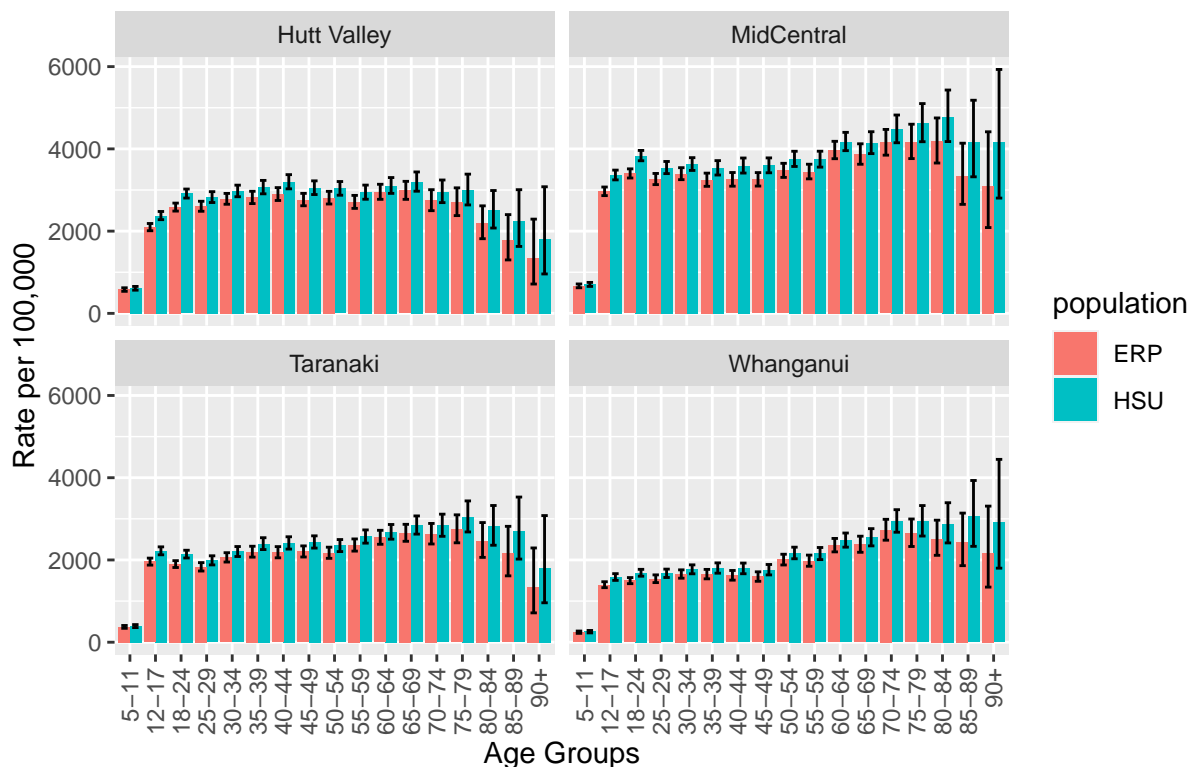
# Capital and Coast, Nelson Marlborough, West Coast, Canterbury, South Canterbury, Southern

HSUvsERP_MFVacc_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_mid2.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 Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)",
labs(y= "Rate per 100,000",
x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))

```


Maori Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)



#pdf(file="Maori Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000).pdf", width = 10

```
ggplot(subset(HSUvsERP_MFVacc_mid2.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 Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)",
  labs(y= "Rate per 100,000",
  x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

dev.off()

#low

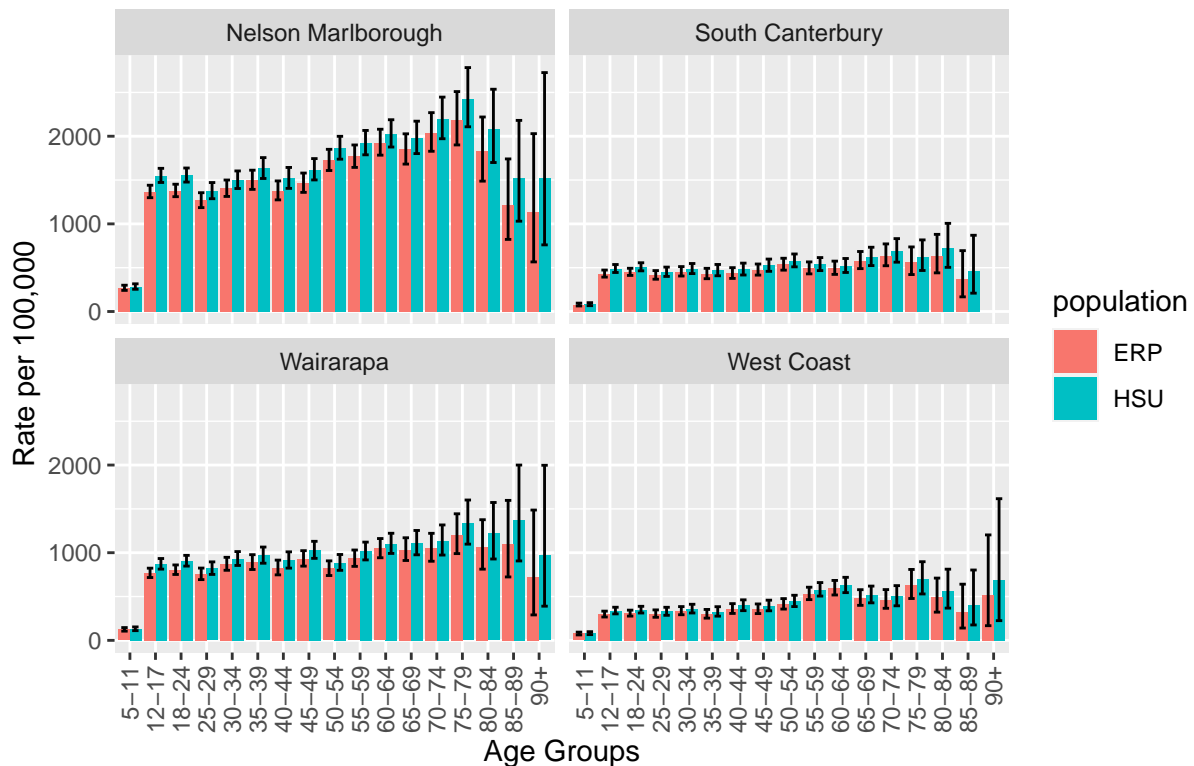
```
HSUvsERP_MFVacc_low.df <- rbind(
  data.frame(HSU_MFVacc_nontot_low.df, population="HSU"),
  data.frame(ERP_MFVacc_nontot_low.df, population="ERP")
)
```

```
ggplot(subset(HSUvsERP_MFVacc_low.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 Fully Vaccinated by Age Group & DHB (Rates approx <3,000 per 100,000)",
```

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

```
## Warning: Removed 2 rows containing missing values (geom_col).
```

Maori Fully Vaccinated by Age Group & DHB (Rates approx <3,000 per 100,000)



```
#pdf(file="Maori Fully Vaccinated by Age Group & DHB (Rates approx <3,000 per 100,000).pdf", width = 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_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Maori Fully Vaccinated by Age Group & DHB (Rates approx <3,000 per 100,000)",
  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
```

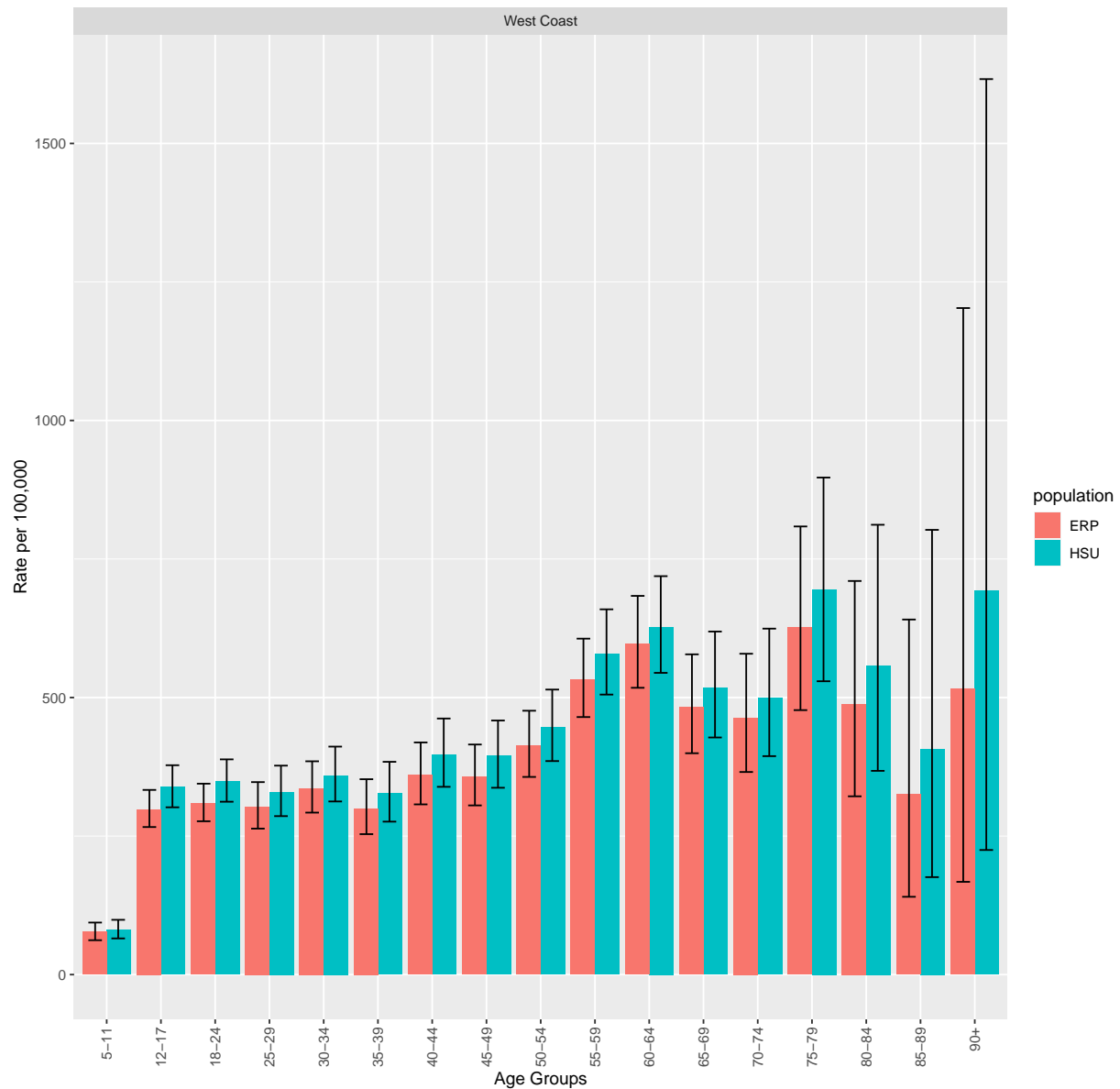
```
HSU_MFVacc_nontot_highest.df <- HSU_MFVacc_nontot.df[HSU_MFVacc_nontot.df$DHB %in% c("Waikato"),]  
HSU_MFVacc_nontot_lowest.df <- HSU_MFVacc_nontot.df[HSU_MFVacc_nontot.df$DHB %in% c("West Coast"),]
```

```
ERP_MFVacc_nontot_highest.df <- ERP_MFVacc_nontot.df[ERP_MFVacc_nontot.df$DHB %in% c("Waikato"),]  
ERP_MFVacc_nontot_lowest.df <- ERP_MFVacc_nontot.df[ERP_MFVacc_nontot.df$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(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_Gamma1Upr), position = position_dodge(width = 0.85),  
  facet_wrap(~DHB) +  
  plot_annotation(title = "Maori Fully Vaccinated by Age Group for West Coast DHB (Lowest Rates per 100  
  labs(y= "Rate per 100,000",  
    x= "Age Groups") &  
  theme(plot.title = element_text(hjust = 0.5))
```

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



```
#pdf(file="Maori 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 Fully Vaccinated by Age Group for West Coast DHB (Lowest Rates per 100
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

```
dev.off()
```

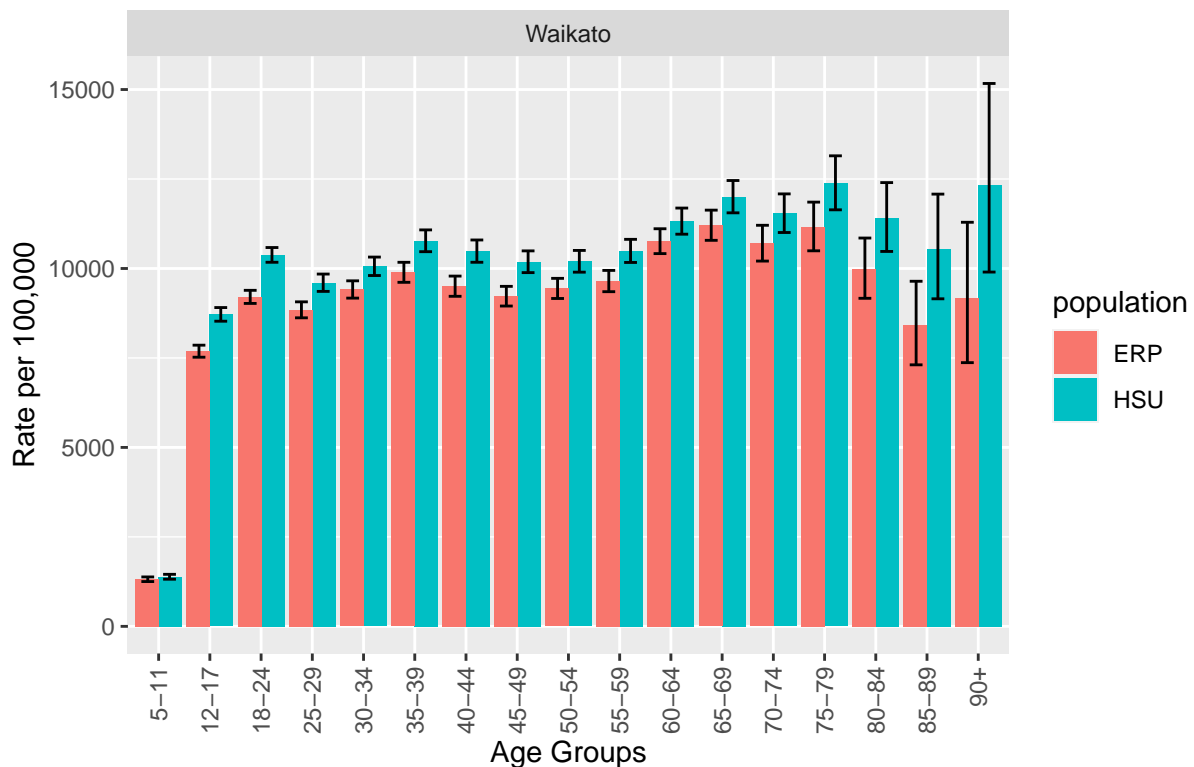
```

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 Fully Vaccinated by Age Group for Waikato DHB (Highest Rates per 100,000)",
  labs(y= "Rate per 100,000",
  x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

Maori Fully Vaccinated by Age Group for Waikato DHB (Highest Rates per 100,000)



```

#pdf(file="Maori 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 Fully Vaccinated by Age Group for Waikato 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

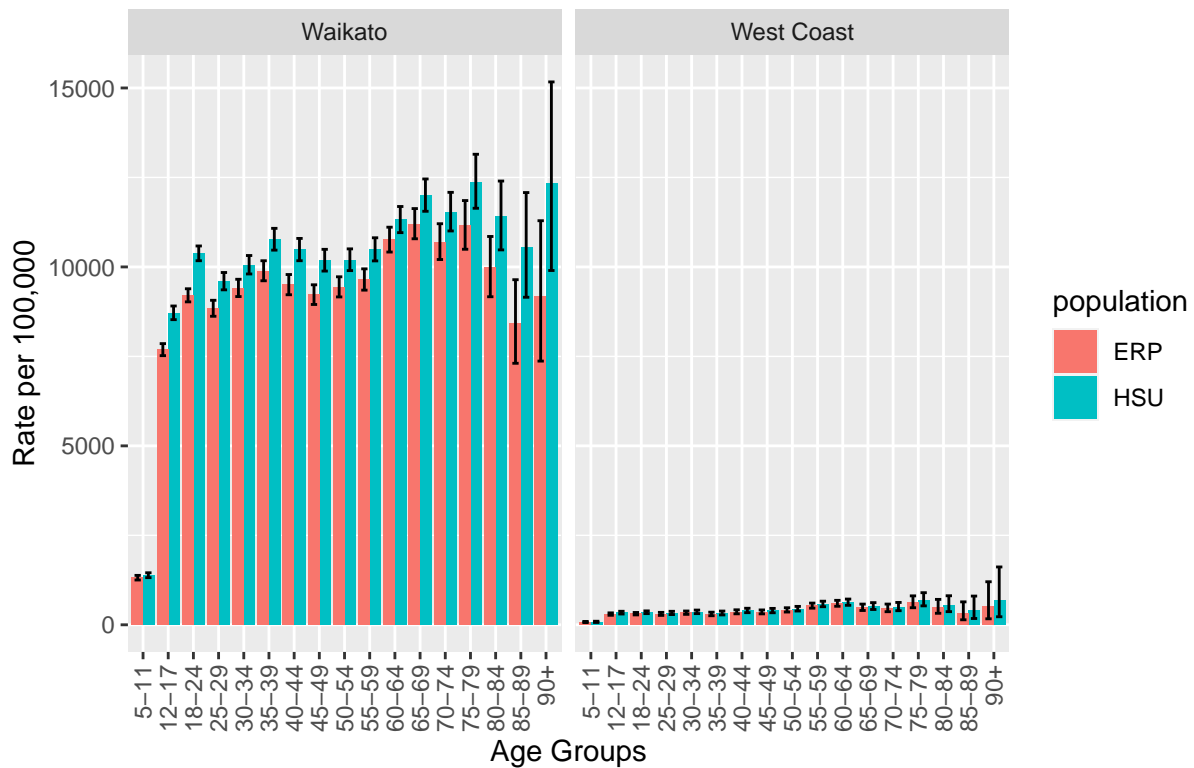
HSU_MFVacc_nontot_lowvshigh.df <- HSU_MFVacc_nontot.df[HSU_MFVacc_nontot.df$DHB %in% c("Waikato", "West Coast"),]
ERP_MFVacc_nontot_lowvshigh.df <- ERP_MFVacc_nontot.df[ERP_MFVacc_nontot.df$DHB %in% c("Waikato", "West Coast"),]

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

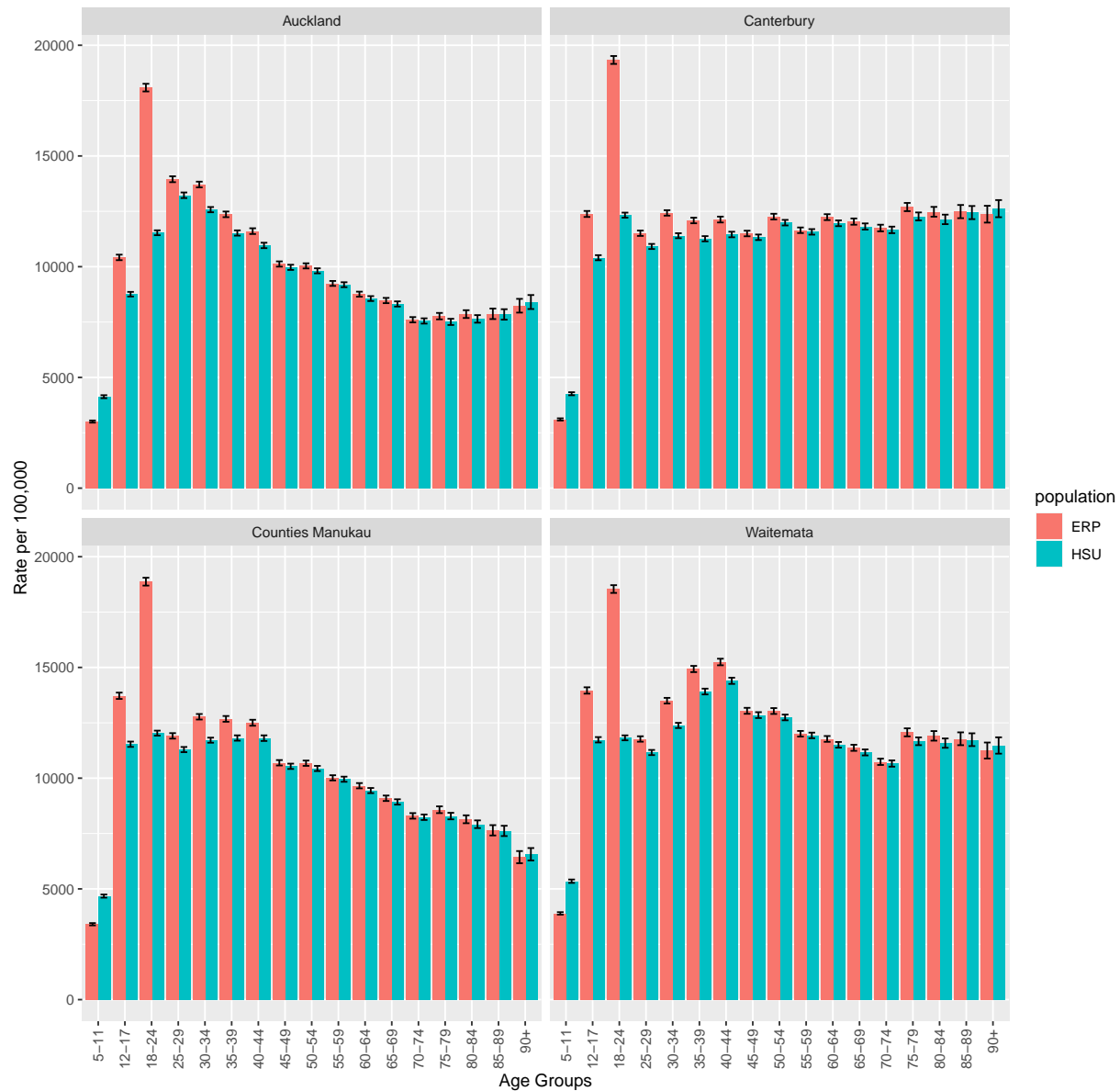
ggplot(subset(HSVsERP_MFVacc_lowvshigh.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, population = population)) +
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position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

```

Maori Fully Vaccinated by Age Group & DHB (Lowest vs. Highest rates per 100,000)



Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <20,000 per 100,000)



```
#pdf(file="Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <20,000 per 100,000).pdf", width
ggplot(subset(HSUvsERP_NMFVacc_high15000.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 = "Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <20,000 per 100,
    labs(y= "Rate per 100,000",
      x= "Age Groups") &
    theme(plot.title = element_text(hjust = 0.5))
dev.off()
```

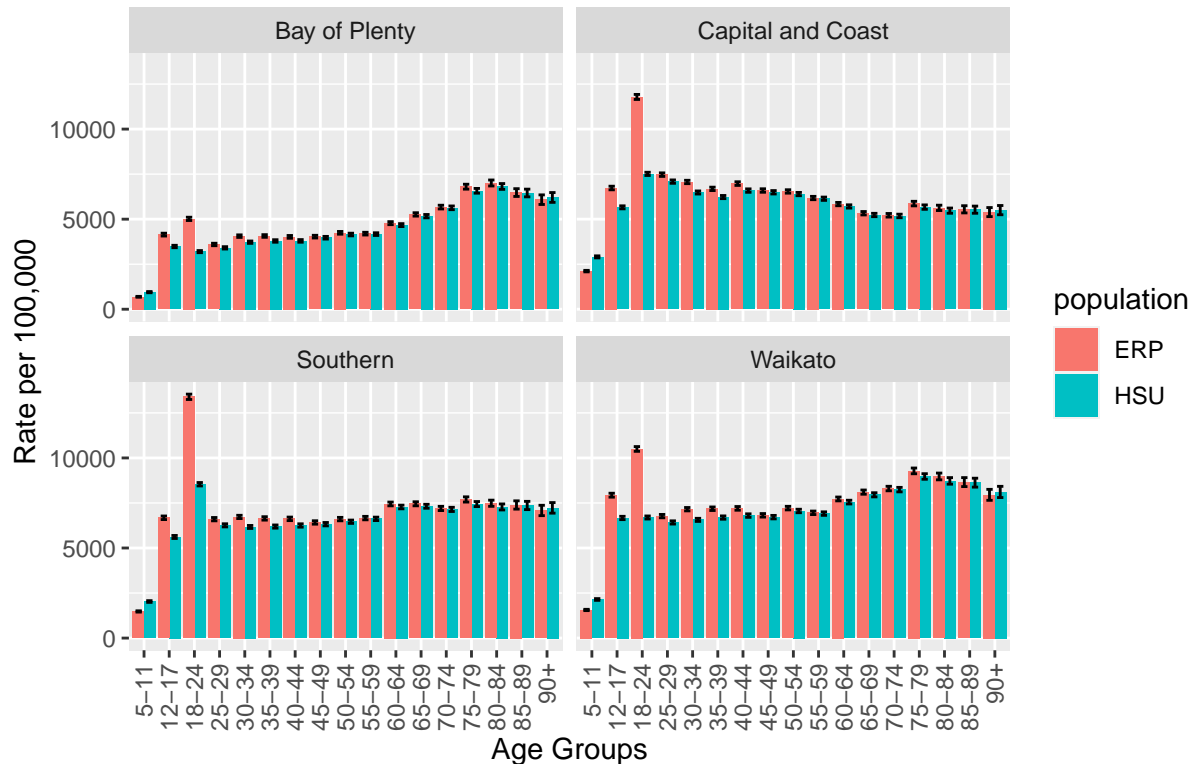


```
# plots for mid range(approx 10,000)
```

```
HSUvsERP_NMFVacc_mid10000.df <- rbind(
  data.frame(HSU_NMFVacc_nontot_mid10000.df, population="HSU"),
  data.frame(ERP_NMFVacc_nontot_mid10000.df, population="ERP")
)
```

```
ggplot(subset(HSUvsERP_NMFVacc_mid10000.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 = "Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <10,000 per 100,000)",
  labs(y= "Rate per 100,000",
    x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

n-Maori Fully Vaccinated by Age Group & DHB (Rates approx <10,000 per 100,000)



```
#pdf(file="Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <10,000 per 100,000).pdf", width=
```

```
ggplot(subset(HSUvsERP_NMFVacc_mid10000.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 = "Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <10,000 per 100,000)",
```

```

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

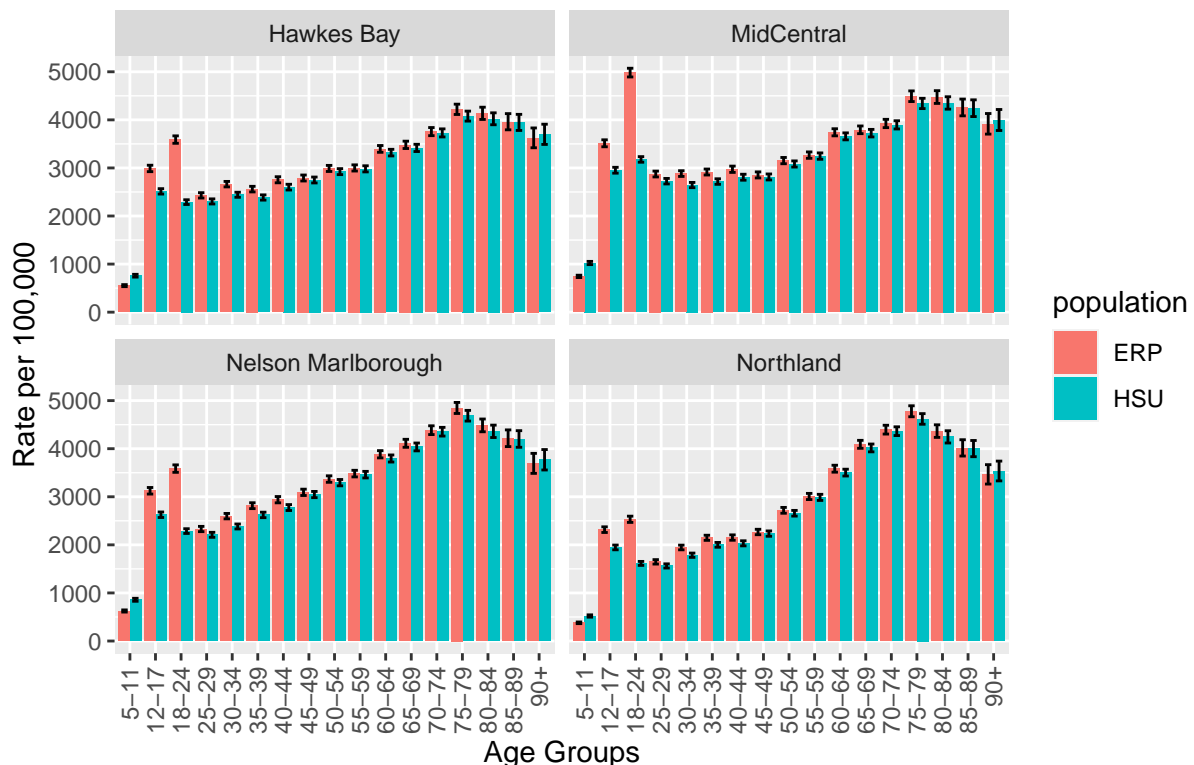
dev.off()

# mid range
HSUvsERP_NMFVacc_mid1.df <- rbind(
  data.frame(HSU_NMFVacc_nontot_mid1.df, population="HSU"),
  data.frame(ERP_NMFVacc_nontot_mid1.df, population="ERP")
)

ggplot(subset(HSVsERP_NMFVacc_mid1.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 = "Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)",
  labs(y= "Rate per 100,000",
       x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)



```

#pdf(file="Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)1.pdf", width=
ggplot(subset(HSVsERP_NMFVacc_mid1.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 = "Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)",
labs(y= "Rate per 100,000",
x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))

dev.off()

```

Capital and Coast, Nelson Marlborough, West Coast, Canterbury, South Canterbury, Southern

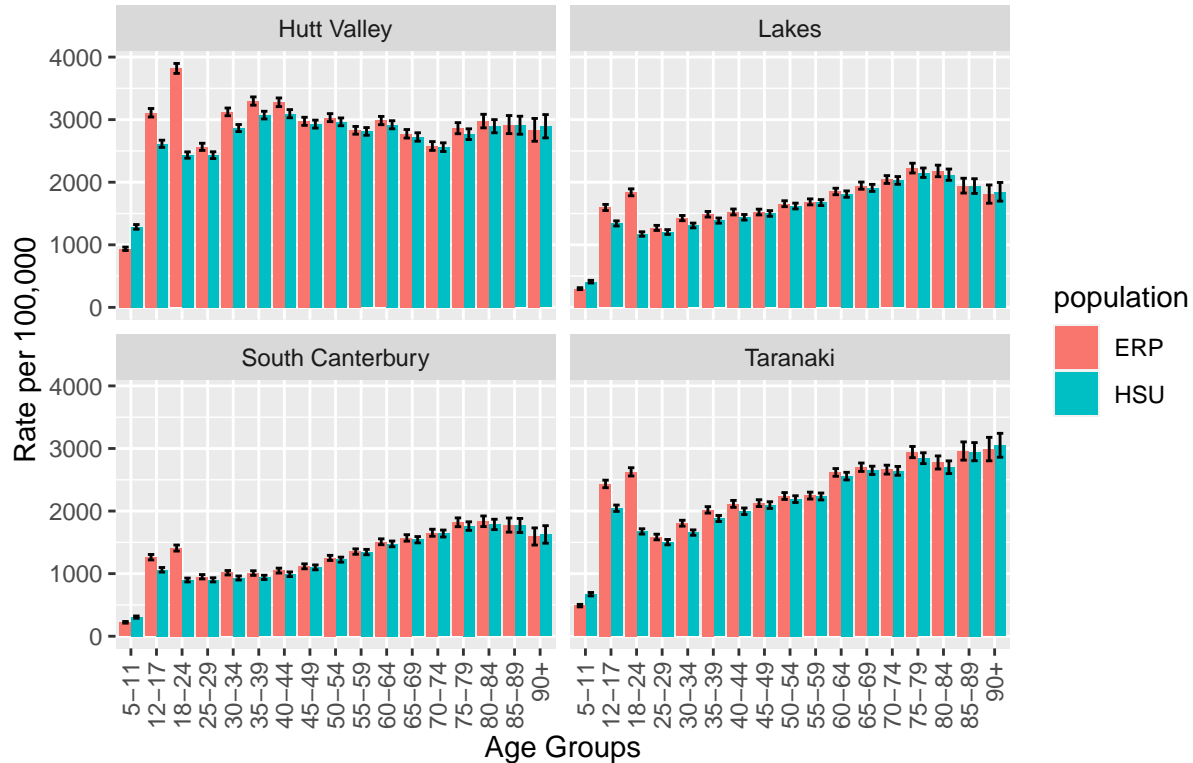
```

HSUvsERP_NMFVacc_mid2.df <- rbind(
  data.frame(HSU_NMFVacc_nontot_mid2.df, population="HSU"),
  data.frame(ERP_NMFVacc_nontot_mid2.df, population="ERP")
)

ggplot(subset(HSVsERP_NMFVacc_mid2.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 = "Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)",
labs(y= "Rate per 100,000",
x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))

```

Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)



#pdf(file="Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)2.pdf", width = 1000, height = 1000)

```
ggplot(subset(HSUvsERP_NMFVacc_mid2.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 = "Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <5,000 per 100,000)",
  labs(y= "Rate per 100,000",
  x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

dev.off()

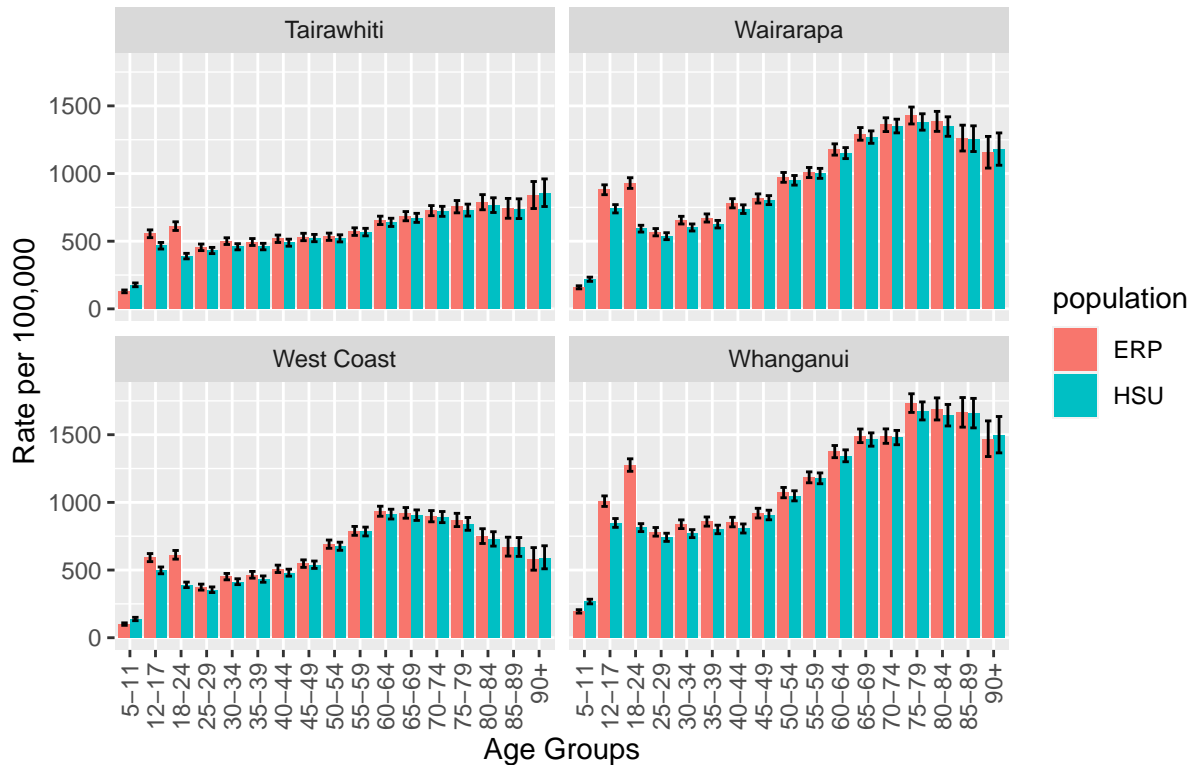
#low

```
HSUvsERP_NMFVacc_low.df <- rbind(
  data.frame(HSU_NMFVacc_nontot_low.df, population="HSU"),
  data.frame(ERP_NMFVacc_nontot_low.df, population="ERP")
)

ggplot(subset(HSUvsERP_NMFVacc_low.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 = "Non-Maori Fully Vaccinated by Age Group & DHB (Rates approx <2,000 per 100,000)",
  labs(y= "Rate per 100,000",
  x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))
```

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

Non-Māori Fully Vaccinated by Age Group & DHB (Rates approx <2,000 per 100,000)



```
#pdf(file="Non-Māori Fully Vaccinated by Age Group & DHB (Rates approx <2,000 per 100,000).pdf", width = 10, height = 10)

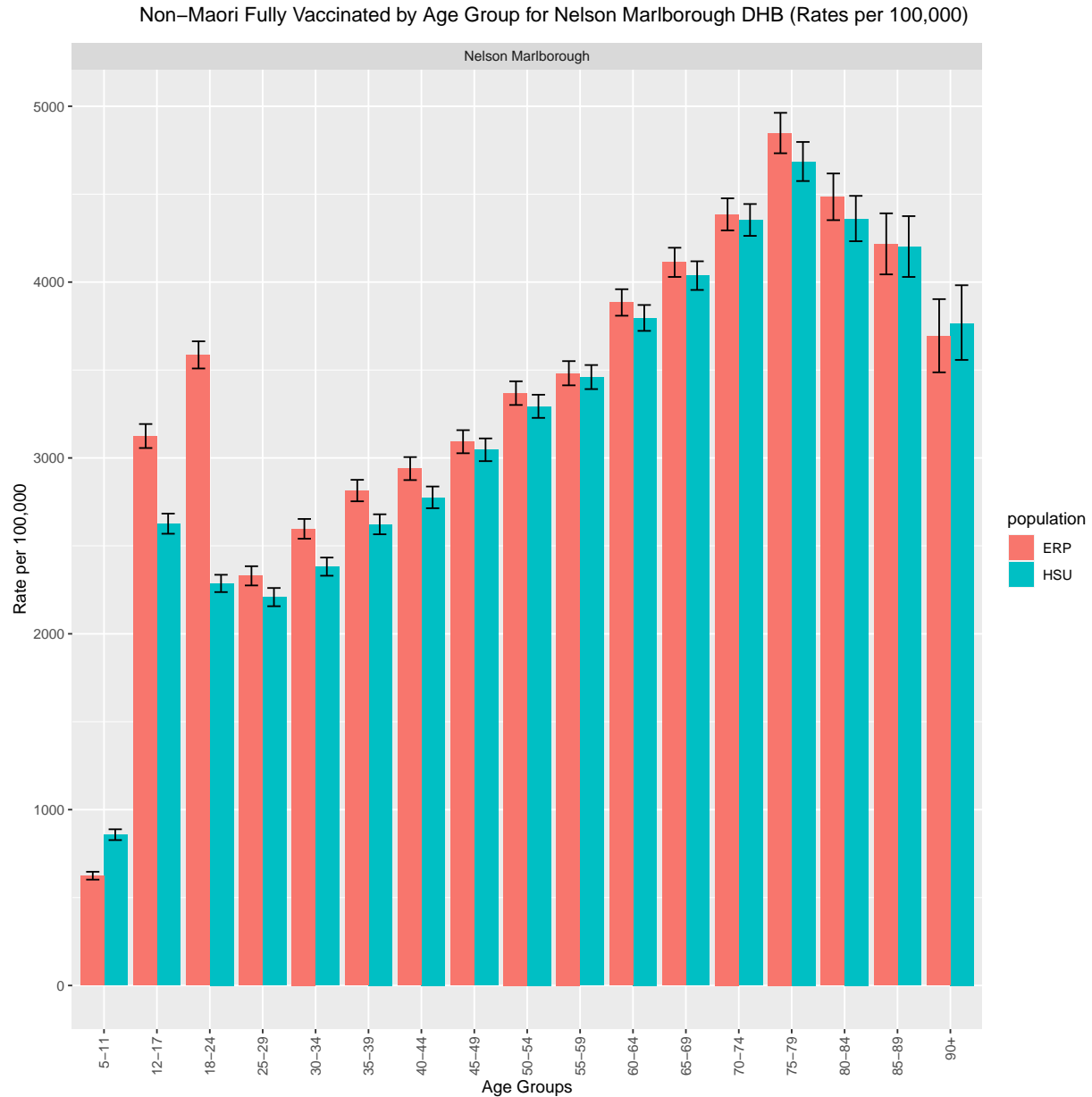
ggplot(subset(HSUvsERP_NMFVacc_low.df), aes(x=factor(AgeGroup, level= level_order), y = RateMult, fill = population)) +
  geom_col(position = position_dodge()) +
  theme(axis.text.x=element_text(angle=90,vjust=0.5,hjust=1)) +
  geom_errorbar(aes(ymin=Rate_Gamma1Lwr, ymax=Rate_Gamma1Upr), position = position_dodge(width = 0.85),
  facet_wrap(~DHB) +
  plot_annotation(title = "Non-Māori Fully Vaccinated by Age Group & DHB (Rates approx <2,000 per 100,000)",
  labs(y= "Rate per 100,000",
       x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

dev.off()
```

presenting lowest vs. highest between Māori and non-māori

```
# separated by rate levels

HSU_NMFVacc_nontot_highestdiff.df <- HSU_NMFVacc_nontot.df[HSU_NMFVacc_nontot.df$DHB %in% c("Nelson Marlborough"),]
```

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

ggplot(subset(HSUvsERP_NMFVacc_highestdiff.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 = "Non-Maori Fully Vaccinated by Age Group for Nelson Marlborough DHB (Rates per
  labs(y= "Rate per 100,000",
        x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

dev.off()
```

```

HSU_MFVacc_nontot_highestdiff.df <- Hsu_MFVacc_nontot.df[HSU_MFVacc_nontot.df$DHB %in% c("Nelson Marlborough DHB"),]

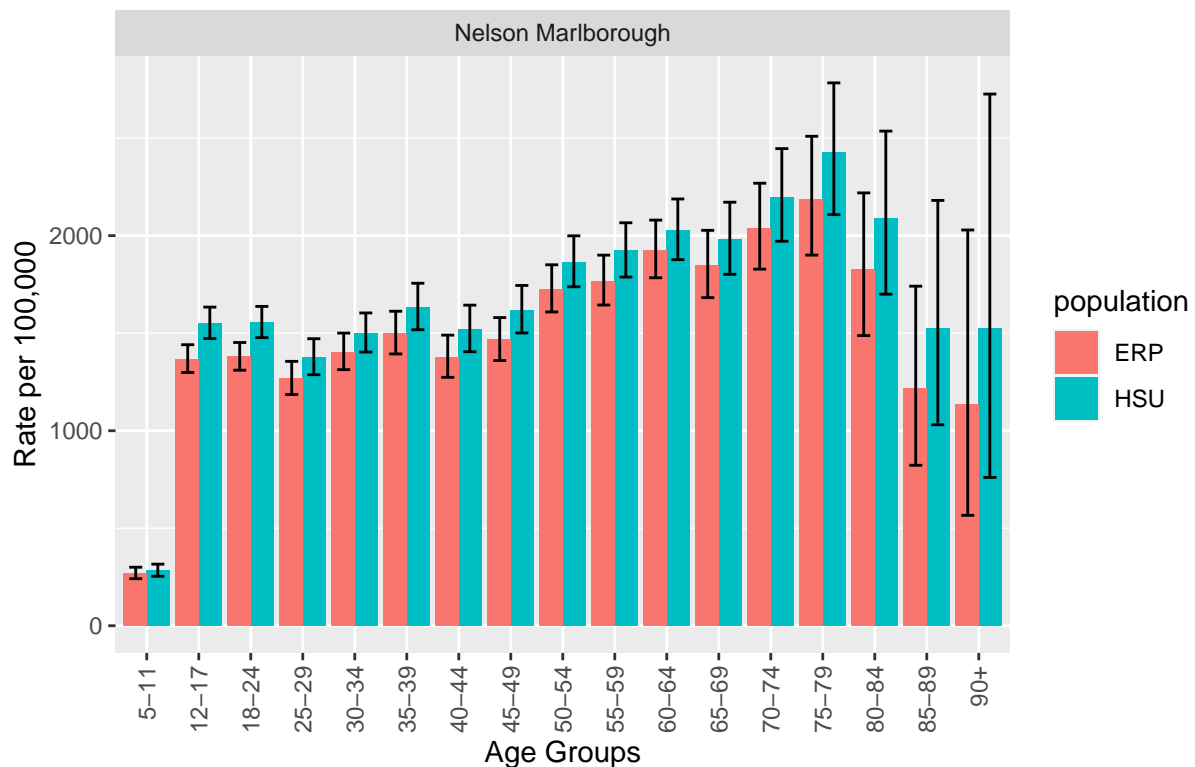
ERP_MFVacc_nontot_highestdiff.df <- ERP_MFVacc_nontot.df[ERP_MFVacc_nontot.df$DHB %in% c("Nelson Marlborough DHB"),]

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 = RateMultipliedBy100000)) +
  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 Fully Vaccinated by Age Group for Nelson Marlborough DHB (Rates per 100,000)",
  labs(y= "Rate per 100,000",
  x= "Age Groups") &
  theme(plot.title = element_text(hjust = 0.5))

```

ori Fully Vaccinated by Age Group for Nelson Marlborough DHB (Rates per 100,0



```

#pdf(file="Maori 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 = RateMultipliedBy100000)) +
  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 Fully Vaccinated by Age Group for Nelson Marlborough DHB (Rates per 100,000)",
labs(y= "Rate per 100,000",
x= "Age Groups") &
theme(plot.title = element_text(hjust = 0.5))
dev.off()

```