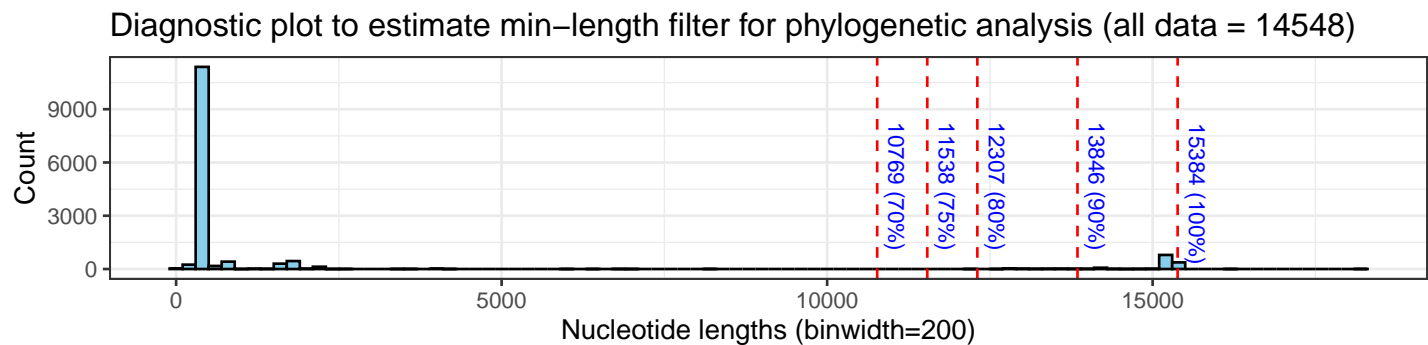
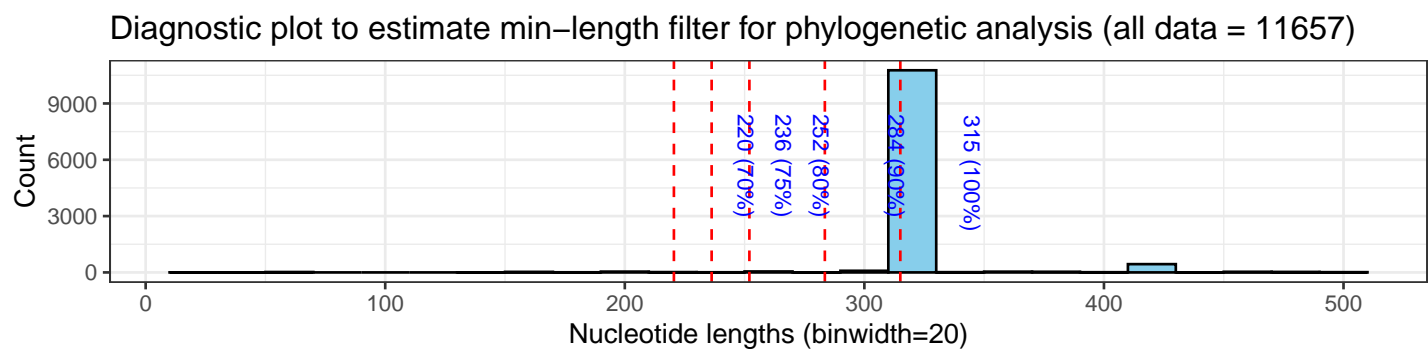


Nextclade Result Parameter Diagnostic Plots

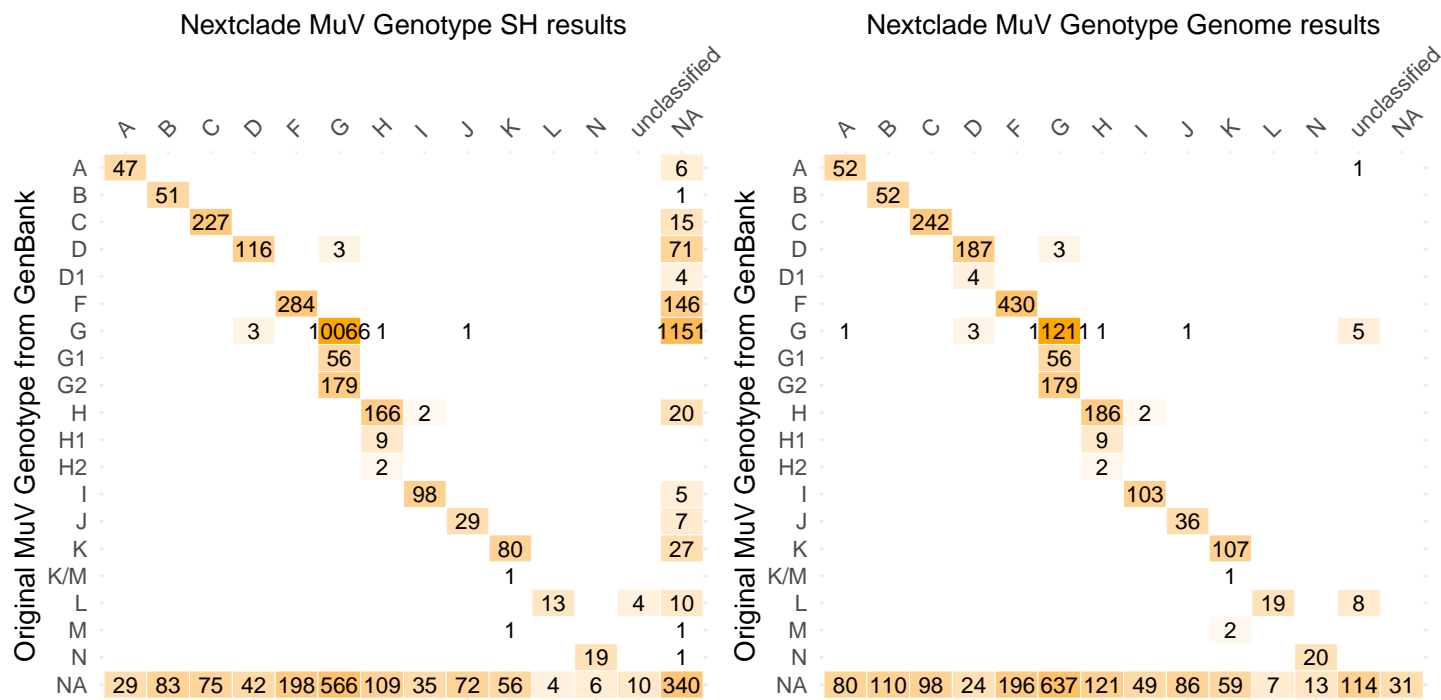
Full Genome



SH Region



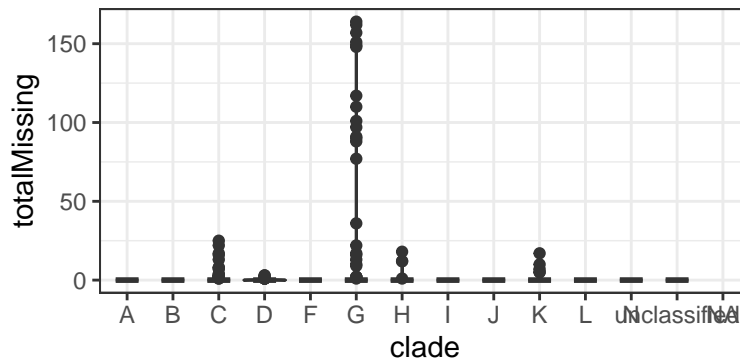
Nextclade compared with GenBank annotations:



SH gene Nextclade Dataset

Missing Data

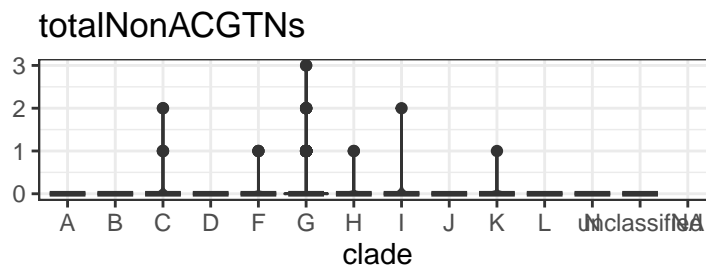
```
--scoreBias 300          # First 300 not penalized
--missingDataThreshold 3000 # Top threshold, scale the next set of missing data from 0 to 100
```



Since this is the SH gene (315nt), we do not reach past the 300 minimum.

Mixed Sites (M)

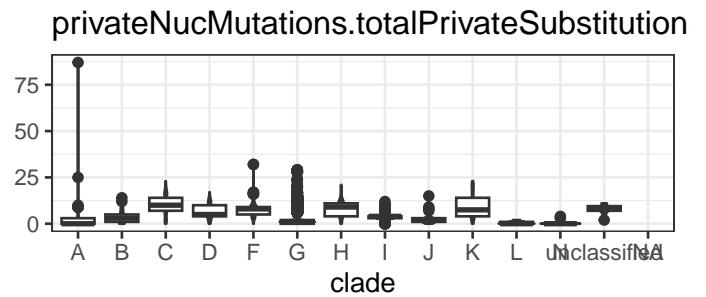
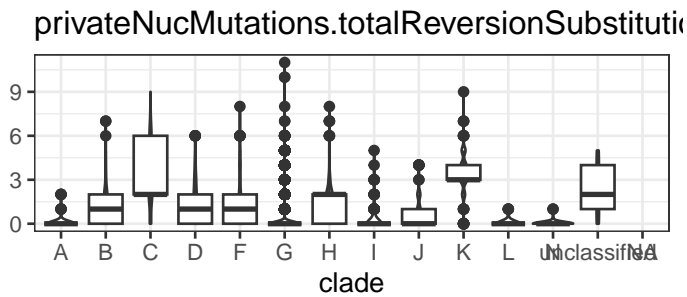
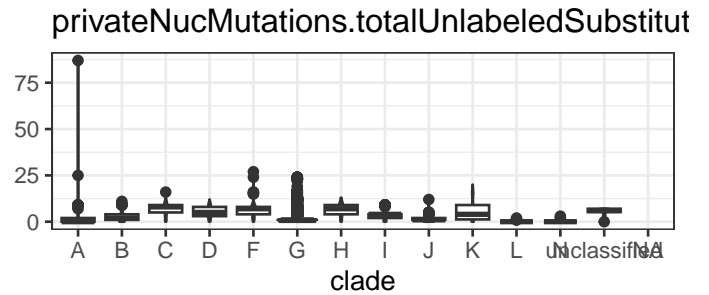
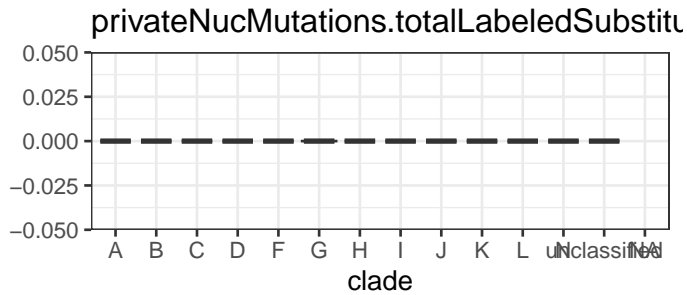
```
--mixedSitesThreshold 10 # More than this number of mixed sites results in a "bad" score
```



Well below the 10 threshold (but once again this is for a reference that is 315nt long).

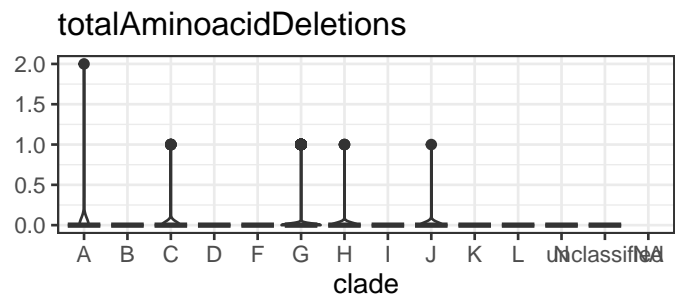
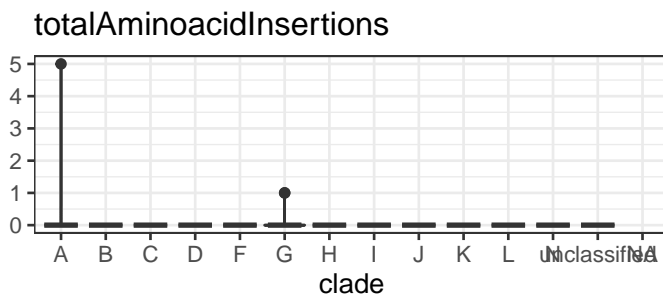
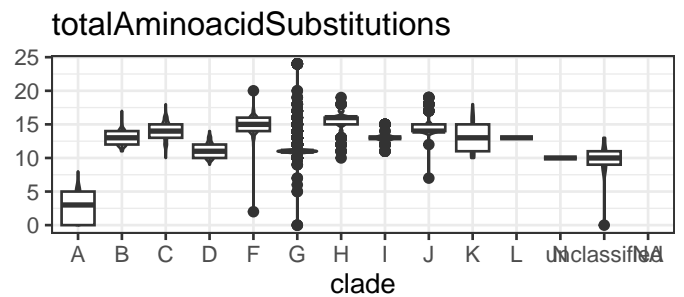
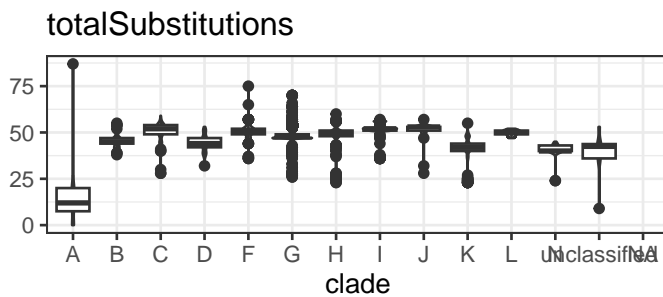
Private Mutations

```
"privateMutations": {
  "enabled": true,
  "typical": 8,
  "cutoff": 24,
  "weightLabeledSubstitutions": 4,
  "weightReversionSubstitutions": 6,
  "weightUnlabeledSubstitutions": 1
},
```



Mutation clusters

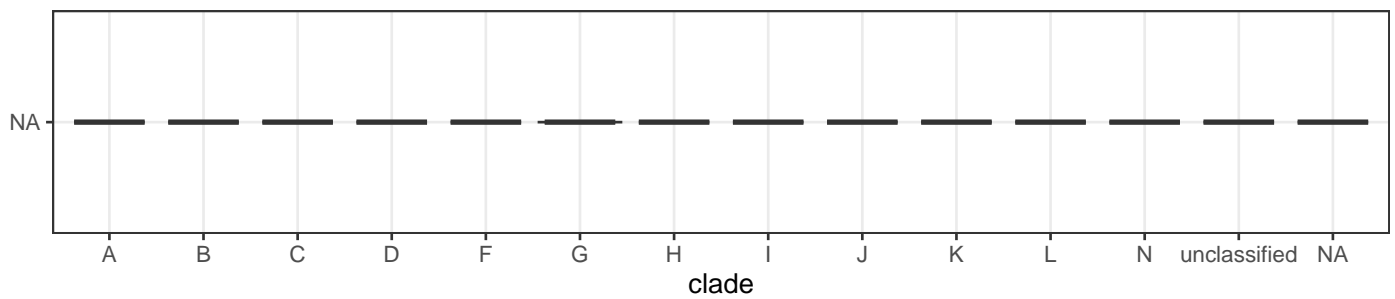
```
"snpcClusters": {
  "enabled": true,
  "windowSize": 100,
  "clusterCutOff": 6,
  "scoreWeight": 50
},
```



Stop Codons

```
"stopCodons": {  
  "enabled": true,  
  "ignoredStopCodons": [  
    {  
      "geneName": "ORF8",  
      "codon": 26  
    },  
    {  
      "geneName": "ORF8",  
      "codon": 67  
    }  
  ]  
}
```

qc.stopCodons.totalStopCodons



Frameshifts

```
"frameShifts": {  
  "enabled": true,  
  "ignoredFrameShifts": [  
    {  
      "geneName": "ORF3a",  
      "codonRange": {  
        "begin": 256,  
        "end": 276  
      }  
    },  
    {  
      "geneName": "ORF3a",  
      "codonRange": {  
        "begin": 258,  
        "end": 276  
      }  
    }  
  ]  
},
```

totalFrameShifts

