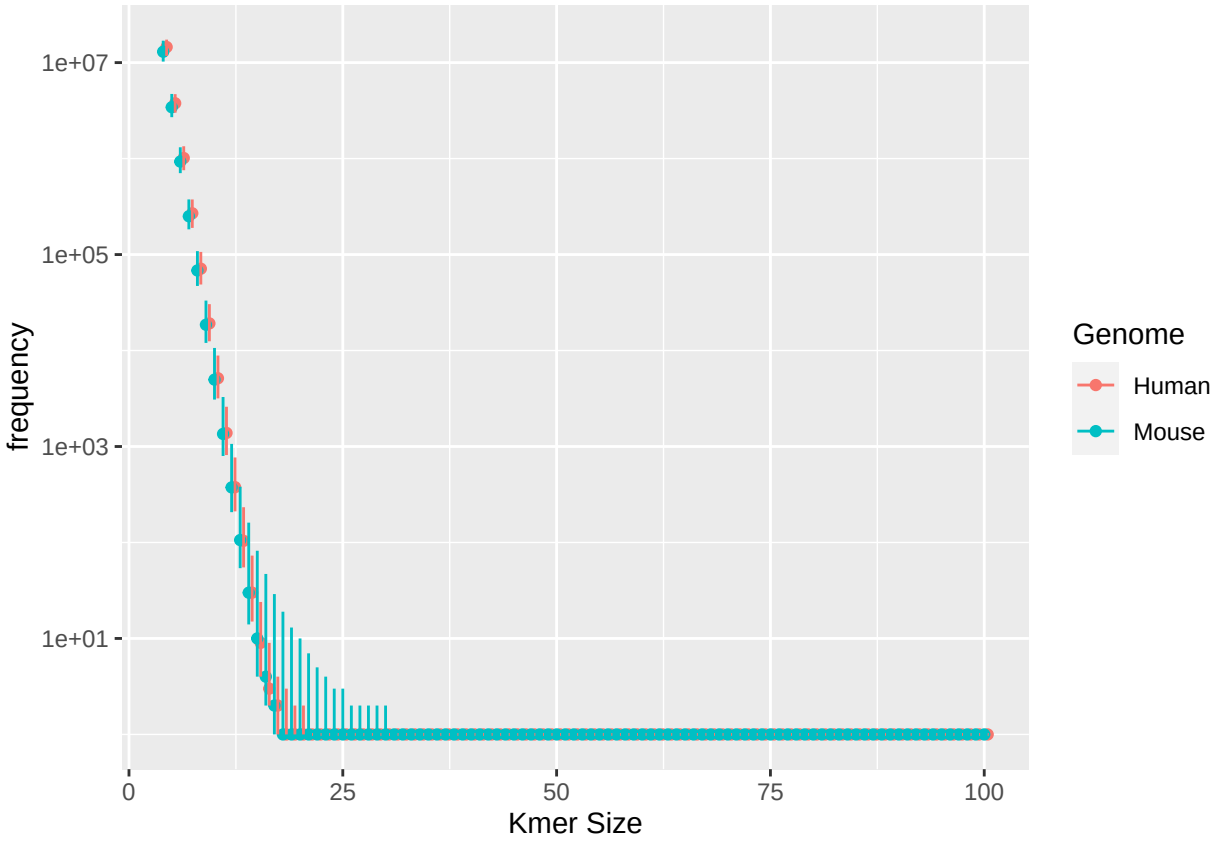
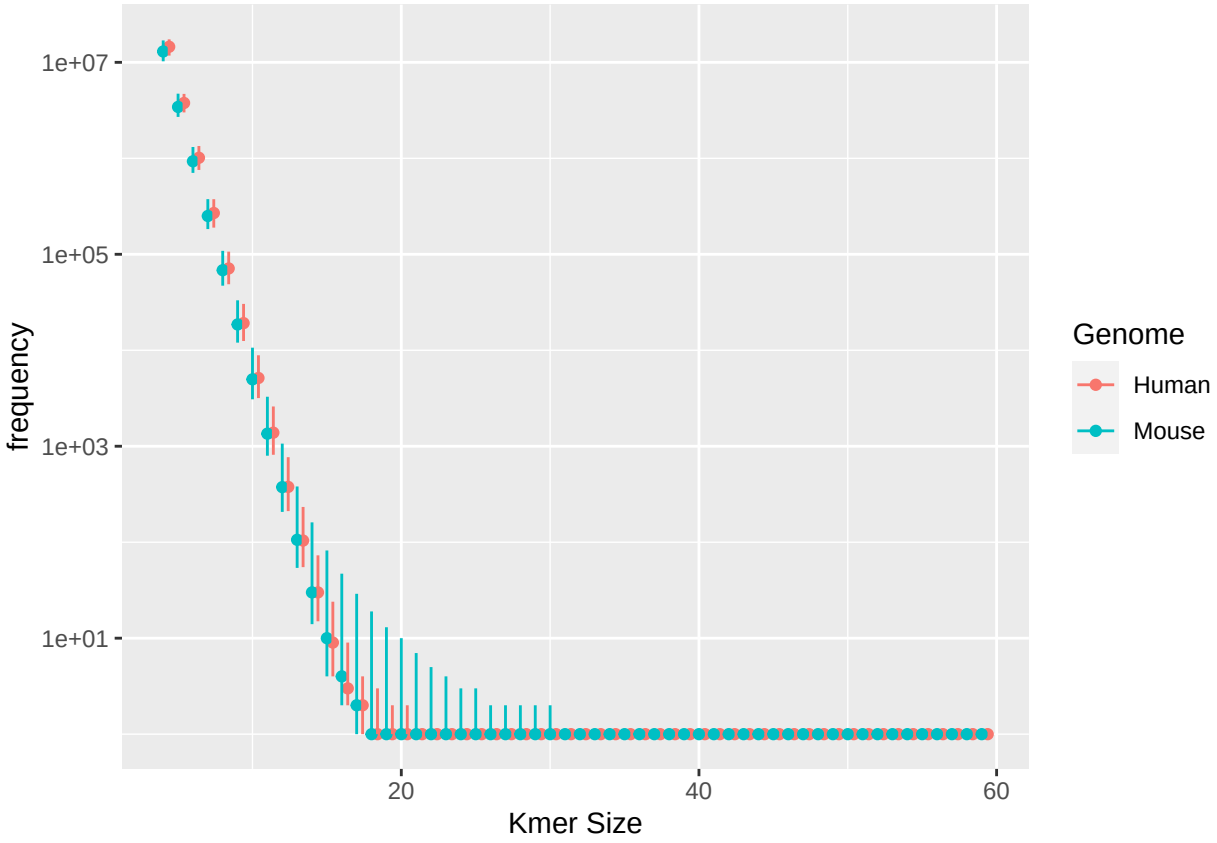
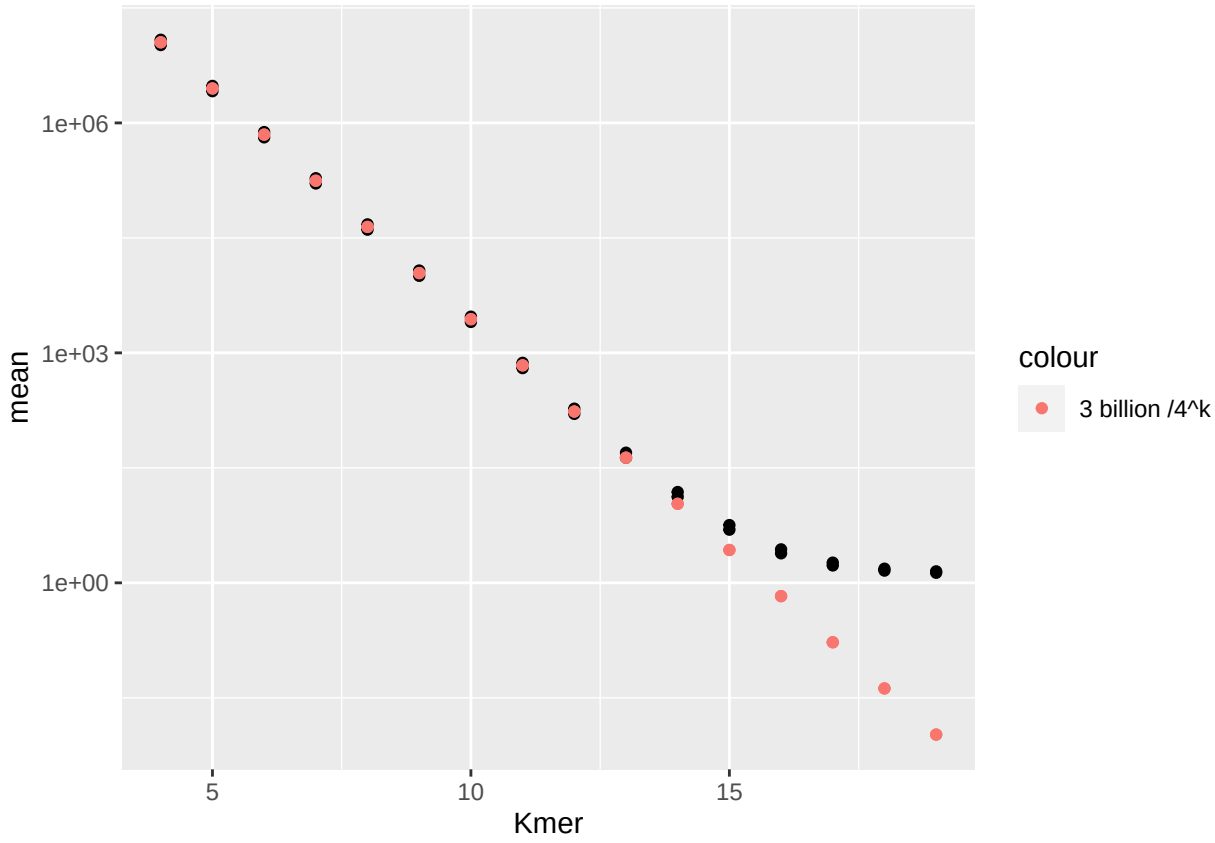
```
quint%>%
  mutate(Kmer=ifelse(Genome=="Human",Kmer+.4,Kmer))%>%
  ggplot()+aes(color=Genome,x=Kmer)+geom_point(aes(y=Q2))+scale_y_log10()+geom_segment(aes(xend=Kmer,y=
```



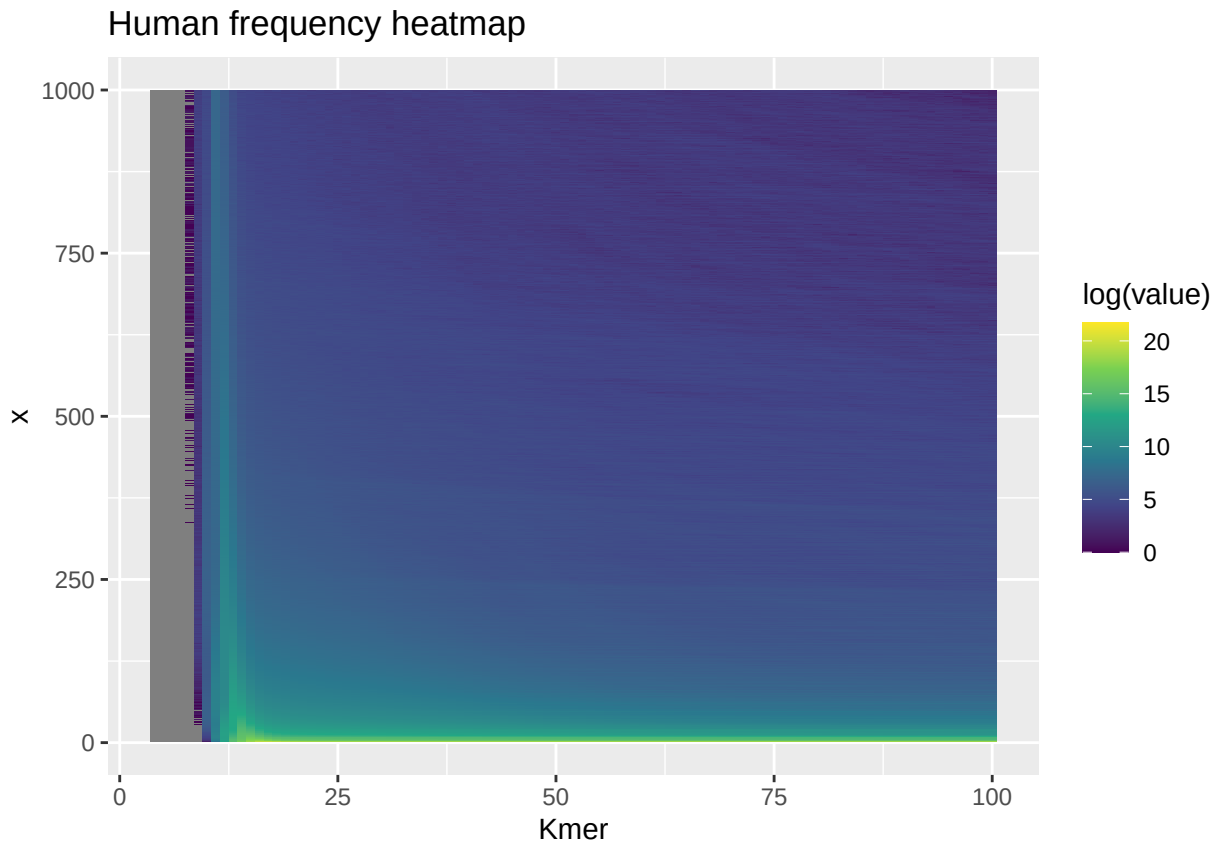

```
quint%>%
  mutate(Kmer=ifelse(Genome=="Human",Kmer+.4,Kmer))%>%
  filter(Kmer<60)%>%
  ggplot()+aes(color=Genome,x=Kmer)+geom_point(aes(y=Q2))+geom_segment(aes(xend=Kmer,y=Q1,yend=Q3))+xla
```



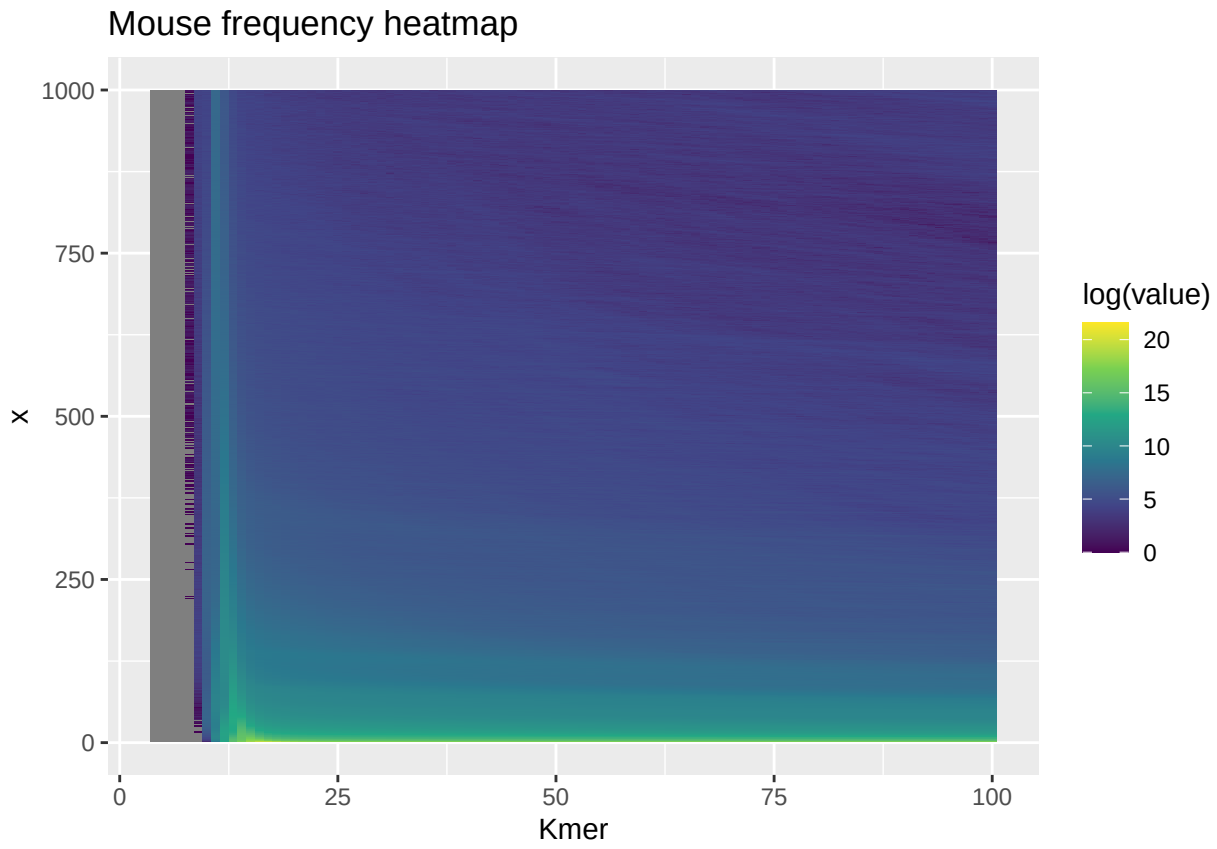

```
#4^k
#so as k increces

#human: 3billion
#mouse: about the same size, 3.1,2.8
#might want to be proportional at a later point
for (i in 0:9){
  break
  print(i)
  ploter=numericnames%>%
    filter((Kmer-1)%/%10==i)%>%
    ggplot(aes(x=x,y=value,color=Genome))+geom_point(alpha=.4)+scale_y_log10()+scale_x_log10()+ggtitle(
  filename=paste("histo of",i*10+1,"mer","to ",i*10+10,"mer")
  ggsave(filename,plot=ploter,device="png")
}




#longerVersion%>%
#  filter(value==0)


numericnamesSumer%>%
  filter(Kmer<20)%>%
  ggplot()+aes(x=Kmer)+geom_point(aes(y=mean))+scale_y_log10()+geom_point(aes(y=random,color="3 billion
```



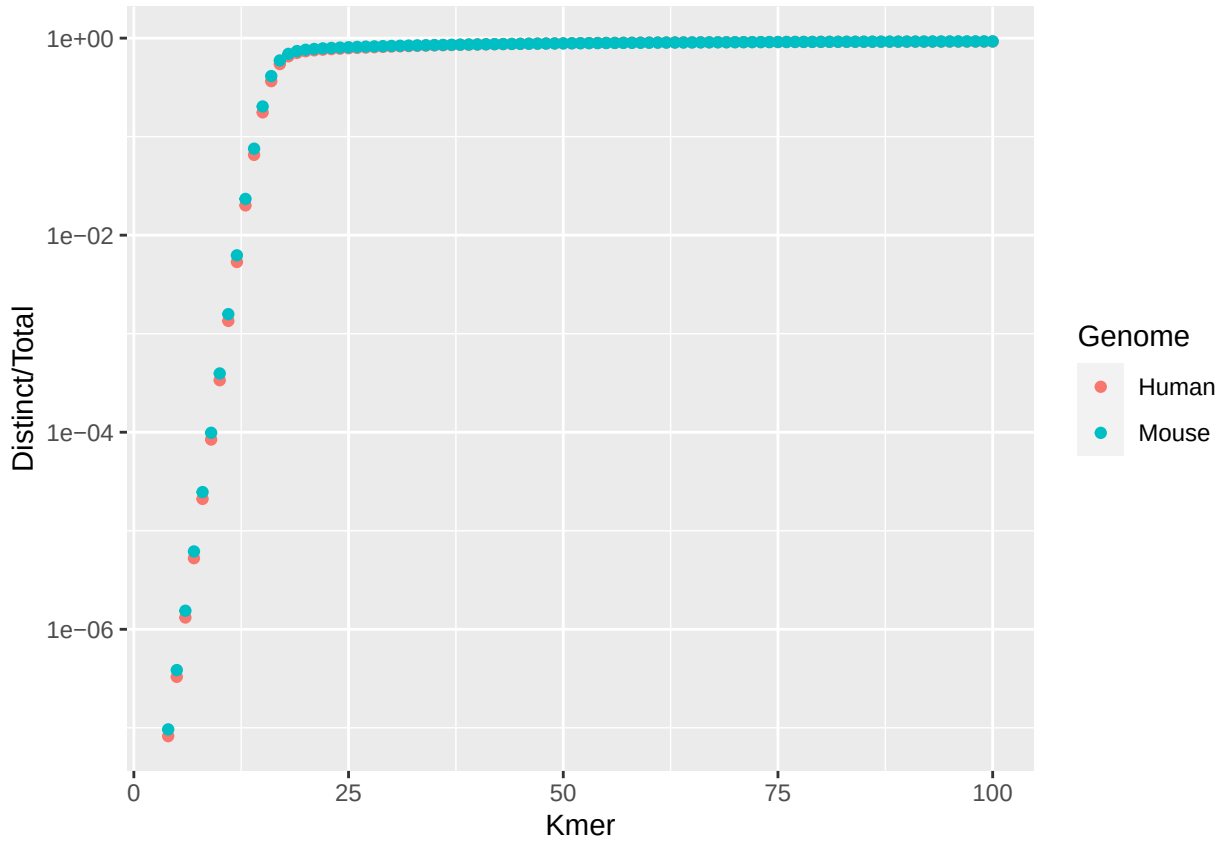

```
#heatmap
numericnames%>%
  filter(Genome=="Human",x<1000)%>%
  ggplot(aes(x=Kmer)) + geom_tile(aes(y=x, fill= log(value)),na.rm=T)+scale_fill_continuous(type = "vir
```



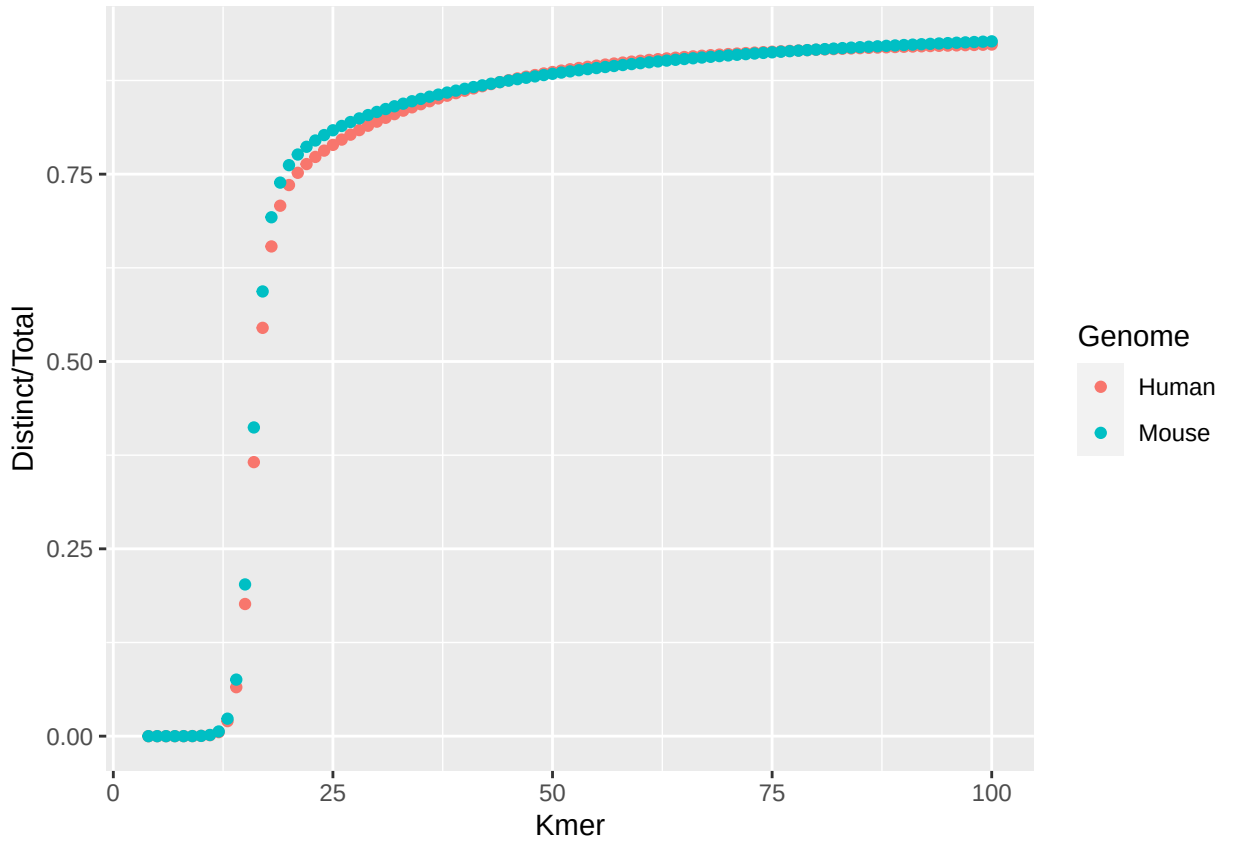

```
numericnames%>%
  filter(Genome=="Mouse",x<1000)%>%
  ggplot(aes(x=Kmer)) + geom_tile(aes(y=x, fill= log(value)),na.rm=T)+scale_fill_continuous(type = "vir
```



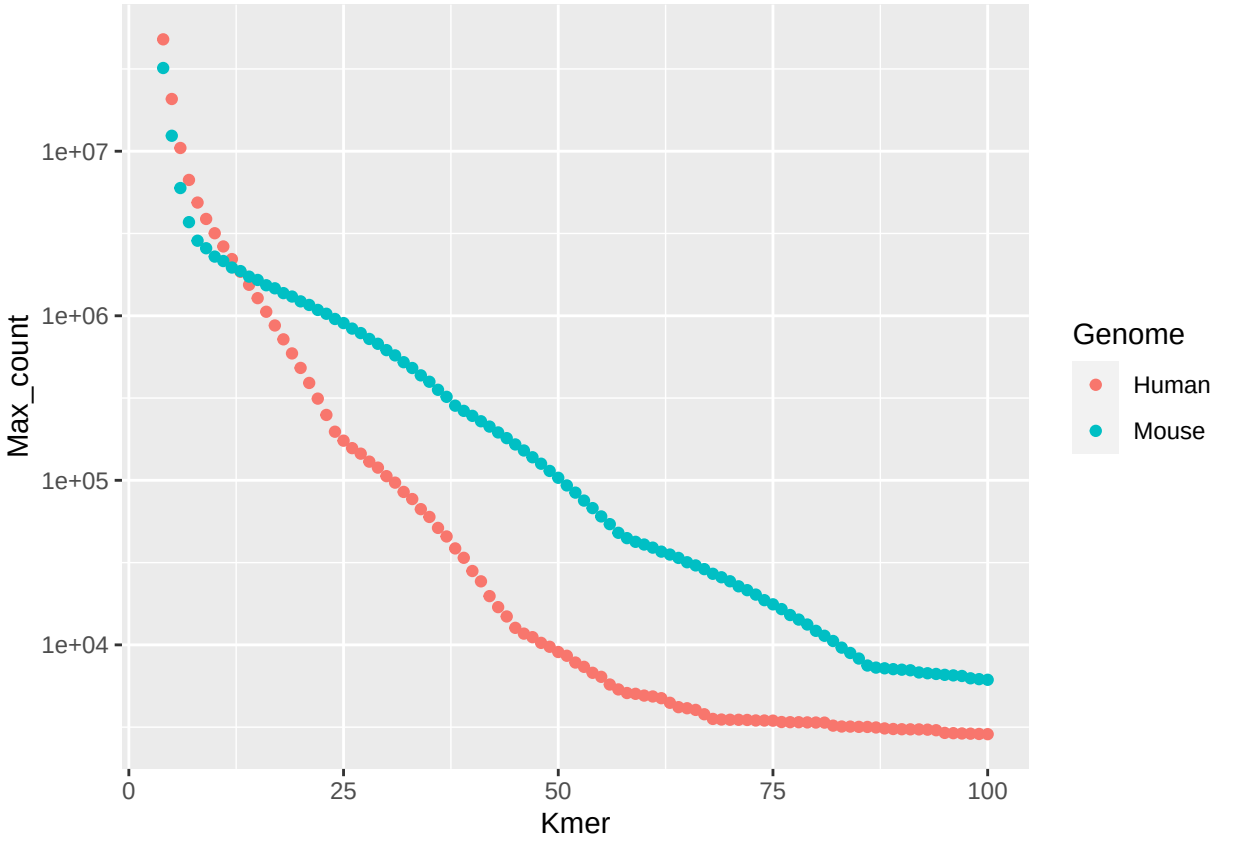

```
#geom_raster

SumTabLonger%>%
  ggplot()+aes(x=Kmer,y=Distinct/Total,color=Genome)+geom_point()+scale_y_log10()
```



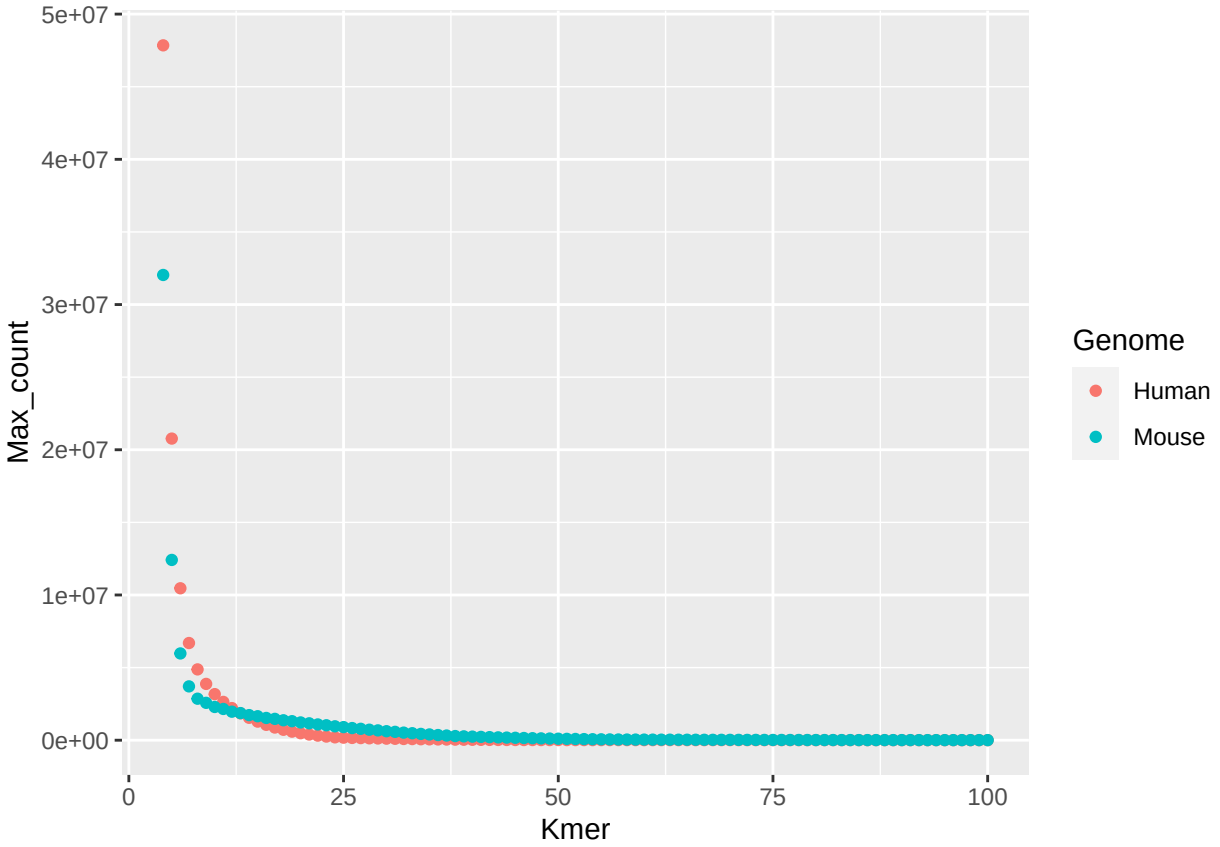

```
SumTabLonger%>%
  ggplot()+aes(x=Kmer,y=Distinct/Total,color=Genome)+geom_point()
```



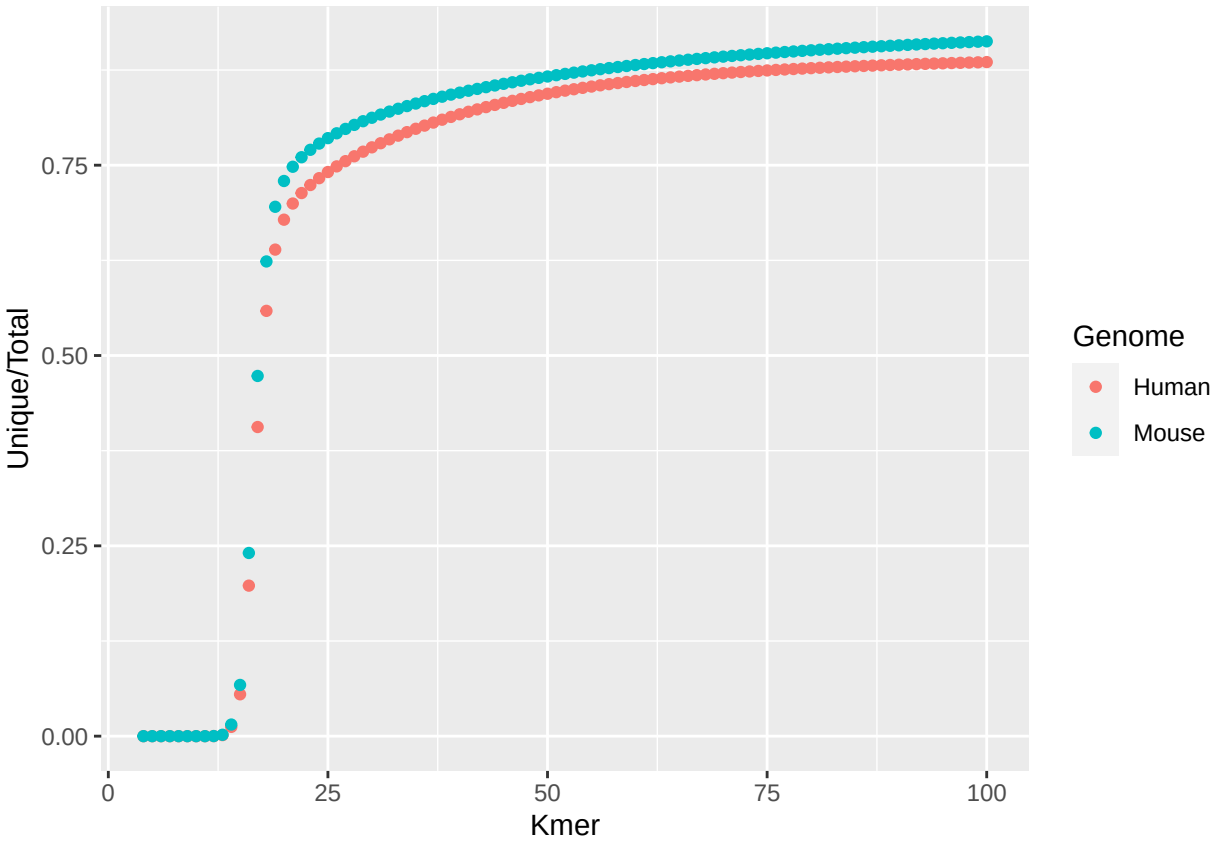

```
SumTabLonger%>%
  ggplot()+aes(x=Kmer,y=Max_count,color=Genome)+geom_point()+scale_y_log10()
```




```
SumTabLonger%>%
  ggplot()+aes(x=Kmer,y=Max_count,color=Genome)+geom_point()
```




```
SumTabLonger%>%
  ggplot()+aes(x=Kmer,y=Unique/Total,color=Genome)+geom_point()
```


Unique/Total
0.00
0.25
0.50
0.75
0
25
50
75
100
Kmer
Genome
Human
Mouse