

# SARS-CoV-2 Guangdong genomic epidemiology

Figure data and plots

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## Process datasets

This section does some consistency checks to makes sure different spreadsheets agree with each other (e.g. no samples have different Ct values or collection dates). If no warnings are printed everything is ok.

Checking Ct values and collection dates...

Figure 1: Cases and Sequences

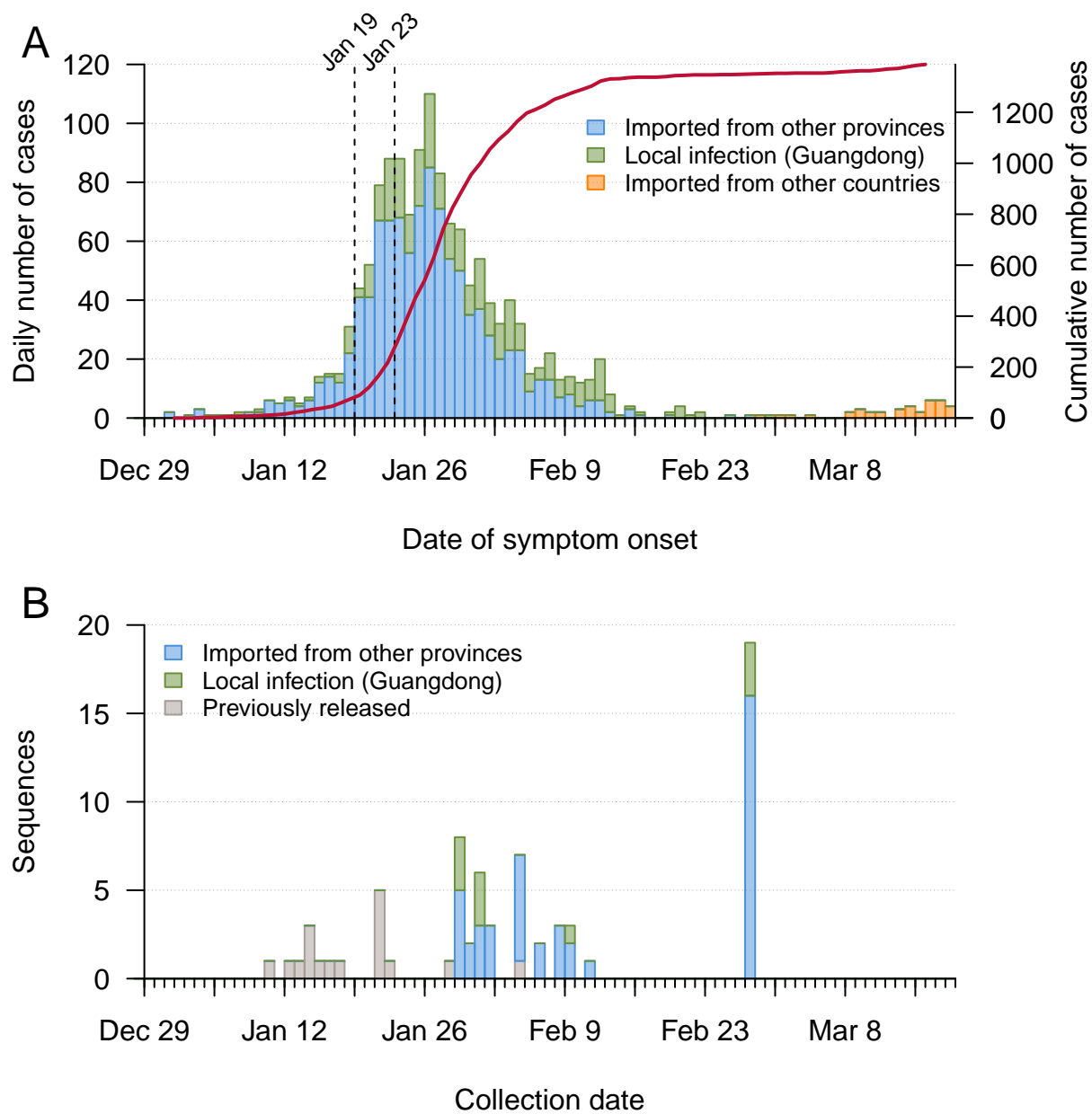


Fig 1 - Non-stacked

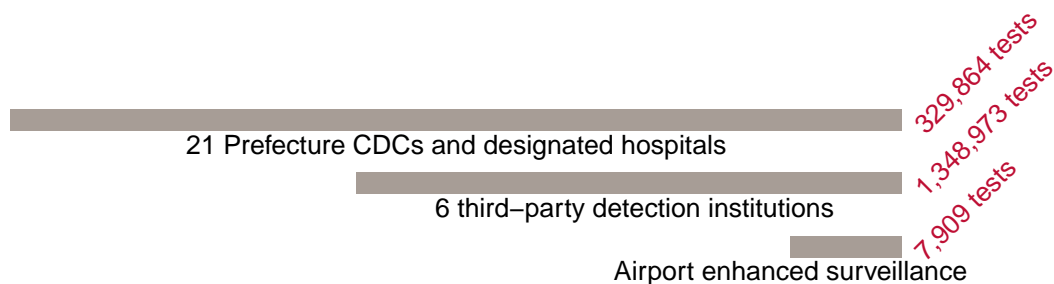
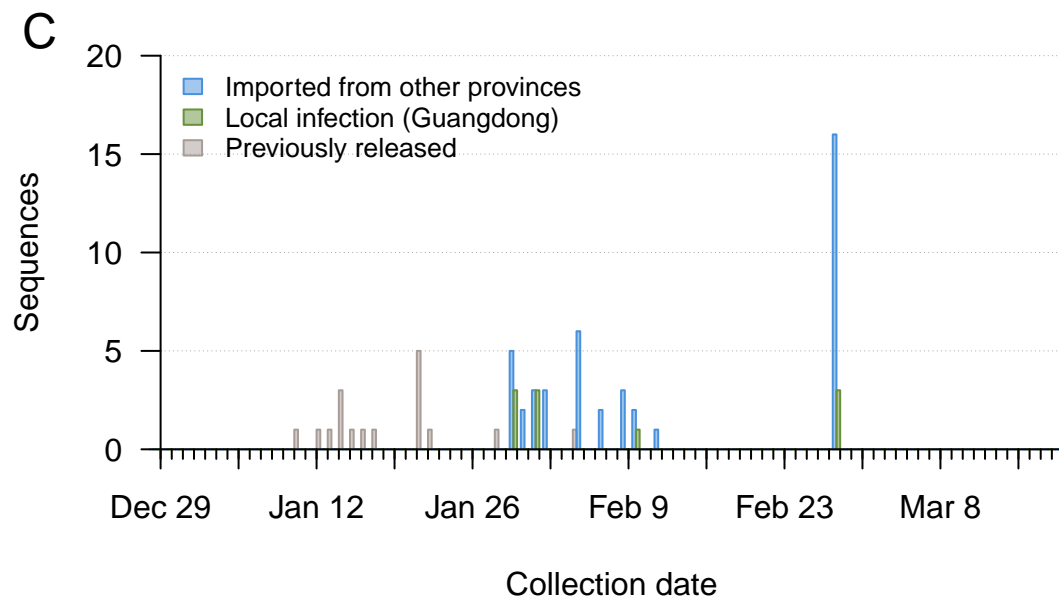
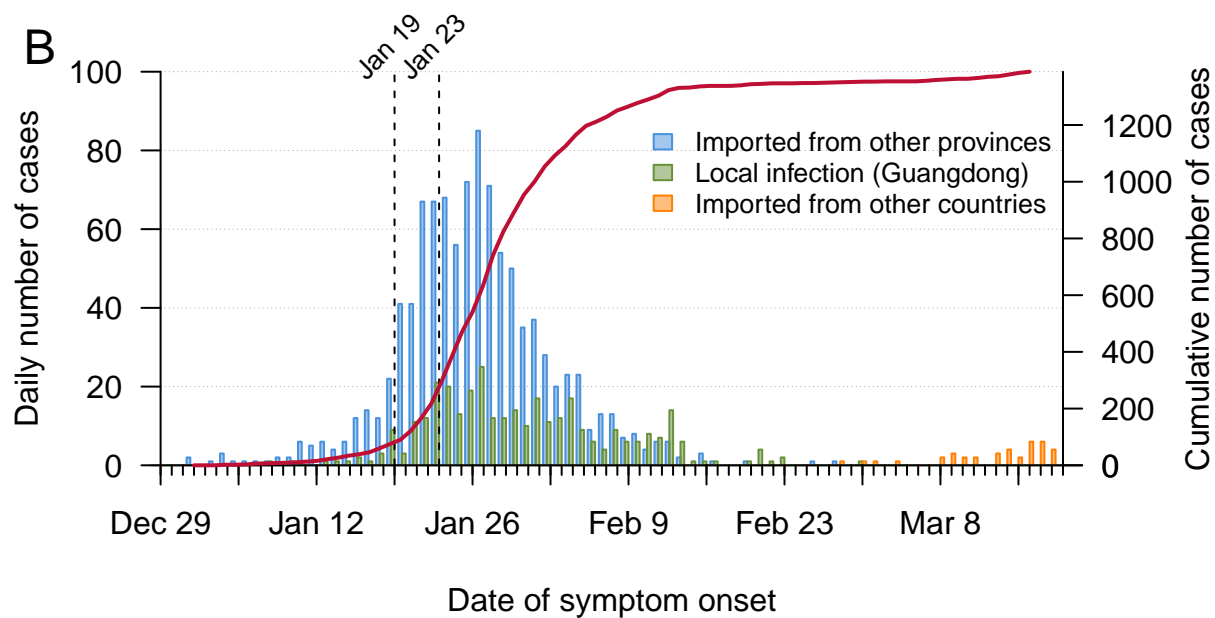
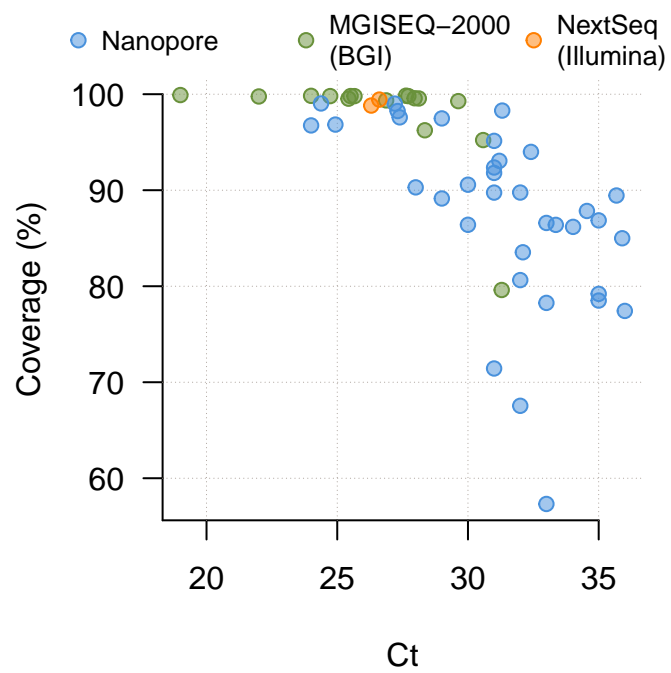
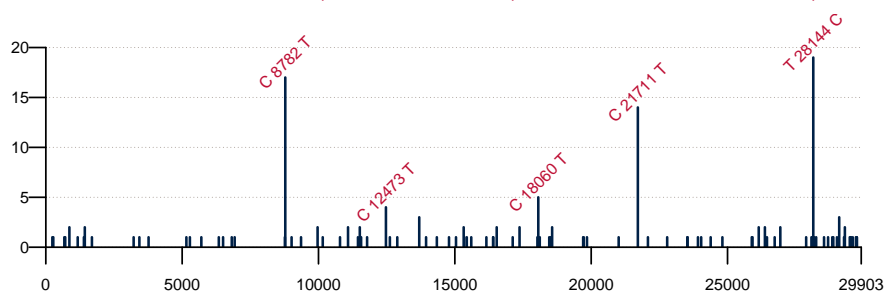
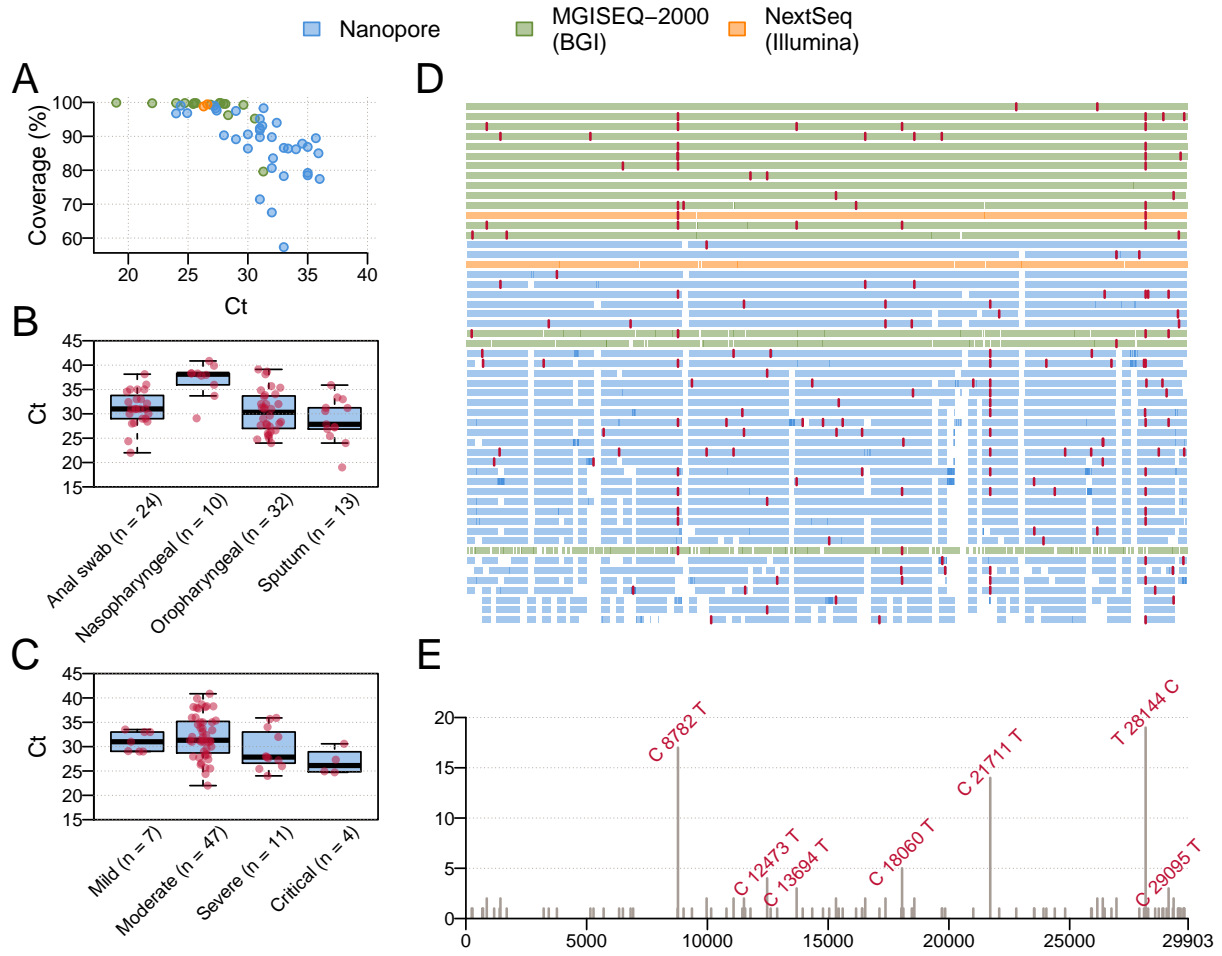


Figure 2: Sequencing Statistics



■ Nanopore
 ■ MGISEQ-2000 (BGI)
 ■ NextSeq (Illumina)





## Kruskal-Wallis H-test

```
##
## Kruskal-Wallis rank sum test
##
## data: ct by symptom
## Kruskal-Wallis chi-squared = 8.9434, df = 3, p-value = 0.03005
##
## Kruskal-Wallis rank sum test
##
## data: ct by sample_type
## Kruskal-Wallis chi-squared = 18.447, df = 3, p-value = 0.0003557
```

**Fig 3A**

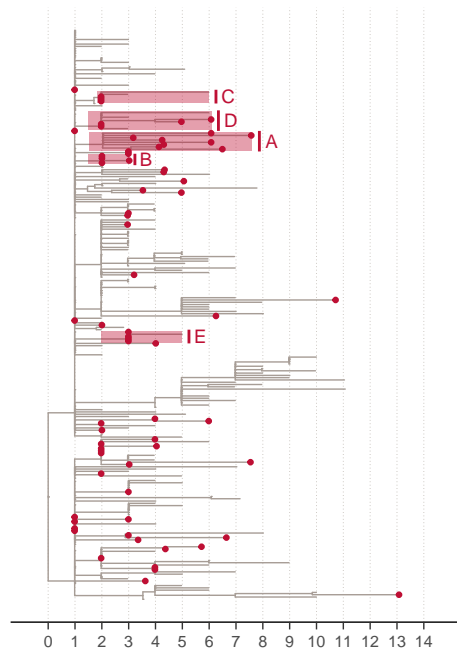
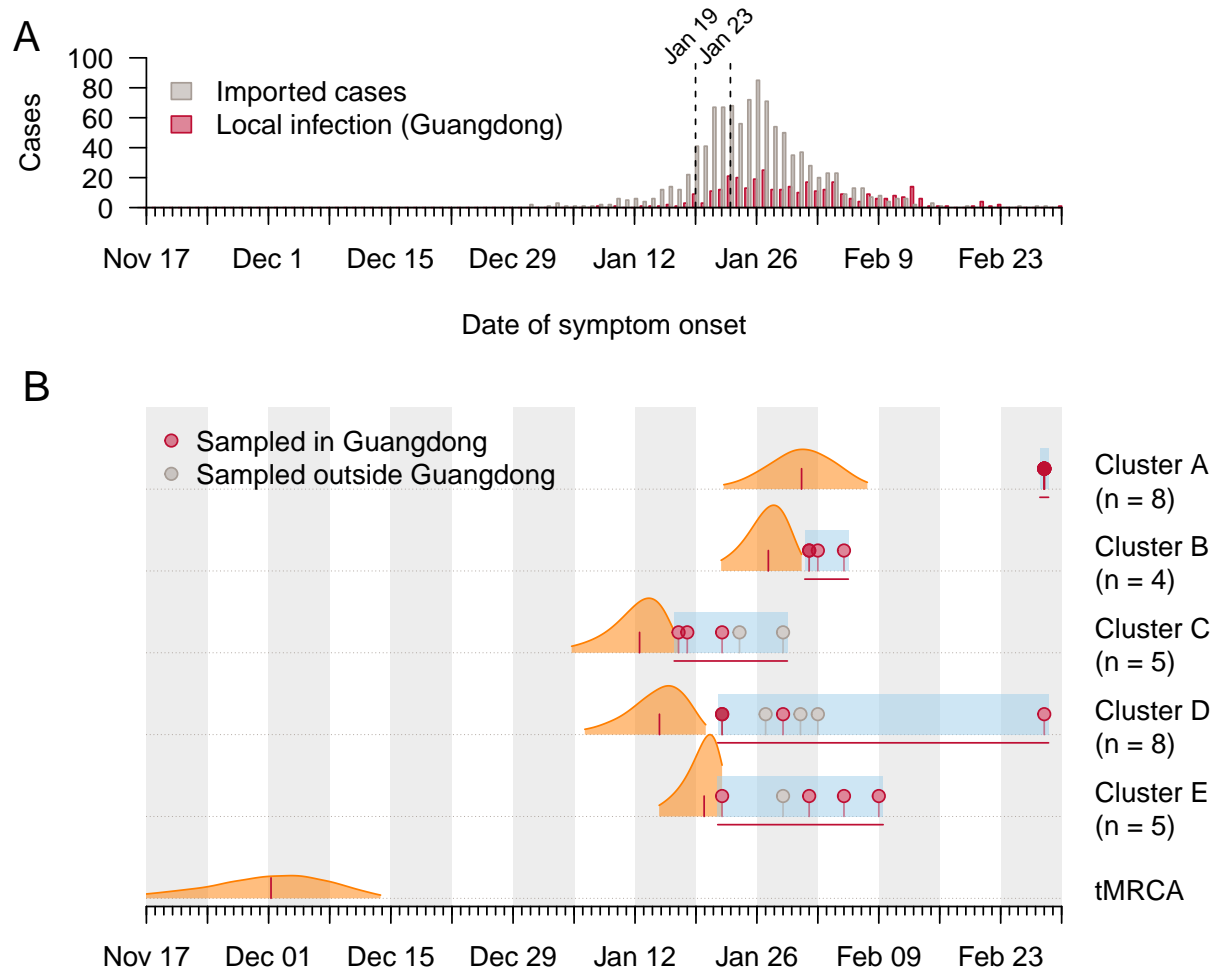
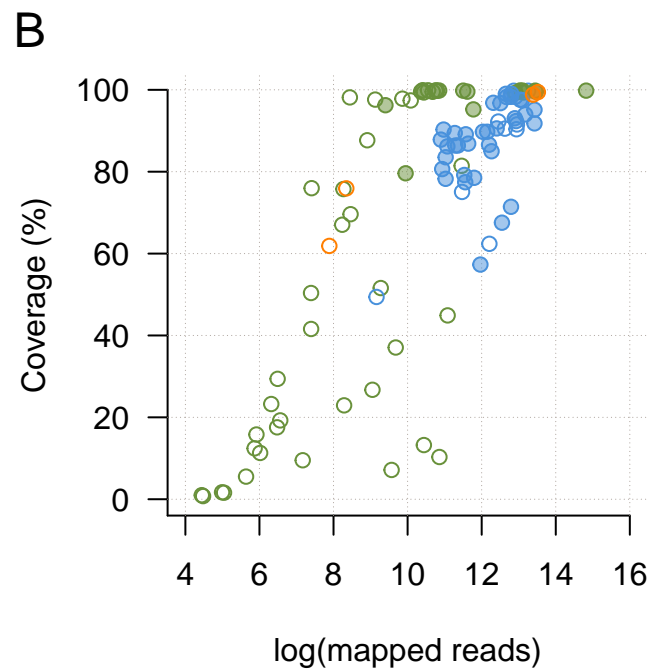
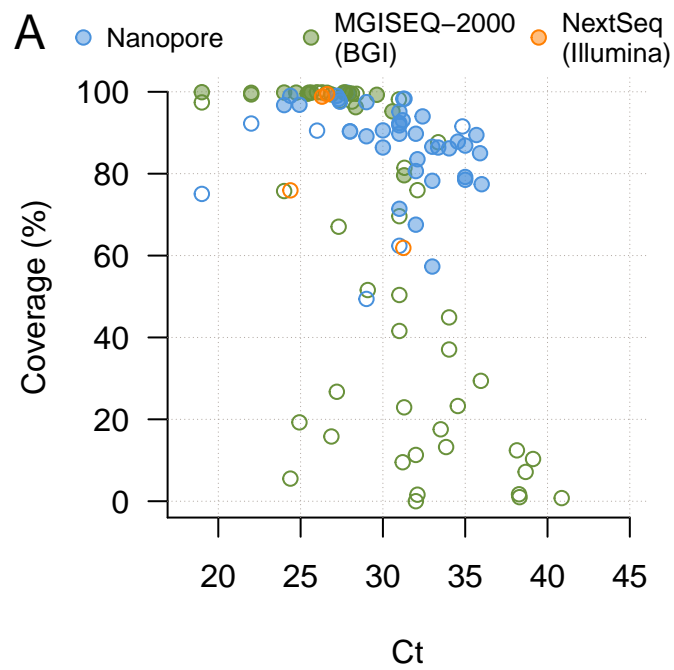


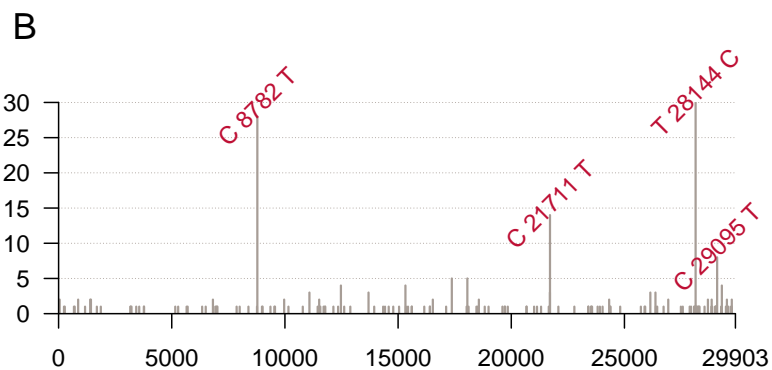
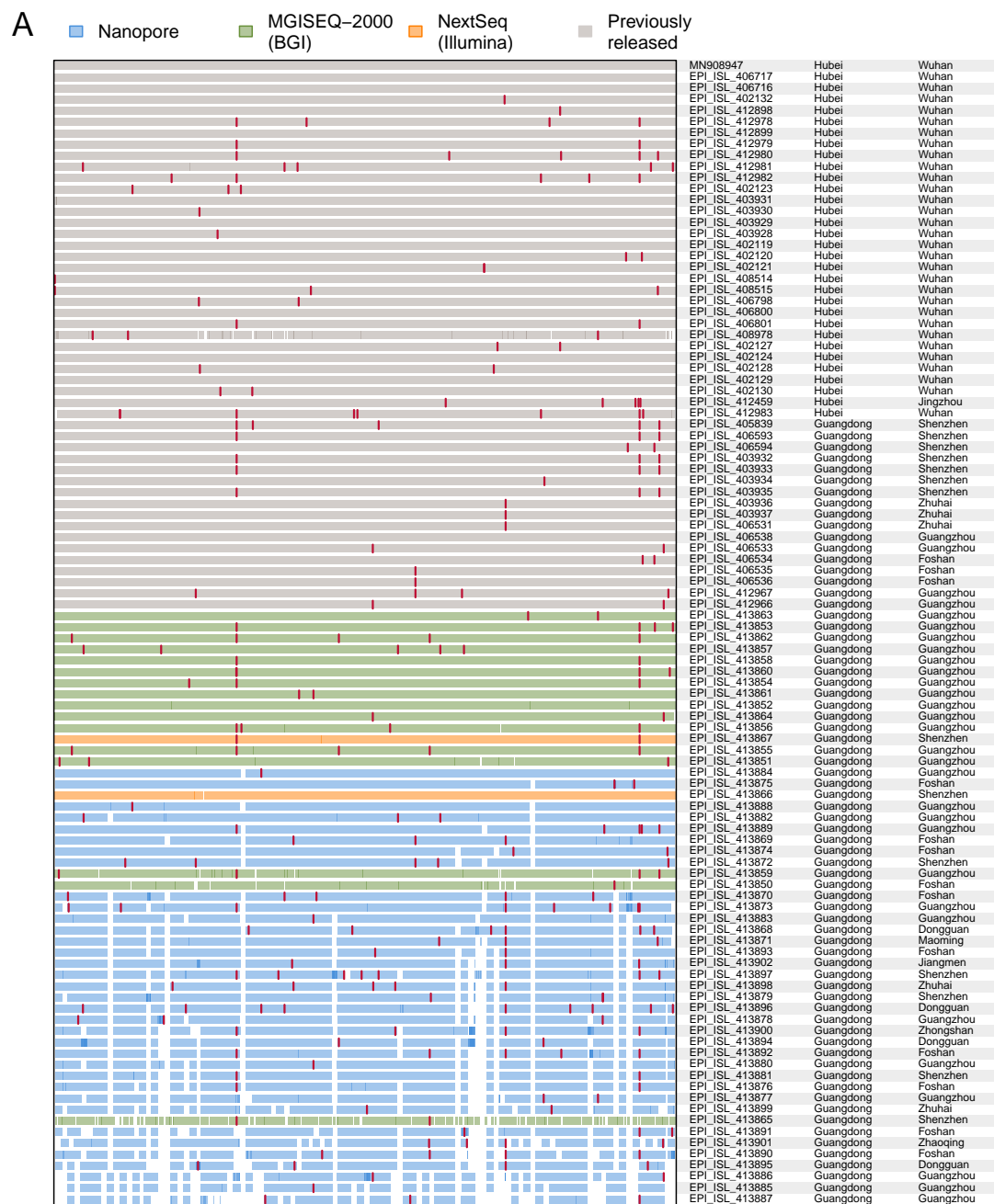
Figure 4 - TaxonSet Ages

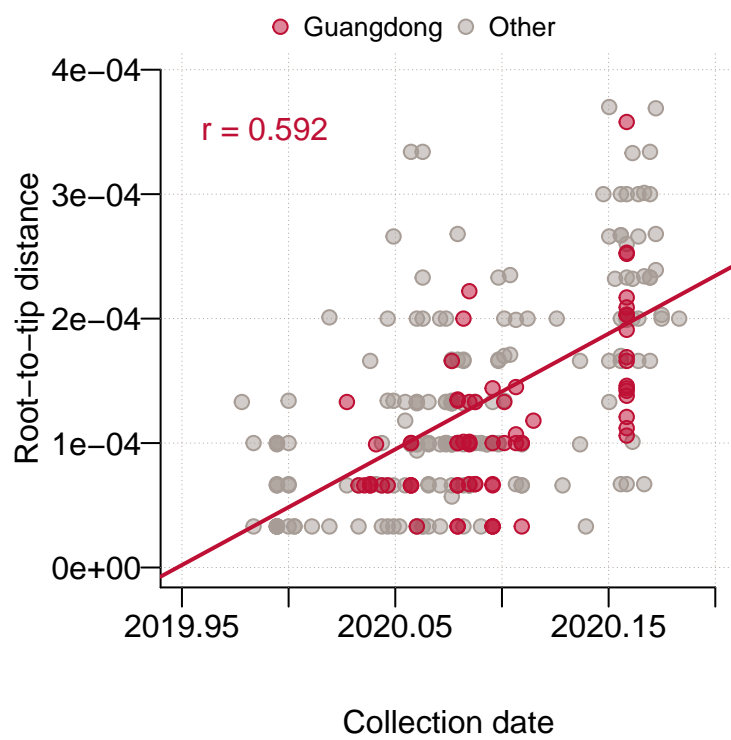


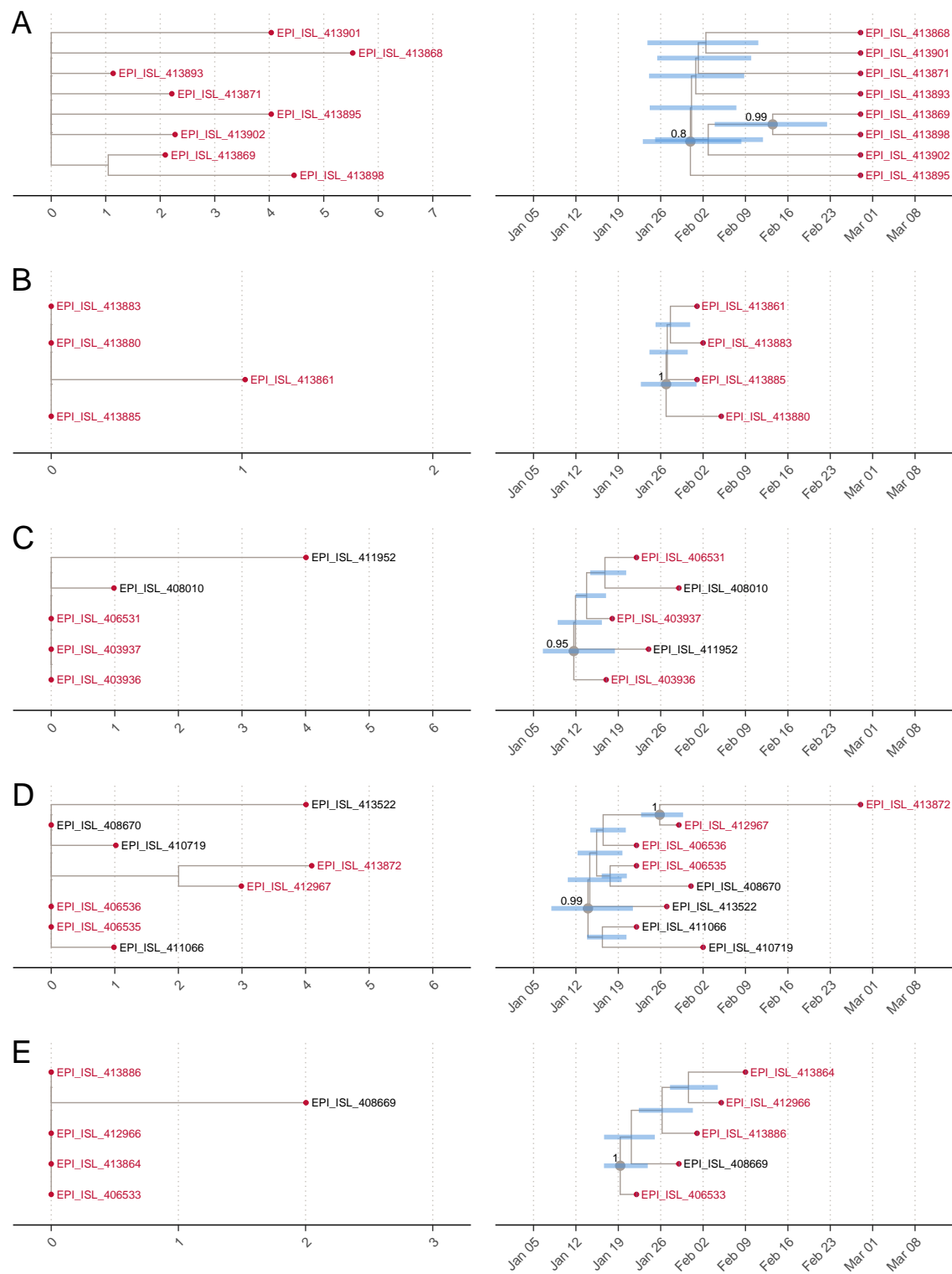


## Supplementary figures (or not included)









## Session info

```
## R version 3.5.1 (2018-07-02)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Sierra 10.12.6
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] lubridate_1.7.4 phytools_0.6-99 maps_3.3.0      ape_5.3
## [5] ggtree_2.1.1     ggplot2_3.2.1  treeio_1.11.2  beastio_0.2.5
## [9] coda_0.19-3      gplots_3.0.1.1 cowplot_1.0.0
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.3          lattice_0.20-38      tidyr_1.0.0
## [4] gtools_3.8.1        assertthat_0.2.1     zeallot_0.1.0
## [7] digest_0.6.23       R6_2.4.1             backports_1.1.5
## [10] evaluate_0.14       pillar_1.4.2         rlang_0.4.2
## [13] lazyeval_0.2.2      gdata_2.18.0         phangorn_2.5.5
## [16] combinat_0.0-8      Matrix_1.2-18        rmarkdown_2.0
## [19] labeling_0.3        stringr_1.4.0        igraph_1.2.4.2
## [22] munsell_0.5.0       compiler_3.5.1       numDeriv_2016.8-1.1
## [25] xfun_0.11           pkgconfig_2.0.3      mnormt_1.5-5
## [28] htmltools_0.4.0     tidyselect_0.2.5     expm_0.999-4
## [31] tibble_2.1.3        quadprog_1.5-8       crayon_1.3.4
## [34] dplyr_0.8.3         withr_2.1.2          MASS_7.3-51.4
## [37] bitops_1.0-6        grid_3.5.1           nlme_3.1-143
## [40] jsonlite_1.6         gtable_0.3.0         lifecycle_0.1.0
## [43] magrittr_1.5         scales_1.1.0         KernSmooth_2.23-16
## [46] tidytree_0.3.1      stringi_1.4.3        farver_2.0.1
## [49] scatterplot3d_0.3-41 rvcheck_0.1.7        vctrs_0.2.1
## [52] fastmatch_1.1-0     RColorBrewer_1.1-2   tools_3.5.1
## [55] glue_1.3.1          purrr_0.3.3          plotrix_3.7-7
## [58] parallel_3.5.1      yaml_2.2.0           colorspace_1.4-1
## [61] BiocManager_1.30.10 caTools_1.17.1.3     animation_2.6
## [64] clusterGeneration_1.3.4 knitr_1.26
```