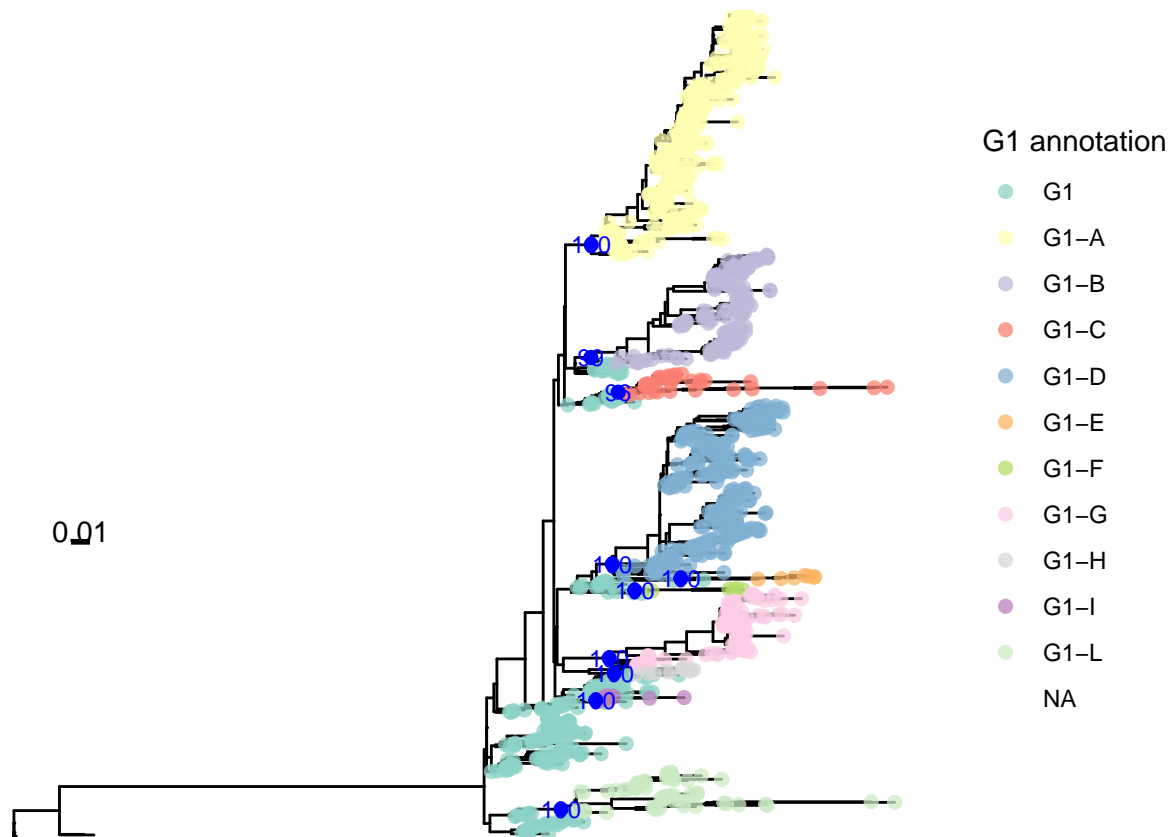


H9_G1_KOR_pairwise_nodedistance

Jiani Chen

9/9/2021

G1 clades defined from annotation files

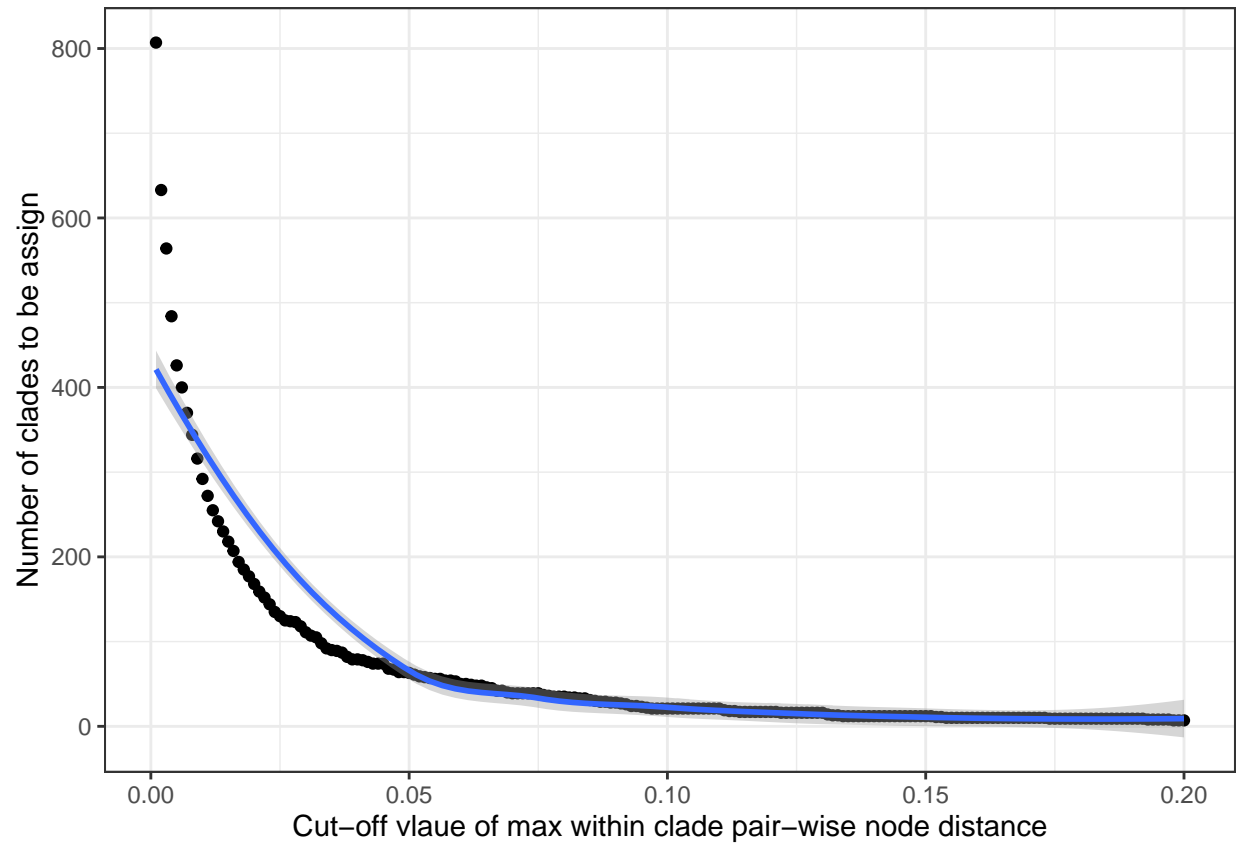


With the assigned clade, calculate the maximal pair-wise node distance within clade

##	clade	max.within.clade.pair.nodedist
## 1	G1-A	0.15301150
## 2	G1-B	0.13781677
## 3	G1-C	0.13020160
## 4	G1-D	0.19205041
## 5	G1-E	0.05739515

## 6	G1-F	0.04719568
## 7	G1-G	0.10645165
## 8	G1-H	0.02182253
## 9	G1-I	0.02052572
## 10	G1-L	0.13336139

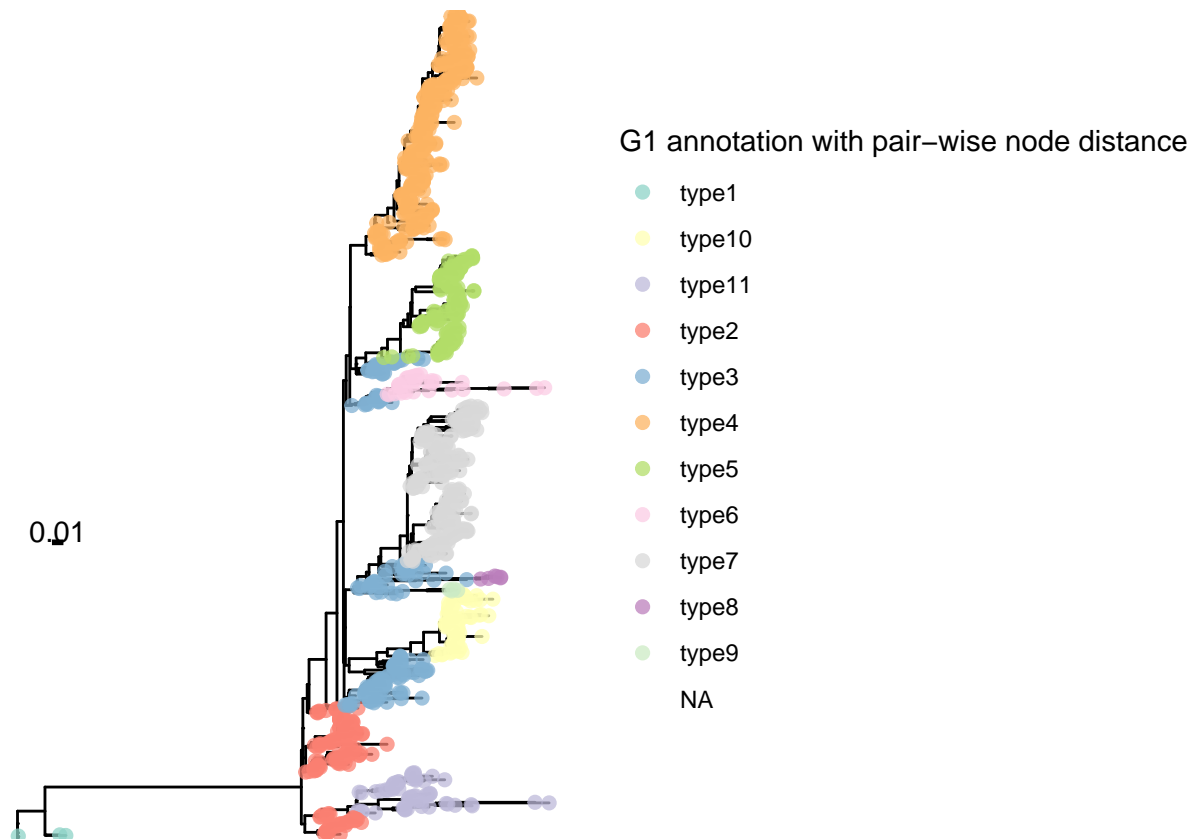
You can also embed plots, for example:



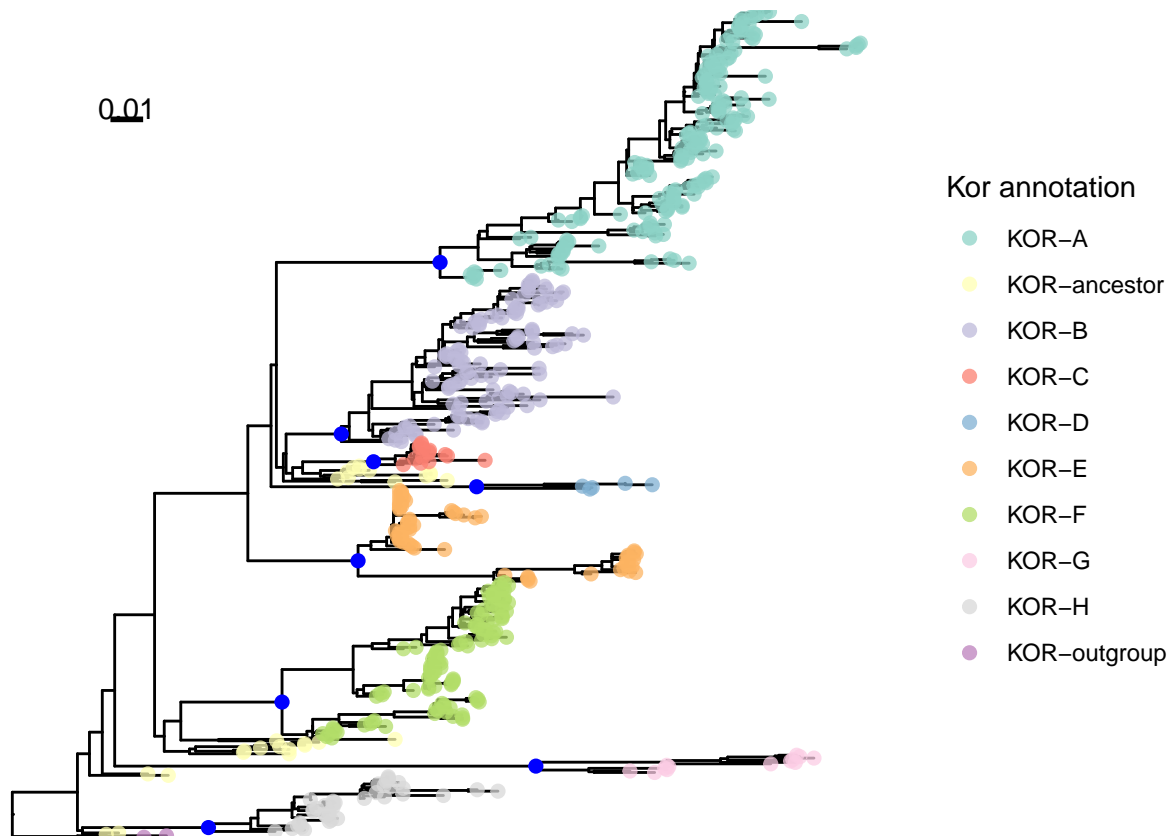
I re-assign the clade with maximal pair-wise node distance 0.16 within clade

Similar results from the clades defined in annotation file

G1-D clade, small propotion of sequences was unable to classified with this approach (type 8, green)



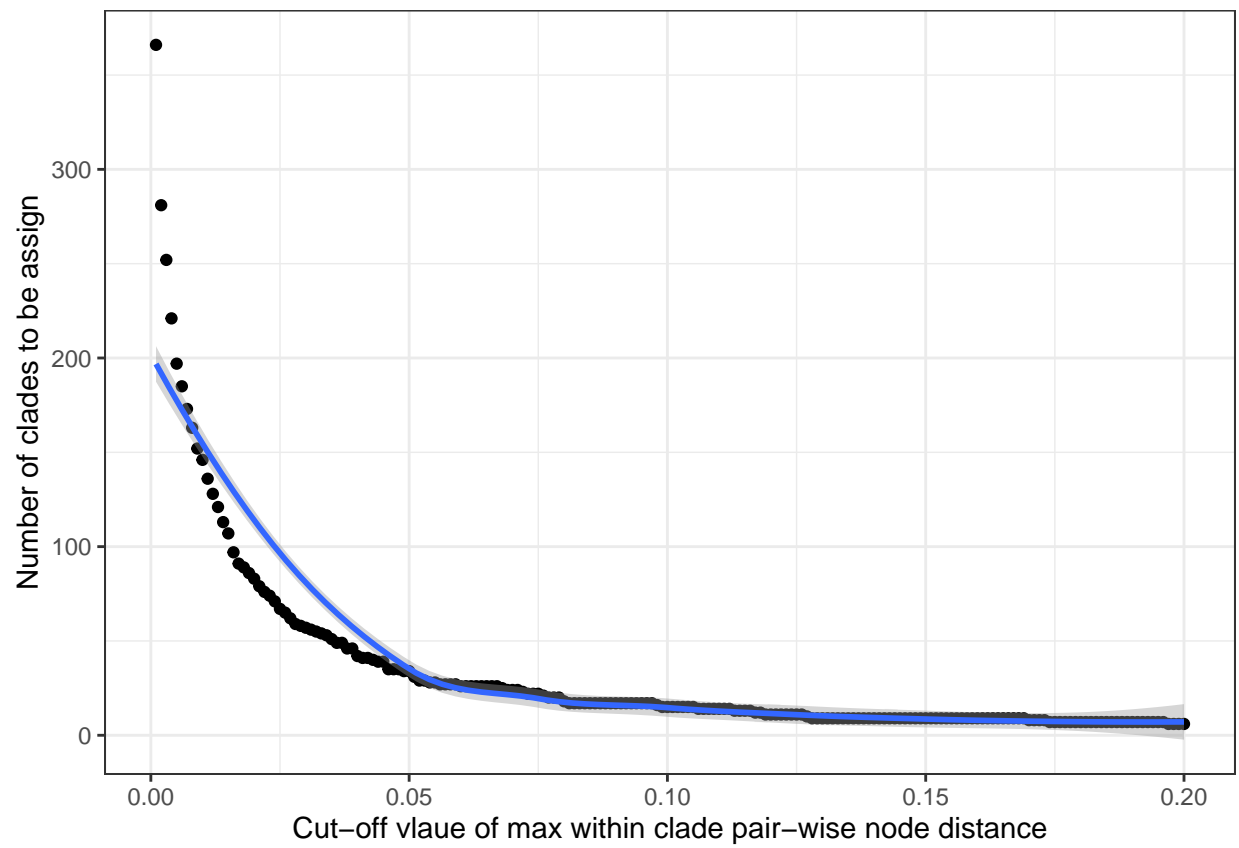
analysis for KOR clade # Kor clades defined from annotation files



With the assigned clade, calculate the maximal pair-wise node distance within clade

```
##   clade max.within.clade.pair.nodedist
## 1 KOR-A 0.173678
## 2 KOR-B 0.097446
## 3 KOR-C 0.016257
## 4 KOR-D 0.079447
## 5 KOR-E 0.118378
## 6 KOR-F 0.126374
## 7 KOR-G 0.116707
## 8 KOR-H 0.079360
```

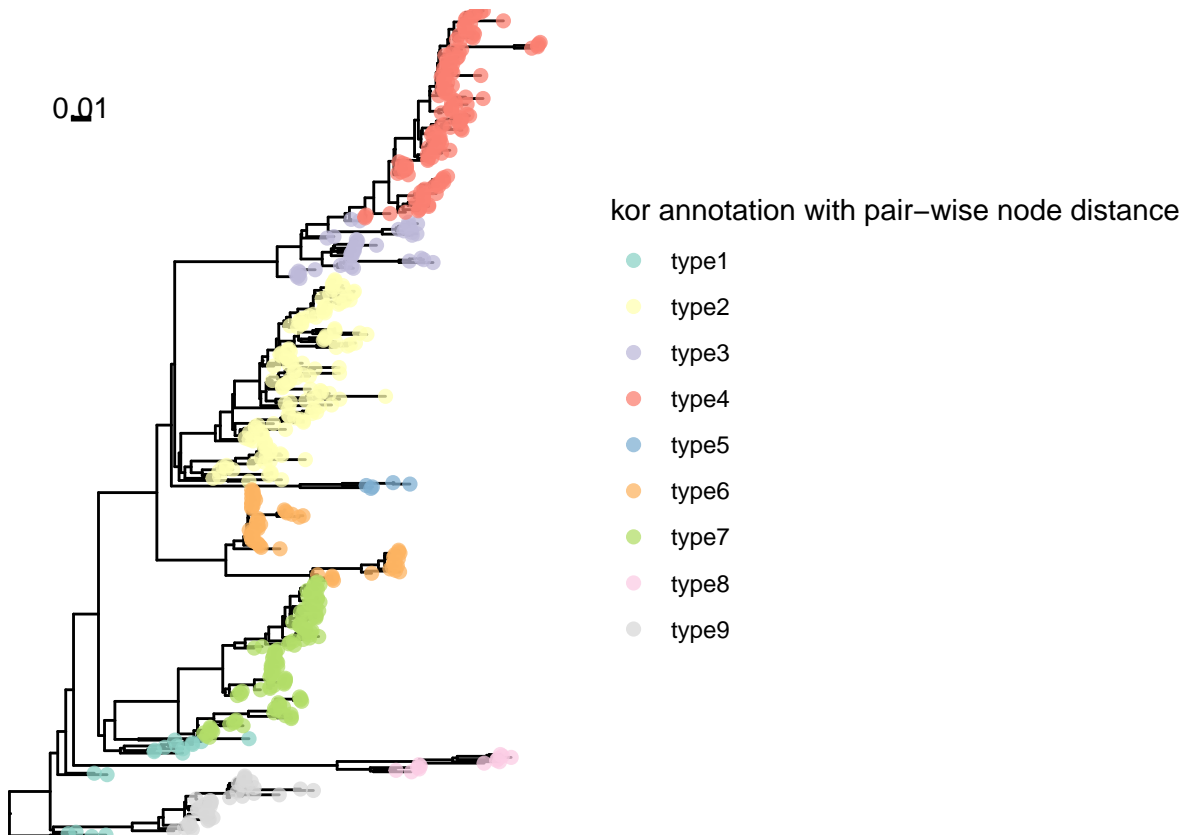
simulation with different maximal within clade pair-wise node distance



I re-assign the clade with maximal pair-wise node distance 0.16 within clade

Similar results from the clades defined in annotation files, only differences in KOR-A

KOR-A was divided into two propotion with pair-wise node distance criteria (type1 and type 3)



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.