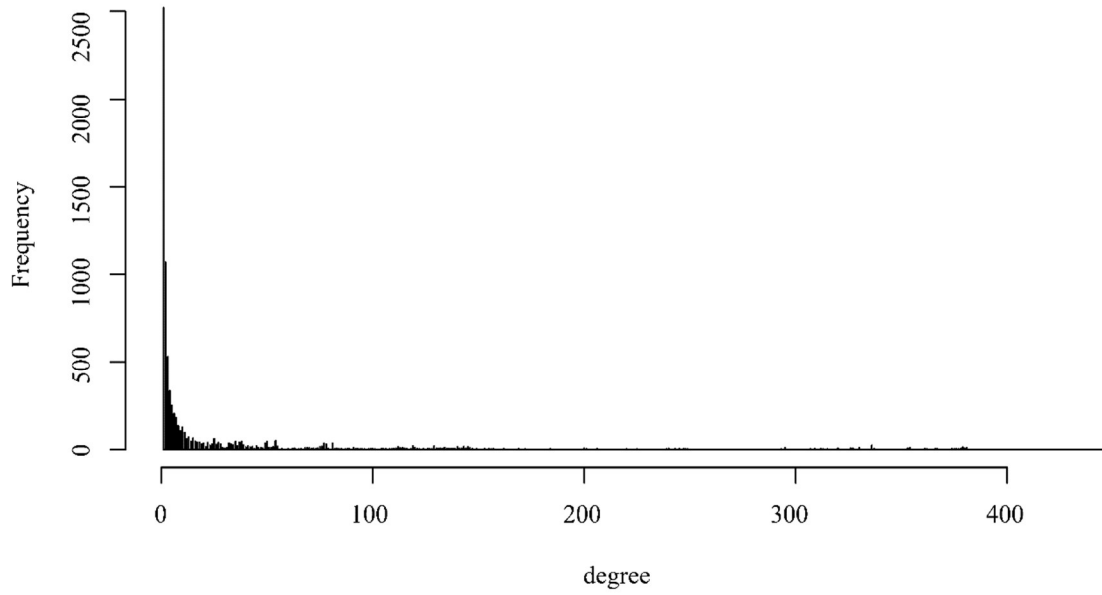## Supplementary Data
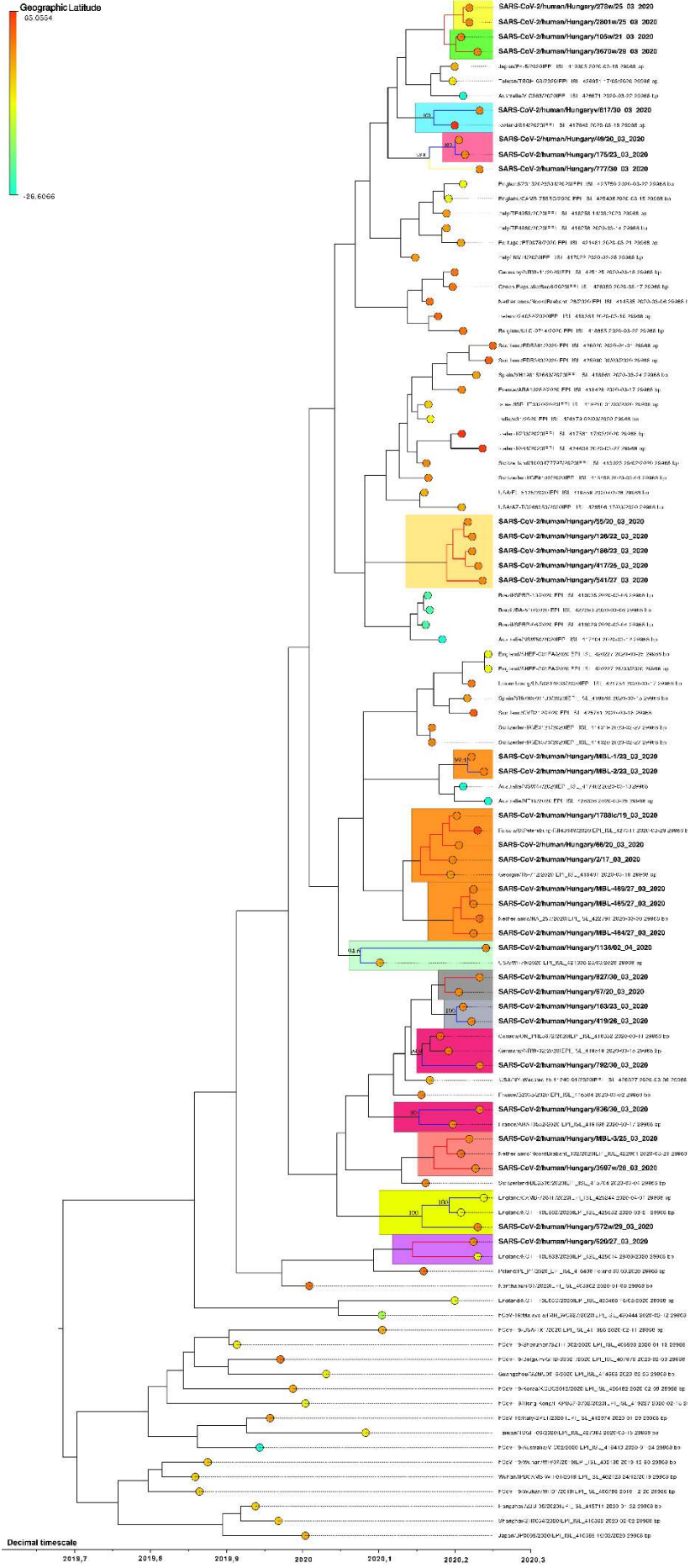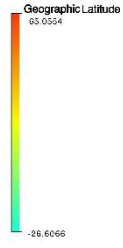
## Degree distribution

Supplementary Figure 1. | Degree distribution representing the haplotype network analysis

Geographic Latitude

65.0554

−26.6066

SARS-CoV-2/human/Hungary/278w/25_03_2020
SARS-CoV-2/human/Hungary/2801w/25_03_2020
SARS-CoV-2/human/Hungary/105w/21_03_2020
SARS-CoV-2/human/Hungary/3670w/29_03_2020

SARS-CoV-2/human/Hungaryv/817/30_03_2020
SARS-CoV-2/human/Hungary/49/20_03_2020
SARS-CoV-2/human/Hungary/175/23_03_2020
SARS-CoV-2/human/Hungary/777/30_03_2020

SARS-CoV-2/human/Hungary/55/20_03_2020
SARS-CoV-2/human/Hungary/126/22_03_2020
SARS-CoV-2/human/Hungary/188/23_03_2020
SARS-CoV-2/human/Hungary/417/25_03_2020
SARS-CoV-2/human/Hungary/541/27_03_2020

SARS-CoV-2/human/Hungary/MBL-1/23_03_2020
SARS-CoV-2/human/Hungary/MBL-2/23_03_2020

SARS-CoV-2/human/Hungary/1788lc/19_03_2020
SARS-CoV-2/human/Hungary/66/20_03_2020
SARS-CoV-2/human/Hungary/2/17_03_2020
SARS-CoV-2/human/Hungary/MBL-469/27_03_2020
SARS-CoV-2/human/Hungary/MBL-465/27_03_2020
SARS-CoV-2/human/Hungary/MBL-464/27_03_2020

SARS-CoV-2/human/Hungary/1138/02_04_2020

SARS-CoV-2/human/Hungary/827/30_03_2020
SARS-CoV-2/human/Hungary/67/20_03_2020
SARS-CoV-2/human/Hungary/163/23_03_2020
SARS-CoV-2/human/Hungary/419/26_03_2020

SARS-CoV-2/human/Hungary/792/30_03_2020

SARS-CoV-2/human/Hungary/836/30_03_2020

SARS-CoV-2/human/Hungary/MBL-3/25_03_2020
SARS-CoV-2/human/Hungary/3597w/26_03_2020

SARS-CoV-2/human/Hungary/572w/29_03_2020

SARS-CoV-2/human/Hungary/620/27_03_2020

Decimal timescale

2019,7   2019,8   2019,9   2020   2020,1   2020,2   2020,3

Supplementary Fig. 2 | Time calibrated phylogenetic and phylogeographic visualization of 105 complete SARS-CoV-2 genomes compared to the 32 Hungarian strains. Sequences of this study are highlighted in bold face, colored clades are representing Nextstrain analysis clustering.
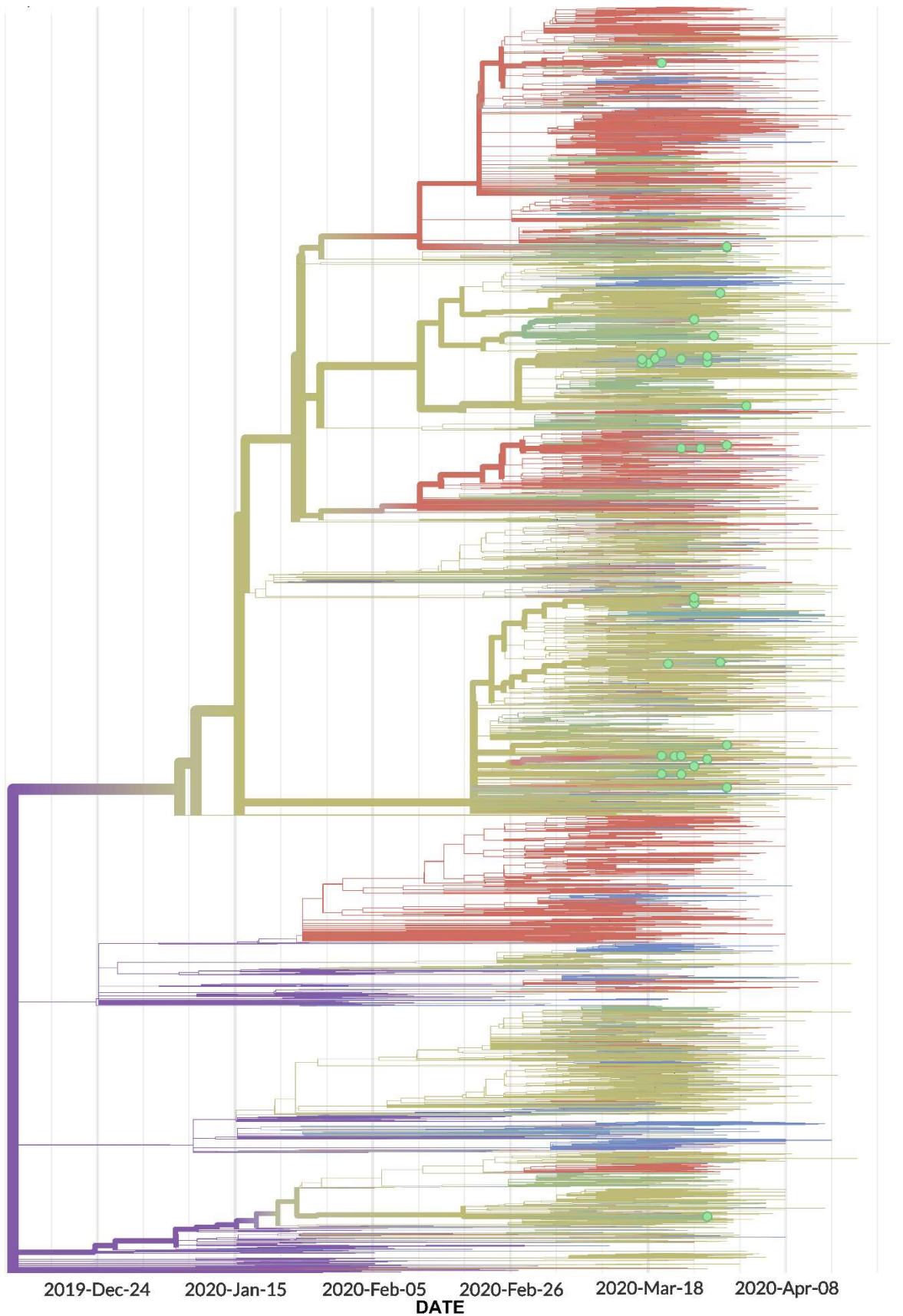
Supplementary Fig. 3 | Visualization of Hungarian sequence dataset with Nextstrain local workflow. Showing 35 (32 from this manuscript and three additional from GISAID database) Hungarian sequences compared to 10,869 genomes sampled between Mar 2020 and Apr 2020.