

Supplementary Tables

Supplementary Table 1. List of designed primers for custom targeted sequencing

Primers	Sequences	Primers	Sequences
CB8-F1-U	GTTGCTAGATTATGTTTGGATGC	DN420-F10-U	TGGTGCTGGGTAGTTTAGCTGCT
CB8-F1-L	GAACCTTCACAGAAATCCATAG	DN420-F10-L	TCTGGTCCCAATATTTAAAAATAGCGGTCGA
DB159-F1-U	GAAGAGTGAAAAGCAAGTTGAAC	DN420-F11-U	TGTGTTTCCACCTACAAGTTTGGACCA
DB159-F1-L	GGTGAAGATTGCCATTAATGTC	DN420-F11-L	TCGTCGACAAAACAACCTGCGC
DB159-F2-U	GGTGTAGTTACAACGTGTCATG	DN420-F12-U	TGTCATTAGCCATTGACGCTTACCCT
DB159-F2-L	CTGATGTGCACATTACATCTGAC	DN420-F12-L	CAGCTGCGTGAGAGCAAGCC
DB159-F3-U	ACGGTATTGGGAACCTGAG	DN420-F13-U	GCGTGCGCGTGTAGAGTGTTT
DB159-F3-L	TGTGACTTGCAGTAATAGCTCATAC	DN420-F13-L	GCAAGTCGCACGTTTGTCGCA
DB159-F4-U	CATTTTGCATCGGACT	DN420-F14-U	CGTTACCCCGCCAATGCAATCG
DB159-F4-L	CTAGCATTGACAACACTCAAGTC	DN420-F14-L	GTCGGTACTCATTGTCATGATGCTGCG
DB159-F5-U	GCACACAAAGATAAGTCAGCTC	DN420-F15-U	TCCTCGAGCTCGTATGGACGA
DB159-F5-L	ACAGTCTGCGTAGGCAATC	DN420-F15-L	GGTCTGAATCGACAAGTAGTGTGCCT
DB159-F6-U	TGATTCATCACAGGGTTCTG	DN420-F16-U	CTGTACATACAGTAACAAATGGGACCTCA
DB159-F6-L	ACCGGTAATGATCTTACTACAGTC	DN420-F16-L	TCTCTCCCAAGCATGAACATTGTGGA
DB159-F7-U	GATAGGATTAGCCAAAAGGTCAC	DN420-F17-U	CAAGTAGCACCGGGTGAGACTGG
DB159-F7-L	GGTTGCCAGGCTTGACTAG	DN420-F17-L	TGTCCTGTCTACAGCAATGCCTGT
DB159-F8-U	TTCCTGGAATGCCGATC	DN420-F18-U	AGTGACACTTGCTGATGCTGGCT
DB159-F8-L	GAAGACAATTGTATTGGATTGTG	DN420-F18-L	GCCAGAAATGTCGCCAAGATCAACA
DB159-F9-U	GGATGGAAAGTGAGTTCAGAG	DN420-F19-U	GGCCCTGGTATATATGGCTCGGC
DB159-F9-L	TGCAGCACCAGCTGTC	DN420-F19-L	ACGACATAGTCTTTAACACCTGAATGCCA
DN420-F1-U	ACCCCGTTGCTTCACCTCAGG	DN420-F20-U	GCCGACGACGACTACTAGCGT
DN420-F1-L	GGAAAACACACAACCACAAAAGACTTAGT	DN420-F20-L	TGACCACATCGAGCGGGTGC
DN420-F2-U	GCGAGCCTATTGGGTTCTCTGT	DN420-F21-U	TGGACACTCCCTAGGGCGGT
DN420-F2-L	GCTTCCGCCACTACACATGCAAA	DN420-F21-L	AGCTCGCTAGTAGCAAGTGAAATCAATGT
DN420-F3-U	GCGCCACTGCTTTCAGCTGG	DN420-F22-U	TCAAGAGTGTGTTAGAGGTACTACCGTACT
DN420-F3-L	GCATGTCAAGTAGTACCACCTGCCT	DN420-F22-L	TGACGTTGTACTGTTTGTAGCAGTACG
DN420-F4-U	AGGGTGTGCTGGTTATACGCTTGA	DN420-F23-U	CAGAAGCCTGTTGATGTGAAGCCAAAA
DN420-F4-L	ACGTCACCCAACTACCAACAGT	DN420-F23-L	ACCGATTTGCATTTCTTAAGAGCAGTCT
DN420-F5-U	ACCATGTGTTTGTGGCGTAATGC	DN420-F24-U	GCAATGTTCAACTTCGTGTTATTGGCC
DN420-F5-L	GCCAAAAACCACTCAGCAGCCA	DN420-F24-L	TGCCACAAGGTTAAATCATTCAGTGT
DN420-F6-U	TCCAAGTGTGACGAGTCTGCTGC	DN420-F25-U	ATGTAAATGCACCTCTTTCAACTGATGGT
DN420-F6-L	ACCACAGAAAACCTCAGGTAGGGC	DN420-F26-L	ACAAGTGGAAGACATCAGCATACTCCT
DN420-F7-U	ACTCTGCTTGGCGCCAGCTT	DN420-F27-U	AGGAGCACTATGTGAGAATTACTGGCT
DN420-F7-L	ACCAACACTACCACATGACCCATTAAGG	DN420-F27-L	CAATGTTCTGGTGGTGTGTAATTGAGC
DN420-F8-U	GGAGCTTCCAACGGGTGTGCA	DN420-F28-U	CTACTGATTCAAGTTTTGCTGCATACA
DN420-F8-L	GCATAGCACACGCAGCAATAGCC	DN420-F28-L	TGCGAATTTATTATCAGCAAGGGGATG
DN420-F9-U	TGATGCTGCTAGACGTGTTGGACA	DN420-F29-U	CGATACATAGTCTACTCTTG
DN420-F9-L	GTCTTCAGACCGCGCCTGCT	DN420-F29-L	GTCATTCTCCTAAGAAGCTA

F: missing fragments after metagenomic sequencing

U: forward primers; L: reverse primers

Supplementary Table 2. List of 63 coronavirus reference genomes extracted from GenBank for read mapping.

Accession number	Virus classification (genus; subgenus)	Virus name
NC_022103.1	Alphacoronavirus; Colacovirus	Bat coronavirus CDPHE15/USA/2006
NC_018871.1	Alphacoronavirus; Decacovirus	Rousettus bat coronavirus HKU10
NC_028814.1	Alphacoronavirus; Decacovirus	BtRf-AlphaCoV/HuB2013
NC_002645.1	Alphacoronavirus; Duvinacovirus	Human coronavirus 229E
NC_028752.1	Alphacoronavirus; Duvinacovirus	Camel/Riyadh/Ry141/2015
NC_032730.1	Alphacoronavirus; Luchacovirus	Lucheng Rn rat coronavirus Lucheng-19
NC_034972.1	Alphacoronavirus; Luchacovirus	Coronavirus AcCoV-JC34
NC_023760.1	Alphacoronavirus; Minacovirus	Mink coronavirus WD1127
NC_030292.1	Alphacoronavirus; Minacovirus	Ferret coronavirus FRCoV-NL-2010
NC_010437.1	Alphacoronavirus; Minunacovirus	Bat coronavirus 1A
NC_010438.1	Alphacoronavirus; Minunacovirus	Miniopterus bat coronavirus HKU8
NC_028811.1	Alphacoronavirus; Myotacovirus	BtMr-AlphaCoV/SAX2011
NC_028833.1	Alphacoronavirus; Nyctacovirus	BtNv-AlphaCoV/SC2013
NC_046964.1	Alphacoronavirus; Nyctacovirus	Bat-CoV/P.kuhl/Italy/3398-19/2015
NC_003436.1	Alphacoronavirus; Pedacovirus	Porcine epidemic diarrhea virus
NC_009657.1	Alphacoronavirus; Pedacovirus	Scotophilus bat coronavirus 512
NC_009988.1	Alphacoronavirus; Rhinacovirus	Rhinolophus bat coronavirus HKU2
NC_028824.1	Alphacoronavirus; Rhinacovirus	BtRf-AlphaCoV/YN2012
NC_005831.2	Alphacoronavirus; Setracovirus	Human Coronavirus NL63
NC_032107.1	Alphacoronavirus; Setracovirus	NL63-related bat coronavirus BtKYNL63-9a
NC_048216.1	Alphacoronavirus; Setracovirus	NL63-related bat coronavirus BtKYNL63-9b
NC_002306.3	Alphacoronavirus; Tegacovirus	Feline infectious peritonitis virus
NC_028806.1	Alphacoronavirus; Tegacovirus	Swine enteric coronavirus Italy/213306/2009
NC_038861.1	Alphacoronavirus; Tegacovirus	Transmissible gastroenteritis virus
AC_000192.1	Betacoronavirus; Embecovirus	Murine hepatitis virus JHM
NC_001846.1	Betacoronavirus; Embecovirus	Murine hepatitis virus MHV-A59 C12
NC_003045.1	Betacoronavirus; Embecovirus	Bovine coronavirus BCoV-ENT
NC_006213.1	Betacoronavirus; Embecovirus	Human coronavirus OC43 ATCC VR-759
NC_006577.2	Betacoronavirus; Embecovirus	Human coronavirus HKU1
NC_012936.1	Betacoronavirus; Embecovirus	Rat coronavirus Parker
NC_017083.1	Betacoronavirus; Embecovirus	Rabbit coronavirus HKU14
NC_026011.1	Betacoronavirus; Embecovirus	Betacoronavirus HKU24 HKU24-R050051
NC_048217.1	Betacoronavirus; Embecovirus	Murine hepatitis virus A59
NC_025217.1	Betacoronavirus; Hibecovirus	Bat Hp-betacoronavirus/Zhejiang2013
NC_009019.1	Betacoronavirus; Merbecovirus	Tylonycteris bat coronavirus HKU4
NC_009020.1	Betacoronavirus; Merbecovirus	Pipistrellus bat coronavirus HKU5
NC_019843.3	Betacoronavirus; Merbecovirus	MERS-related coronavirus HCoV-EMC/2012
NC_038294.1	Betacoronavirus; Merbecovirus	Betacoronavirus England 1 H123990006
NC_039207.1	Betacoronavirus; Merbecovirus	Erinaceus/VMC/DEU/2012
NC_009021.1	Betacoronavirus; Nobecovirus	Rousettus bat coronavirus HKU9
NC_030886.1	Betacoronavirus; Nobecovirus	Rousettus bat coronavirus GCCDC1 356
NC_004718.3	Betacoronavirus; Sarbecovirus	SARS-CoV Tor2
NC_014470.1	Betacoronavirus; Sarbecovirus	Bat coronavirus BM48-31/BGR/2008
NC_045512.2	Betacoronavirus; Sarbecovirus	SARS-CoV-2 Wuhan-Hu-1
NC_011547.1	Deltacoronavirus; Buldecovirus	Bulbul coronavirus HKU11-934
NC_011549.1	Deltacoronavirus; Buldecovirus	Thrush coronavirus HKU12-600
NC_011550.1	Deltacoronavirus; Buldecovirus	Munia coronavirus HKU13-3514
NC_016991.1	Deltacoronavirus; Buldecovirus	White-eye coronavirus HKU16
NC_016992.1	Deltacoronavirus; Buldecovirus	Sparrow coronavirus HKU17
NC_016993.1	Deltacoronavirus; Buldecovirus	Magpie-robin coronavirus HKU18
NC_016994.1	Deltacoronavirus; Buldecovirus	Night-heron coronavirus HKU19
NC_016995.1	Deltacoronavirus; Buldecovirus	Wigeon coronavirus HKU20
NC_016996.1	Deltacoronavirus; Buldecovirus	Common moorhen coronavirus HKU21
NC_039208.1	Deltacoronavirus; Buldecovirus	Porcine coronavirus HKU15 HKU15-155
NC_046965.1	Gammacoronavirus	Canada goose coronavirus CambridgeBay2017
NC_010646.1	Gammacoronavirus; Cegacovirus	Beluga Whale coronavirus SW1
NC_001451.1	Gammacoronavirus; Igacovirus	Avian infectious bronchitis virus
NC_010800.1	Gammacoronavirus; Igacovirus	Turkey coronavirus
NC_048213.1	Gammacoronavirus; Igacovirus	Infectious bronchitis virus Ind-TN92-03
NC_048214.1	Gammacoronavirus; Igacovirus	Duck coronavirus DK/GD/27/2014
NC_034440.1	NA	Bat coronavirus PREDICT/PDF-2180
NC_046954.1	NA	Rodent coronavirus RtMruf-CoV-2/JL2014
NC_048212.1	NA	Bat coronavirus

Supplementary Table 3: Origin of the 111 genomes of *Sarbecovirus* analysed in this study

Host species	Virus name	Accession number	Country / province	Reference
<i>Aselliscus stoliczkanus</i>	As6526	KY417142 ¹	Yunnan (China)	Hu et al. (2017)
<i>Homo sapiens</i>	SARS-CoV	NC_004718 ¹	Canada	He et al. (2004)
<i>Homo sapiens</i>	SARS-CoV-2	NC_045512 ¹	Hubei (China)	Wu et al. (2020)
<i>Manis javanica</i>	MjGuangdong*	EPI_ISL_410721 ²	Guangdong (China)	Xiao et al. (2020)
<i>Manis javanica</i>	MjGuangxi*	EPI_ISL_410539 ²	Guangxi (China)	Lam et al. (2020)
<i>Rhinolophus acuminatus</i>	RacCS203	MW251308 ¹	Thailand	Wacharapluesadee et al. (2021)
<i>Rhinolophus affinis</i>	Ra21CB8	This study	Vietnam	This study
<i>Rhinolophus affinis</i>	Ra22DB107	This study	Vietnam	This study
<i>Rhinolophus affinis</i>	Ra22DB163	This study	Vietnam	This study
<i>Rhinolophus affinis</i>	Ra22QT77	This study	Vietnam	This study
<i>Rhinolophus affinis</i>	RaGD2017F	OK017792 ¹	Guangdong (China)	Wu et al. (2023)
<i>Rhinolophus affinis</i>	RaLYRa11*	KF569996 ¹	Yunnan (China)	He et al. (2014)
<i>Rhinolophus affinis</i>	RaTG13	MN996532 ¹	Yunnan (China)	Zhou P. et al. (2020)
<i>Rhinolophus affinis</i>	RaTG15 = Ra7909	OL674077 ¹	Yunnan (China)	Guo et al. (2021)
<i>Rhinolophus affinis</i>	RaYN2018A*	MK211375 ¹	Yunnan (China)	Han et al. (2019)
<i>Rhinolophus affinis</i>	RaYN2018B*	MK211376 ¹	Yunnan (China)	Han et al. (2019)
<i>Rhinolophus affinis</i>	RaYN2018C*	MK211377 ¹	Yunnan (China)	Han et al. (2019)
<i>Rhinolophus affinis</i>	RaYN2018D*	MK211378 ¹	Yunnan (China)	Han et al. (2019)
<i>Rhinolophus blasii</i>	RbBM48-31*	NC_014470 ¹	Bulgaria	Drexler et al. (2010)
<i>Rhinolophus cornutus</i>	Rc-o319	LC556375 ¹	Japan	Murakami et al. (2020)
<i>Rhinolophus cornutus</i>	Rckw8	LC663793 ¹	Japan	Murakami et al. (2022)
<i>Rhinolophus ferrumequinum</i> ¹¹	Rf1	DQ412042 ¹	Hubei (China)	Li et al. (2005)
<i>Rhinolophus ferrumequinum</i> ¹¹	Rf4092	KY417145 ¹	Yunnan (China)	Hu et al. (2017)
<i>Rhinolophus ferrumequinum</i> ¹¹	RfLN2020B	OK017795 ¹	Liaoning (China)	Wu et al. (2023)
<i>Rhinolophus ferrumequinum</i> ¹¹	RfJiyuan-84*	KY770860 ¹	Henan (China)	Lin et al. (2017)
<i>Rhinolophus ferrumequinum</i> ¹¹	RfSKB20-50	ON378802 ¹	South Korea	Lo et al. (2022)
<i>Rhinolophus ferrumequinum</i> ¹¹	RfV273*	DQ648856 ¹	Yunnan (China)	Tang et al. (2006)
<i>Rhinolophus ferrumequinum</i> ¹¹	RfYNLF/31C*	KP886808 ¹	Yunnan (China)	Lau et al. (2015)
<i>Rhinolophus hipposideros</i>	RhGB01*	MW719567 ¹	United Kingdom	Crook et al. (2021)
<i>Rhinolophus hipposideros</i>	RhKhosta2*	MZ190138 ¹	Russia	Alkhovsky et al. (2022)
<i>Rhinolophus macrotis</i> ¹²	Rmac279*	DQ648857 ¹	Yunnan (China)	Tang et al. (2006)
<i>Rhinolophus malayanus</i>	RmBANAL52*	EPI_ISL_4302644 ²	Vientiane P. (Laos)	Temmam et al. (2022)
<i>Rhinolophus malayanus</i>	RmBANAL247*	EPI_ISL_4302648 ²	Vientiane P. (Laos)	Temmam et al. (2022)
<i>Rhinolophus malayanus</i>	RmYN02*	EPI_ISL_412977 ²	Yunnan (China)	Zhou H. et al. (2020)
<i>Rhinolophus malayanus</i>	RmYN07*	EPI_ISL_1699447 ²	Yunnan (China)	Zhou et al. (2021)
<i>Rhinolophus marshalli</i>	RmaBANAL236*	EPI_ISL_4302647 ²	Vientiane P. (Laos)	Temmam et al. (2022)

<i>Rhinolophus pusillus</i>	Rp22DB159	This study	Vietnam	This study
<i>Rhinolophus pearsonii</i>	Rpe3	DQ071615 ¹	Guangxi (China)	Li et al. (2005)
<i>Rhinolophus pusillus</i>	RpBANAL103*	EPI_ISL_4302645 ²	Vientiane P. (Laos)	Temmam et al. (2022)
<i>Rhinolophus pusillus</i>	RpF46*	KU973692 ¹	Yunnan (China)	Wang et al. (2017)
<i>Rhinolophus pusillus</i>	RpHN2021A*	OK017803 ¹	Hunan (China)	Wu et al. (2023)
<i>Rhinolophus pusillus</i>	RpHN2021G*	OK017805 ¹	Hunan (China)	Wu et al. (2023)
<i>Rhinolophus pusillus</i>	RpJCC9*	OK287355 ¹	Yunnan (China)	unpublished
<i>Rhinolophus pusillus</i>	RpPrC31*	EPI_ISL_1098866 ²	Yunnan (China)	Li et al. (2021)
<i>Rhinolophus pusillus</i>	RpShaanxi2011	JX993987 ¹	Shaanxi (China)	Yang et al. (2013)
<i>Rhinolophus pusillus</i>	RpYN06*	EPI_ISL_1699446 ²	Yunnan (China)	Zhou et al. (2021)
<i>Rhinolophus pusillus</i>	RpYN2021*	OK017806 ¹	Yunnan (China)	Wu et al. (2023)
<i>Rhinolophus pusillus</i>	RpVZC45*	MG772933 ¹	Zhejiang (China)	Hu et al. (2018)
<i>Rhinolophus pusillus</i>	RpZXC21*	MG772934 ¹	Zhejiang (China)	Hu et al. (2018)
<i>Rhinolophus shameli</i>	RshSTT200	EPI_ISL_852605 ²	Cambodia	Delaune et al. (2021)
<i>Rhinolophus siamensis</i>	RsiGX2019A	OK017859	Guangxi (China)	Wu et al. (2023)
<i>Rhinolophus siamensis</i>	RsiJX2021D	OK017860	Jiangxi (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	Rs56	MW681002 ¹	Guangdong (China)	Li et al. (2022)
<i>Rhinolophus sinicus</i>	Rs3367	KC881006 ¹	Yunnan (China)	Ge et al. (2013)
<i>Rhinolophus sinicus</i>	Rs4081	KY417143 ¹	Yunnan (China)	Hu et al. (2017)
<i>Rhinolophus sinicus</i>	Rs4084	KY417144 ¹	Yunnan (China)	Hu et al. (2017)
<i>Rhinolophus sinicus</i>	Rs4231	KY417146 ¹	Yunnan (China)	Hu et al. (2017)
<i>Rhinolophus sinicus</i>	Rs4237	KY417147 ¹	Yunnan (China)	Hu et al. (2017)
<i>Rhinolophus sinicus</i>	Rs4247	KY417148 ¹	Yunnan (China)	Hu et al. (2017)
<i>Rhinolophus sinicus</i>	Rs4255	KY417149 ¹	Yunnan (China)	Hu et al. (2017)
<i>Rhinolophus sinicus</i>	Rs4874	KY417150 ¹	Yunnan (China)	Hu et al. (2017)
<i>Rhinolophus sinicus</i>	Rs7327	KY417151 ¹	Yunnan (China)	Hu et al. (2017)
<i>Rhinolophus sinicus</i>	Rs9401	KY417152 ¹	Yunnan (China)	Hu et al. (2017)
<i>Rhinolophus sinicus</i>	RsAH2021A	OK017807 ¹	Anhui (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsAnlong103*	KY770858 ¹	Guizhou (China)	Lin et al. (2017)
<i>Rhinolophus sinicus</i>	RsFJ2021D	OK017809 ¹	Fujian (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsFJ2021M	OK017811 ¹	Fujian (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsGD2016B	OK017812 ¹	Guangdong (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsGD2017L	OK017818 ¹	Guangdong (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsGD2017M	OK017819 ¹	Guangdong (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsGD2017Q	OK017823 ¹	Guangdong (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsGD2017W	OK017824 ¹	Guangdong (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsGD2019B	OK017826 ¹	Guangdong (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsGD2019D	OK017827 ¹	Guangdong (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsGD2019E	OK017828 ¹	Guangdong (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsHKU3-1*	DQ022305 ¹	Hong-Kong (China)	Lau et al. (2005)

<i>Rhinolophus sinicus</i>	RsHKU3-7*	GQ153542 ¹	Hong-Kong (China)	Lau et al. (2010)
<i>Rhinolophus sinicus</i>	RsHKU3-12*	GQ153547 ¹	Hong-Kong (China)	Lau et al. (2010)
<i>Rhinolophus sinicus</i>	RsHN2021C	OK017832 ¹	Hunan (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsHN2021D	OK017833 ¹	Hunan (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsHN2021E	OK017834 ¹	Hunan (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsHN2021F	OK017835 ¹	Hunan (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsHuB2013*	KJ473814 ¹	Hubei (China)	Wu et al. (2016)
<i>Rhinolophus sinicus</i>	RsJX2021AC	OK017836 ¹	Jiangxi (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsJX2021C	OK017837 ¹	Jiangxi (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsJX2021G	OK017838 ¹	Jiangxi (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsJX2021J	OK017839 ¹	Jiangxi (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsJX2021K	OK017840 ¹	Jiangxi (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsJX2021N	OK017843 ¹	Jiangxi (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsJX2021O	OK017844 ¹	Jiangxi (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsJX2021P	OK017845 ¹	Jiangxi (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsKMC6	OK287354 ¹	Yunnan (China)	unpublished
<i>Rhinolophus sinicus</i>	RsSHC014	KC881005 ¹	Yunnan (China)	Ge et al. (2013)
<i>Rhinolophus sinicus</i>	RsYN2016A	OK017847 ¹	Yunnan (China)	Wu et al. (2023)
<i>Rhinolophus sinicus</i>	RsYN2020C	OK017853 ¹	Yunnan (China)	Wu et al. (2023)
<i>Rhinolophus</i> sp.	RspHB2020E	OK017802 ¹	Hubei (China)	Wu et al. (2023)
<i>Rhinolophus</i> sp.	RspKY72*	KY352407 ¹	Kenya	Tao and Tong (2019)
<i>Rhinolophus</i> sp.	RspSC2018*	MK211374 ¹	Sichuan (China)	Han et al. (2019)
<i>Rhinolophus stheno</i> ^{T3}	RstYN03*	EPI_ISL_1699443 ²	Yunnan (China)	Zhou et al. (2021)
<i>Rhinolophus stheno</i> ^{T3}	RstYN04*	EPI_ISL_1699444 ²	Yunnan (China)	Zhou et al. (2021)
<i>Rhinolophus stheno</i> ^{T3}	RstYN09*	EPI_ISL_1699449 ²	Yunnan (China)	Zhou et al. (2021)
<i>Rhinolophus thomasi</i>	Rt17DN420	This study	Vietnam	This study
<i>Rhinolophus thomasi</i>	Rt21LC92	This study	Vietnam	This study
<i>Rhinolophus thomasi</i>	Rt22CB395	This study	Vietnam	This study
<i>Rhinolophus thomasi</i>	Rt22DB31	This study	Vietnam	This study
<i>Rhinolophus thomasi</i>	Rt22LC378	This study	Vietnam	This study
<i>Rhinolophus thomasi</i>	Rt22QB8	This study	Vietnam	This study
<i>Rhinolophus thomasi</i>	Rt22QB78	This study	Vietnam	This study
<i>Rhinolophus thomasi</i>	Rt22QT124	This study	Vietnam	This study
<i>Rhinolophus thomasi</i>	Rt22SL9	This study	Vietnam	This study
<i>Rhinolophus thomasi</i>	Rt22SL115	This study	Vietnam	This study

*original name slightly modified to be consistent with other names and to facilitate interpretations; 1: NCBI; 2: GISAID.

Taxonomic issues (Burgin et al., 2020) = T1: currently *Rhinolophus nippon*; T2: currently *Rhinolophus episcopus*; T3: currently *Rhinolophus microglobosus*.

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Supplementary Table 4. Synonymous nucleotide composition at four-fold (4X) and two-fold (2X) degenerate third codon-positions.

Genomes	4X-A	4X-C	4X-G	4X-U	2X-A	2X-G	2X-C	2X-U
RbBM4831	25.1	17.1	9.1	48.8	54.8	45.2	35.8	64.2
RhGB01	26.7	17.7	11.5	44.1	52.7	47.3	36.2	63.8
RhKhosta2	27.9	16.7	10.6	44.9	53.7	46.3	34.2	65.8
RspKY72	26.3	15.3	9.2	49.2	58.4	41.6	32.3	67.7
As6526	28.9	17.0	8.6	45.4	56.9	43.1	38.9	61.1
Ra21CB8	29.2	17.0	8.3	45.5	57.4	42.6	39.1	60.9
Ra22DB107	28.9	16.7	8.4	46.1	56.9	43.1	38.4	61.6
Ra22DB163	28.2	17.2	8.8	45.8	54.8	45.2	38.1	61.9
RaGD2017F	28.6	16.7	8.6	46.1	57.1	42.9	39.4	60.6
RaLYRa11	28.0	16.5	8.7	46.7	57.1	42.9	37.1	62.9
RaYN2018A	29.0	16.5	8.5	46.1	56.7	43.3	39.3	60.7
RaYN2018B	28.9	16.8	8.3	46.0	56.8	43.2	38.5	61.5
RaYN2018C	28.9	17.0	8.5	45.6	56.4	43.6	39.1	60.9
RaYN2018D	28.9	16.9	8.7	45.5	56.6	43.4	39.2	60.8
Rf1	27.7	17.6	9.5	45.3	58.0	42.0	39.8	60.2
Rf4092	28.9	16.6	8.9	45.7	55.6	44.4	39.8	60.2
RfJiyuan84	27.6	17.8	9.5	45.2	58.6	41.4	39.7	60.3
RfLN2020B	27.9	16.8	9.5	45.8	57.6	42.4	39.4	60.6
RfSKB2050	27.7	16.6	9.5	46.1	58.0	42.0	39.4	60.6
RfV273	28.0	17.4	9.5	45.1	58.1	41.9	40.3	59.7
RfYNLF31C	28.7	17.1	8.5	45.7	56.7	43.3	37.3	62.7
Rmac279	28.4	17.1	9.1	45.4	56.6	43.4	40.6	59.4
RmYN07	27.9	16.5	9.1	46.5	56.5	43.5	38.0	62.0
Rpe3	29.8	16.2	8.5	45.6	56.6	43.4	38.5	61.5
RpF46	28.6	16.9	8.9	45.6	56.1	43.9	38.4	61.6
RpShaanxi	28.1	17.6	10.2	44.1	56.3	43.7	42.2	57.8
Rs3367	29.0	16.7	8.5	45.9	56.6	43.4	38.4	61.6
Rs4081	28.7	17.2	8.9	45.2	56.4	43.6	38.6	61.4
Rs4084	29.0	16.6	8.3	46.2	56.0	44.0	39.2	60.8
Rs4231	28.9	17.0	8.5	45.6	56.1	43.9	38.3	61.7
Rs4237	28.8	16.7	8.8	45.7	57.0	43.0	38.2	61.8
Rs4247	29.2	16.7	8.5	45.6	55.8	44.2	38.3	61.7
Rs4255	28.5	17.1	8.9	45.5	56.4	43.6	38.7	61.3
Rs4874	28.9	17.0	8.7	45.3	56.5	43.5	37.8	62.2
Rs56	28.1	16.3	9.3	46.2	57.1	42.9	38.3	61.7
Rs7327	29.2	17.0	8.1	45.7	56.0	44.0	38.6	61.4
Rs9401	29.2	16.8	8.2	45.8	56.2	43.8	38.0	62.0
RsAH2021A	28.0	16.4	9.1	46.5	56.2	43.8	38.2	61.8
RsAnlong103	28.6	16.5	8.7	46.2	56.0	44.0	38.9	61.1
RsFJ2021D	27.9	16.1	9.8	46.2	57.4	42.7	38.2	61.8
RsFJ2021M	27.8	16.3	9.7	46.3	57.5	42.5	38.4	61.6
RsGD2016B	27.9	16.7	9.8	45.6	57.5	42.5	38.4	61.6
RsGD2017L	28.4	16.5	9.2	45.9	56.9	43.1	38.8	61.2
RsGD2017M	28.2	16.5	9.2	46.2	56.0	44.0	38.1	61.9
RsGD2017Q	32.2	18.4	8.7	40.8	63.5	36.5	44.9	55.1
RsGD2017W	28.8	16.6	8.7	45.9	56.6	43.4	39.4	60.6
RsGD2019B	28.8	16.4	9.0	45.8	56.8	43.2	39.1	60.9
RsGD2019D	29.0	16.6	8.9	45.6	56.9	43.1	38.9	61.1
RsGD2019E	28.9	16.7	8.8	45.6	56.8	43.2	39.1	60.9
RsHKU31	27.8	16.6	9.9	45.6	57.1	42.9	38.4	61.6
RsHKU312	27.8	16.5	9.6	46.1	57.1	42.9	38.5	61.5
RsHKU37	27.5	16.3	10.1	46.0	56.9	43.1	37.9	62.1
RsHN2021C	28.1	17.1	9.3	45.6	56.8	43.2	39.6	60.4
RsHN2021D	28.8	16.5	8.9	45.9	58.5	41.5	40.0	60.0
RsHN2021E	28.3	16.8	9.0	45.9	56.7	43.3	40.1	59.9
RsHN2021F	28.8	16.9	9.1	45.2	56.7	43.3	41.2	58.8
RsHuB2013	28.6	17.0	9.0	45.4	55.3	44.7	41.6	58.4
RsiGX2019A	28.4	15.9	9.1	46.6	56.9	43.1	40.4	59.6

RsiJX2021D	28.5	16.7	8.9	45.9	55.9	44.1	39.3	60.7
RsJX2021AC	27.5	17.0	9.4	46.0	55.9	44.1	37.6	62.4
RsJX2021C	27.7	16.8	9.3	46.2	56.7	43.3	39.2	60.8
RsJX2021G	27.8	16.2	9.5	46.5	56.7	43.3	37.6	62.4
RsJX2021J	28.5	16.3	9.3	45.9	56.2	43.8	38.3	61.7
RsJX2021K	27.8	16.1	9.4	46.8	56.1	43.9	37.4	62.6
RsJX2021N	28.7	16.2	9.0	46.1	57.4	42.6	38.1	61.9
RsJX2021O	27.7	16.1	9.9	46.3	56.3	43.7	38.3	61.7
RsJX2021P	27.7	15.8	9.8	46.7	55.9	44.1	38.0	62.0
RsKMC6	28.5	16.1	8.9	46.4	56.3	43.7	38.2	61.8
RspHB2020E	27.5	16.5	9.4	46.6	57.7	42.3	37.4	62.6
RspSC2018	27.5	17.0	9.6	46.0	56.7	43.3	37.3	62.7
RsSHC014	29.3	16.8	8.2	45.7	56.5	43.5	38.8	61.2
RstYN03	28.4	16.5	8.6	46.5	57.0	43.0	38.4	61.6
RstYN09	28.1	16.3	8.7	46.9	56.9	43.1	37.2	62.8
RsYN2016A	28.9	16.8	8.3	45.9	56.6	43.4	38.8	61.2
RsYN2020C	28.7	17.0	8.6	45.7	56.5	43.5	38.9	61.1
Rt17DN420	27.9	14.9	8.9	48.2	59.6	40.4	30.7	69.3
Rt21LC92	28.7	16.1	8.9	46.3	57.6	42.4	39.3	60.7
Rt22CB395	29.0	16.6	8.6	45.8	57.6	42.4	39.4	60.6
Rt22DB31	28.6	16.7	8.6	46.1	56.8	43.2	38.1	61.9
Rt22LC378	28.7	16.5	8.7	46.1	56.7	43.3	38.8	61.2
Rt22QB78	28.2	16.2	8.6	47.0	57.3	42.7	34.9	65.1
Rt22QB8	28.2	15.7	8.7	47.4	57.6	42.4	34.9	65.2
Rt22QT124	28.5	15.9	8.6	47.1	57.9	42.1	34.4	65.6
Rt22SL115	28.9	16.2	8.7	46.2	57.7	42.3	37.1	62.9
Rt22SL9	29.3	16.6	8.2	45.9	56.9	43.1	37.3	62.7
SARS-CoV	28.6	16.6	8.4	46.4	56.0	44.0	37.8	62.2
Rp22DB159	29.2	14.5	7.1	49.2	64.6	35.4	33.5	66.5
RpHN2021A	29.0	14.8	7.6	48.7	62.4	37.6	33.2	66.8
RpHN2021G	28.7	14.4	7.8	49.1	62.2	37.8	35.1	64.9
RpJCC9	29.0	14.4	7.7	48.9	63.4	36.6	34.5	65.5
RpPrC31	29.3	14.5	7.2	49.0	63.5	36.5	33.8	66.2
RpVZC45	28.5	14.2	8.0	49.3	61.7	38.3	33.6	66.4
RpVZXC21	28.6	14.5	7.8	49.1	62.5	37.5	33.9	66.1
RpYN2021	28.7	14.8	7.6	48.9	62.7	37.3	34.3	65.7
MjGuangdong	29.9	13.6	6.2	50.3	67.6	32.4	33.9	66.1
MjGuangxi	30.0	13.8	6.7	49.4	67.5	32.5	34.7	65.3
Ra22QT77	29.1	14.0	6.6	50.4	68.8	31.2	31.5	68.5
RacCS203	29.1	14.2	6.9	49.8	66.7	33.3	32.9	67.1
RaTG13	29.2	13.5	6.4	50.9	67.1	32.9	32.4	67.6
RmaBANAL236	29.3	13.4	6.5	50.8	67.8	32.2	32.7	67.3
RmBANAL247	28.7	13.7	7.0	50.5	68.0	32.0	32.3	67.7
RmBANAL52	28.9	13.3	6.5	51.2	67.9	32.1	32.8	67.2
RmYN02	29.2	13.8	6.9	50.1	67.4	32.6	32.1	67.9
RpBANAL103	29.6	13.5	6.4	50.6	67.6	32.5	32.9	67.1
RpYN06	28.9	14.0	6.5	50.7	67.3	32.7	32.4	67.6
RshSTT200	29.3	13.8	6.4	50.6	68.5	31.5	31.9	68.1
SARS-CoV-2	29.0	13.7	6.5	50.9	67.8	32.2	31.6	68.4
Rc-o319	31.1	16.1	8.6	44.2	59.6	40.4	38.7	61.3
Rckw8	31.7	16.0	8.7	43.6	59.4	40.6	38.8	61.2
Ra7909	24.1	19.1	9.8	47.0	57.9	42.1	32.6	67.4
RstYN04	24.4	19.2	9.6	46.8	57.7	42.3	32.8	67.2

Supplementary Table 5. Five sliding window bootstrap (SWB) analyses performed on an alignment of 111 *Sarbecovirus* genomes (length: 30,103 nt).

	Window Size (nt)	Step (nt)	WB sub-datasets	SWB bipartitions ¹	SuperTRI matrix ²	BBC bipartitions ³	SARS-CoV-2 bipartitions ⁴
1	400	50	595	633,785	1,298,453	2,452	216
2	500	50	593	505,978	1,124,693	2,366	210
3	600	50	591	411,978	985,475	2,348	217
4	1000	50	583	233,005	706,224	2,115	189
5	2000	50	563	97,968	450,416	1,661	165

¹: Number of bipartitions (with window bootstrap percentages [WBP] calculated for each WB subdatasets) obtained under the SWB program (Hassanin et al., 2022);

²: Number of characters in the MRP matrix reconstructed using LFG (Hassanin et al., 2022) and SuperTRI (Ropiquet et al., 2009) programs;

³: Number of SWB bipartitions including at least one WBP $\geq 50\%$ selected under the BBC program using the SWB file as input (Hassanin et al., 2022);

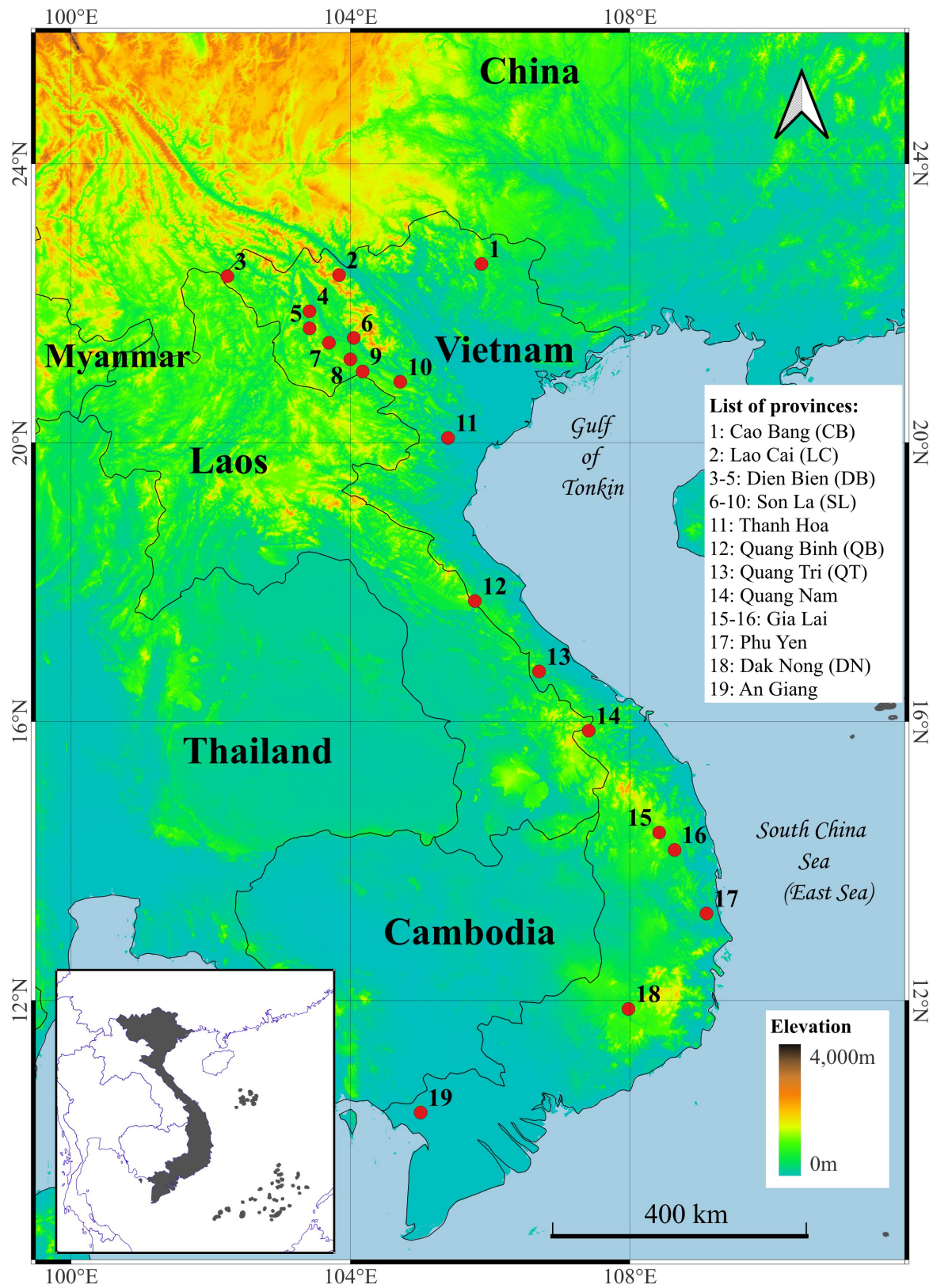
⁴: Number of BBC bipartitions including SARS-CoV-2.

Supplementary Table 6. Origin of *Rhinolophus pusillus* sequences of cytochrome c oxidase subunit 1 gene (CO1) identical to that of the bat hosting Rp22DB159

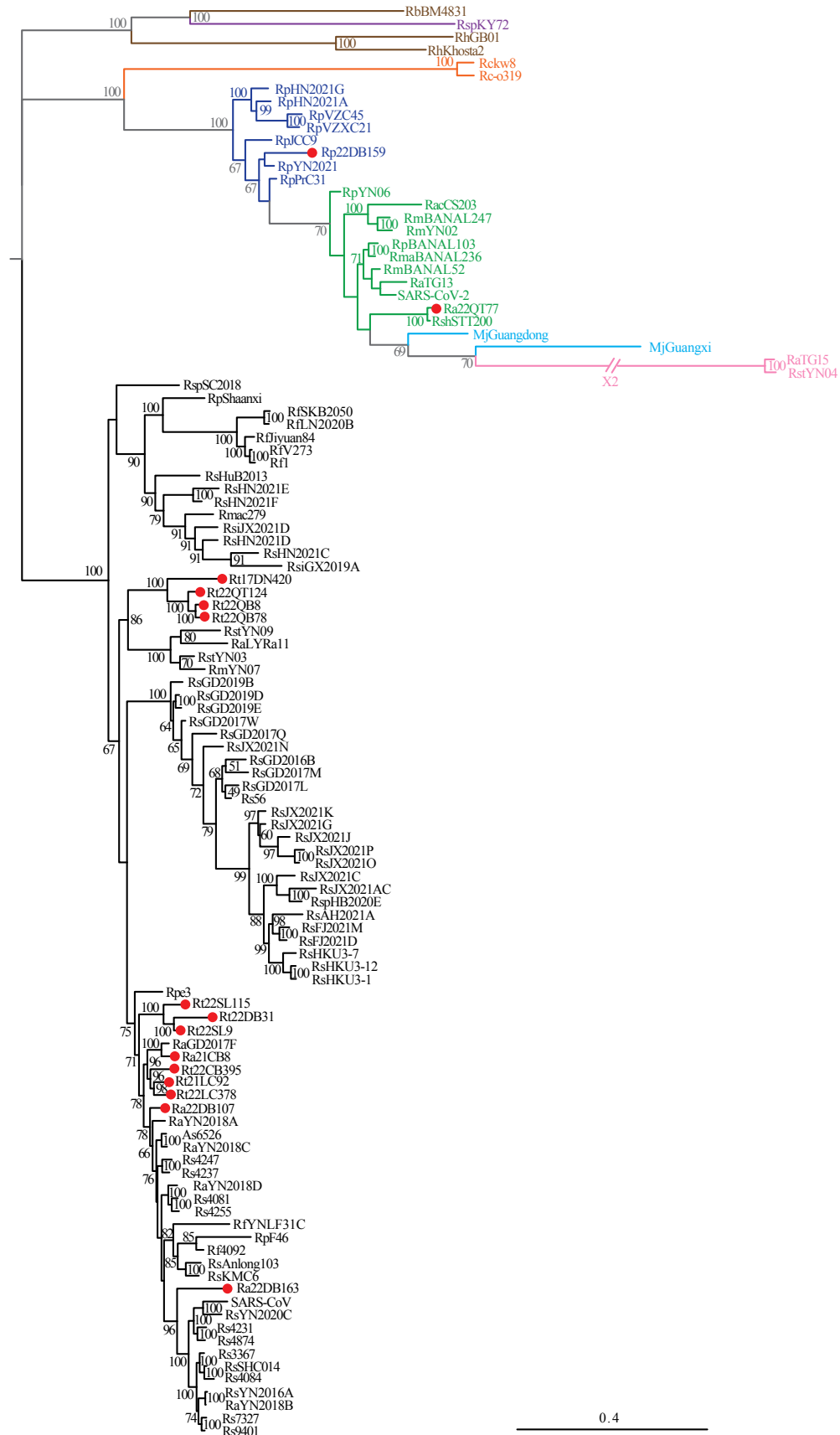
GenBank accession numbers	latitude	Longitude
OK562941, OK562942, OK562943, OK562946	24.62 N	102.16 E
OK562956	22.64 N	100.81 E
DB159	22.39 N	102.24 E

Supplementary Figures

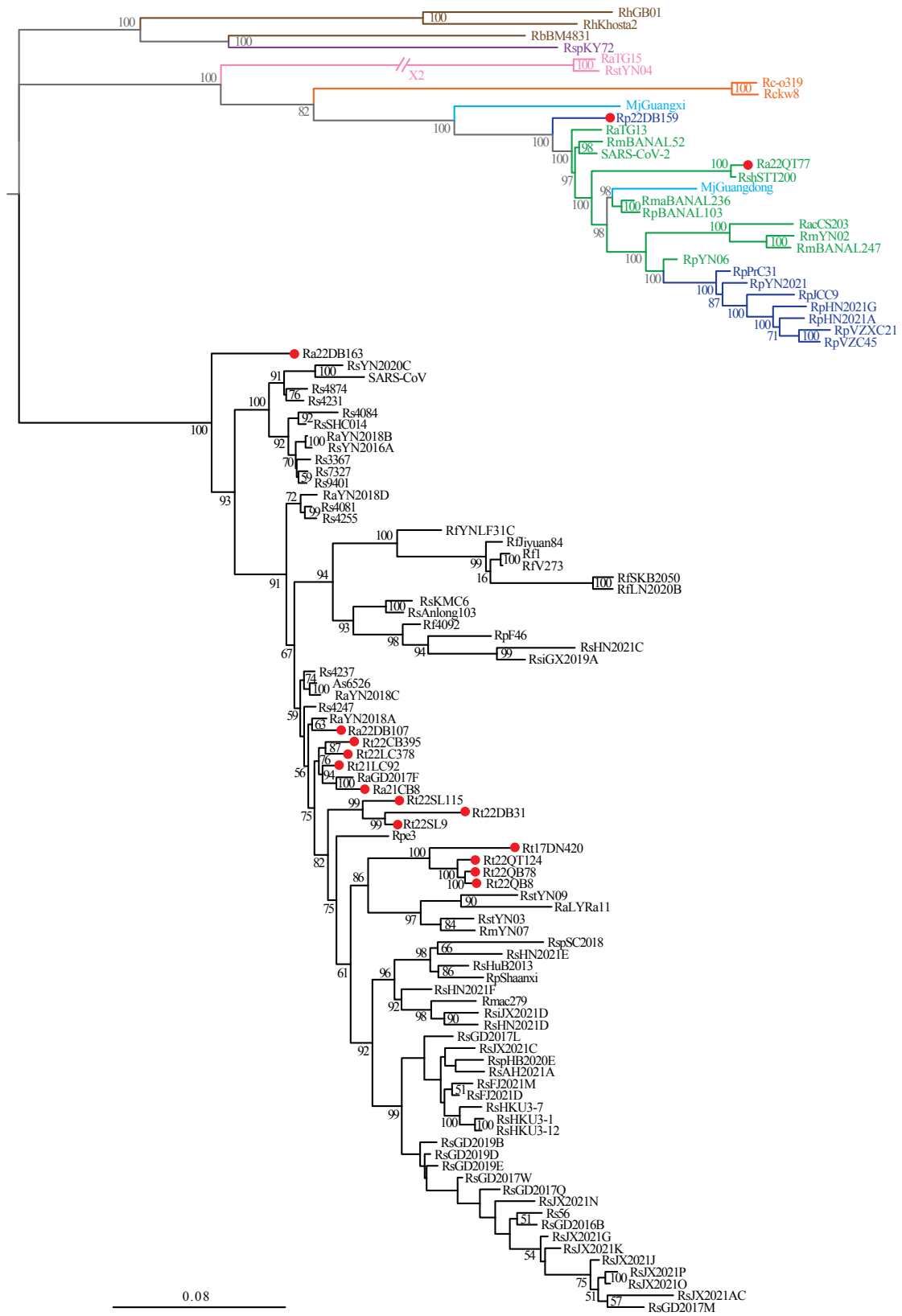
Supplementary Figure 1. Locations in Vietnam (numbered from 1 to 19) where bats were sampled for this study.



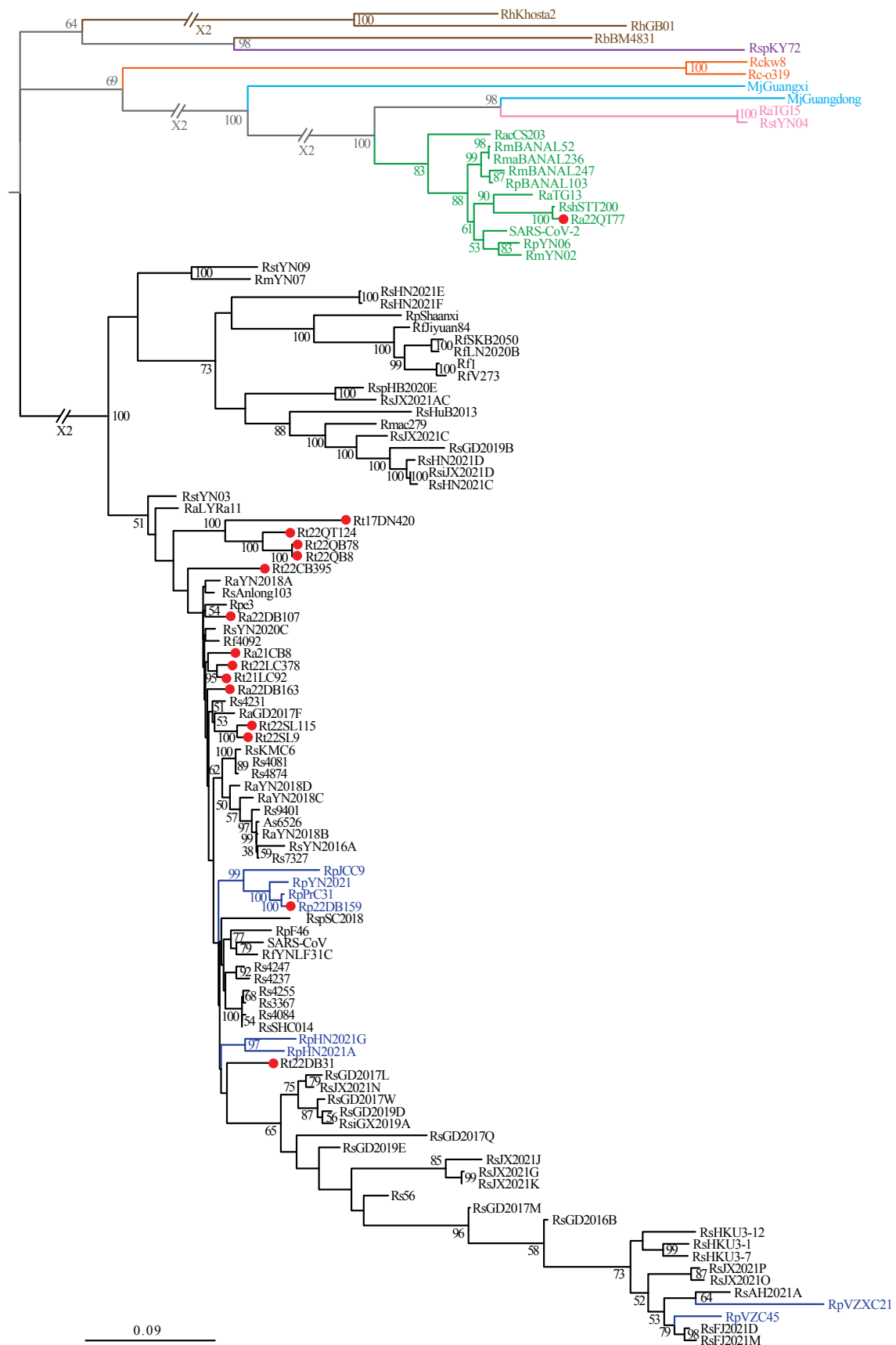
Supplementary Figure 2. Maximum Likelihood tree based on a nucleotide alignment of 111 full *Sarbecovirus* genomes. The tree was reconstructed with RAXML using a different GTR model for the four partitions corresponding to the three codon positions and non-coding regions. Bootstrap percentages higher than 50% are indicated at the nodes.



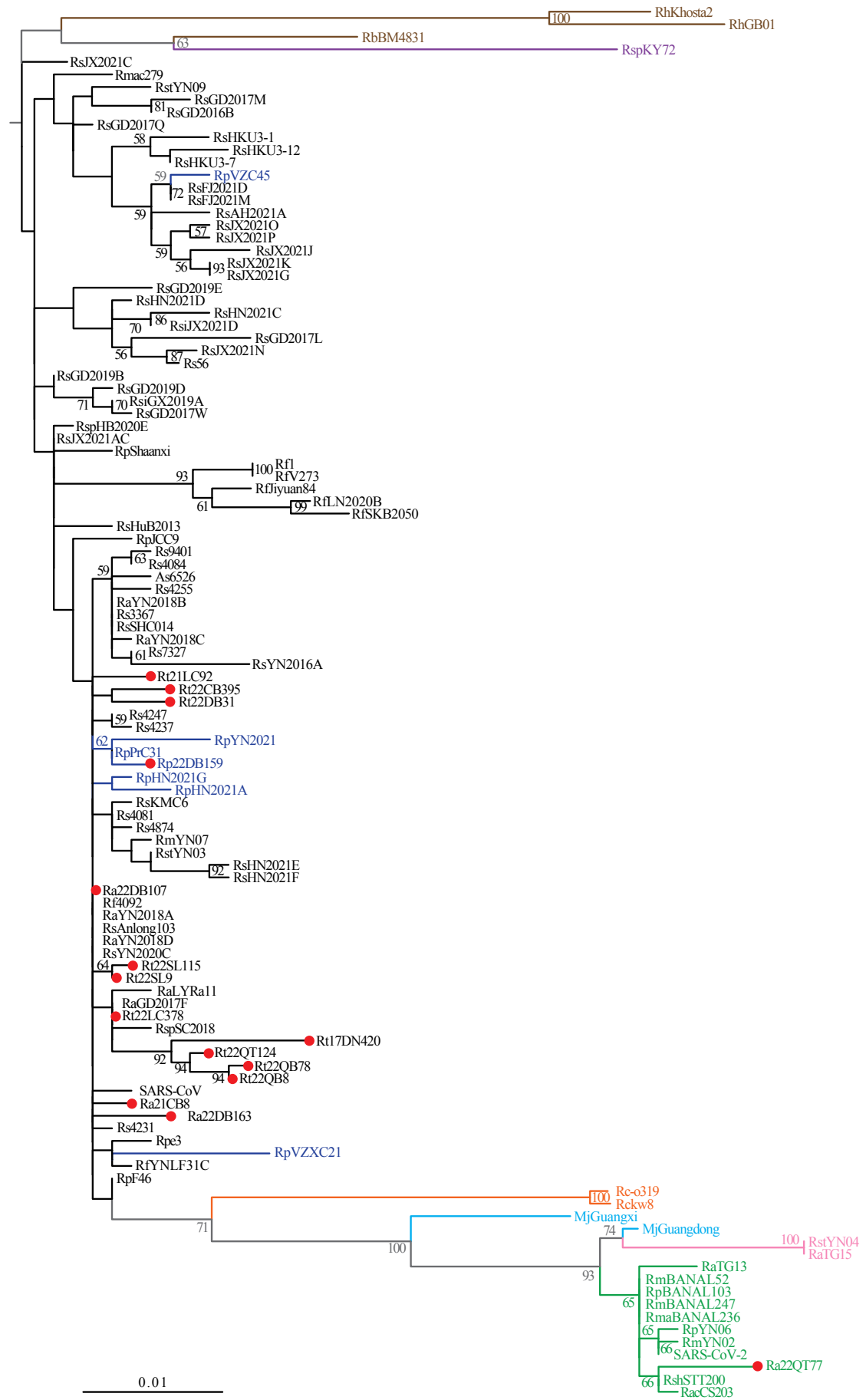
Supplementary Figure 3. Maximum Likelihood tree based on a protein alignment of 111 full *Sarbecovirus* genomes. The tree was reconstructed with RAxML using the LG model.



Supplementary Figure 4. Maximum Likelihood tree based on a RdRp gene alignment of 111 sarbecoviruses. The tree was reconstructed with RAxML using a different GTR model for the three partitions corresponding to the three codon positions. Bootstrap percentages higher than 50% are indicated at the nodes.



Supplementary Figure 5. Maximum Likelihood tree based on a RdRp protein alignment of 111 sarbecoviruses. The tree was reconstructed with RAXML using the LG model. Bootstrap percentages higher than 50% are indicated at the nodes.

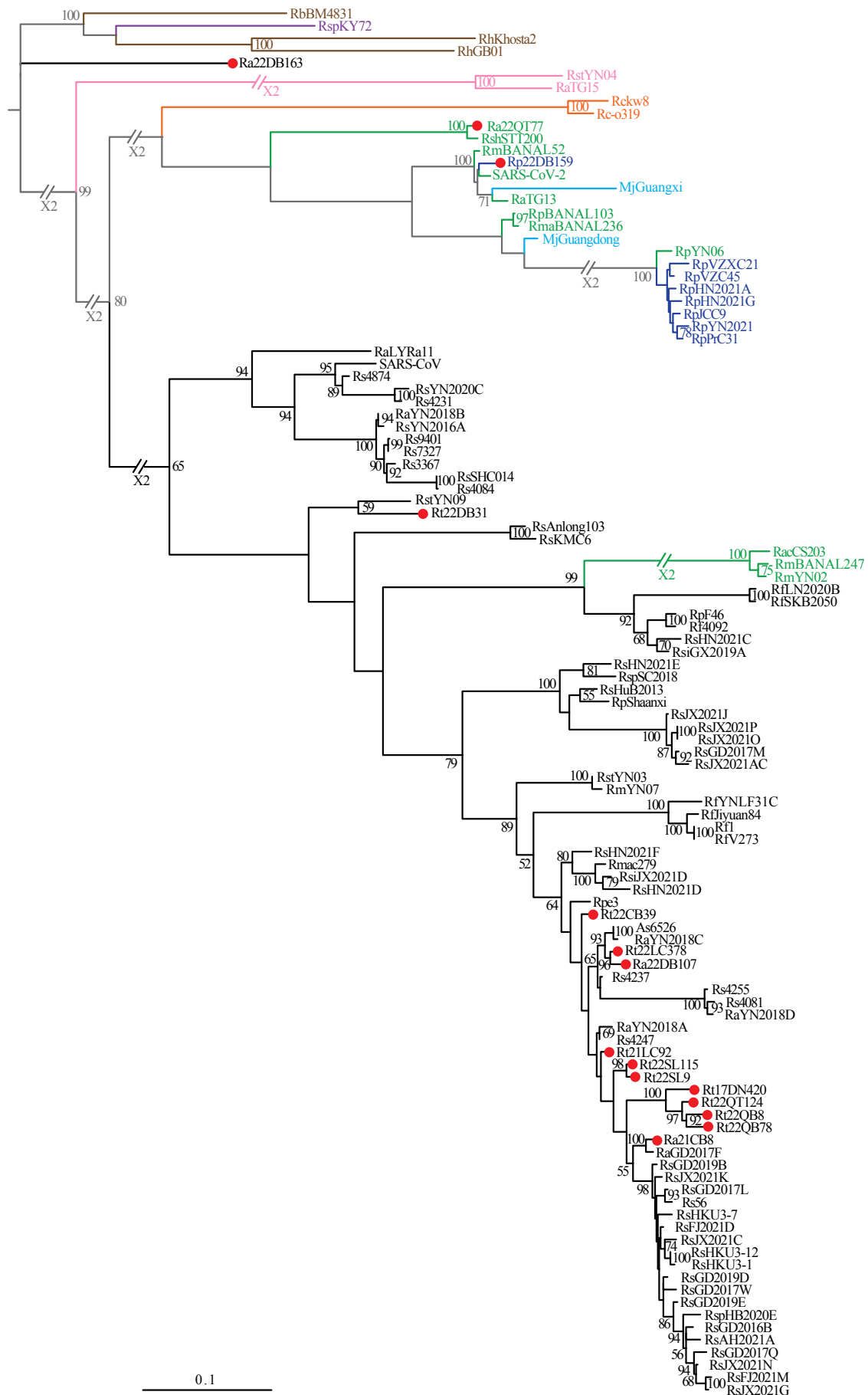


Phylogenetic tree showing the relationships between various SARS-CoV-2 sequences. The tree is rooted at the top left and branches out to the right. The sequences are color-coded by source: human (black), animal (red), and environmental (green). The tree shows that the sequences are highly similar, with many branches having bootstrap values of 100. The sequences are grouped into several clusters, including a large cluster of human sequences, a cluster of animal sequences, and a cluster of environmental sequences. The tree also shows the relationship between the sequences and the reference sequence, RaTG15. The scale bar at the bottom indicates a distance of 0.5.

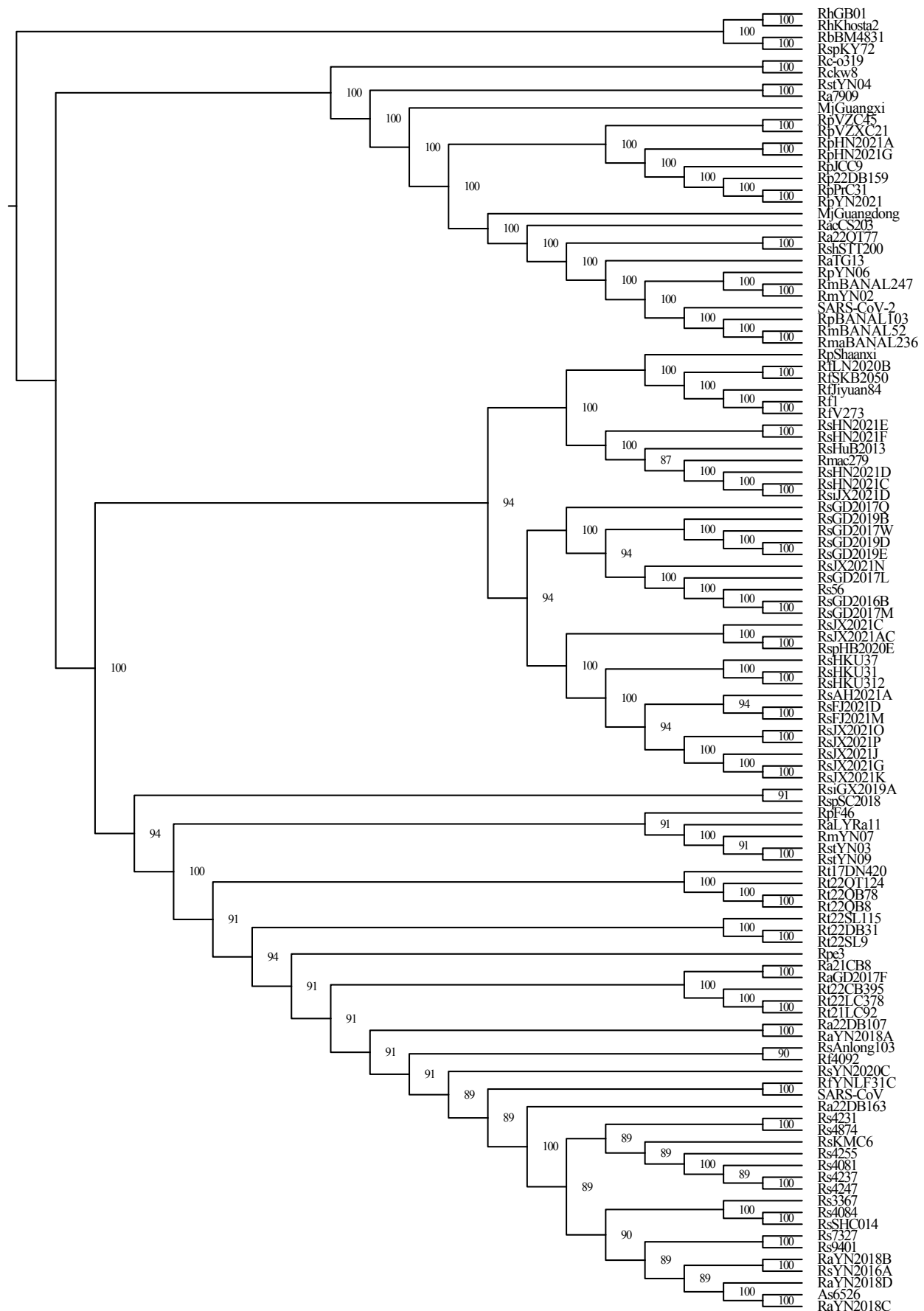
Sequences shown include:

- RbBM4831
- RspKY72
- RhGB01
- RhKhosta2
- RaTG15
- RstYN04
- Ra22DB163
- Ra4874
- SARS-CoV
- RsYN2020C
- Ra4231
- Rs3367
- RsSHC014
- Ra4084
- RsYN2016A
- RaYN2018B
- Ra9401
- Ra7327
- RaLYRa11
- Rt22DB31
- RstYN09
- RfLN2020B
- RfSKB2050
- RsiGX2019A
- RshN2021C
- Rpf46
- Rf4092
- RacCS203
- RmBANAL247
- RmYN02
- Rc-o319
- Rckw8
- RpYN06
- RpLCC9
- RpYN2021
- RpPrC31
- RpHN2021G
- RpHN2021A
- RpVZXC21
- RpVZC45
- MjGuangdong
- RpBANAL103
- RmaBANAL236
- RshSTT200
- Ra22Q177
- RmBANAL52
- Rp22DB159
- SARS-CoV-2
- RaTG13
- MjGuangxi
- RsKMC6
- RsAnlong103
- RpShaanxi
- RshuB2013
- RshN2021E
- RspSC2018
- RsJX2021AC
- RsgD2017M
- RsJX2021J
- RsJX2021P
- RsJX2021O
- RmYN07
- RstYN03
- RfYNLF31C
- RfIyuan84
- RfV273
- RfI
- Rt17DN420
- Rt22Q1124
- Rt22QB78
- Rt22QB8
- Rpe3
- RshN2021F
- Rmac279
- RsiJX2021D
- RshN2021D
- Rt22SL115
- Rt22SL9
- Rt22CB395
- Rt21LC92
- Ra4247
- RaYN2018A
- Ra4237
- Ra4255
- Ra4081
- RaYN2018D
- Ra22DB107
- Rt22LC378
- As6526
- RaYN2018C
- RaGD2017F
- RaCB821S
- RsHKU3-7
- RsJX2021K
- RsgD2017W
- RsgD2019D
- RsgD2019E
- RsgD2019B
- RsgD2017L
- Ra56
- RsHKU3-12
- RsHKU3-1
- RsfJ2021D
- RsJX2021C
- RspHB2020E
- RsgD2016B
- RsaH2021A
- RsJX2021G
- RsfJ2021M
- RsgD2017Q
- RsJX2021N

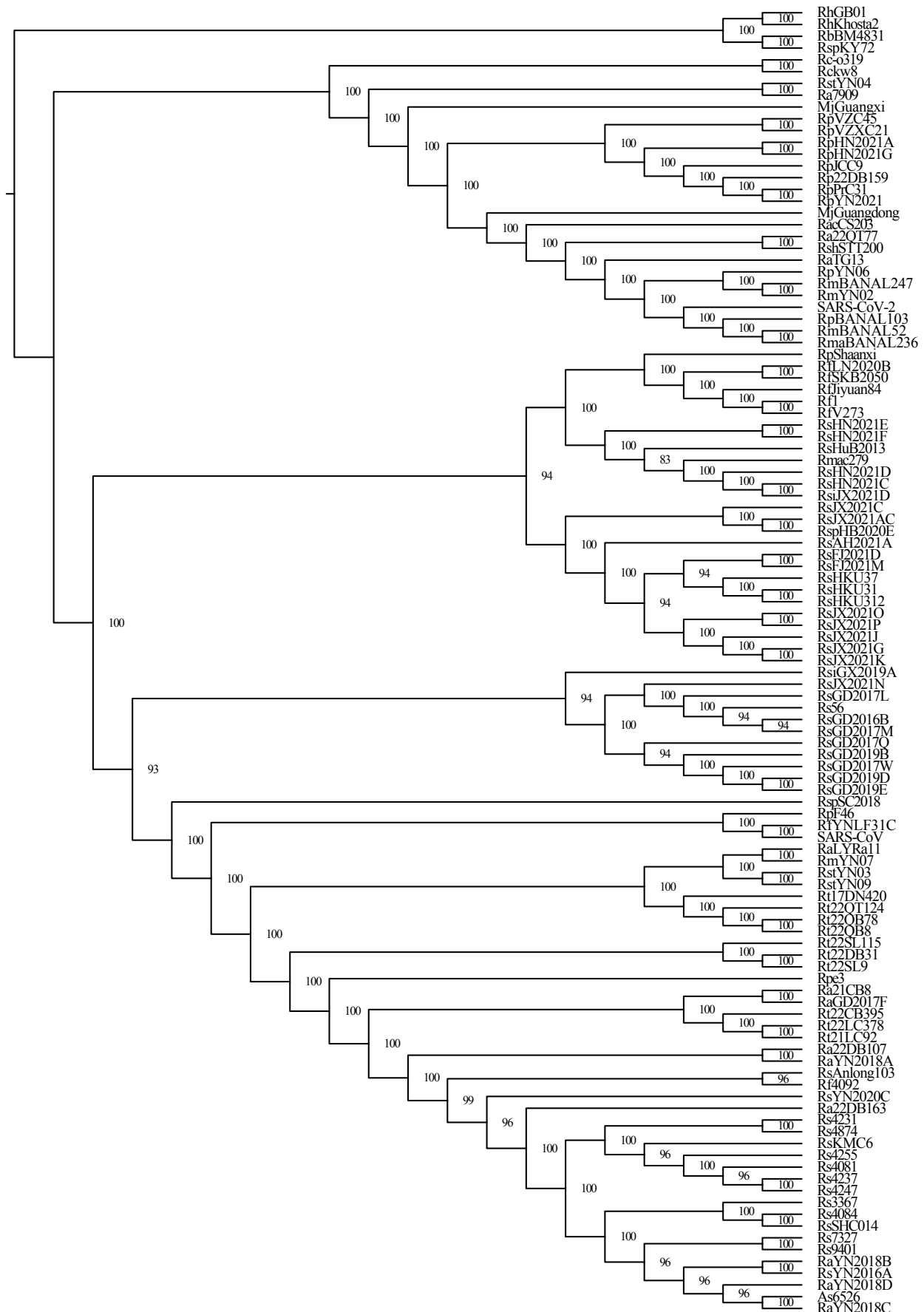
Supplementary Figure 7. Maximum Likelihood tree based on a Spike protein alignment of 111 sarbecoviruses. The tree was reconstructed with RAXML using the LG model. Bootstrap percentages higher than 50% are indicated at the nodes.



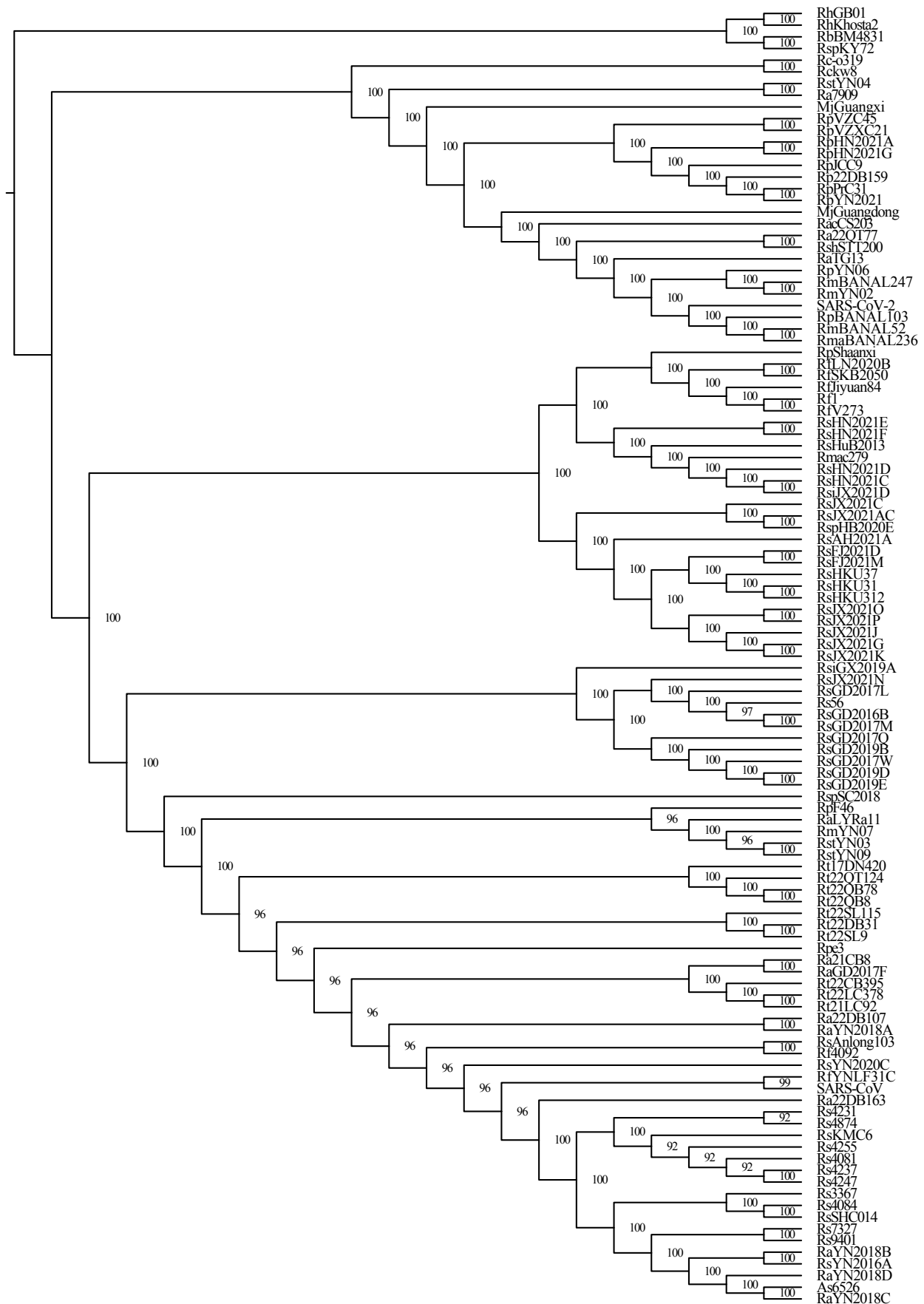
Supplementary Figure 8. SuperTRI bootstrap 50% majority-rule consensus tree reconstructed from the SWB analysis based on a sliding window of 400 nucleotides moving in step of 50 nucleotides. The MRP file used for the bootstrap analysis (weighted parsimony, 1000 replicates) includes 1,298,453 characters.



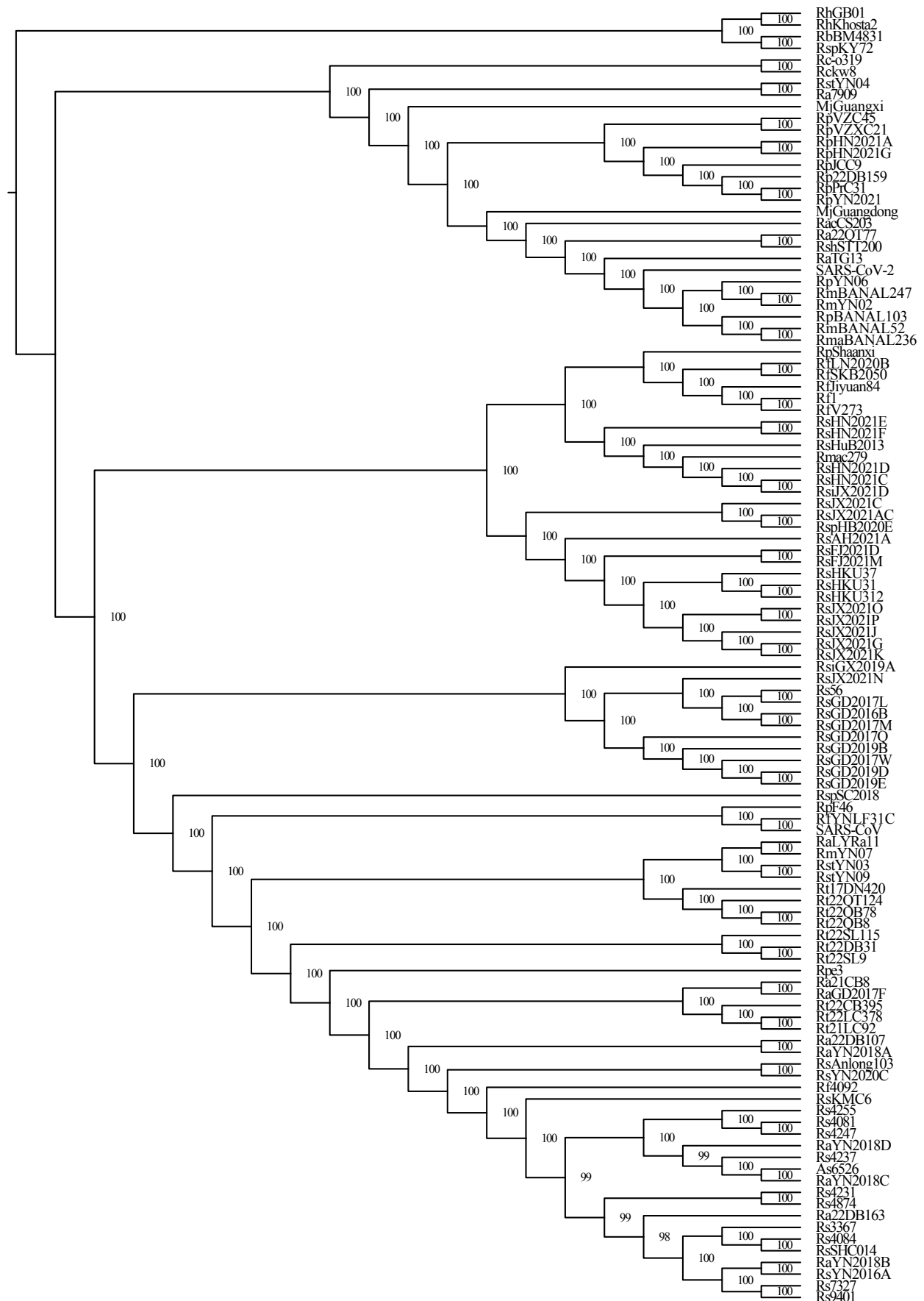
Supplementary Figure 9. SuperTRI bootstrap 50% majority-rule consensus tree reconstructed from the SWB analysis based on a sliding window of 500 nucleotides moving in step of 50 nucleotides. The MRP file used for the bootstrap analysis (weighted parsimony, 1000 replicates) includes 1,124,693 characters.



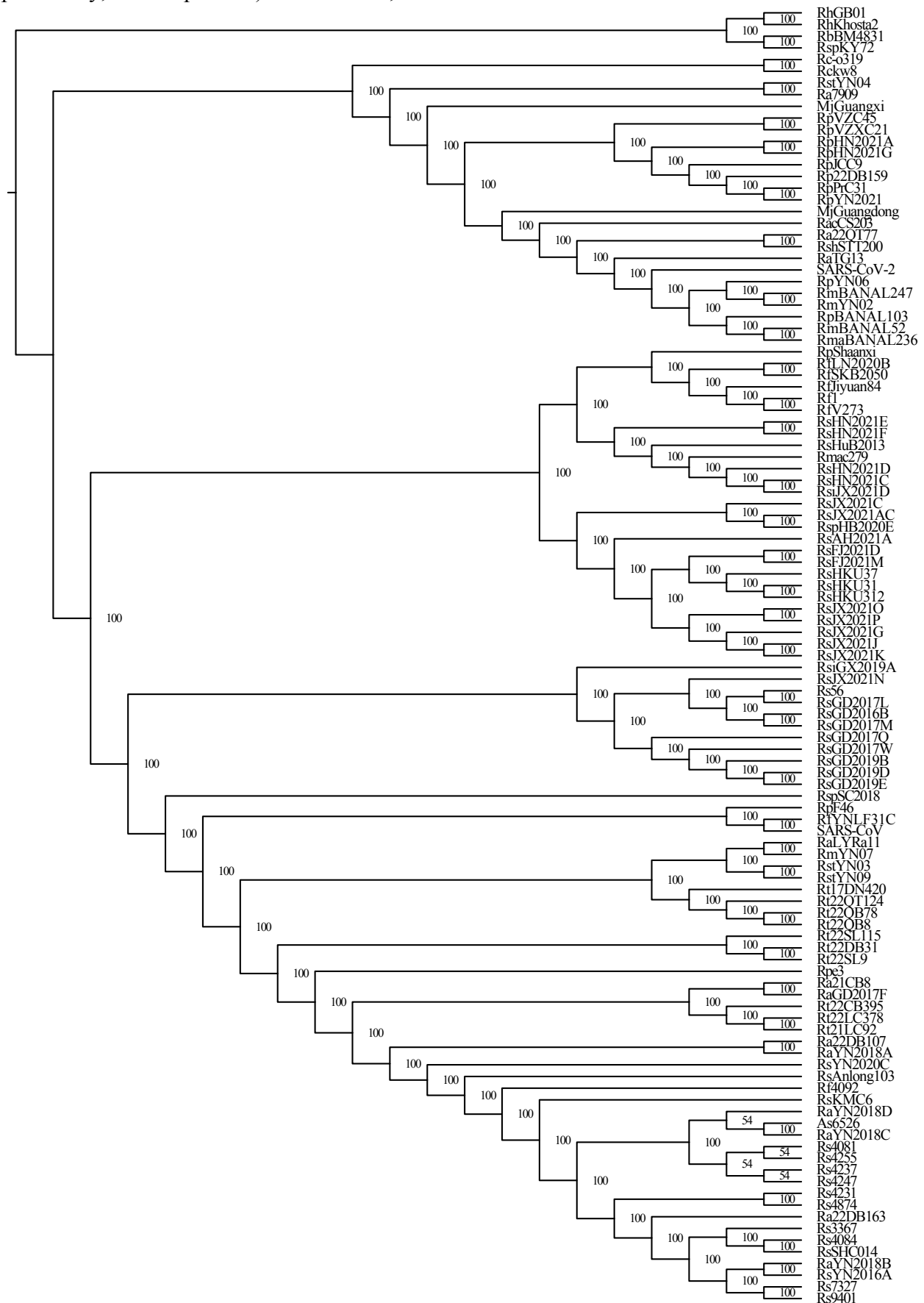
Supplementary Figure 10. SuperTRI bootstrap 50% majority-rule consensus tree reconstructed from the SWB analysis based on a sliding window of 600 nucleotides moving in step of 50 nucleotides. The MRP file used for the bootstrap analysis (weighted parsimony, 1000 replicates) includes 985,475 characters.



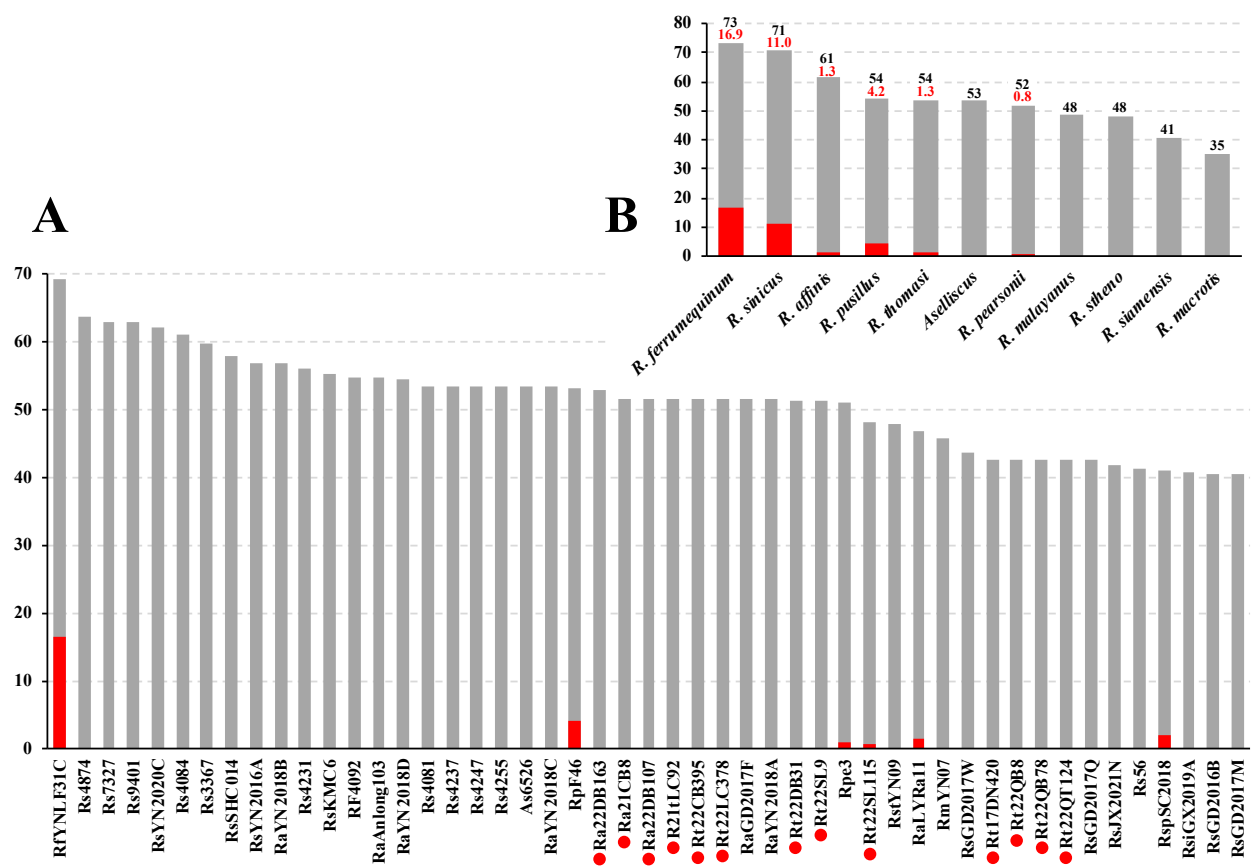
Supplementary Figure 11. SuperTRI bootstrap 50% majority-rule consensus tree reconstructed from the SWB analysis based on a sliding window of 1,000 nucleotides moving in step of 50 nucleotides. The MRP file used for the bootstrap analysis (weighted parsimony, 1000 replicates) includes 706,224 characters.



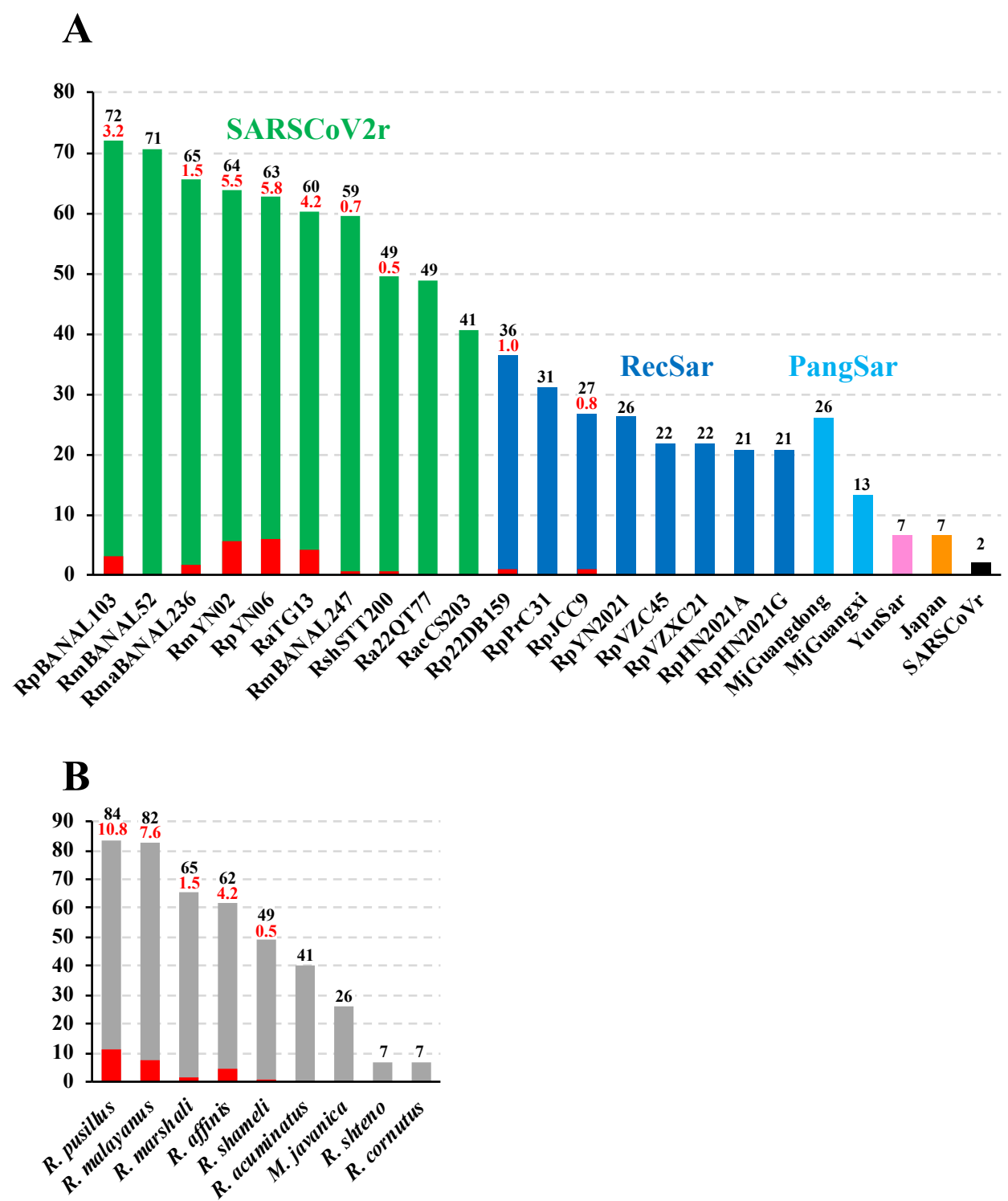
Supplementary Figure 12. SuperTRI bootstrap 50% majority-rule consensus tree reconstructed from the SWB analysis based on a sliding window of 2,000 nucleotides moving in step of 50 nucleotides. The MRP file used for the bootstrap analysis (weighted parsimony, 1000 replicates) includes 450,416 characters.



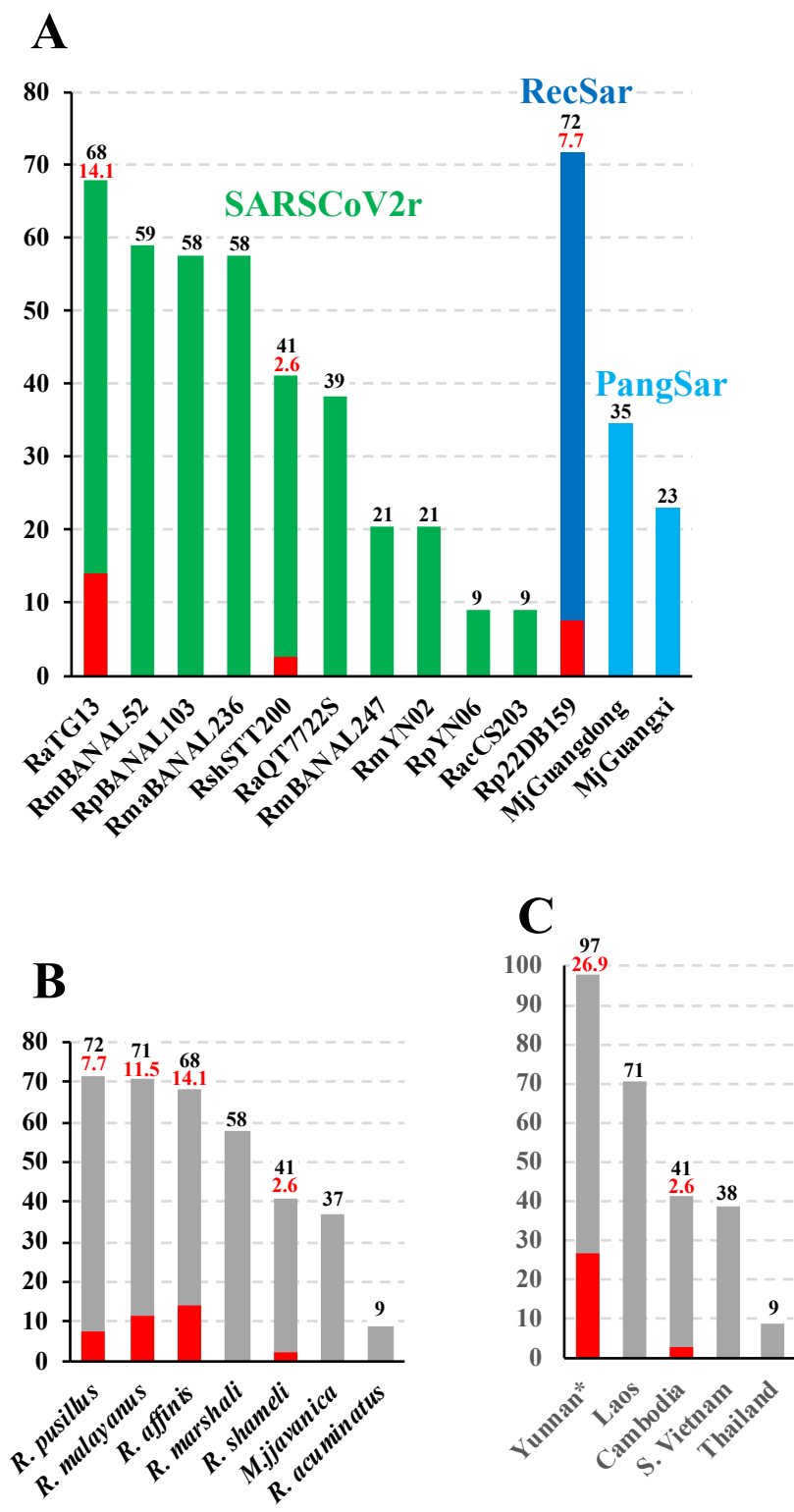
Supplementary Figure 13. Virus (A) and host species (B) contributions calculated for the phylogenetic barcode of SARS-CoV. Grey histograms indicate the total percentages of phylogenetic contribution (C_T), whereas red histograms indicate the percentages of exclusive phylogenetic contribution (C_E), i.e., due to direct ancestry.



Supplementary Figure 14. Virus (A) and host species (B) contributions calculated for the phylogenetic barcode of SARS-CoV-2. The coloured histograms (except those in red) indicate the total percentages of phylogenetic contribution (C_T), whereas red histograms indicate the percentages of exclusive phylogenetic contribution (C_E), i.e., due to direct ancestry.



Supplementary Figure 15. Virus (A), host species (B), and geographic (C) contributions calculated for the Spike gene of SARS-CoV-2. The coloured histograms (except those in red) indicate the total percentages of phylogenetic contribution (C_T), whereas red histograms indicate the percentages of exclusive phylogenetic contribution (C_E), i.e., due to direct ancestry.



Supplementary Figure 16. Bootstrap 50% majority-rule consensus tree reconstructed from a genomic fragment of 400 nucleotides. The genomic fragment corresponds to bipartition G in Fig. 6, i.e., positions 1200-1599 in the nucleotide alignment of the Spike gene. The analysis was computed using the maximum parsimony method and 1,000 bootstrap replicates. Bootstrap percentages are indicated at the nodes.

