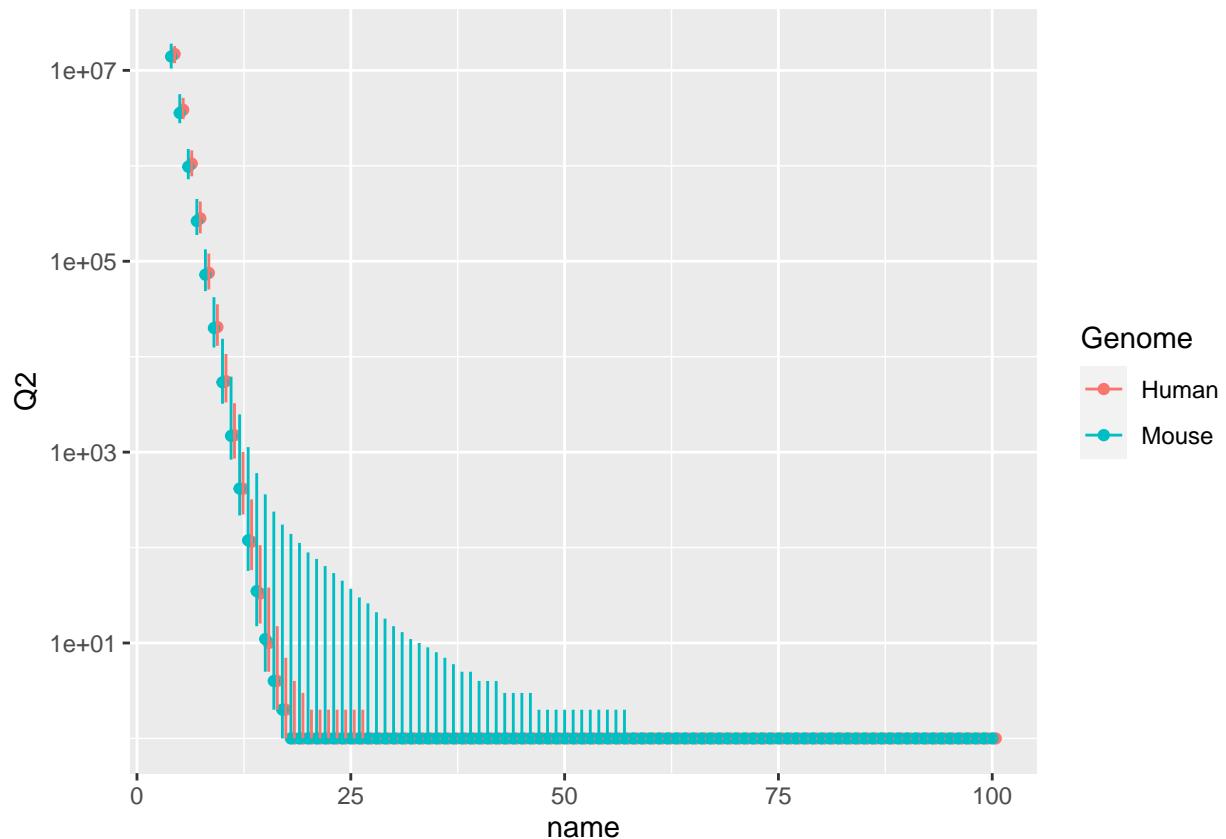


```

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

```



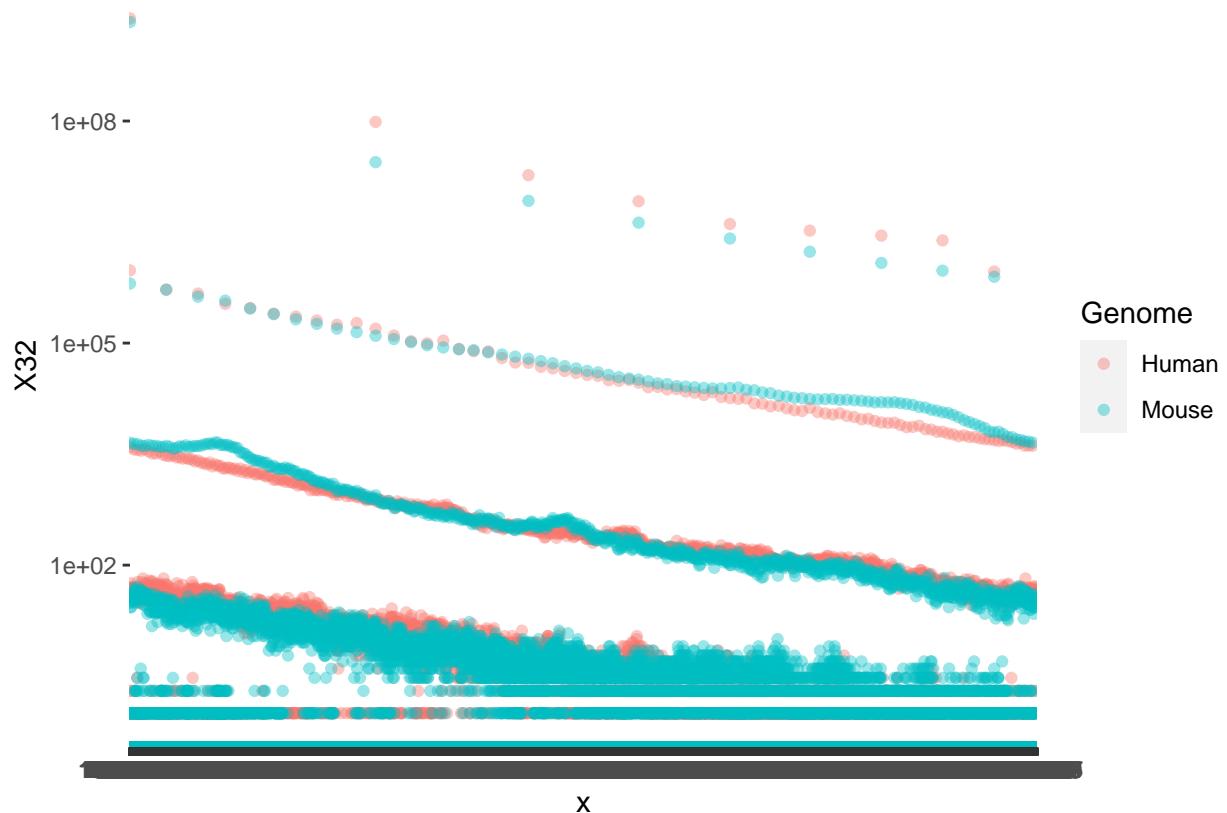
```

#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

Dataframe%>%
  ggplot(aes(x=x,y=X32,color=Genome))+geom_point(alpha=.4)+scale_y_log10()

```



```
longerVersion%>%
  filter(value!=0)
```

```
## # A tibble: 1,319,489 x 5
##   Genome     x name      value  weighted
##   <chr>    <dbl> <chr>     <dbl>     <dbl>
## 1 Human      1 X11      2638      2638
## 2 Human      1 X12     257757    257757
## 3 Human      1 X13    4267981   4267981
## 4 Human      1 X14   37984112  37984112
## 5 Human      1 X15  171077907  171077907
## 6 Human      1 X16  615097747  615097747
## 7 Human      1 X17 1263212344 1263212344
## 8 Human      1 X18 1737852949 1737852949
## 9 Human      1 X19 1988073244 1988073244
## 10 Human     1 X20 2110409768 2110409768
## # ... with 1,319,479 more rows
```

```
#8450895/9054271
```

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

