VC_Bench_Poster_Figures

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A BUNCH OF PREPROCESSING

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --
## v ggplot2 3.3.3     v purrr   0.3.4
## v tibble  3.1.0     v dplyr   1.0.5
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.1
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(RColorBrewer)
library(reshape2)
```

```
##
## Attaching package: 'reshape2'
## The following object is masked from 'package:tidyr':
##
##     smiths
```

```
bench_df<- read.csv("~/Desktop/NoyesLab/All_Benchmarks.csv")
#bench_df


###Dataset Fixing
bench_df$Dataset_num<-ifelse(bench_df$Dataset=="M0.5",0.5,
                         ifelse(bench_df$Dataset=="M1",1,
                                ifelse(bench_df$Dataset=="M5",5,
                                       ifelse(bench_df$Dataset=="M10",10,
                                              ifelse(bench_df$Dataset=="M15",15,
                                                     ifelse(bench_df$Dataset=="M25",25,50))))))
bench_df$Dataset_f<-factor(bench_df$Dataset, levels=c("M0.5","M1","M5","M10","M15","M25","M50"))

###Subset Fixing
bench_df$Subset_num<-ifelse(bench_df$Subset=="S5",5,
                            ifelse(bench_df$Subset=="S15",15,
                                   ifelse(bench_df$Subset=="S25",25,35)))
bench_df$Subset<-ifelse(bench_df$Subset=="S5","5 Genomes",
                        ifelse(bench_df$Subset=="S15","15 Genomes",
```

```
                                ifelse(bench_df$Subset=="S25","25 Genomes","35 Genomes")))

bench_df$Subset_f<-factor(bench_df$Subset, levels=c("5 Genomes","15 Genomes","25 Genomes","35 Genomes"))


###Variant Caller Fixing
bench_df$VCaller<-ifelse(bench_df$VCaller=="FB_Out","FreeBayes",
                         ifelse(bench_df$VCaller=="GATK_Out","GATK",
                                ifelse(bench_df$VCaller=="Disco_Out","DiscoSNP++","MetaSNV")))
bench_df$VCaller_f<-factor(bench_df$VCaller,levels=c("MetaSNV","GATK","FreeBayes","DiscoSNP++"))




cbbPalette<-rev(brewer.pal(n=4,name = "Dark2"))
```

Making color palettes

```
cbbPalette<-rev(brewer.pal(n=4,name = "Dark2"))
VCPalette<-rev(brewer.pal(n=7,name = "Dark2"))
VC_light_palette<-rev(brewer.pal(n=7,name = "BuGn"))
```

SUBSET AS A FACET

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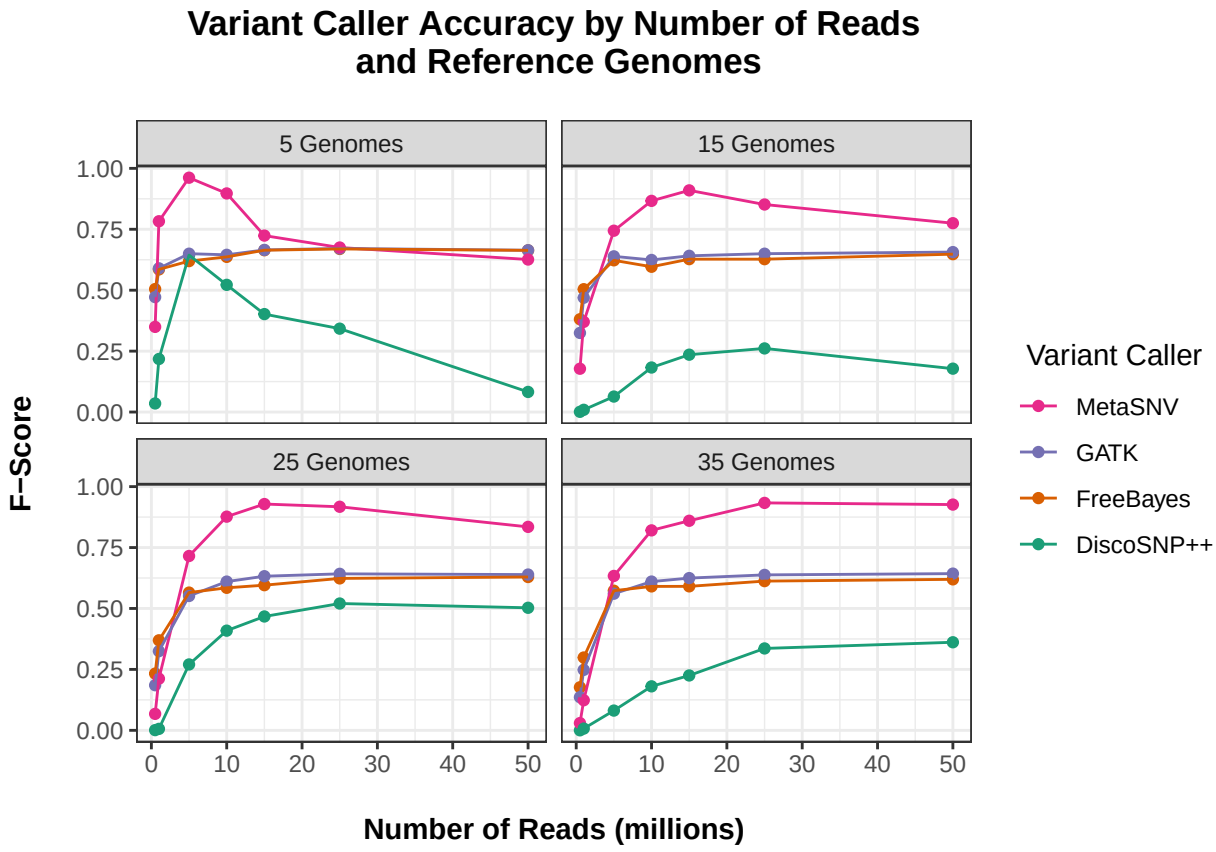
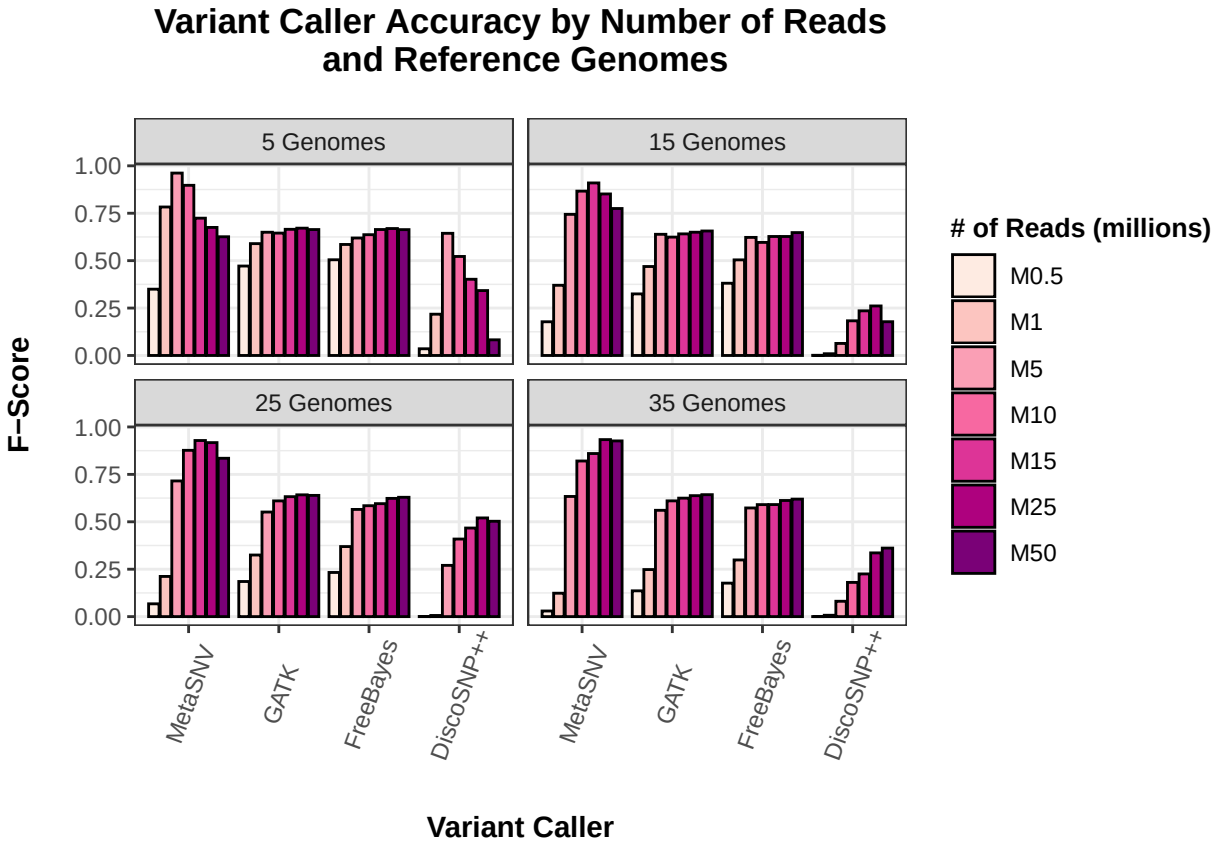
```
###MUST INCLUDE
#1A
ggplot(bench_df,aes(x=Dataset_num,y=F.score,colour=VCaller_f,group=VCaller_f)) +
  geom_point() + geom_line() + facet_wrap(~Subset_f,nrow=2) +
  ggtitle("Variant Caller Accuracy by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reads (millions)") + ylab("F-Score") + labs(col="Variant Caller") +
  scale_color_manual(values=cbbPalette) + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold") +
        annotate("text",  x=30, y = 0.5,label="HELLO WORLD", vjust=1, hjust=1))
```




```
###MUST INCLUDE
```

1A

```
###Reasonably good
#1B
ggplot(bench_df,aes(x=VCaller_f,y=F.score,fill=Dataset_f,group=Dataset_f)) +
  geom_col(colour="black",position="dodge2") + facet_wrap(~Subset_f,nrow=2) +
  ggtitle("Variant Caller Accuracy by Number of Reads\n and Reference Genomes") +
  xlab("Variant Caller") + ylab("F-Score") + labs(fill="# of Reads (millions)") +
  scale_fill_brewer(palette = "RdPu") + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.text.x = element_text(size=9,angle=70,vjust = 0.6),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold"))
```



1B

VARIANT CALLER AS A FACET

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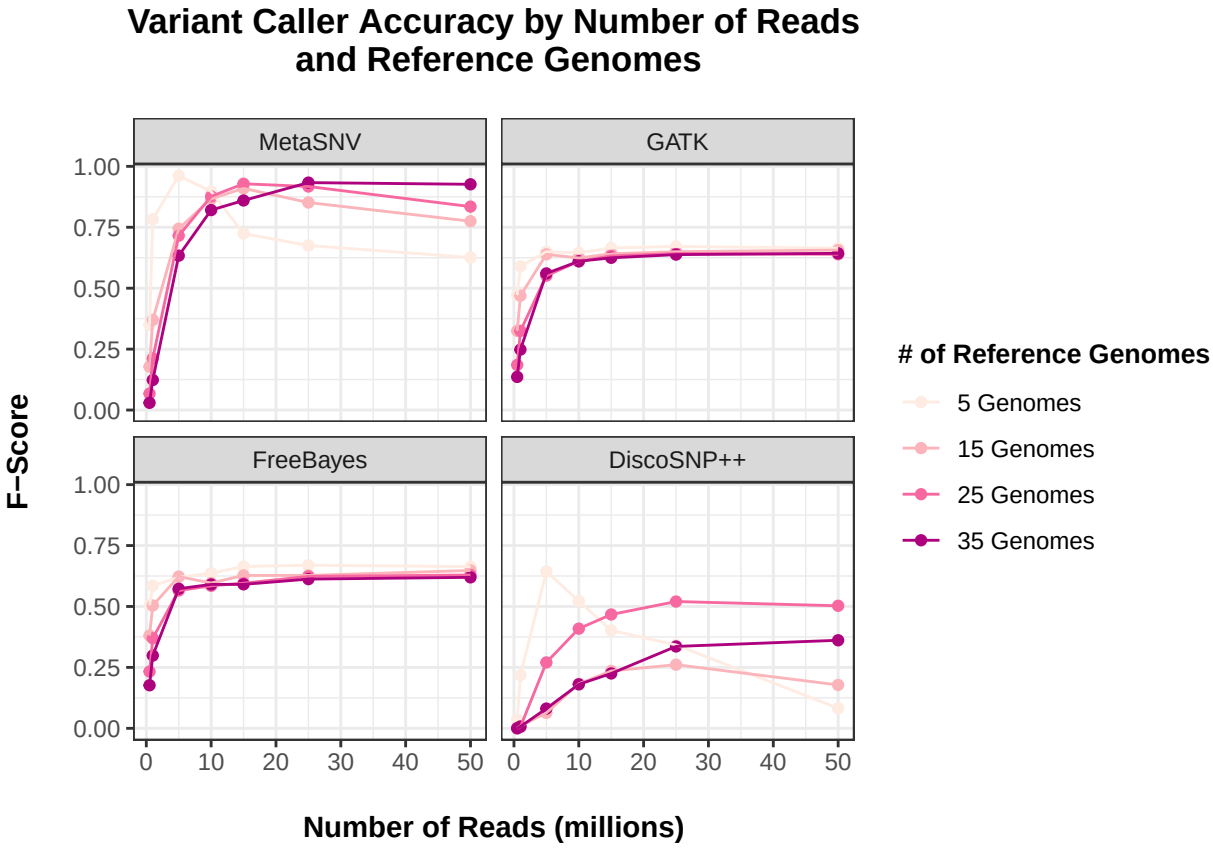
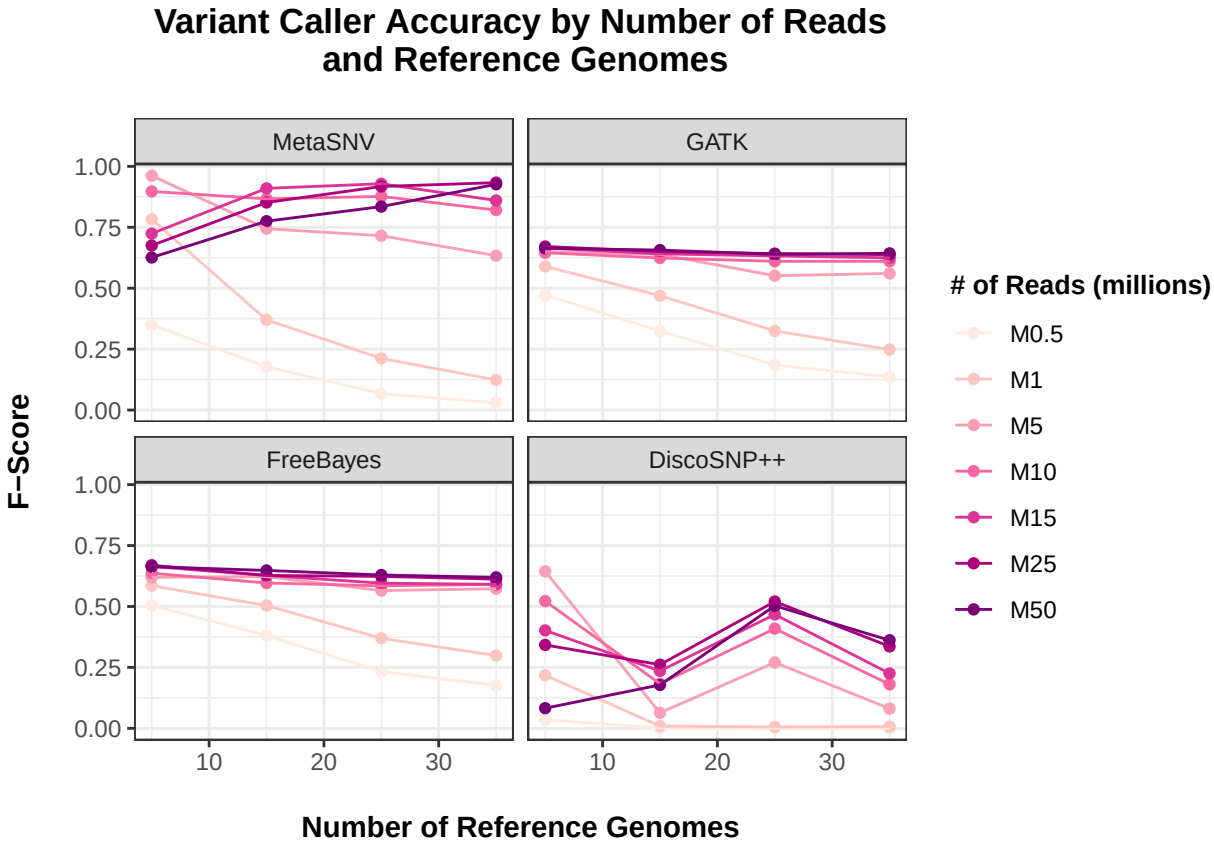
```
#####CONSIDER USING EITHER LINE GRAPHS
###This one is BETTER
#2A
ggplot(bench_df,aes(x=Dataset_num,y=F.score,colour=Subset_f,group=Subset_f)) +
  geom_point() + geom_line() + facet_wrap(~VCaller_f,nrow=2) +
  ggtitle("Variant Caller Accuracy by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reads (millions)") + ylab("F-Score") + labs(col="# of Reference Genomes") +
  scale_color_brewer(palette = "RdPu") + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold"))
```



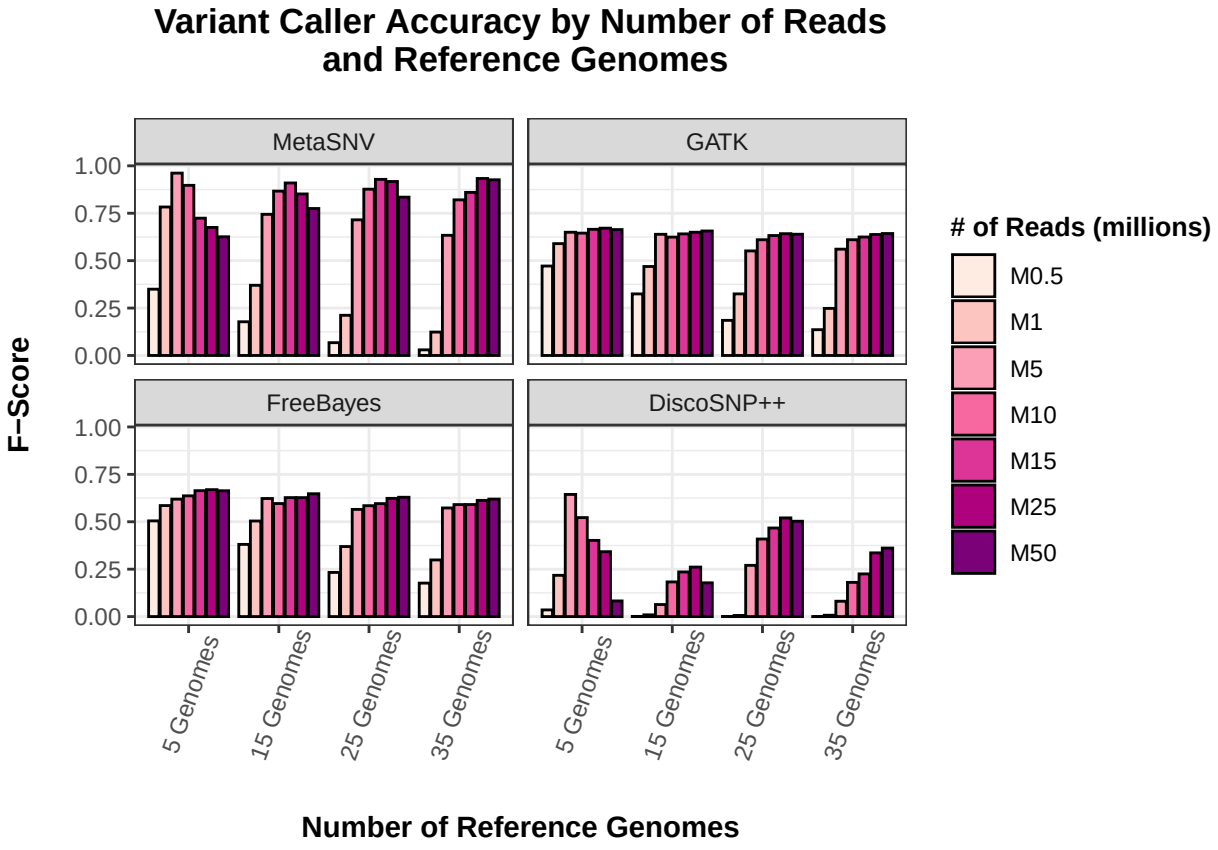
2A

```
###This is also good
#2B
ggplot(bench_df,aes(x=Subset_num,y=F.score,colour=Dataset_f,group=Dataset_f)) +
  geom_point() + geom_line() + facet_wrap(~VCaller_f,nrow=2) +
  ggtitle("Variant Caller Accuracy by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reference Genomes") + ylab("F-Score") + labs(col="# of Reads (millions)") +
  scale_color_brewer(palette = "RdPu") + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold"))
```



2B

```
#Barplot version is less good but viable
#2C
ggplot(bench_df,aes(x=Subset_f,y=F.score,fill=Dataset_f,group=Dataset_f)) +
  geom_col(colour="black",position="dodge2") + facet_wrap(~VCaller_f,nrow=2) +
  ggtitle("Variant Caller Accuracy by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reference Genomes") + ylab("F-Score") + labs(fill="# of Reads (millions)") +
  scale_fill_brewer(palette = "RdPu") + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.text.x = element_text(size=9,angle=70,vjust = 0.6),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold"))
```



2C

DATASET AS A FACET

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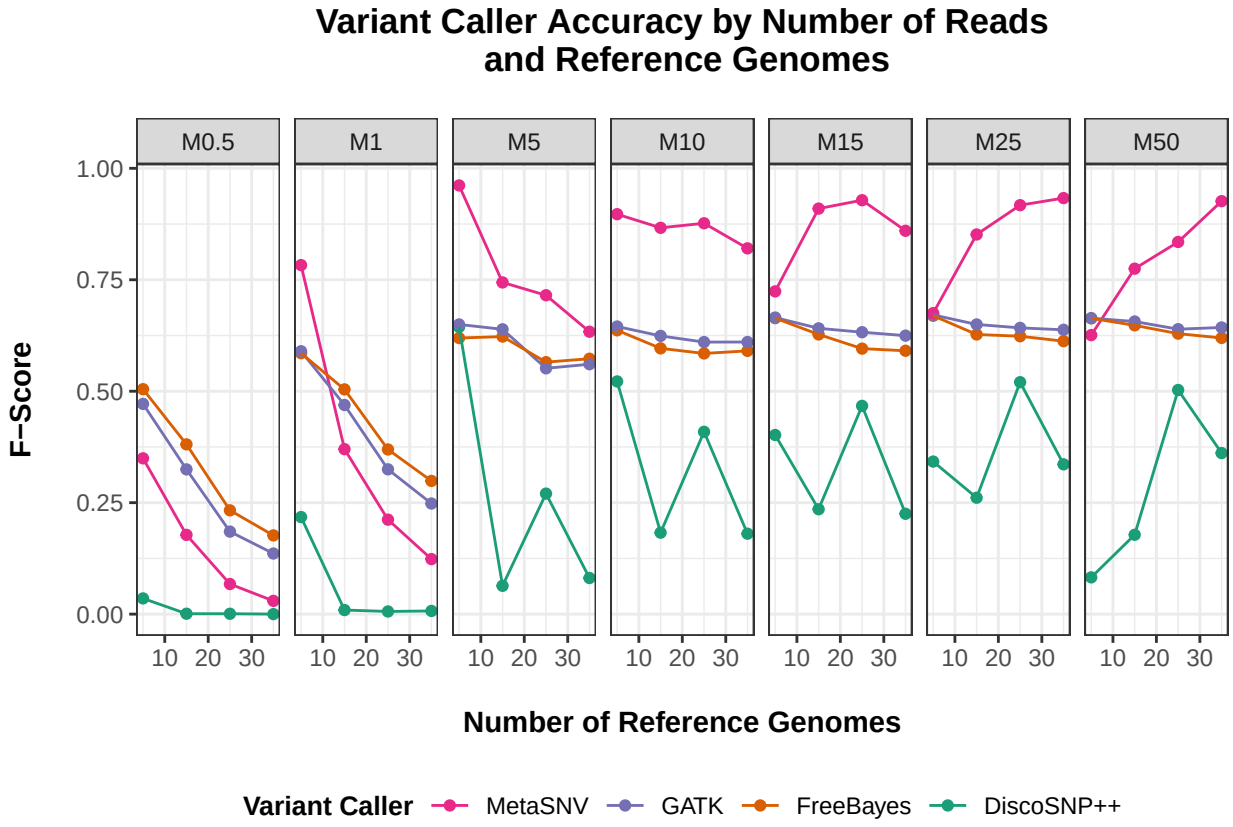
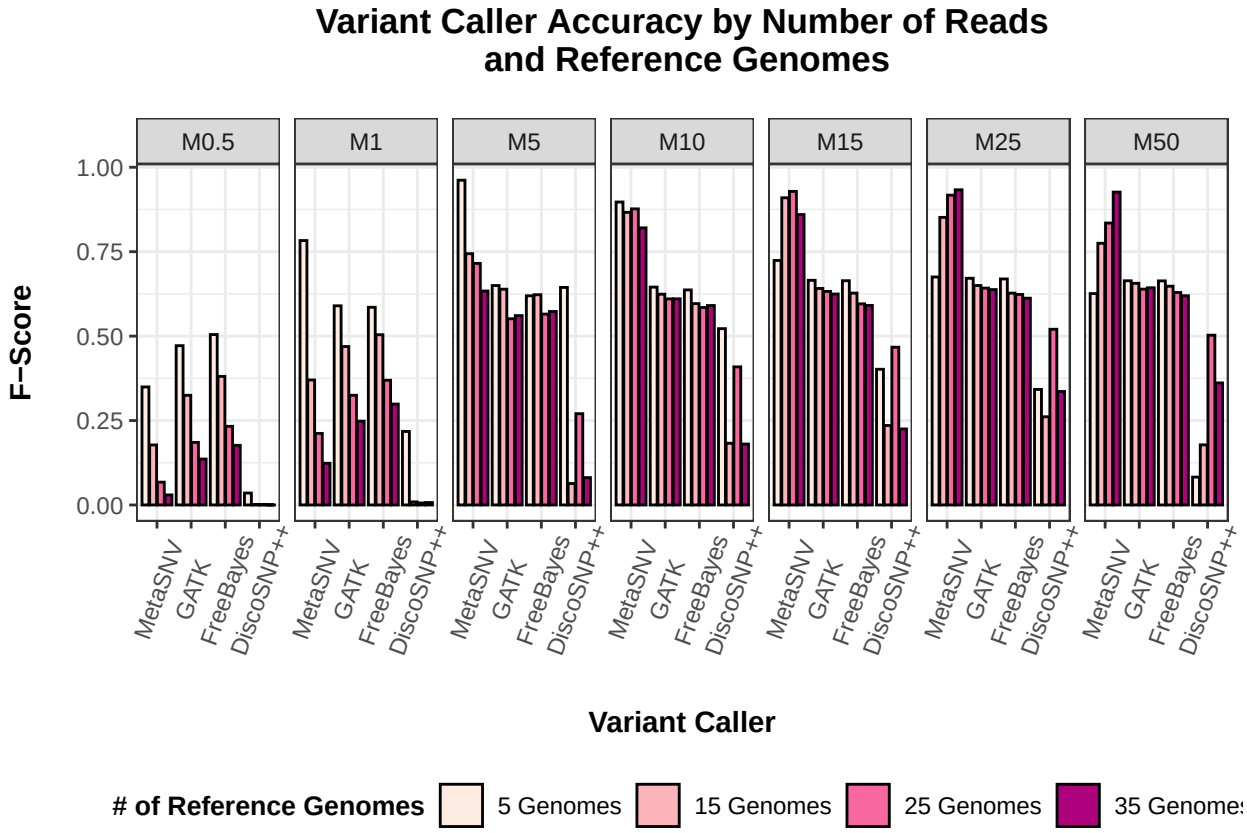
```
###INCLUDE THIS ONE IF POSSIBLE -- GOOD STORY HERE
#3A
ggplot(bench_df,aes(x=Subset_num,y=F.score,colour=VCaller_f,group=VCaller_f)) +
  geom_point() + geom_line() + facet_wrap(~Dataset_f,nrow=1) +
  ggtitle("Variant Caller Accuracy by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reference Genomes") + ylab("F-Score") + labs(col="Variant Caller") +
  scale_color_manual(values=cbbPalette) + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold"), legend.position = "bottom")
```



3A

```
#3B
ggplot(bench_df,aes(x=VCaller_f,y=F.score,fill=Subset_f,group=Subset_f)) +
  geom_col(colour="black",position="dodge2") + facet_wrap(~Dataset_f,nrow=1) +
  ggtitle("Variant Caller Accuracy by Number of Reads\n and Reference Genomes") +
  xlab("Variant Caller") + ylab("F-Score") + labs(fill="# of Reference Genomes") +
  scale_fill_brewer(palette = "RdPu") + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.text.x = element_text(size=9,angle=70,vjust = 0.6),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold"), legend.position = "bottom")
```

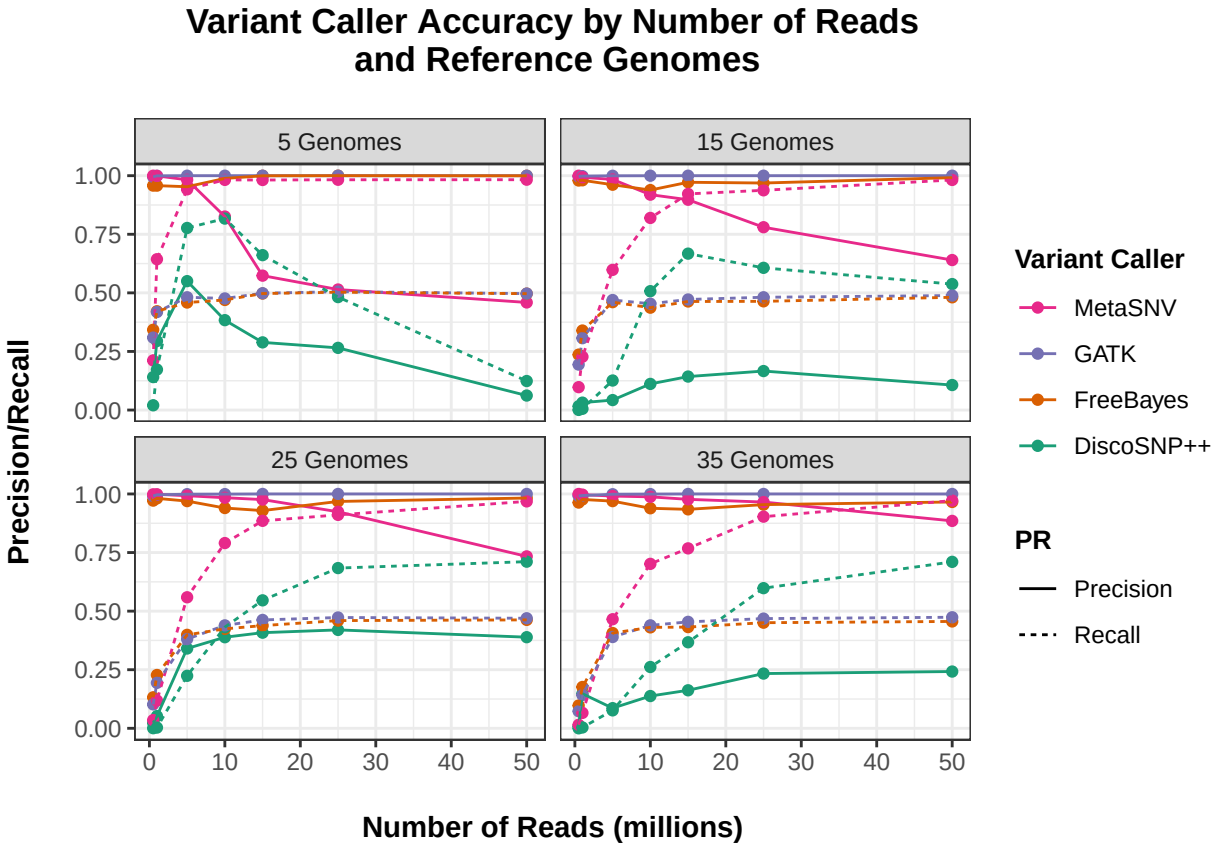


3B

Figures using Precision/Recall

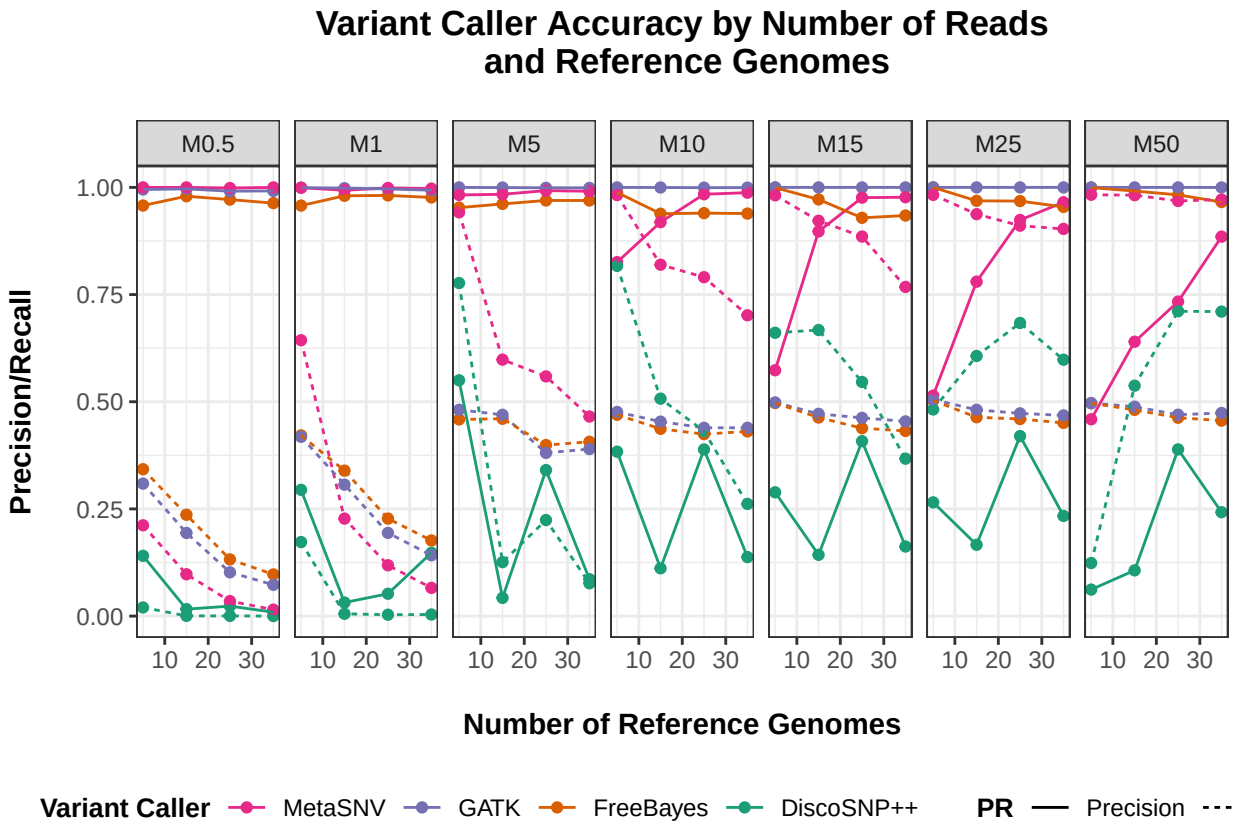
```
bench_melt<-gather(bench_df,"PR","PR_value",7:8)

ggplot(bench_melt,aes(x=Dataset_num,y=PR_value,colour=VCaller_f,group=interaction(VCaller_f,PR))) +
  geom_point() + geom_line(aes(linetype=PR)) + facet_wrap(~Subset_f,nrow=2) +
  ggtitle("Variant Caller Accuracy by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reads (millions)") + ylab("Precision/Recall") + labs(col="Variant Caller") +
  scale_color_manual(values=cbbPalette) + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold") )
```



1PR

```
ggplot(bench_melt,aes(x=Subset_num,y=PR_value,colour=VCaller_f,group=interaction(VCaller_f,PR)) ) +
  geom_point() + geom_line(aes(linetype=PR)) + facet_wrap(~Dataset_f,nrow=1) +
  ggtitle("Variant Caller Accuracy by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reference Genomes") + ylab("Precision/Recall") + labs(col="Variant Caller") +
  scale_color_manual(values=cbbPalette) + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold"), legend.position = "bottom") #+
```

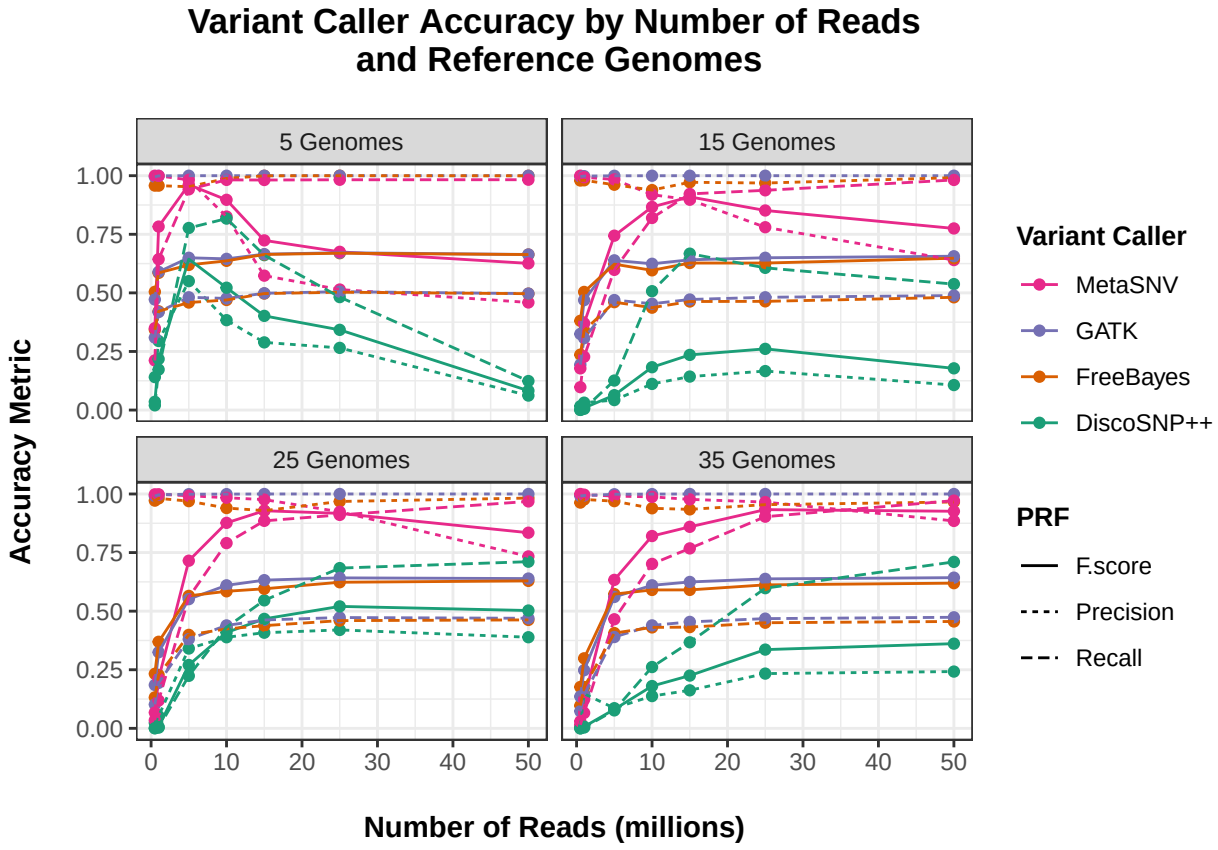



```
  #guides(fill=guide_legend(nrow=2,byrow=TRUE))
```

3PR

```
bench_super_melt<-gather(bench_df,"PRF","PRF_value",7:9)

ggplot(bench_super_melt,aes(x=Dataset_num,y=PRF_value,colour=VCaller_f,group=interaction(VCaller_f,PRF))
  geom_point() + geom_line(aes(linetype=PRF)) + facet_wrap(~Subset_f,nrow=2) +
  ggtitle("Variant Caller Accuracy by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reads (millions)") + ylab("Accuracy Metric") + labs(col="Variant Caller") +
  scale_color_manual(values=cbbPalette) + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold") )
```



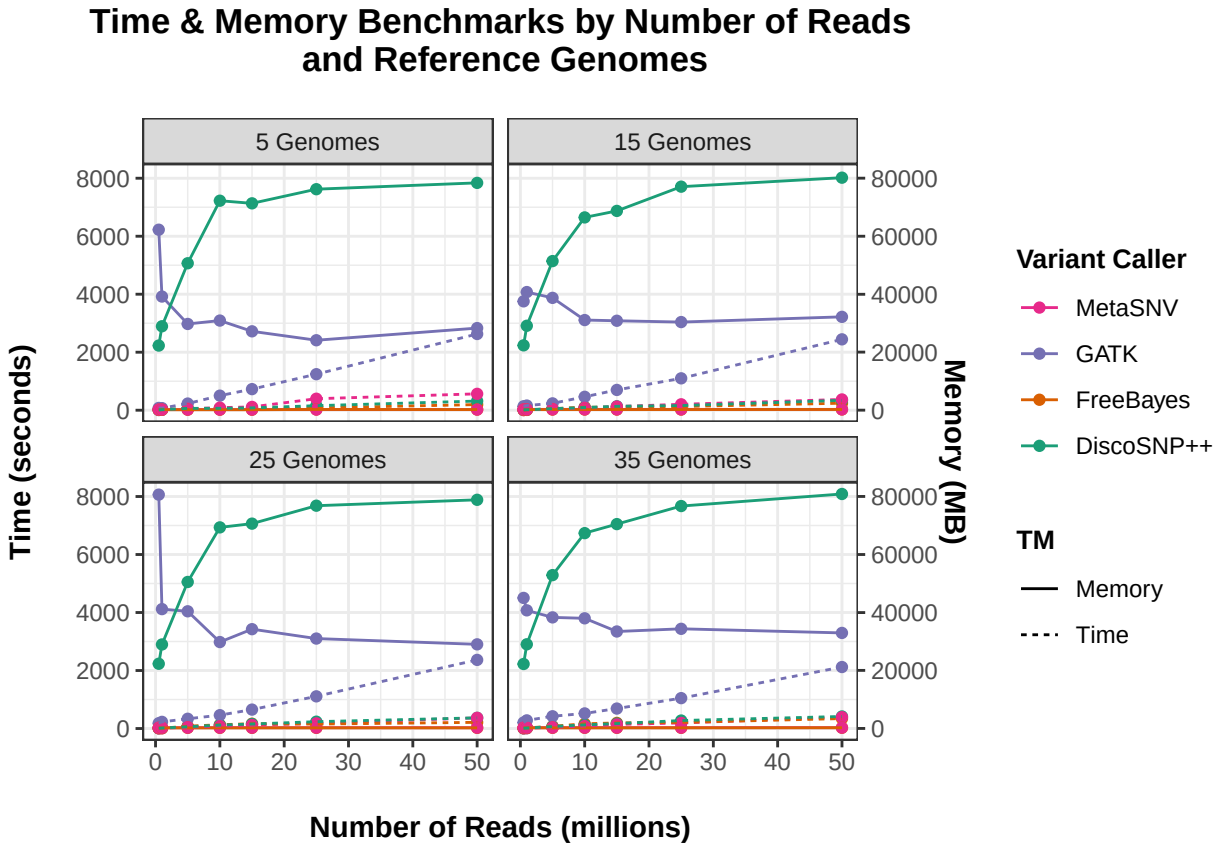
1PRF

Time and Memory Benchmarks

These ones aren't that good

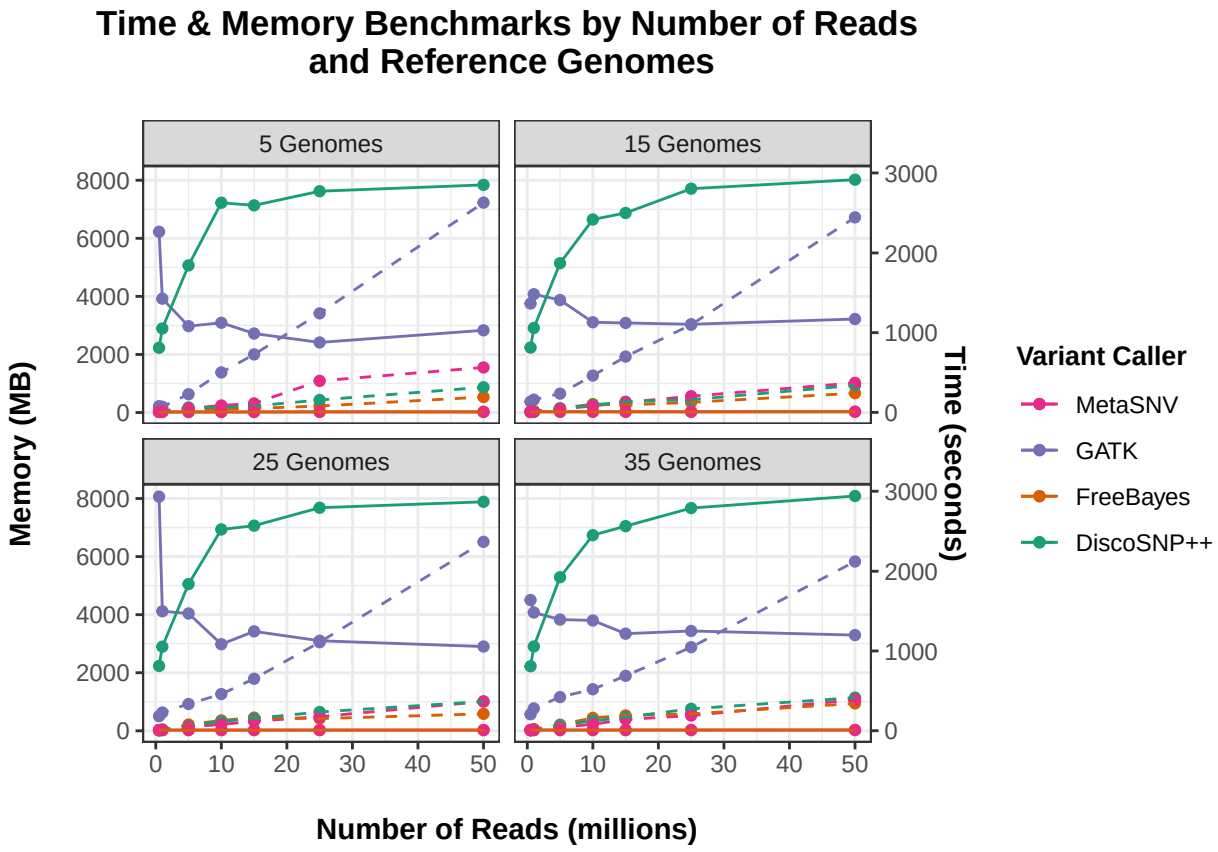
```
tm_df<-gather(bench_df,"TM","TM_value",10:11)

#Scaled axis, unscaled data
ggplot(tm_df,aes(x=Dataset_num,y=TM_value,colour=VCaller_f,group=interaction(VCaller_f,TM))) +
  geom_point() + geom_line(aes(linetype=TM)) + facet_wrap(~Subset_f,nrow=2) +
  ggtitle("Time & Memory Benchmarks by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reads (millions)") + ylab("Time (seconds)") + labs(col="Variant Caller") +
  scale_y_continuous(name="Time (seconds)", sec.axis = sec_axis(~ 10*., name="Memory (MB)")) +
  scale_color_manual(values=cbbPalette) + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold") )
```



TM1

```
#Scaled axis and data
ggplot(bench_df) +
  geom_point(mapping = aes(x=Dataset_num,y=Time*2.75,colour=VCaller_f)) +
  geom_line(mapping = aes(x=Dataset_num,y=Time*2.75,colour=VCaller_f),linetype=2) +
  geom_point(mapping = aes(x=Dataset_num,y=Memory,colour=VCaller_f)) +
  geom_line(mapping = aes(x=Dataset_num,y=Memory,colour=VCaller_f),linetype=1) +
  facet_wrap(~Subset_f,nrow=2) +
  ggtitle("Time & Memory Benchmarks by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reads (millions)") + ylab("Time (seconds)") + labs(col="Variant Caller") +
  scale_y_continuous(name="Memory (MB)", sec.axis = sec_axis(~ ./2.75, name="Time (seconds)")) +
  scale_color_manual(values=cbbPalette) + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold") )
```



TM2

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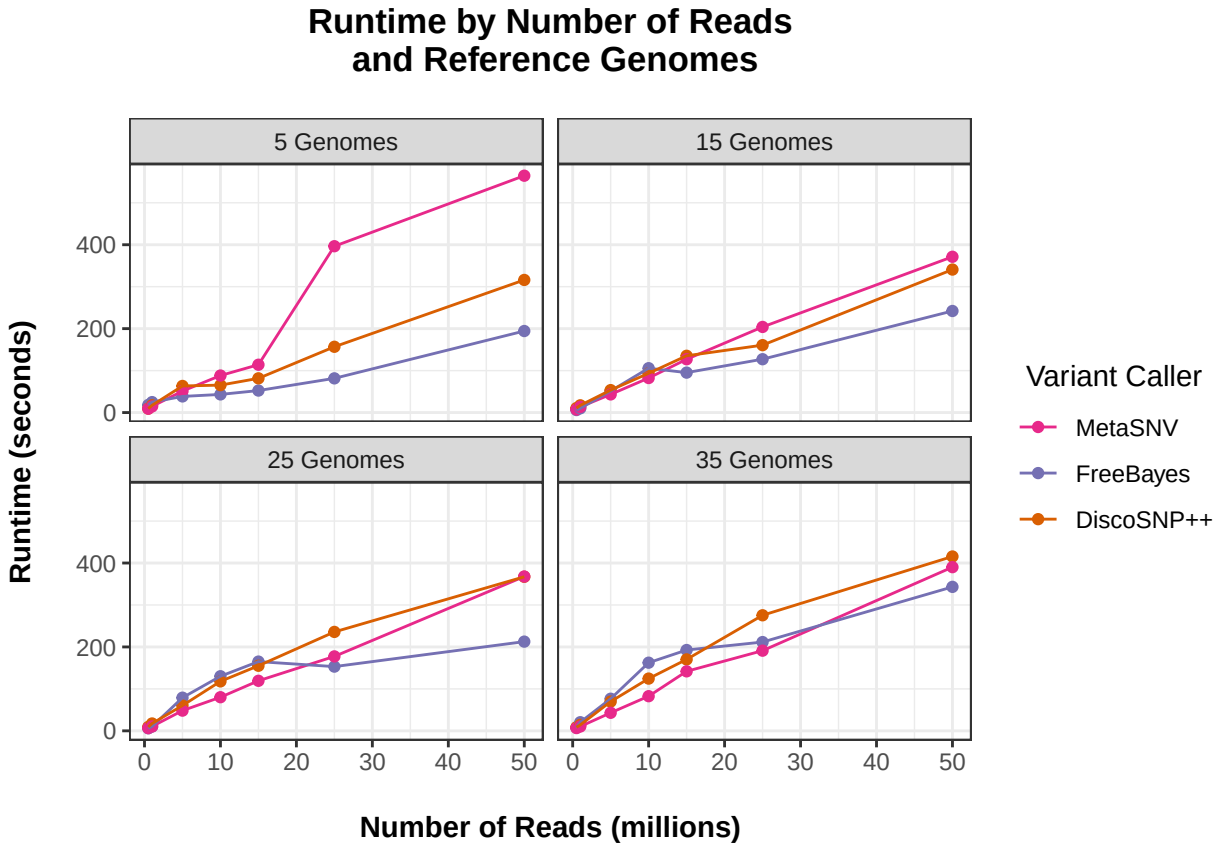
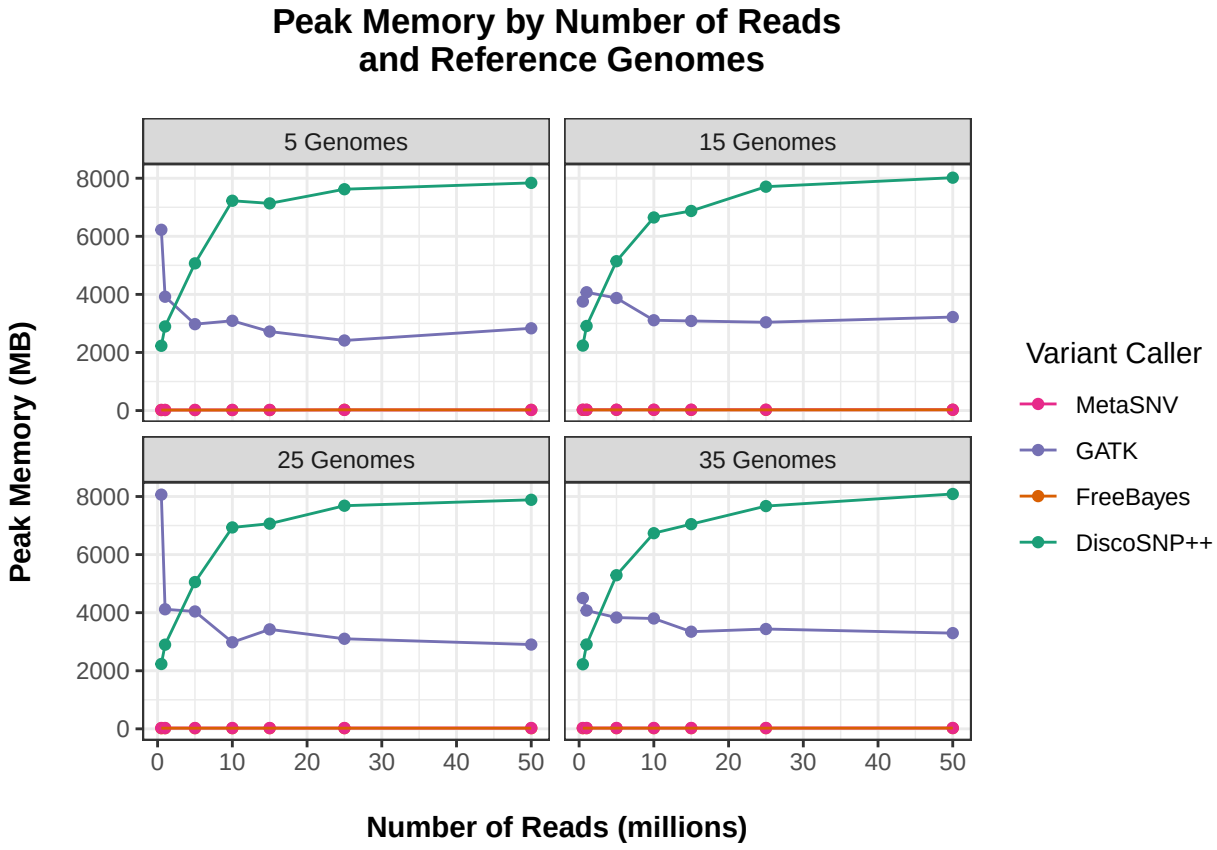
These are Fab

```
ggplot(bench_df[bench_df$VCaller!="GATK",],aes(x=Dataset_num,y=Time,colour=VCaller_f,group=VCaller_f)) +
  geom_point() + geom_line() + facet_wrap(~Subset_f,nrow=2) +
  ggtitle("Runtime by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reads (millions)") + ylab("Runtime (seconds)") + labs(col="Variant Caller") +
  scale_color_manual(values=cbbPalette) + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold") +
        annotate("text",  x=30, y = 0.5,label="HELLO WORLD", vjust=1, hjust=1))
```



T1

```
ggplot(bench_df,aes(x=Dataset_num,y=Memory,colour=VCaller_f,group=VCaller_f)) +
  geom_point() + geom_line() + facet_wrap(~Subset_f,nrow=2) +
  ggtitle("Peak Memory by Number of Reads\n and Reference Genomes") +
  xlab("Number of Reads (millions)") + ylab("Peak Memory (MB)") + labs(col="Variant Caller") +
  scale_color_manual(values=cbbPalette) + theme_bw() +
  theme(plot.title = element_text(hjust=0.5,size=13,face="bold",margin=margin(0,0,15,0)),
        axis.title.x = element_text(face="bold",margin=margin(15,0,0,0)),
        axis.title.y = element_text(face="bold",margin=margin(0,15,0,0)),
        legend.title = element_text(size = 10, face = "bold") +
        annotate("text",  x=30, y = 0.5,label="HELLO WORLD", vjust=1, hjust=1))
```


Peak Memory by Number of Reads
and Reference Genomes
5 Genomes
15 Genomes
25 Genomes
35 Genomes
Peak Memory (MB)
8000
6000
4000
2000
0
0
10
20
30
40
50
Number of Reads (millions)
Variant Caller
MetaSNV
GATK
FreeBayes
DiscoSNP++

M1