
Supplementary information

A molnupiravir-associated mutational signature in global SARS-CoV-2 genomes

In the format provided by the authors and unedited

Supplementary Information

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SUPPLEMENTAL TABLE

Data Availability

GISAID Identifier: EPI_SET_230110wz

doi: [10.55876/gis8.230110wz](https://doi.org/10.55876/gis8.230110wz)

All genome sequences and associated metadata in this dataset are published in GISAID's EpiCoV database. To view the contributors of each individual sequence with details such as accession number, Virus name, Collection date, Originating Lab and Submitting Lab and the list of Authors, visit [10.55876/gis8.230110wz](https://gisaid.org/WIV04)

Data Snapshot

- EPI_SET_230110wz is composed of 7,748,305 individual genome sequences.
- The collection dates range from 2020-01-01 to 2022-12-29;
- Data were collected in 213 countries and territories;
- All sequences in this dataset are compared relative to hCoV-19/Wuhan/WIV04/2019 (WIV04), the official reference sequence employed by GISAID (EPI_ISL_402124). Learn more at <https://gisaid.org/WIV04>.

SUPPLEMENTAL TABLE

Data Availability

GISAID Identifier: EPI_SET_230110db

doi: [10.55876/gis8.230110db](https://doi.org/10.55876/gis8.230110db)

All genome sequences and associated metadata in this dataset are published in GISAID's EpiCoV database. To view the contributors of each individual sequence with details such as accession number, Virus name, Collection date, Originating Lab and Submitting Lab and the list of Authors, visit [10.55876/gis8.230110db](https://gisaid.org/WIV04)

Data Snapshot

- EPI_SET_230110db is composed of 6,701,432 individual genome sequences.
- The collection dates range from 2010-12-06 to 2021-12-31;
- Data were collected in 207 countries and territories;
- All sequences in this dataset are compared relative to hCoV-19/Wuhan/WIV04/2019 (WIV04), the official reference sequence employed by GISAID (EPI_ISL_402124). Learn more at <https://gisaid.org/WIV04>.

SUPPLEMENTAL TABLE

Data Availability

GISAID Identifier: EPI_SET_230622mw

doi: [10.55876/gis8.230622mw](https://doi.org/10.55876/gis8.230622mw)

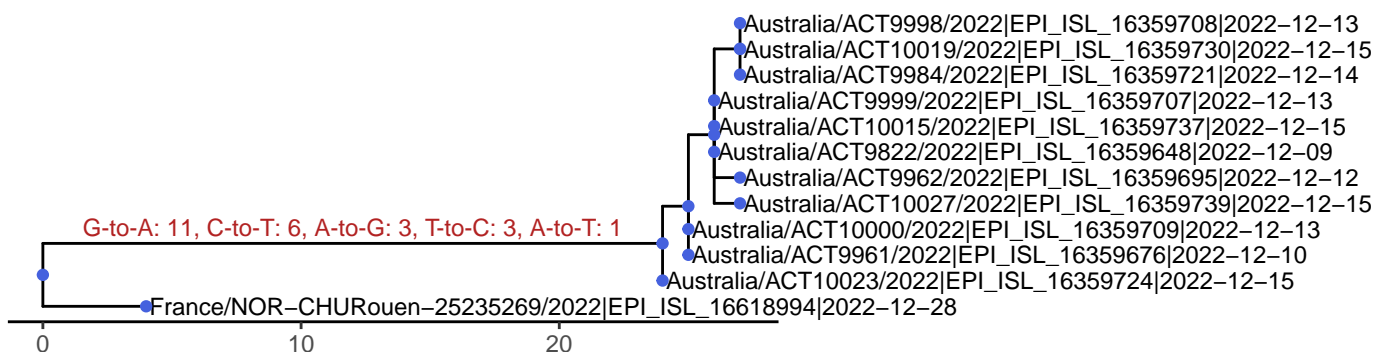
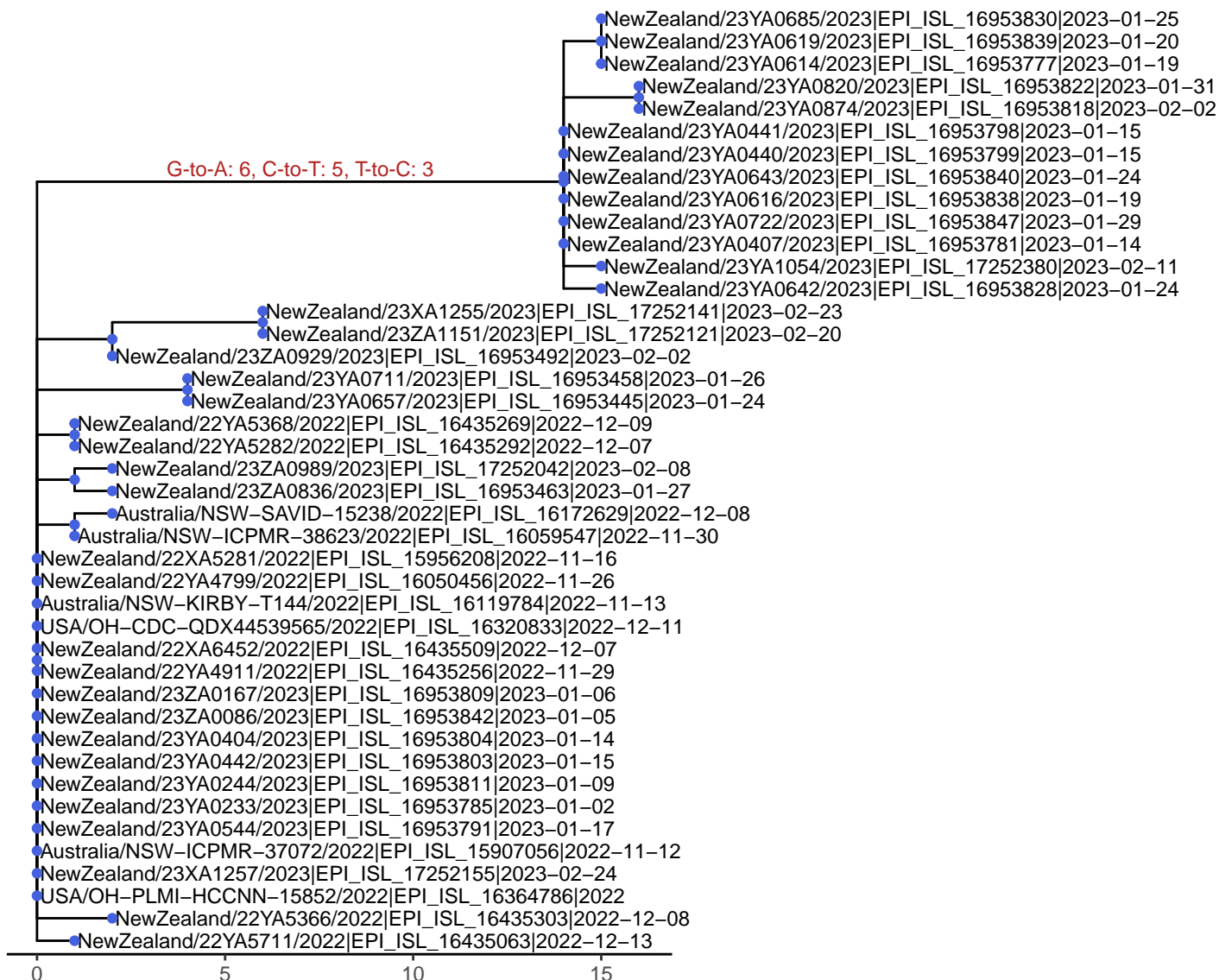
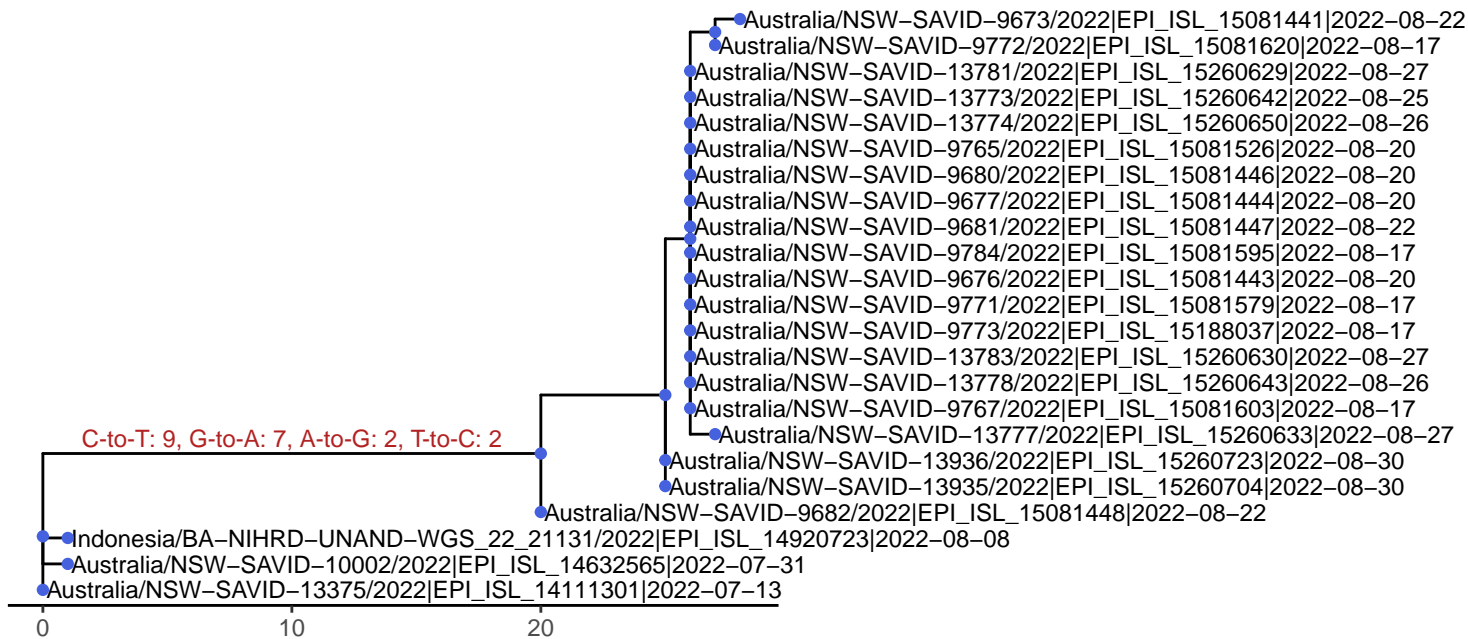
All genome sequences and associated metadata in this dataset are published in GISAID's EpiCoV database. To view the contributors of each individual sequence with details such as accession number, Virus name, Collection date, Originating Lab and Submitting Lab and the list of Authors, visit [10.55876/gis8.230622mw](https://gisaid.org/230622mw)

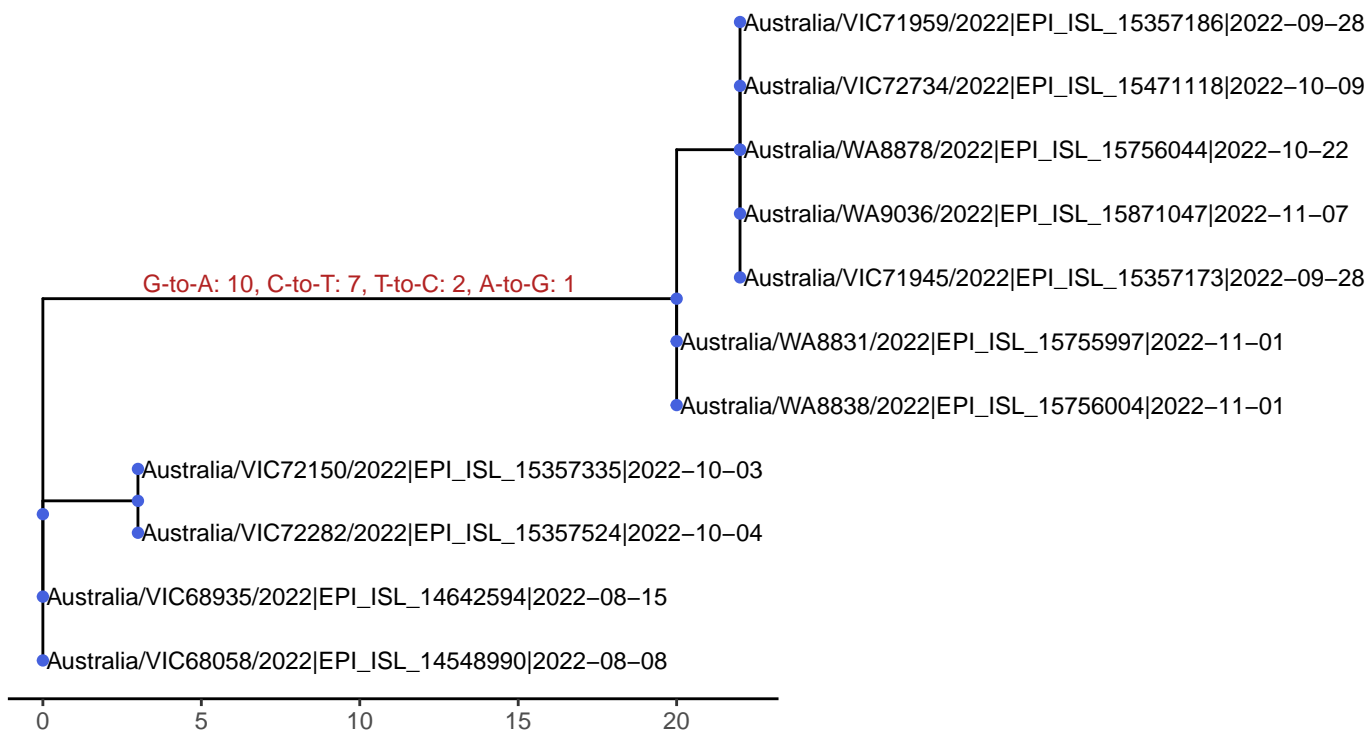
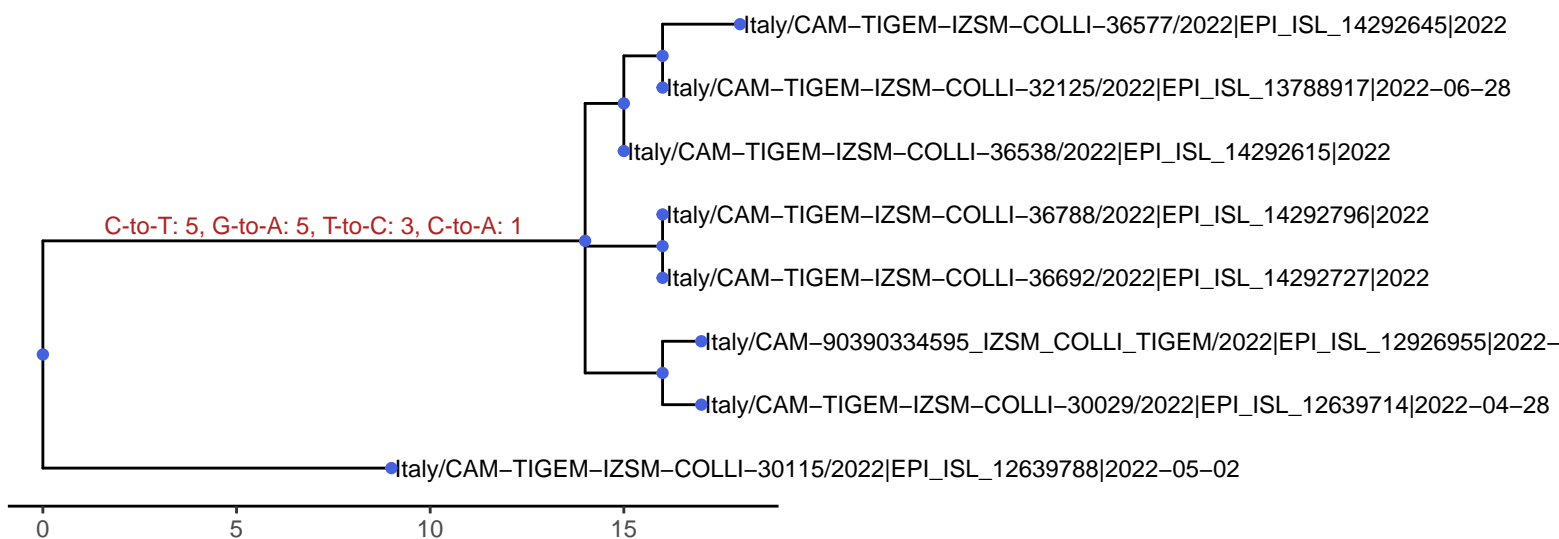
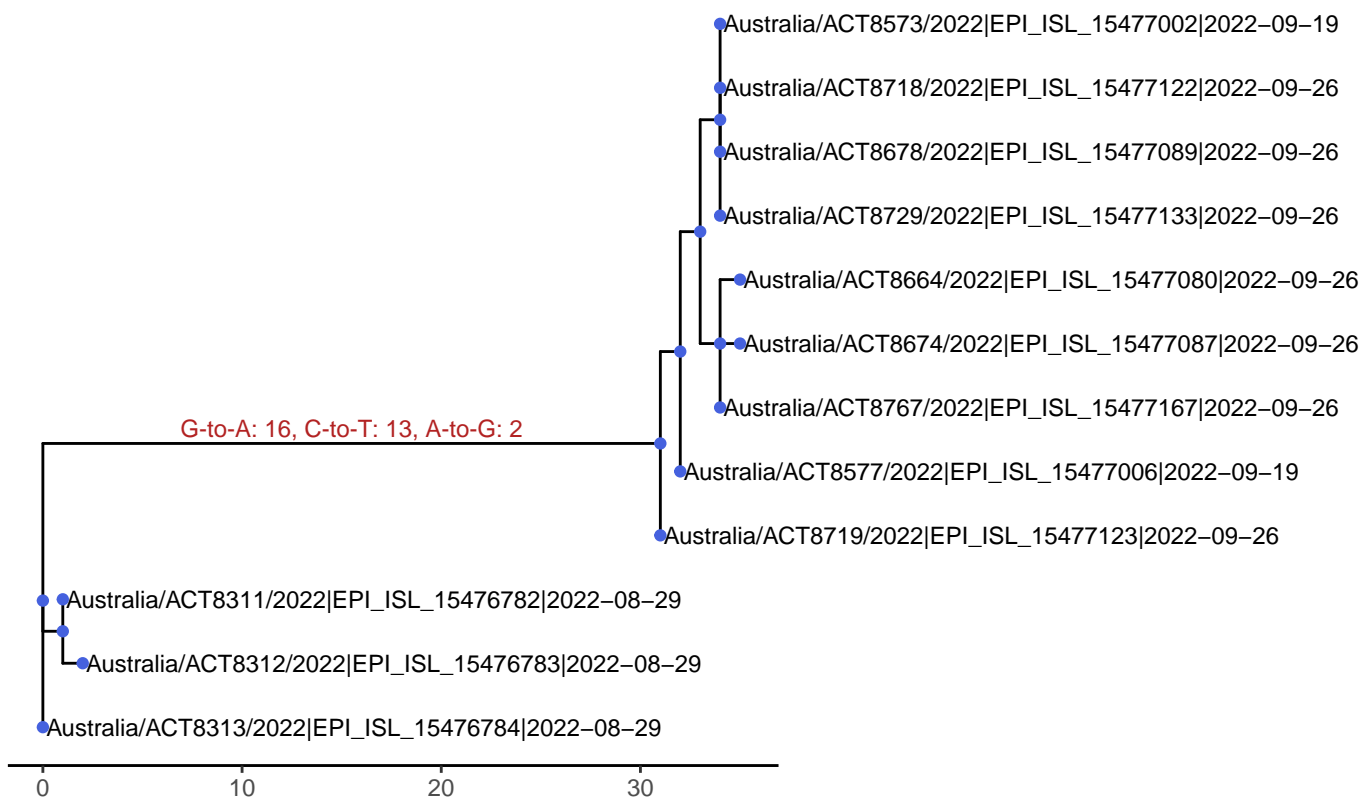
Data Snapshot

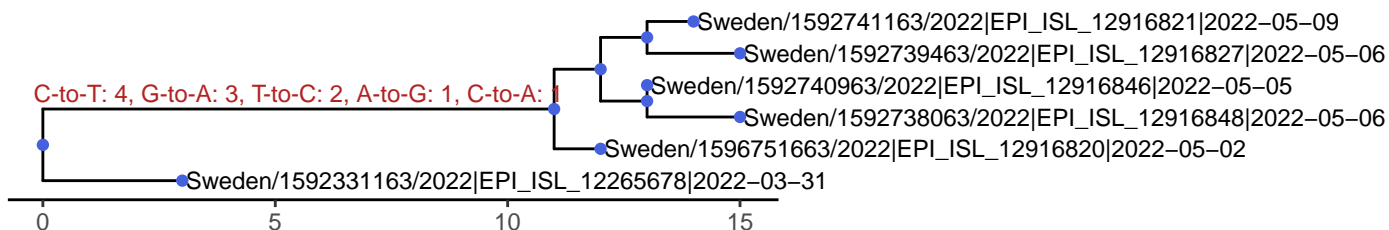
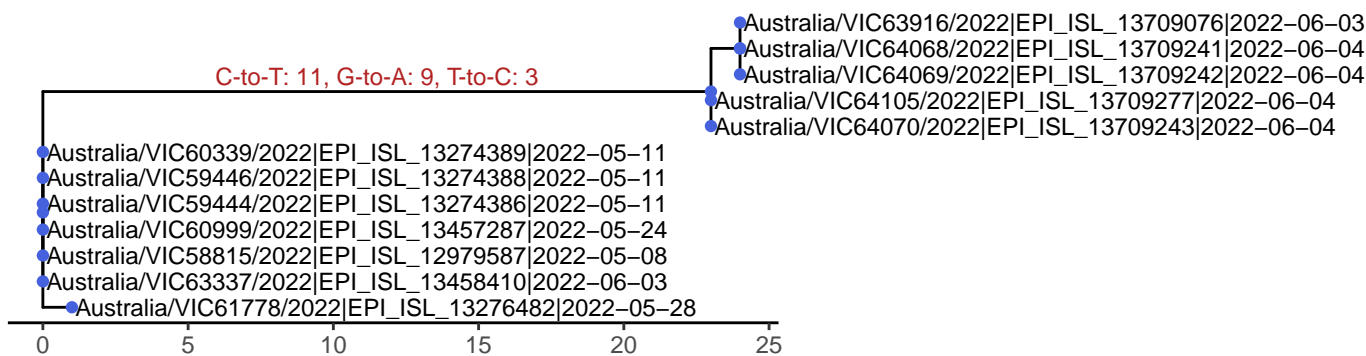
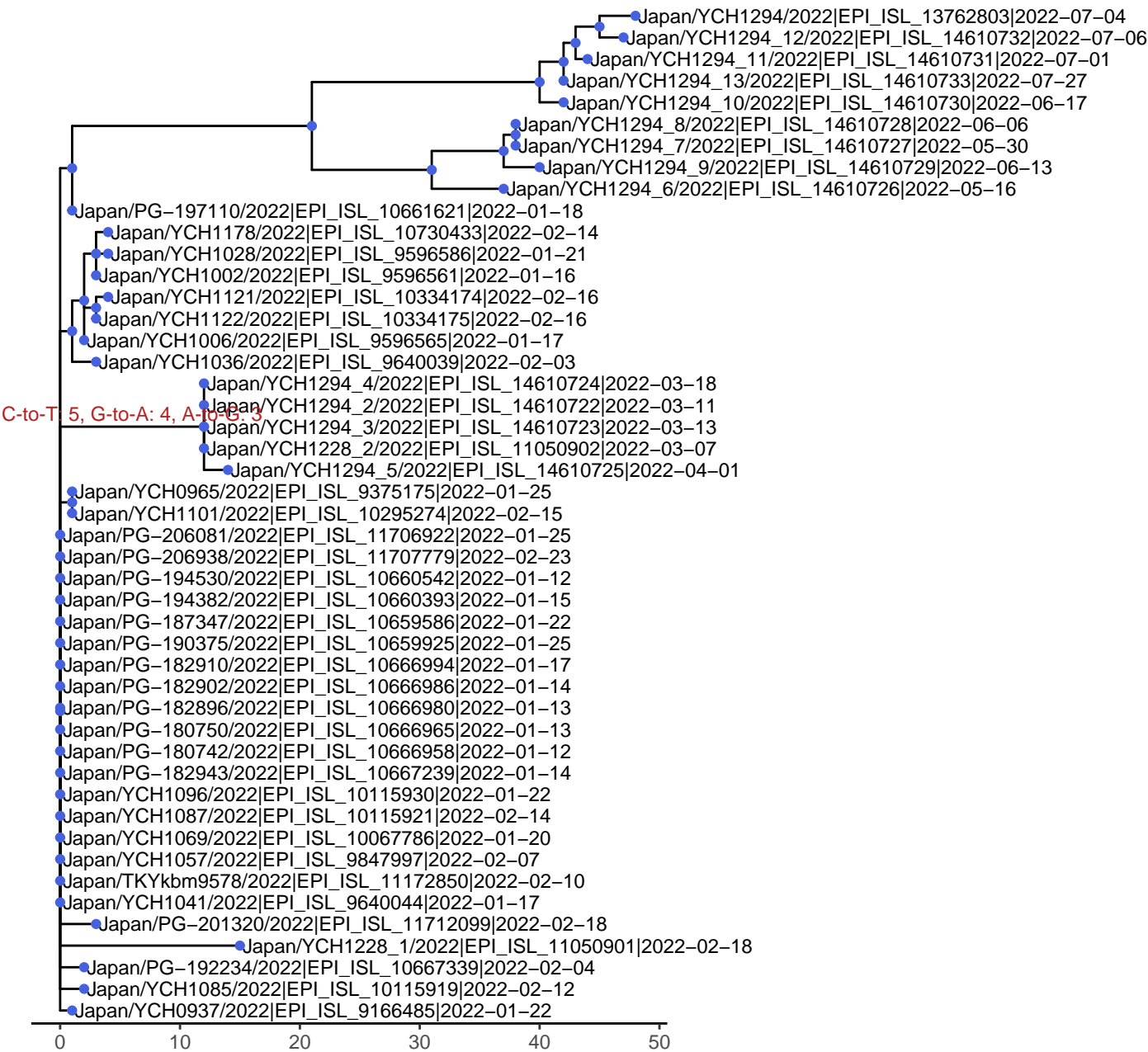
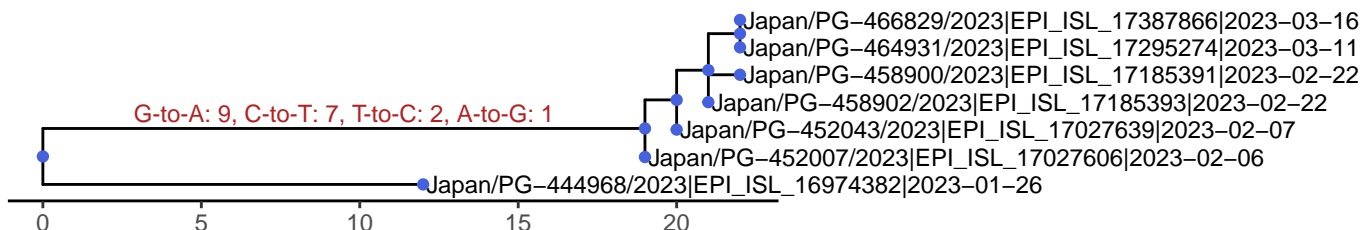
- EPI_SET_230622mw is composed of 1,122,676 individual genome sequences.
- The collection dates range from 2020-01-01 to 2023-06-17;
- Data were collected in 172 countries and territories;
- All sequences in this dataset are compared relative to hCoV-19/Wuhan/WIV04/2019 (WIV04), the official reference sequence employed by GISAID (EPI_ISL_402124). Learn more at <https://gisaid.org/WIV04>.

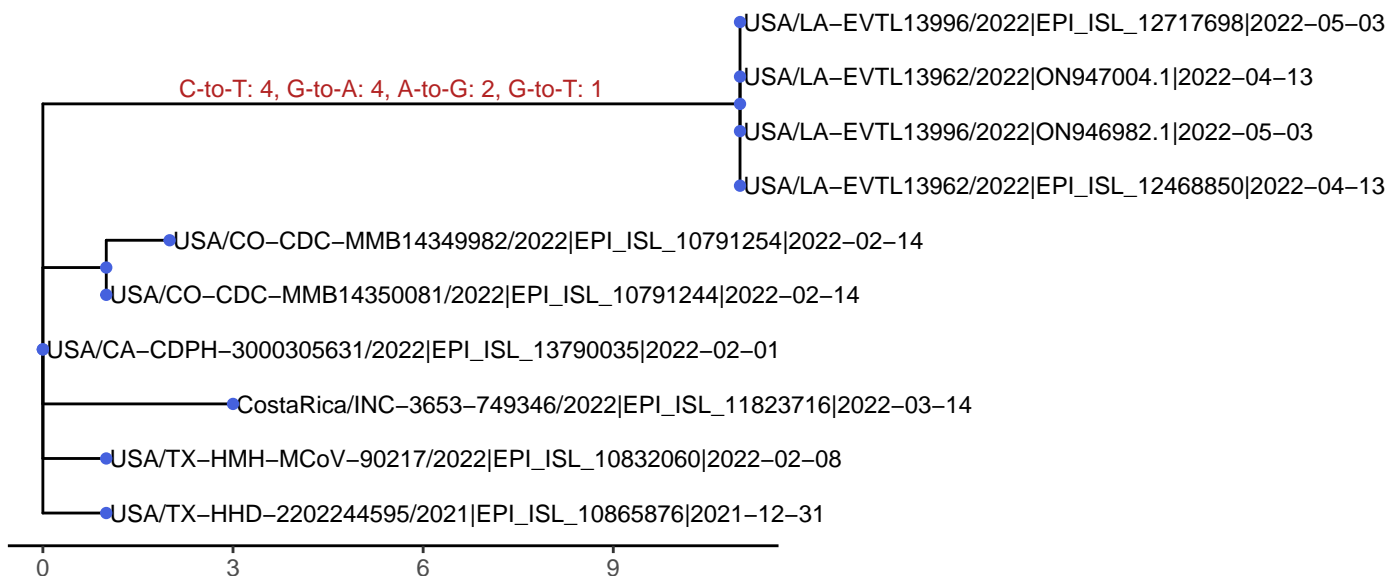
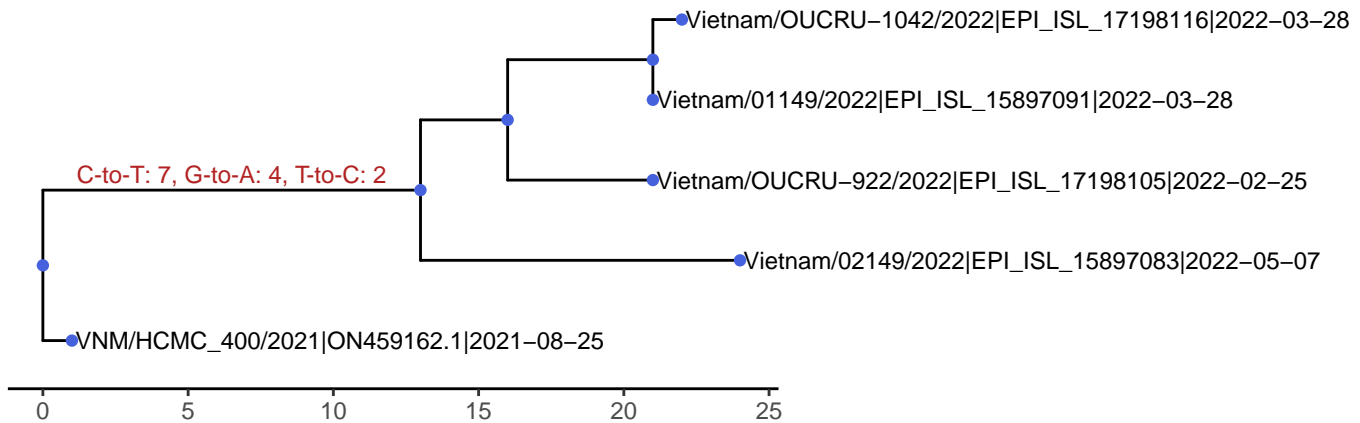
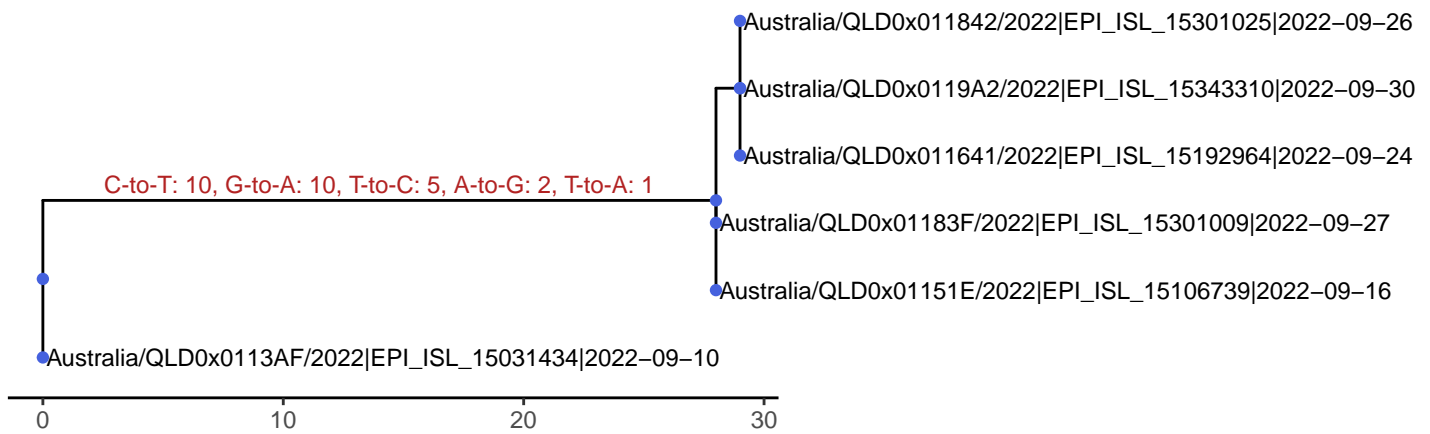
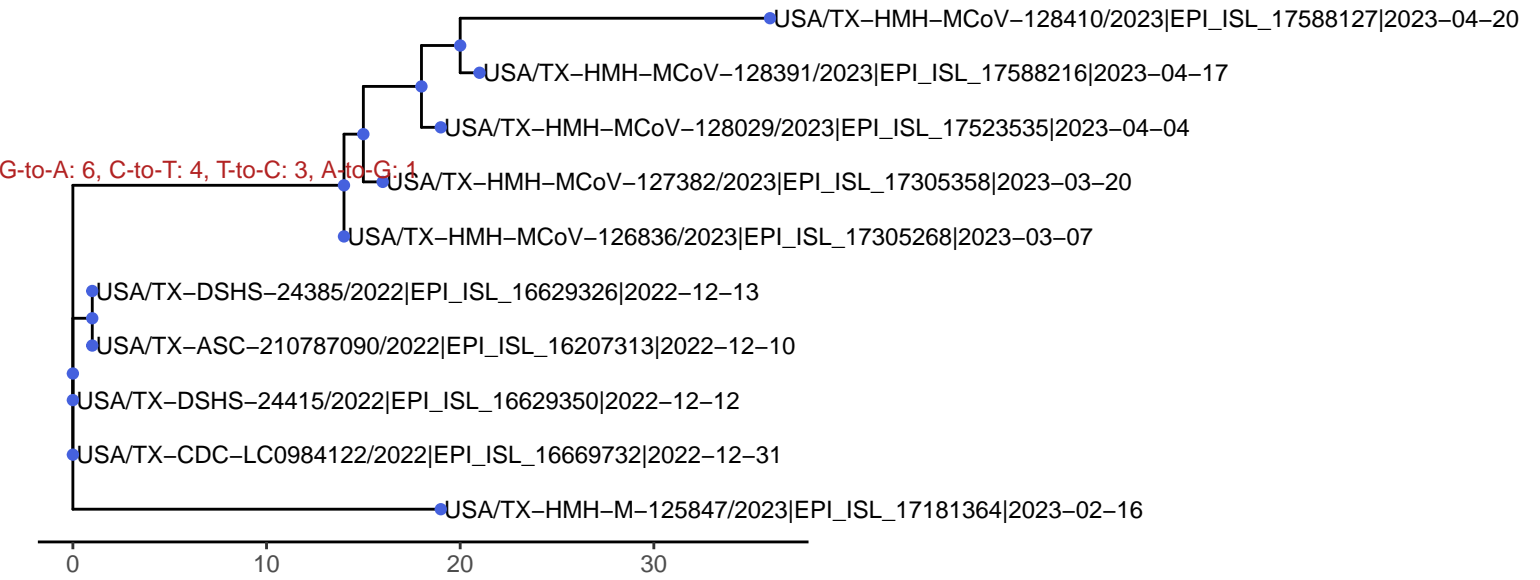
Cluster trees

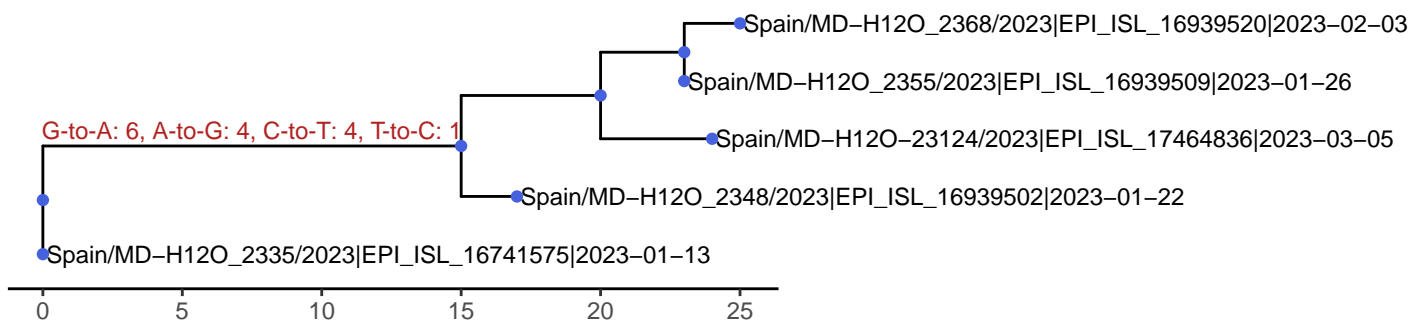
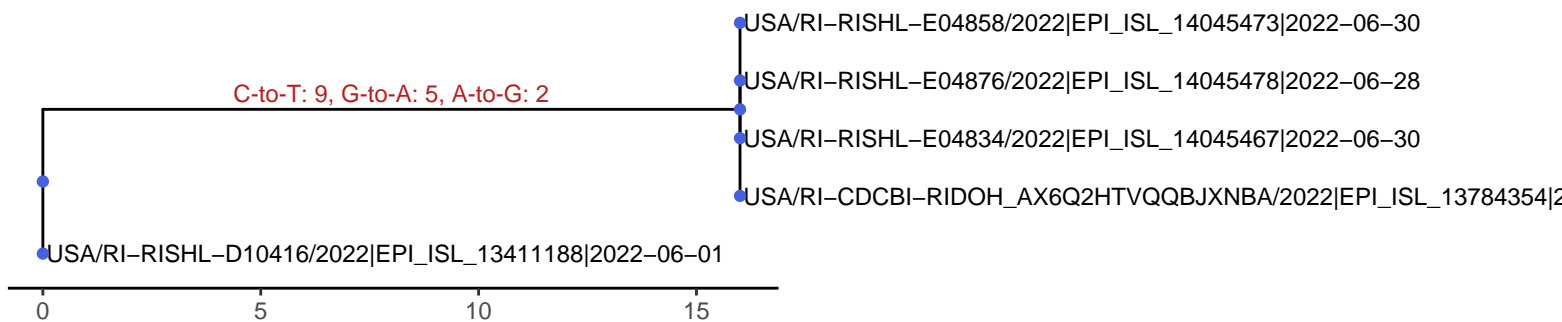
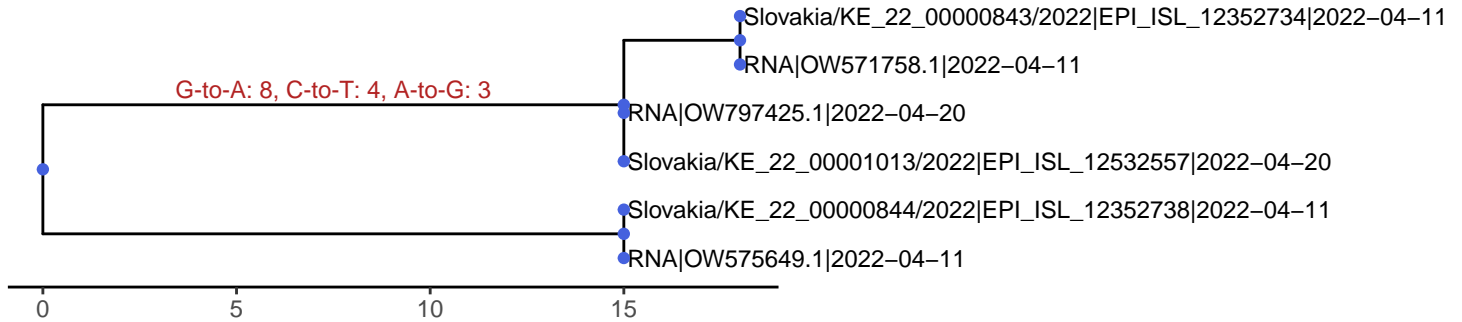
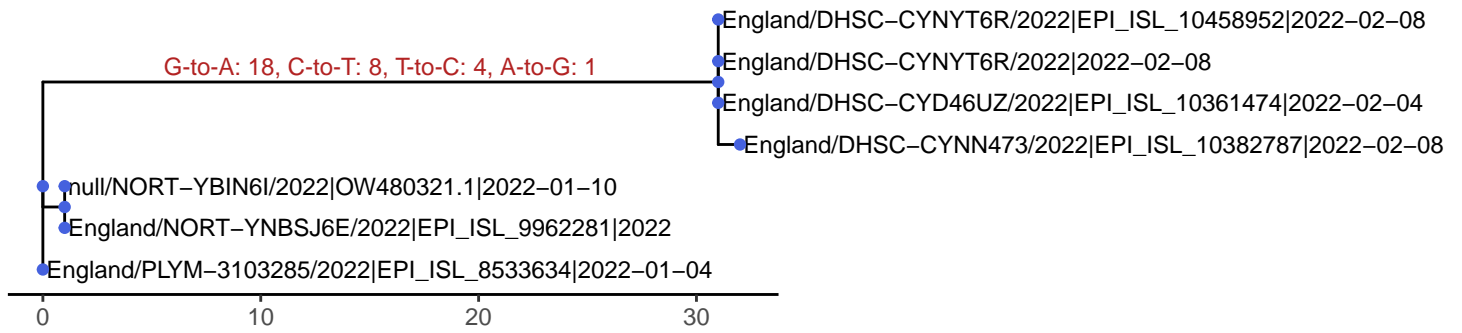
The following pages contain trees for high G-to-A branches with at least 3 descendant sequences. Note that in some cases, multiple descendants may represent single patients sampled multiple times.











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Japan/PG-443716/2023|EPI_ISL_17047241|2023-01-26
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Japan/PG-446071/2023|EPI_ISL_17047305|2023-02-01
Japan/TKYmbc36281/2023|EPI_ISL_17172535|2023-02-08
Japan/PG-442527/2023|EPI_ISL_16972384|2023-01-16
Japan/TKYkbm83657/2023|EPI_ISL_16828517|2023-01-12

C-to-T: 13, G-to-A: 13, A-to-G: 3, T-to-C: 1

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Japan/PG-439688/2023|EPI_ISL_16994641|2023-01-17
Japan/PG-439689/2023|EPI_ISL_16994642|2023-01-17
Japan/PG-449494/2023|EPI_ISL_16994655|2023-01-18

Japan/PG-455075/2023|EPI_ISL_17103193|2023-02-13
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