

ViReport v0.0.1

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1 Input Dataset

The analysis was conducted on a dataset containing 188 sequences. The average sequence length was 29802.441489361703, with a standard deviation of 398.1848733754408. The earliest sample date was 2013-07-24, the median sample date was 2020-01-23, and the most recent sample date was 2020-02-28.

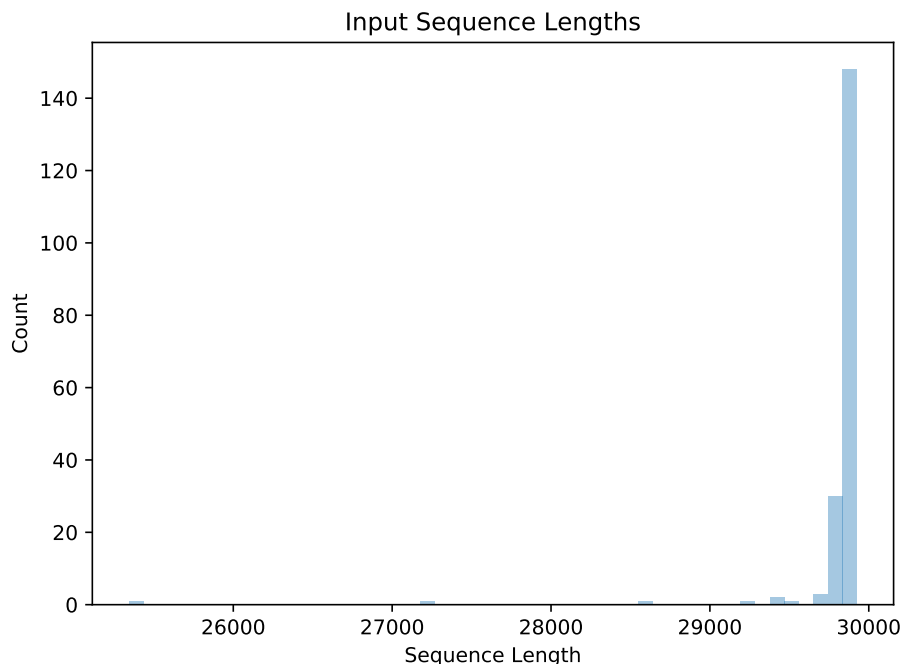


Figure 1: Distribution of input sequence lengths

2 Preprocessed Dataset

The input dataset was preprocessed such that sequences were given safe names: non-letters/digits in sequence IDs were converted to underscores. After preprocessing, the dataset contained 188 sequences. The average sequence length was 29802.441489361703, with a standard deviation of 398.1848733754408. The earliest sample date was 2013-07-24, the median sample date was 2020-01-23, and the most recent sample date was 2020-02-28.

3 Multiple Sequence Alignment

Multiple sequence alignment was performed using MAFFT (Katoh & Standley, 2013) in automatic mode. There were 30379 positions (16955 invariant) and 166 unique sequences in the multiple sequence alignment. Pairwise distances were computed from the multiple sequence alignment using the tn93 tool of HIV-TRACE (Pond et al., 2018). The average pairwise sequence distance was 0.00023931959492795083, with a standard deviation of 0.000241191693733296.

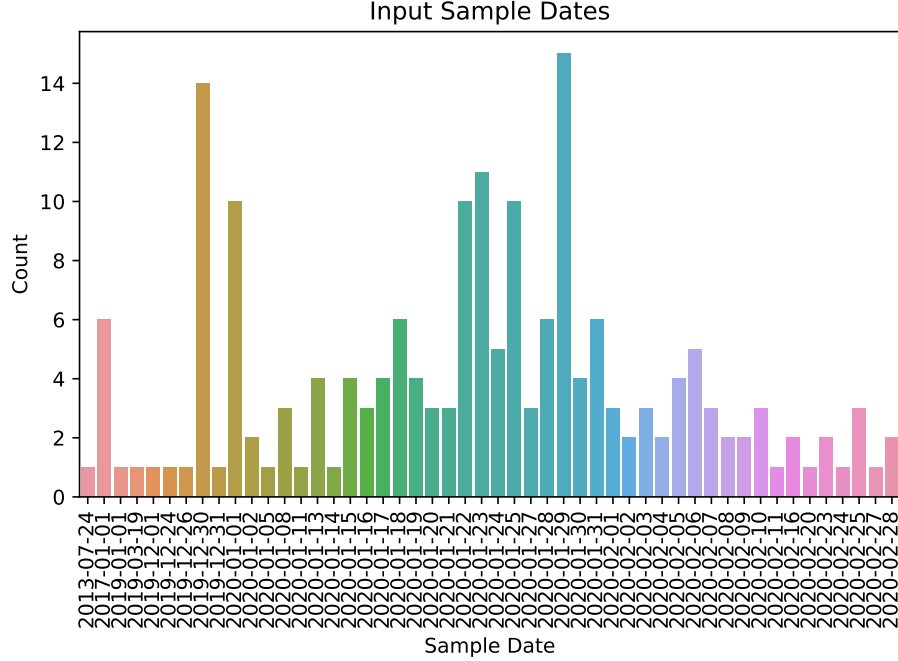


Figure 2: Distribution of input sample dates

4 Phylogenetic Inference

A maximum-likelihood phylogeny was inferred under the General Time-Reversible (GTR) model (Tavare, 1986) using FastTree 2 (Price et al., 2010) using a Gamma20-based likelihood. The inferred phylogeny was MinVar-rooted using FastRoot (Mai et al., 2017). Pairwise distances were computed from the phylogeny using TreeSwift (Moshiri, 2020). The maximum pairwise phylogenetic distance (i.e., tree diameter) was 0.003576486000000001, and the average pairwise phylogenetic distance was 0.0004088191522249731, with a standard deviation of 0.00040730380089063823.

5 Phylogenetic Dating

The rooted phylogeny was dated using treedater (Volz & Frost, 2017). The height of the dated tree was 0.2730446270571233 days, so given that the most recent sample was collected on 2020-02-28, the estimated time of the most recent common ancestor (tMRCA) was 2020-02-27.

6 Transmission Clustering

Transmission clustering was performed using TreeN93 (Moshiri, 2018) using pairwise phylogenetic distances. The total number of singletons (i.e., non-clustered individuals) was 111, and the total number of clusters (excluding singletons) was 21. The average cluster size (excluding singletons) was 3.1904761904761907, with a standard deviation of 1.3316315670580536, and the maximum and minimum cluster sizes were 6 and 2, respectively.

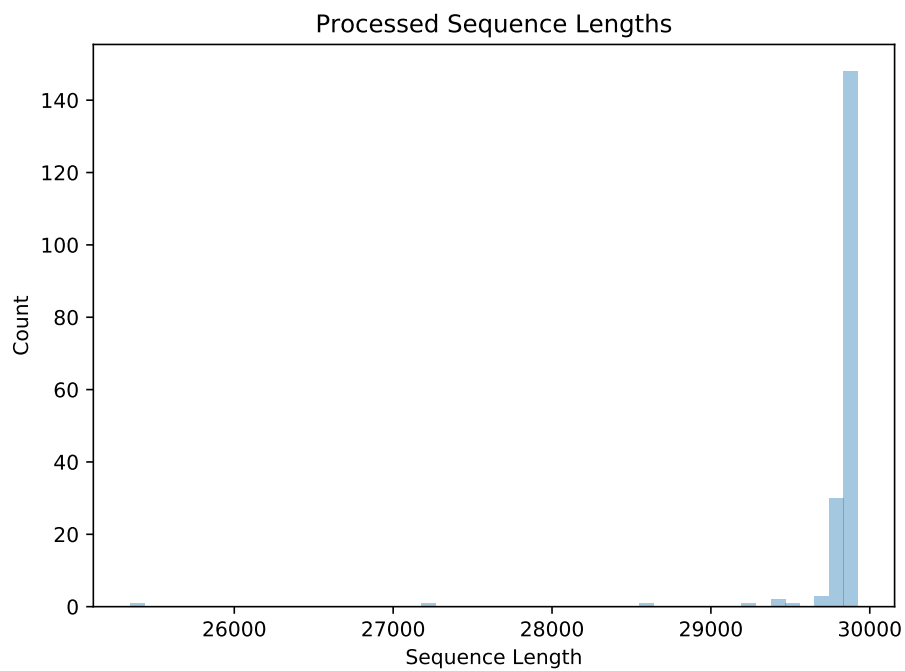


Figure 3: Distribution of preprocessed sequence lengths

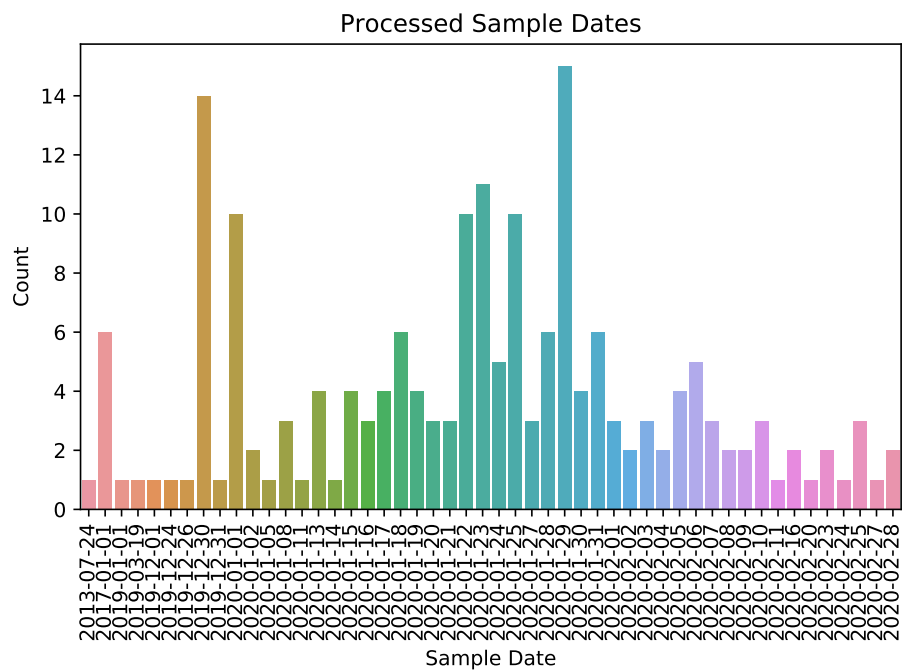


Figure 4: Distribution of preprocessed sample dates

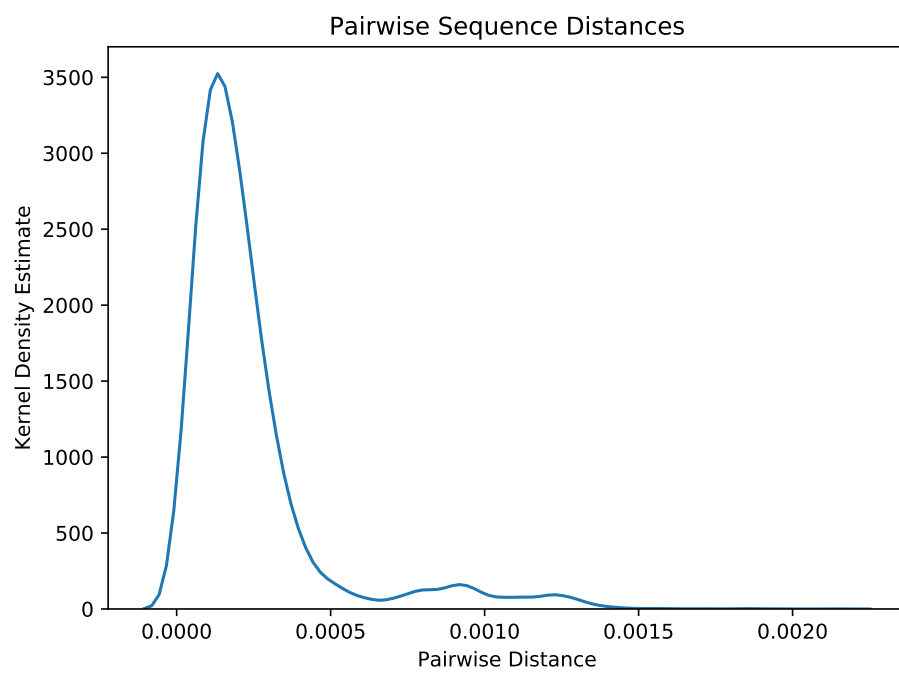


Figure 5: Distribution of pairwise sequence distances

BetaCoV_Nepal_61_2020_EPI_ISL_410301
 BetaCoV_USA_IL1_2020_EPI_ISL_404253
 BetaCoV_Guangdong_20SF014_2020_EPI_ISL_403934
 BetaCoV_Shenzhen_SZTH_004_2020_EPI_ISL_406595
 BetaCoV_Shenzhen_SZTH_003_2020_EPI_ISL_406594
 BetaCoV_Foshan_20SF207_2020_EPI_ISL_406534
 BetaCoV_USA_MA1_2020_EPI_ISL_409067
 BetaCoV_Canada_ON_PHL2445_2020_EPI_ISL_413014
 BetaCoV_Canada_ON_VIDO_01_2020_EPI_ISL_413015
 BetaCoV_USA_CA3_2020_EPI_ISL_408008
 BetaCoV_USA_CA4_2020_EPI_ISL_408009
 BetaCoV_Singapore_3_2020_EPI_ISL_407988
 BetaCoV_France_IDF0571_2020_EPI_ISL_411218
 BetaCoV_France_IDF0515_2020_EPI_ISL_408430
 BetaCoV_France_IDF0515_isl_2020_EPI_ISL_410984
 BetaCoV_Chongqing_IVDC_CQ_001_2020_EPI_ISL_408481
 BetaCoV_Shandong_IVDC_SD_001_2020_EPI_ISL_408482
 BetaCoV_Wuhan_HBCDC_HB_05_2020_EPI_ISL_412981
 BetaCoV_Canada_BC_37_0_2_2020_EPI_ISL_412965
 BetaCoV_Australia_NSW05_2020_EPI_ISL_412975
 BetaCoV_Italy_SPL1_2020_EPI_ISL_412974
 BetaCoV_Italy_INMI1_isl_2020_EPI_ISL_410545
 BetaCoV_England_03_2020_EPI_ISL_412116
 BetaCoV_Australia_VIC01_2020_EPI_ISL_406844
 BetaCoV_South_Korea_KUMC02_2020_EPI_ISL_413018
 BetaCoV_South_Korea_KUMC01_2020_EPI_ISL_413017
 BetaCoV_South_Korea_SNUJ01_2020_EPI_ISL_411929
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 BetaCoV_Singapore_9_2020_EPI_ISL_410715
 BetaCoV_Singapore_10_2020_EPI_ISL_410716
 BetaCoV_Singapore_5_2020_EPI_ISL_410536
 BetaCoV_Sweden_01_2020_EPI_ISL_411951
 BetaCoV_USA_CA2_2020_EPI_ISL_406036
 BetaCoV_France_IDF0386_2020_EPI_ISL_411220
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 BetaCoV_France_IDF0386_2020_EPI_ISL_411219
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 BetaCoV_France_IDF0373_2020_EPI_ISL_406597
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 BetaCoV_Singapore_8_2020_EPI_ISL_410714
 BetaCoV_Wuhan_WH05_2020_EPI_ISL_408978
 BetaCoV_Italy_INMI1_cs_2020_EPI_ISL_410546
 BetaCoV_Brazil_SPBR_02_2020_EPI_ISL_413016
 BetaCoV_Japan_Hu_DP_Kng_19_027_2020_EPI_ISL_412969
 BetaCoV_Hong_Kong_VB20026565_2020_EPI_ISL_412030
 BetaCoV_Japan_Hu_DP_Kng_19_020_2020_EPI_ISL_412968
 BetaCoV_Hefei_2_2020_EPI_ISL_412026
 BetaCoV_Wuhan_Hu_1_2019_EPI_ISL_402125
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 BetaCoV_Italy_CDG1_2020_EPI_ISL_412973
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 BetaCoV_Finland_FIN_25_2020_EPI_ISL_412971
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 BetaCoV_Guangdong_20SF174_2020_EPI_ISL_406531
 BetaCoV_Guangdong_20SF028_2020_EPI_ISL_403936
 BetaCoV_Guangdong_20SF040_2020_EPI_ISL_403937
 BetaCoV_Sydney_2_2020_EPI_ISL_408976
 BetaCoV_Wuhan_IVDC_HB_envF13_20_2020_EPI_ISL_408514
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 BetaCoV_Singapore_2_2020_EPI_ISL_407987
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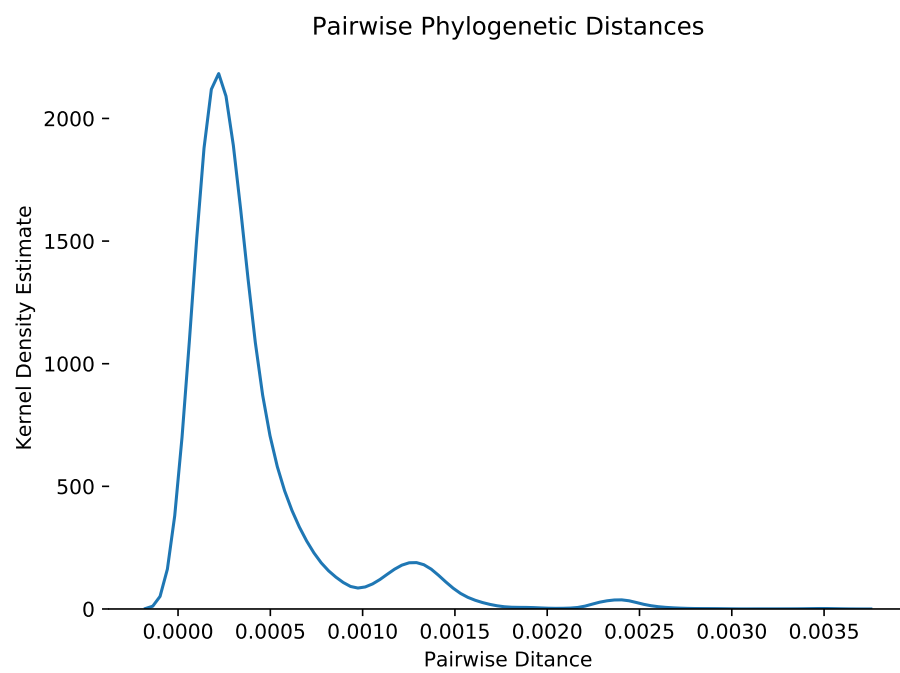
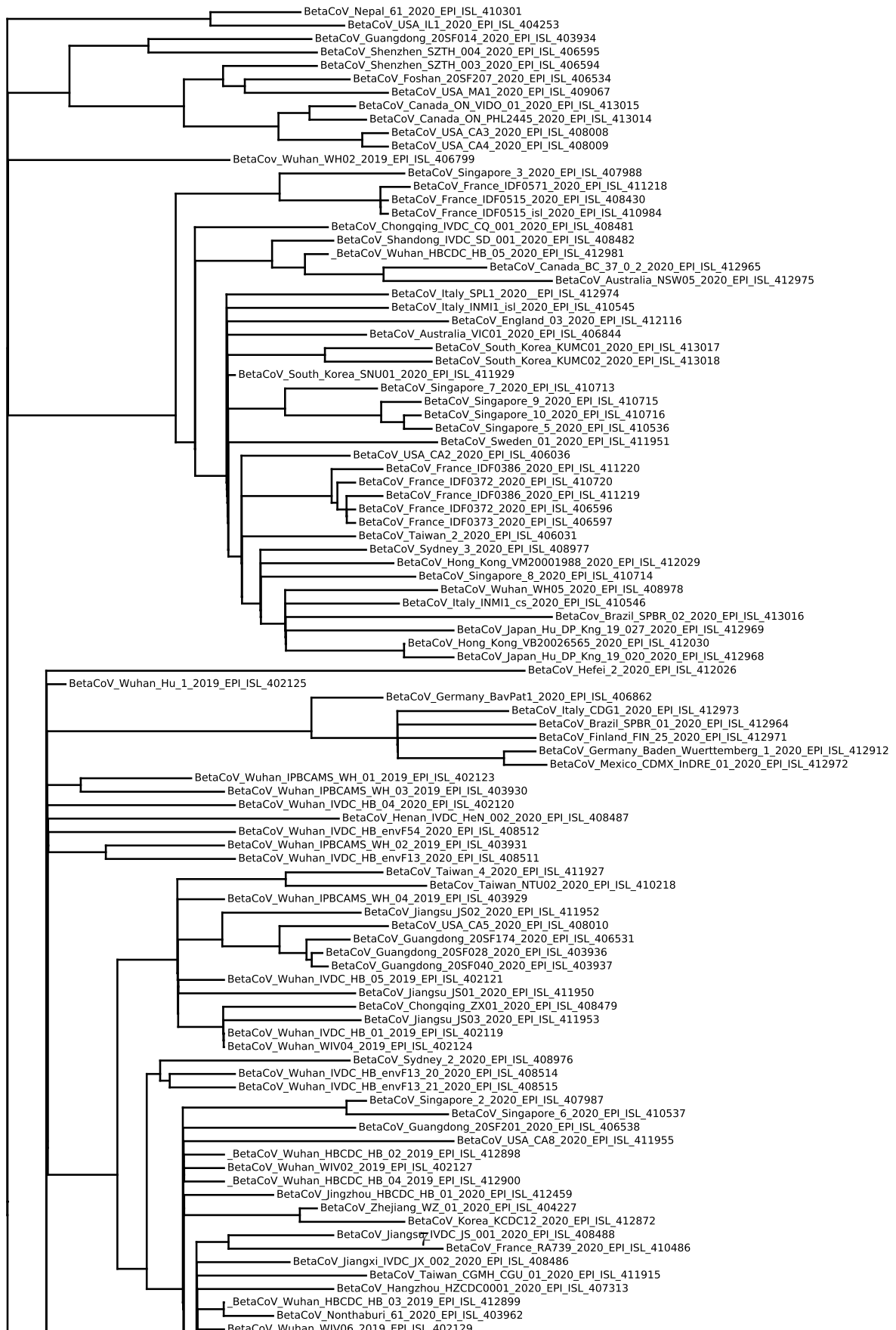


Figure 7: Distribution of pairwise phylogenetic distances



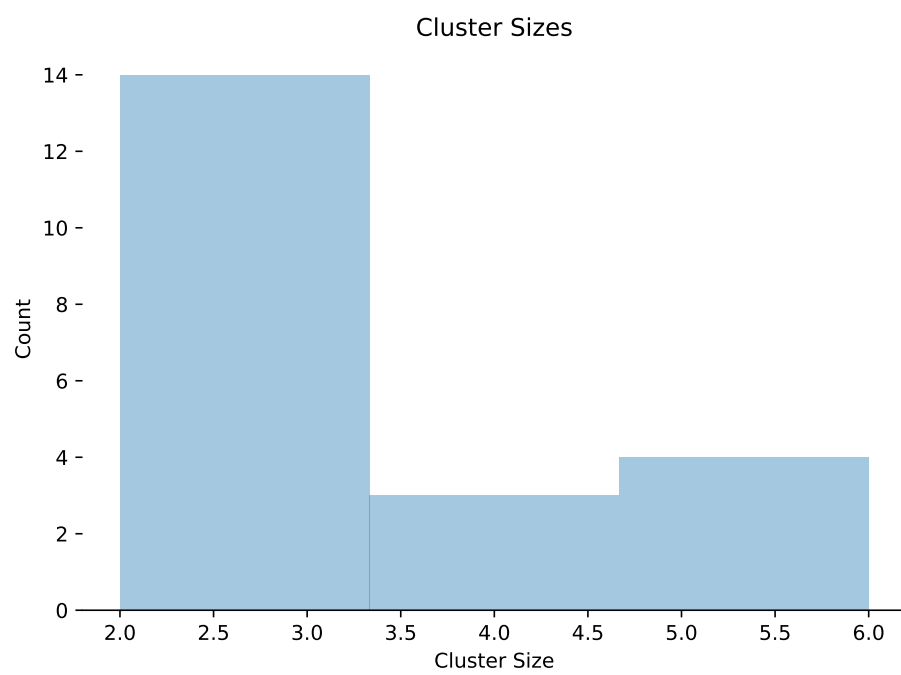


Figure 9: Distribution of cluster sizes (excluding singletons)