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Supplemental Information

High-Density Amplicon Sequencing Identifies Community Spread and Ongoing Evolution of SARS-CoV-2 in the Southern United States

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Supplemental Information

Includes

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Table S1

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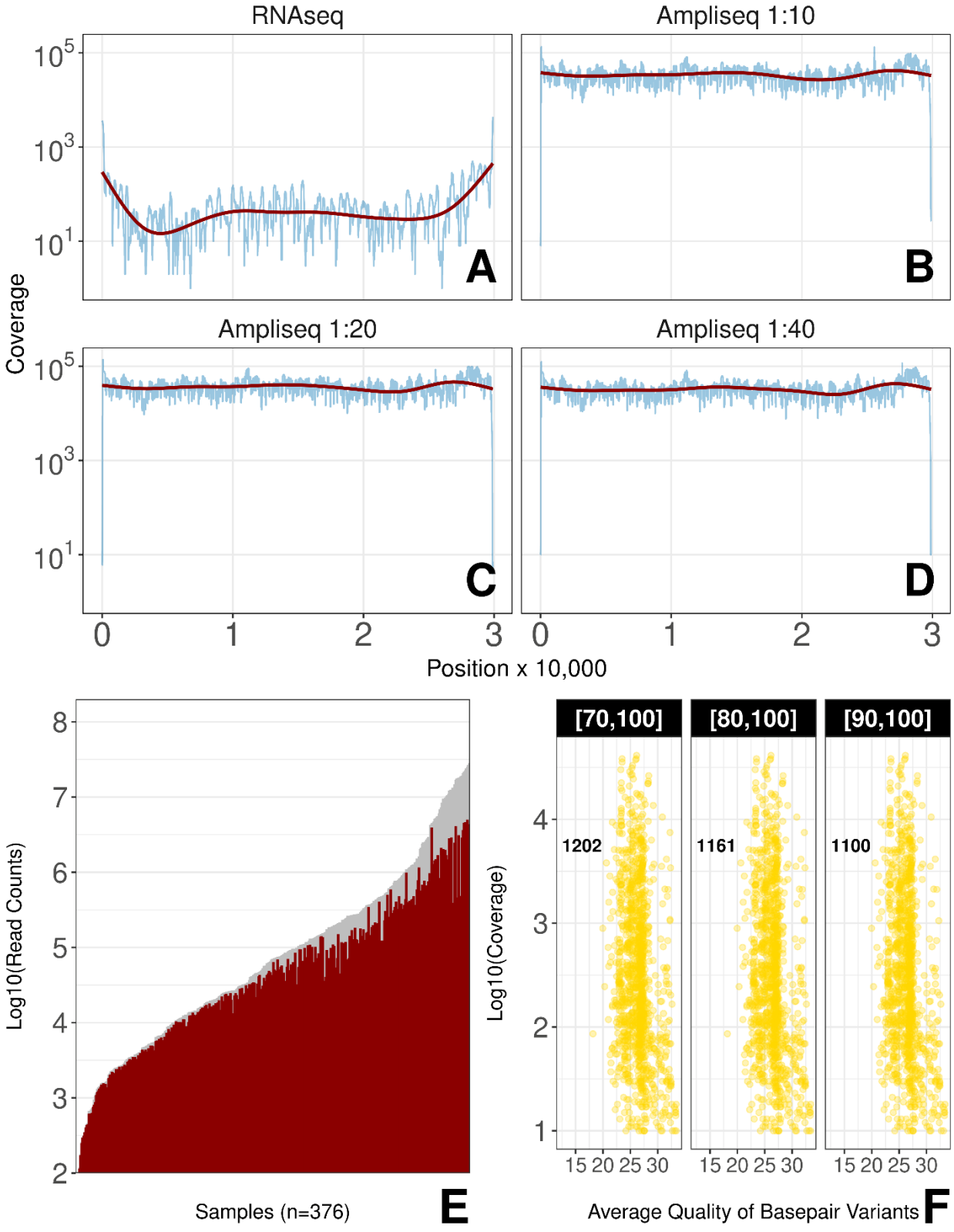
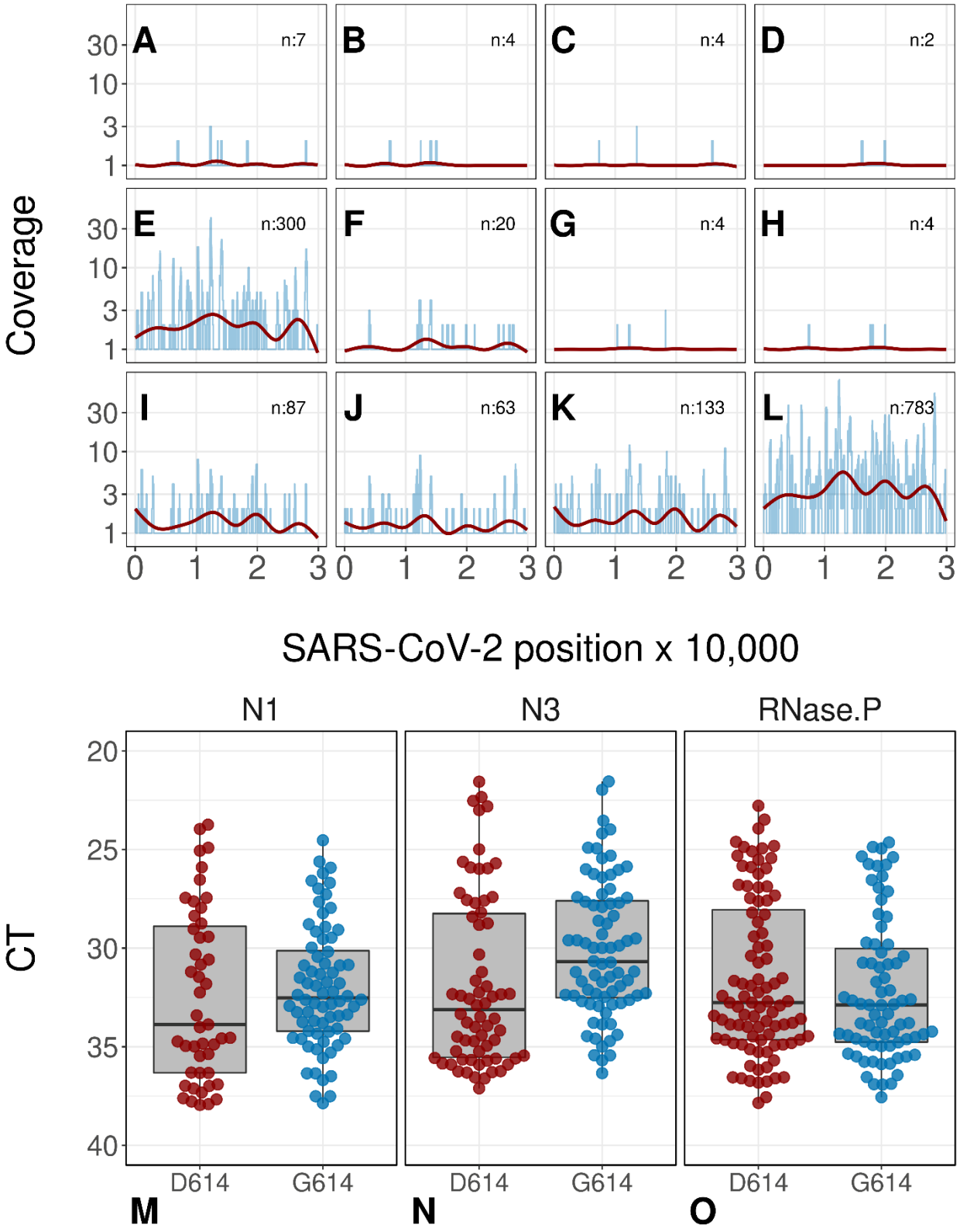
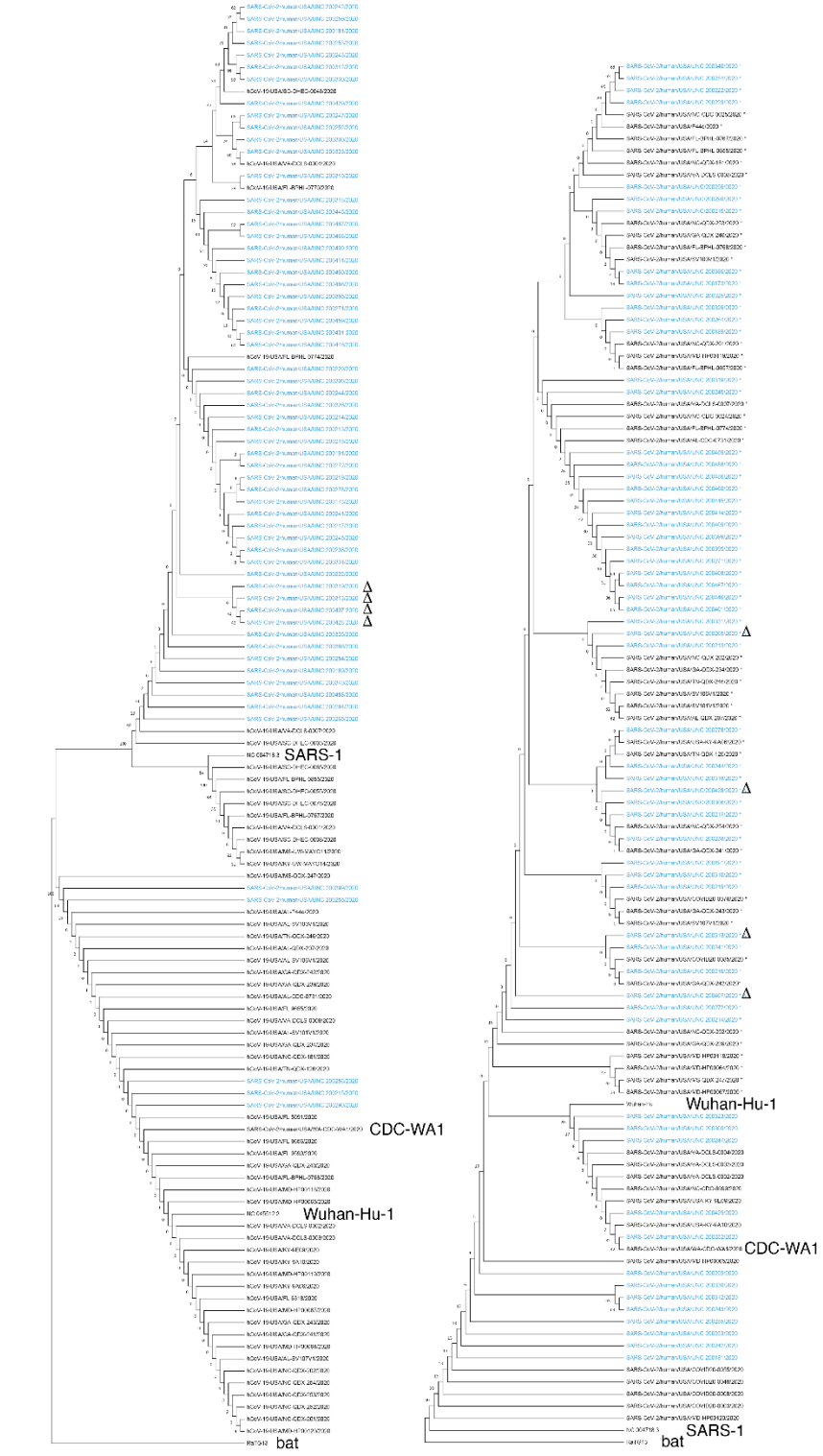
Supplemental Figure S1



Supplemental Figure S2



Supplemental Figure S3



A genome B spike

Supplemental Figure Legends

Supplemental Figure S1

Panels A-D show coverage comparison of targeted (AmpliSeq) and non-targeted sequencing of the BEI reference material (NR-52285, strain SARS-CoV-2/human/USA-WA1/2020). Sample types, RNA seq or dilutions of input RNA, are listed on top. Coverage is shown on the vertical and genome position on the horizontal axis; Loess-regression line is shown in red. (E) Log-base 10 of the total read counts of all samples used in this study. (F) The average quality of base-pair variants called by sequencing was plotted based on increasing coverage reads. Related to **Figure 1**.

Supplemental Figure S2

Panels A-N shows the coverage analysis of unknown cases that had at least one read mapped to the reference sequence NC_045512. The number of reads is shown on the vertical axis and genome position on the horizontal axis; Loess-regression line is shown in red. The insert label indicates the total number of reads. Panels M-O depict PCR cycle CT of D614 and G614 isolates using the SARS-CoV-2 N1 and N3 primers. RNaseP was used as an internal control for total RNA. Shown is a beeplot of Raw CT numbers obtained by real-time RT-qPCR using CDC primers N1 and N3, as well as RNAseP, which serves as a control for reverse transcription. Lower CT values signify a higher genome copy number per sample. CT values are shown on the vertical and the SNV variant G614D (ancestral, red) or G614G (recent, blue) on the horizontal axis. Related to **Figure 1** and **Figure 2**.

Supplemental Figure S3

Phylogenetic analysis. A. Neighbor-joining tree of whole SARS-CoV-2 genomes from the southeastern United States (from GenBank and GISAID) The bat coronavirus genome strain RaTG13 was used as an outlier to root the tree. Average nucleotide difference is shown for the two major branches and the difference between SARS (NC_004718.3) and SARS-CoV-2. B. Neighbor-joining tree based on amino acids for S protein. Support values are listed at the major branch points. Colors indicate geographic regions. Additional genome sequences and protein sequences are from GISAID and GenBank. Related to **Figure 2**.

Table S1

Information on complete genomes

Name	Accession	Collection Date	GISAID clade
Batch 1			
BankIt2330137 SARS-CoV-2/human/USA/UNC_200173/2020	MT300186	March 19th, 2020,	B.1 (*GH*),
BankIt2331121 SARS-CoV-2_Human_UNC_200191_2020	MT308702	March 23rd, 2020,	B.1.2 (*GH*)
BankIt2331639 SARS-CoV-2_human_UNC_200181_2020	MT308703	March 23rd, 2020,	A.3 (*S*)
BankIt2331651 SARS-CoV-2_human_UNC_200189_2020	MT308704	March 23rd, 2020,	B.1.2 (*GH*)
Batch 2			
SUB7503826 SARS_CoV-2_Human_UNC_200213_2020	MT522852	March 25th, 2020,	B.1 (*GH*)
SUB7503826 SARS_CoV-2_Human_UNC_200214_2020	MT522853	March 30th, 2020,	B.1 (*GH*)
SUB7503826 SARS_CoV-2_Human_UNC_200215_2020	MT522854	March 31st, 2020,	B.1 (*GH*)
SUB7503826 SARS_CoV-2_Human_UNC_200216_2020	MT522855	March 30th, 2020,	B.1 (*GH*)
Batch 3			
SUB7504586 SARS_CoV-2_Human_UNC_200217_2020	MT528598	March 25th, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200219_2020	MT528599	March 30th, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200229_2020	MT528631	March 31st, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200238_2020	MT528600	April 1st , 2020,	B.1.3 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200241_2020	MT528601	March 21st ,2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200242_2020	MT528602	March 20th ,2020,	A.3 (*S*)
SUB7504586 SARS_CoV-2_Human_UNC_200243_2020	MT528603	March 20th, 2020,	A.3 (*S*)
SUB7504586 SARS_CoV-2_Human_UNC_200244_2020	MT528604	March 19th, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200245_2020	MT528605	March 31st, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200247_2020	MT528606	March 26th, 2020,	A.1 (*S*)
SUB7504586 SARS_CoV-2_Human_UNC_200252_2020	MT528627	March 23rd, 2020,	A.1 (*S*)
SUB7504586 SARS_CoV-2_Human_UNC_200253_2020	MT528628	March 22nd, 2020,	A.3 (*S*)
SUB7504586 SARS_CoV-2_Human_UNC_200254_2020	MT528607	March 28th, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200255_2020	MT528608	March 28th, 2020,	A.3 (*S*)
SUB7504586 SARS_CoV-2_Human_UNC_200256_2020	MT528609	March 27th, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200259_2020	MT528610	March 30th, 2020,	A.3 (*S*)
SUB7504586 SARS_CoV-2_Human_UNC_200264_2020	MT528611	April 6th, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200271_2020	MT528612	April 6th, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200272_2020	MT528613	April 1st, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200278_2020	MT528614	April 2nd, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200290_2020	MT528615	April 3rd, 2020,	B.1 (*GH*)
SUB7504586 SARS_CoV-2_Human_UNC_200300_2020	MT528616	March 18th, 2020,	A.1 (*S*)
SUB7504586 SARS_CoV-2_Human_UNC_200306_2020	MT528617	March 24th, 2020,	B.1 (*G*)
SUB7504586 SARS_CoV-2_Human_UNC_200310_2020	MT528618	March 26th, 2020,	B.1 (*G*)
SUB7504586 SARS_CoV-2_Human_UNC_200312_2020	MT528619	March 25th, 2020,	A.3 (*S*)

SUB7504586	SARS_CoV-2_Human_UNC_200318_2020	MT528620	March 18th, 2020,	B.1.37 (*GH*)
SUB7504586	SARS_CoV-2_Human_UNC_200319_2020	MT528621	March 23rd, 2020,	B.1.2 (*GH*)
SUB7504586	SARS_CoV-2_Human_UNC_200323_2020	MT528622	March 26th, 2020,	A.1 (*S*)
SUB7504586	SARS_CoV-2_Human_UNC_200325_2020	MT528623	March 23rd, 2020,	B.1 (*GH*)
SUB7504586	SARS_CoV-2_Human_UNC_200326_2020	MT528624	March 30th, 2020,	B.1 (*GH*)
SUB7504586	SARS_CoV-2_Human_UNC_200330_2020	MT528626	March 20th, 2020,	A.3 (*S*)
SUB7504586	SARS_CoV-2_Human_UNC_200331_2020	MT528625	March 19th, 2020,	B.1 (*GH*)
SUB7504586	SARS_CoV-2_Human_UNC_200340_2020	MT528629	March 28th, 2020,	B.1 (*GH*)
SUB7504586	SARS_CoV-2_Human_UNC_200386_2020	MT528630	March 30th, 2020,	B.1 (*GH*)
SUB7536347	SARS_CoV-2_Human_UNC_200459_2020	MT551604	April10th, 2020,	B.1 (*GH*)
SUB7536347	SARS_CoV-2_Human_UNC_200460_2020	MT551605	April 10th, 2020,	B.1 (*GH*)
SUB7536347	SARS_CoV-2_Human_UNC_200467_2020	MT551606	April 10th, 2020,	B.1 (*GH*)
SUB7536347	SARS_CoV-2_Human_UNC_200468_2020	MT551607	April 10th, 2020,	B.1 (*GH*)
SUB7536347	SARS_CoV-2_Human_UNC_200486_2020	MT551608	April 10th, 2020,	B.1 (*GH*)
SUB7536347	SARS_CoV-2_Human_UNC_200488_2020	MT551609	April 10th, 2020,	B.1 (*GH*)
SUB7539666	SARS_CoV-2_Human_UNC_200222_2020	MT554052	March 31st, 2020,	B.1 (*GH*)
SUB7540664	SARS_CoV-2_Human_UNC_200429_2020	MT557568	March 6th, 2020,	A (*S*)
SUB7540664	SARS_CoV-2_Human_UNC_200445_2020	MT557569	May 14th, 2020,	B.1 (*GH*)
SUB7540664	SARS_CoV-2_Human_UNC_200446_2020	MT557570	May 14th, 2020,	B.1 (*GH*)
SUB7544178	SARS_CoV-2_Human_UNC_200395_2020	MT559800	April 8th, 2020,	B.1 (*GH*)
SUB7544178	SARS_CoV-2_Human_UNC_200399_2020	MT559801	April 8th,2020,	B.1 (*GH*)
SUB7544178	SARS_CoV-2_Human_UNC_200401_2020	MT559802	April 7th,2020,	B.1 (*GH*)
SUB7544178	SARS_CoV-2_Human_UNC_200409_2020	MT559803	April 8th, 2020,	B.1 (*GH*)
SUB7552904	SARS_CoV-2_Human_UNC_200414_2020	MT565495	April 8th, 2020,	B.1 (*GH*)
SUB7552904	SARS_CoV-2_Human_UNC_200407_2020	MT565496	April 8th, 2020,	B.1.2 (*GH*)
SUB7552904	SARS_CoV-2_Human_UNC_200428_2020	MT565497	April 7th, 2020,	B.1.2 (*GH*)
SUB7552904	SARS_CoV-2_Human_UNC_200313_2020	MT565498	March 24th,2020,	B.1.2 (*GH*)
SUB7552904	SARS_CoV-2_Human_UNC_200265_2020	MT565499	April 3rd, 2020,	B.1.2 (*GH*)

Supplemental Table S1

Table of complete SARS-CoV-2 genomes deposited in this study. Shown are sequence file names, accession numbers, date of sequencing, and GISAID clade. Related to **Figure 1**, **Figure 2**, and **Figure 3**.