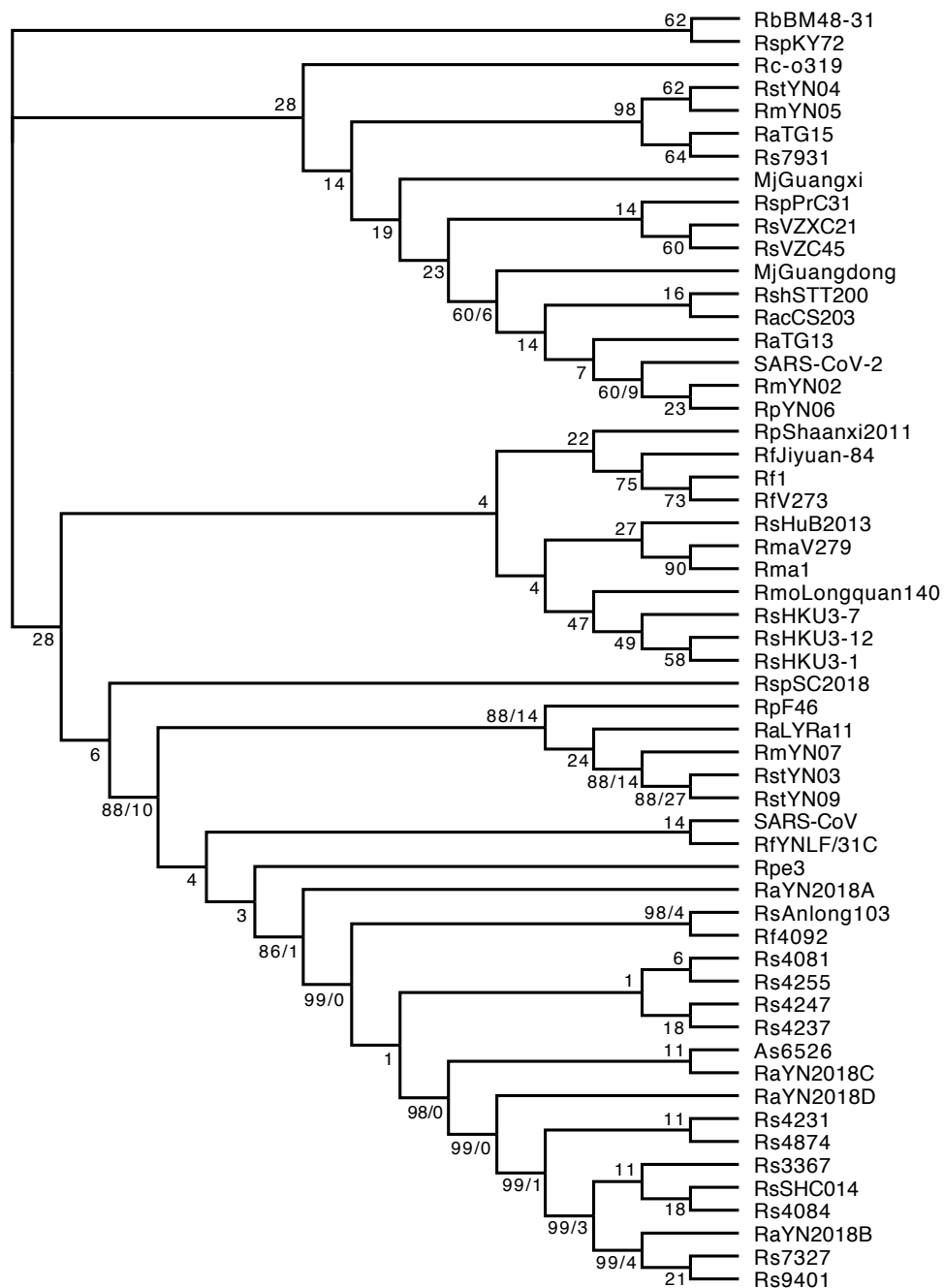


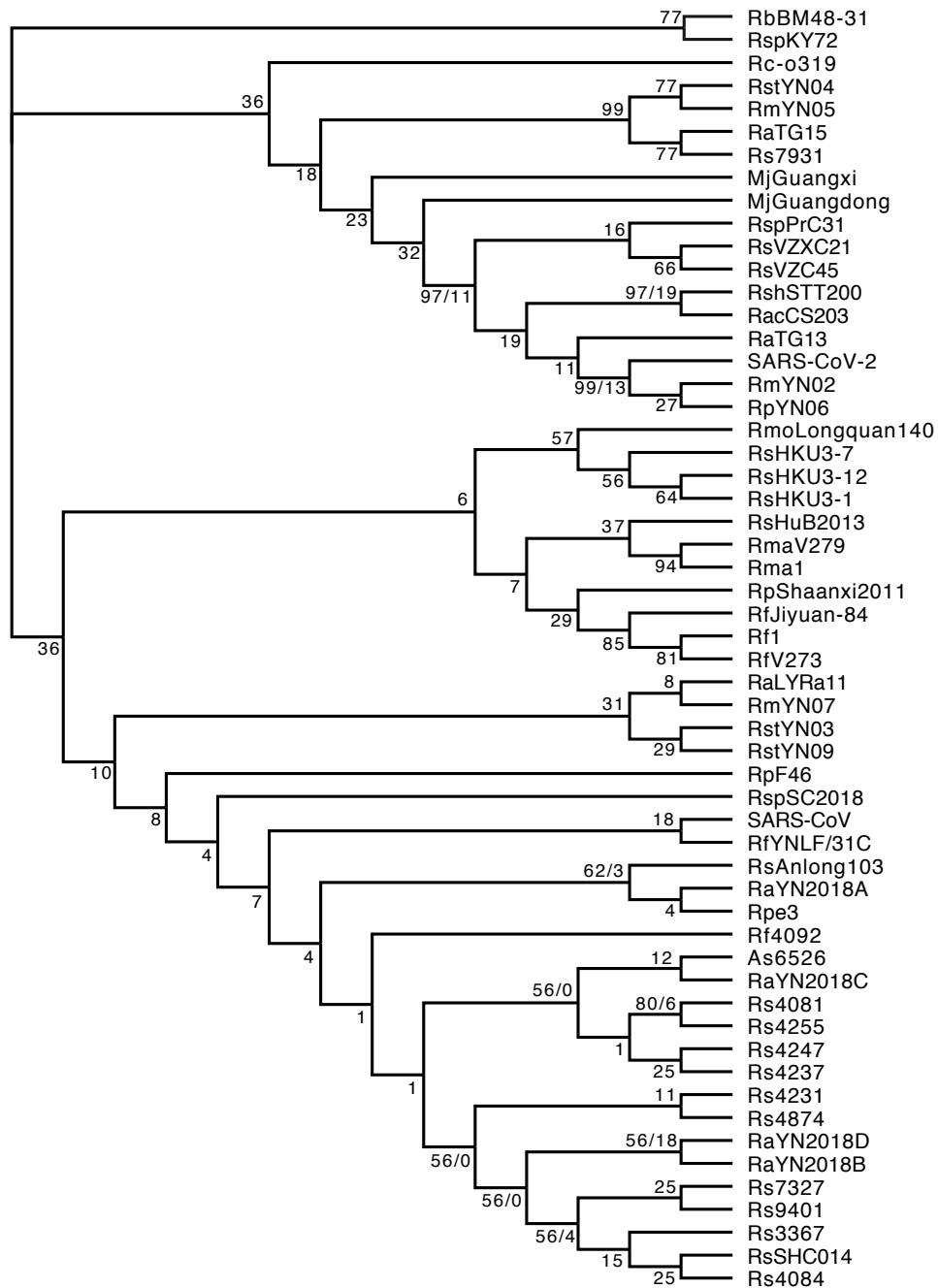
**Figure S1: SuperTRI bootstrap 50%-majority-rule consensus (SB) trees reconstructed from bootstrap log files generated from the four SWB analyses based on different window sizes (250, 500, 1000, and 2000 nt).**

The values at the nodes are mean bootstrap percentages (MBP) calculated under SuperTRI v57 (Ropiquet et al., 2009). All SuperTRI bootstrap percentages (SBP) calculated with the MRP matrix under PAUP\* (Swofford, 2003) were equal to 100% (not shown), except for nodes for which the SBP value is indicated at the left of the slash.

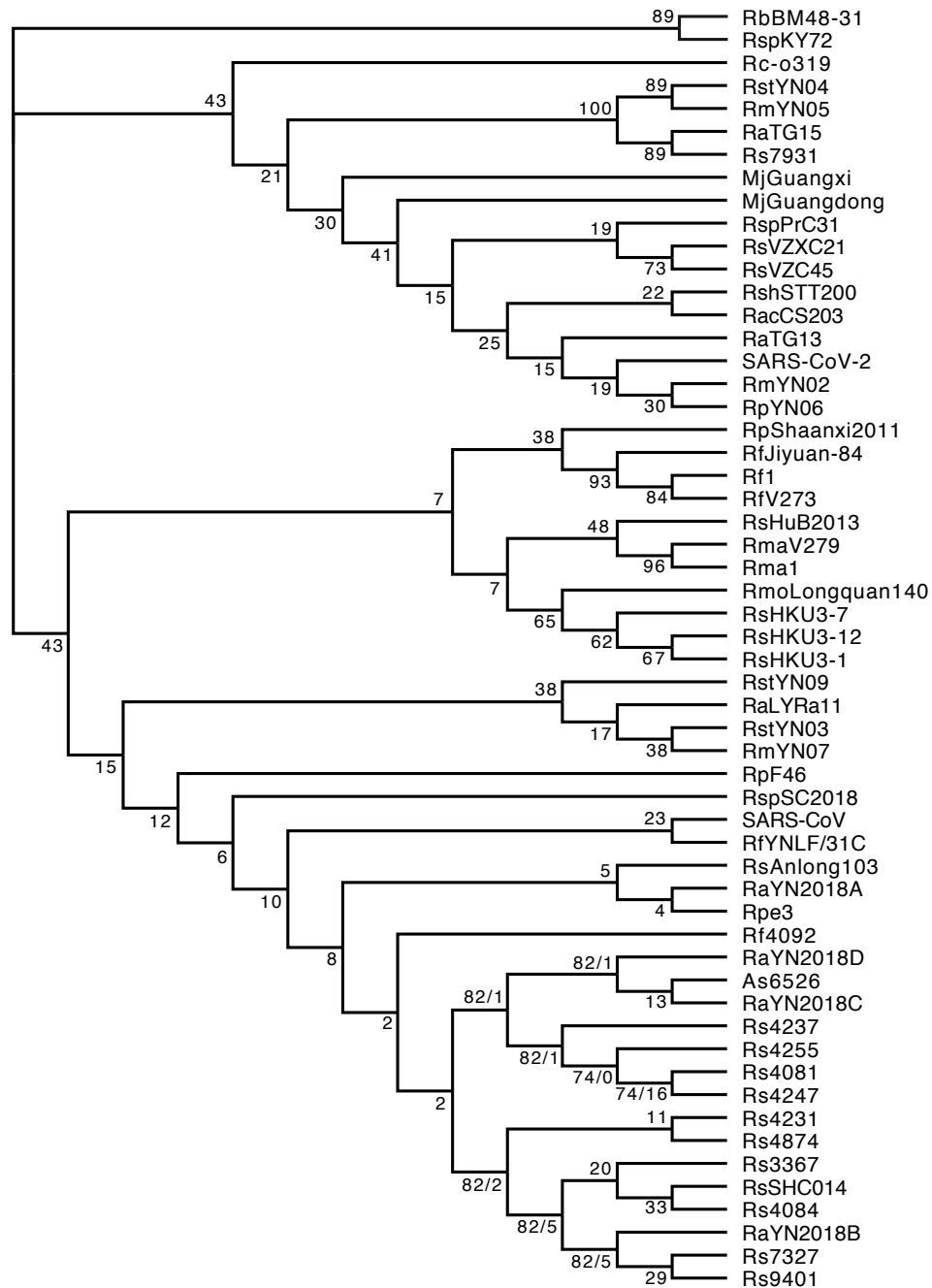
**A. SuperTRI bootstrap 50%-majority-rule consensus (SB) trees reconstructed from bootstrap log files generated from the SWB analysis based on a window of 250 nucleotides.**



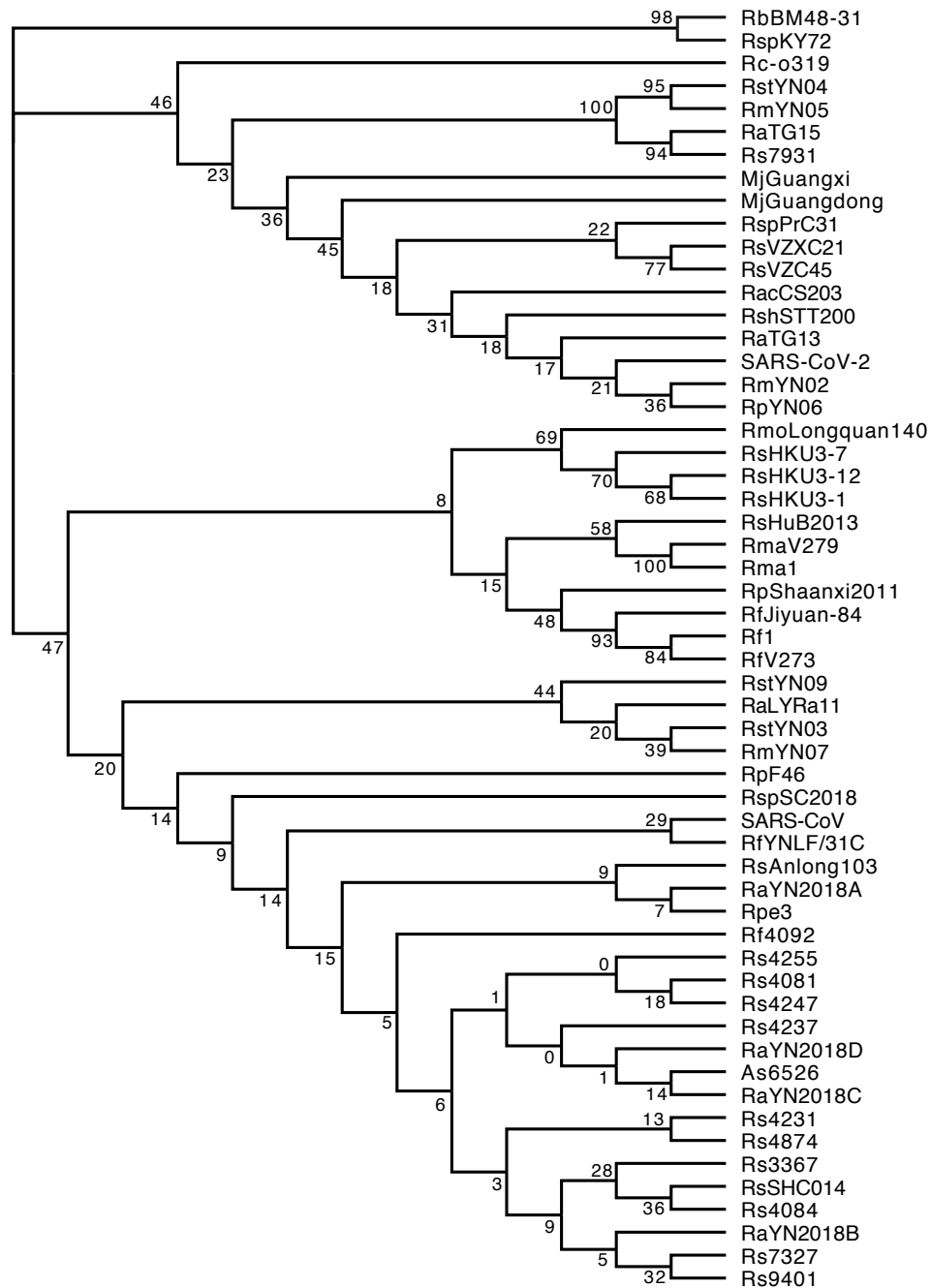
**B. SuperTRI bootstrap 50%-majority-rule consensus (SB) trees reconstructed from bootstrap log files generated from the SWB analysis based on a window of 500 nucleotides.**



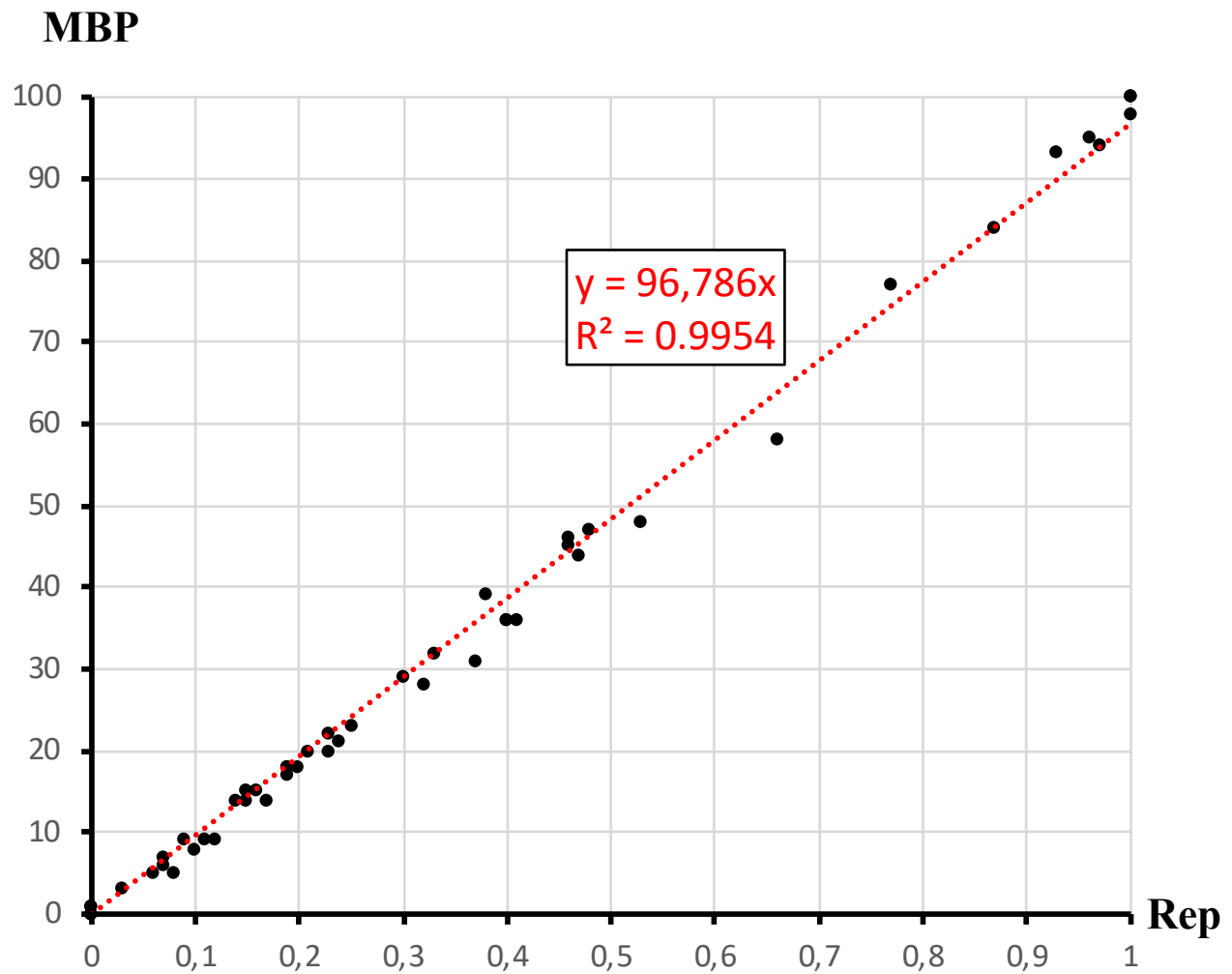
**C. SuperTRI bootstrap 50%-majority-rule consensus (SB) trees reconstructed from bootstrap log files generated from the SWB analyses based on the sliding window of 1000 nucleotides.**



**D. SuperTRI bootstrap 50%-majority-rule consensus (SB) trees reconstructed from bootstrap log files generated from the SWB analysis based a window of 2000 nucleotides.**



**Figure S2: Comparison between Mean Bootstrap Percentage (MBP) and reproducibility index (Rep) for all nodes of the tree of Figure 3.**  
The linear regression is reported in red.

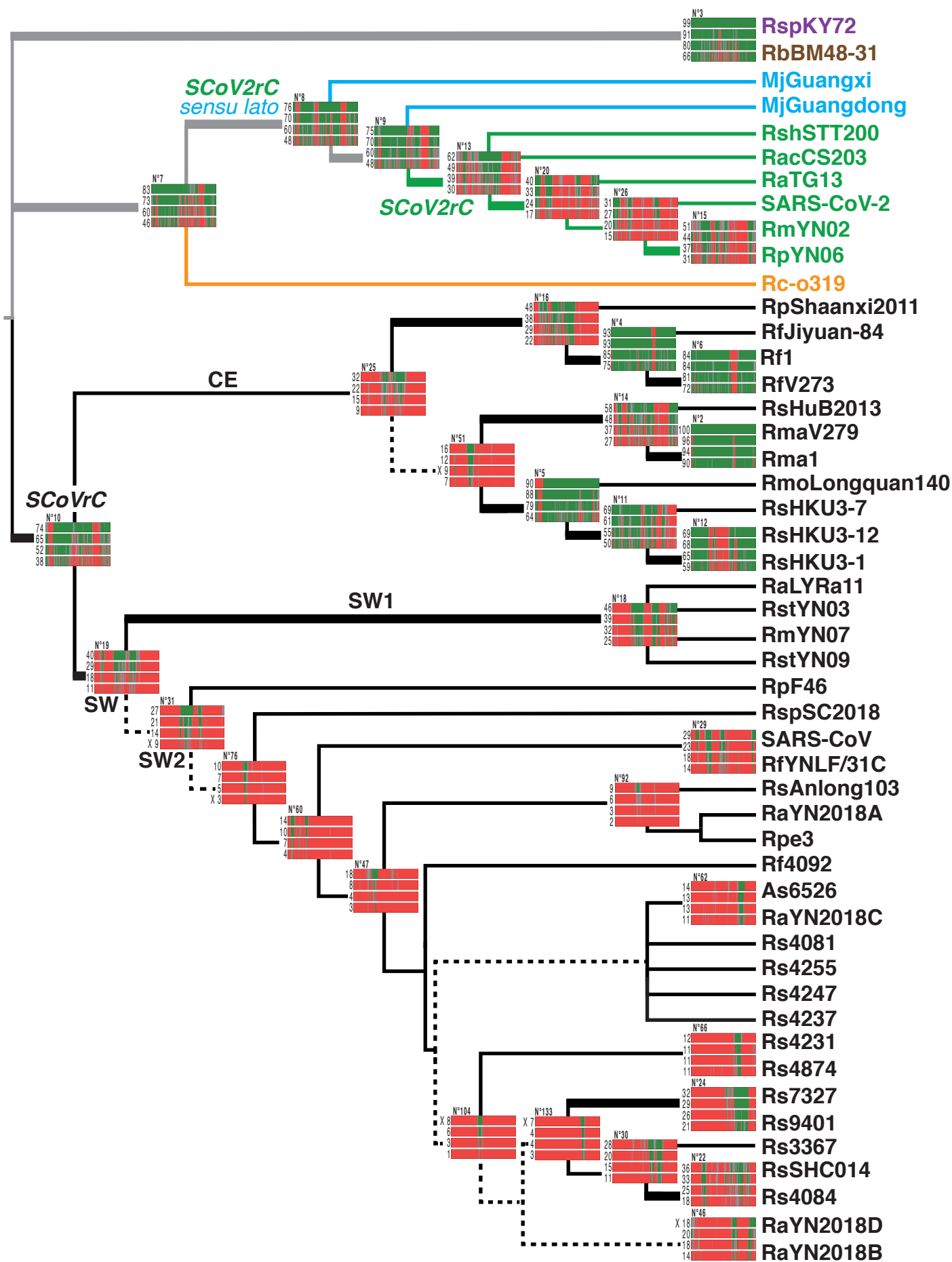


**Figure S3: Synthesis tree showing the most reliable relationships reconstructed from SWB analyses of a reduced alignment of 49 *Sarbecovirus* genomes.**

Bootstrap analyses were conducted on an alignment of 49 *Sarbecovirus* genomes (28,845 nt) using the SWB program and four different window sizes (250, 500, 1000 or 2000 nt).

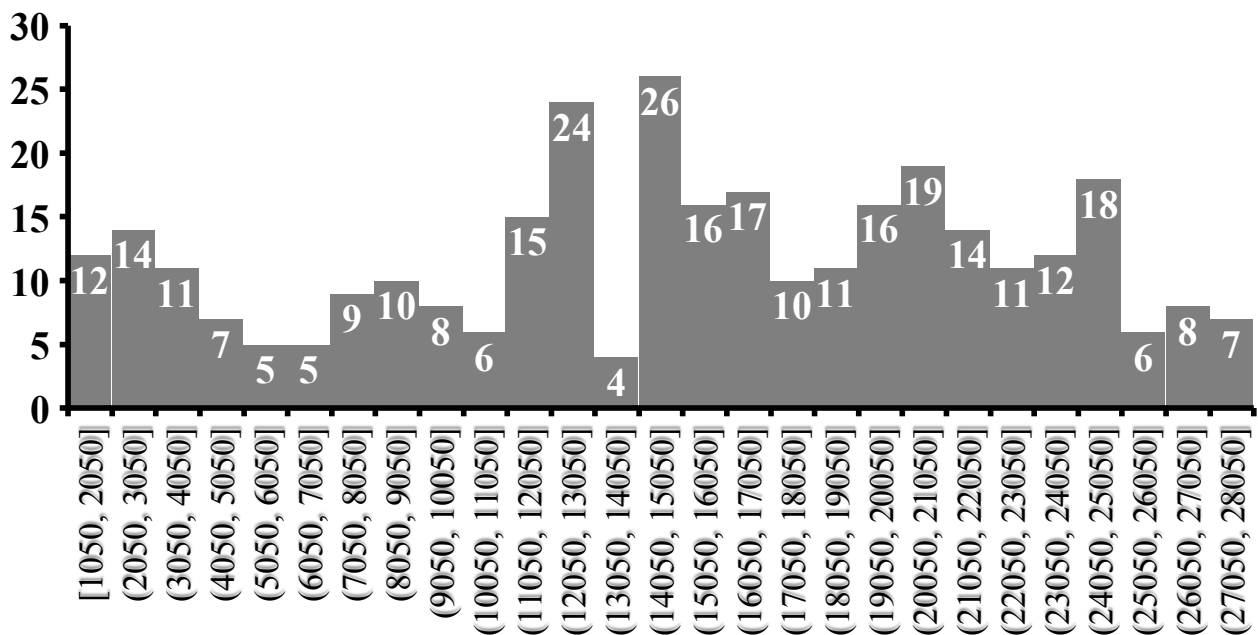
The tree shown here is a 75% majoritary-rule consensus tree of the four SB trees reconstructed using four different window sizes. The nodes were recovered in all the four SB trees, except those indicated by dash branches, which were found monophyletic in only three of the four SB analyses. The GB barcodes were constructed for all nodes showing at least one Bootstrap Percentage (BP)  $\geq 70\%$  in the four SWB analyses using different window sizes. Thick branches highlight the nodes that were supported by Mean Bootstrap Percentage (MBP)  $\geq 33\%$  with a window size of 2000 nt.

The colours of sarbecoviruses indicate to which group of synonymous nucleotide composition they belong (Hassanin, in review): black for SARS-CoV related coronaviruses (*SCoVrC*); green for coronaviruses related to SARS-CoV-2 (*SCoV2rC*); light blue for the two pangolin viruses (*PangSar*); dark blue for the three bat *RecSar* viruses showing evidence of genomic recombination between *SCoV2rC* and *SCoVrC*; red for the four divergent bat viruses from Yunnan (*YunSar*); and orange for the bat virus from Japan.



**Figure S4: Recombination break-points counted in genomic intervals of 1000 nt and deduced from the 5'- and 3'-ends of GRPSs characterized for the 11 viruses of the SCoV2rC *sensu lato* lineage.**

The genomic regions containing robust phylogenetic signal (GRPSs) were characterized using the SWB analysis based on a window of 2000 nt (see main text and **Figure 1** for more details).





**Table S1: Origin of the *Sarbecovirus* genomes used in this study**

<b>Virus name</b>	<b>Accession number</b>	<b>Host species</b>	<b>Geographic origin</b>	<b>Reference</b>
SARS-CoV	NC_004718 <sup>1</sup>	<i>Homo sapiens</i>	Canada	He et al. (2004)
As6526	KY417142 <sup>1</sup>	<i>Aselliscus stoliczkanus</i>	Yunnan (China)	Hu et al. (2017)
RaLYRa11*	KF569996 <sup>1</sup>	<i>Rhinolophus affinis</i>	Yunnan (China)	He et al. (2014)
RaYN2018A*	MK211375 <sup>1</sup>	<i>Rhinolophus affinis</i>	Yunnan (China)	Han et al. (2019)
RaYN2018B*	MK211376 <sup>1</sup>	<i>Rhinolophus affinis</i>	Yunnan (China)	Han et al. (2019)
RaYN2018C*	MK211377 <sup>1</sup>	<i>Rhinolophus affinis</i>	Yunnan (China)	Han et al. (2019)
RaYN2018D*	MK211378 <sup>1</sup>	<i>Rhinolophus affinis</i>	Yunnan (China)	Han et al. (2019)
Rf1	DQ412042 <sup>1</sup>	<i>Rhinolophus ferrumequinum</i> <sup>T1</sup>	Hubei (China)	Li et al. (2005)
Rf4092	KY417145 <sup>1</sup>	<i>Rhinolophus ferrumequinum</i> <sup>T1</sup>	Yunnan (China)	Hu et al. (2017)
RfJiyuan-84*	KY770860 <sup>1</sup>	<i>Rhinolophus ferrumequinum</i> <sup>T1</sup>	Henan (China)	Lin et al. (2017)
RfV273*	DQ648856 <sup>1</sup>	<i>Rhinolophus ferrumequinum</i> <sup>T1</sup>	Yunnan (China)	Tang et al. (2006)
RfYNLF/31C*	KP886808 <sup>1</sup>	<i>Rhinolophus ferrumequinum</i> <sup>T1</sup>	Yunnan (China)	Lau et al. (2015)
RmYN07*	EPI_ISL_1699447 <sup>2</sup>	<i>Rhinolophus malayanus</i>	Yunnan (China)	Zhou et al. (2021)
Rma1*	DQ412043 <sup>1</sup>	<i>Rhinolophus macrotis</i> <sup>T2</sup>	Hubei (China)	Li et al. (2005)
RmaV279*	DQ648857 <sup>1</sup>	<i>Rhinolophus macrotis</i> <sup>T2</sup>	Yunnan (China)	Tang et al. (2006)
RmoLongquan140*	KF294457 <sup>1</sup>	<i>Rhinolophus monoceros</i> <sup>T3</sup>	Zhejiang (China)	Lin et al. (2017)
RpF46*	KU973692 <sup>1</sup>	<i>Rhinolophus pusillus</i>	Yunnan (China)	Wang et al. (2017)
RpShaanxi2011	JX993987 <sup>1</sup>	<i>Rhinolophus pusillus</i>	Shaanxi (China)	Yang et al. (2013)
Rpe3	DQ071615 <sup>1</sup>	<i>Rhinolophus pearsoni</i>	Guangxi (China)	Li et al. (2005)
Rs3367	KC881006 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Ge et al. (2013)
Rs4081	KY417143 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Hu et al. (2017)
Rs4084	KY417144 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Hu et al. (2017)
Rs4231	KY417146 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Hu et al. (2017)
Rs4237	KY417147 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Hu et al. (2017)
Rs4247	KY417148 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Hu et al. (2017)
Rs4255	KY417149 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Hu et al. (2017)
Rs4874	KY417150 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Hu et al. (2017)
Rs7327	KY417151 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Hu et al. (2017)
Rs9401	KY417152 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Hu et al. (2017)
RsAnlong103*	KY770858 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Guizhou (China)	Lin et al. (2017)
RsHKU3-1*	DQ022305 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Hong-Kong (China)	Lau et al. (2005)
RsHKU3-7*	GQ153542 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Hong-Kong (China)	Lau et al. (2010)
RsHKU3-12*	GQ153547 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Hong-Kong (China)	Lau et al. (2010)
RsHuB2013*	KJ473814 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Hubei (China)	Wu et al. (2016)
RsSHC014	KC881005 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Yunnan (China)	Ge et al. (2013)
RstYN03*	EPI_ISL_1699443 <sup>2</sup>	<i>Rhinolophus stheno</i> <sup>T4</sup>	Yunnan (China)	Zhou et al. (2021)
RstYN09*	EPI_ISL_1699449 <sup>2</sup>	<i>Rhinolophus stheno</i> <sup>T4</sup>	Yunnan (China)	Zhou et al. (2021)
RspSC2018*	MK211374 <sup>1</sup>	<i>Rhinolophus</i> sp.	Sichuan (China)	Han et al. (2019)
<b>SARS-CoV-2</b>	NC_045512 <sup>1</sup>	<i>Homo sapiens</i>	Hubei (China)	Wu et al. (2020)
<b>RaTG13</b>	MN996532 <sup>1</sup>	<i>Rhinolophus affinis</i>	Yunnan (China)	Zhou P. et al. (2020)

<b>RacCS203</b>	MW251308 <sup>1</sup>	<i>Rhinolophus acuminatus</i>	Thailand	Wacharapluesadee et al. (2021)
<b>RmYN02*</b>	EPI_ISL_412977 <sup>2</sup>	<i>Rhinolophus malayanus</i>	Yunnan (China)	Zhou H. et al. (2020)
<b>RpYN06*</b>	EPI_ISL_1699446 <sup>2</sup>	<i>Rhinolophus pusillus</i>	Yunnan (China)	Zhou et al. (2021)
<b>RshSTT200</b>	EPI_ISL_852605 <sup>2</sup>	<i>Rhinolophus shameli</i>	Cambodia	Delaune et al. (2021)
<b>MjGuangdong*</b>	EPI_ISL_410721 <sup>2</sup>	<i>Manis javanica</i>	Guangdong (China)	Xiao et al. (2020)
<b>MjGuangxi*</b>	EPI_ISL_410539 <sup>2</sup>	<i>Manis javanica</i>	Guangxi (China)	Lam et al. (2020)
<b>RsZXC21*</b>	MG772934 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Zhejiang (China)	Hu et al. (2018)
<b>RsZC45*</b>	MG772933 <sup>1</sup>	<i>Rhinolophus sinicus</i>	Zhejiang (China)	Hu et al. (2018)
<b>RpPrC31*</b>	EPI_ISL_1098866 <sup>2</sup>	<i>Rhinolophus pusillus</i>	Yunnan (China)	Li et al. (2021)
<b>RaTG15</b>	GWHBAUP01000001 <sup>3</sup>	<i>Rhinolophus affinis</i>	Yunnan (China)	Guo et al. (2021)
<b>Rst7931</b>	GWHBAUS01000001 <sup>3</sup>	<i>Rhinolophus stheno</i> <sup>T4</sup>	Yunnan (China)	Guo et al. (2021)
<b>RmYN05</b>	EPI_ISL_1699445 <sup>2</sup>	<i>Rhinolophus malayanus</i>	Yunnan (China)	Zhou et al. (2021)
<b>RstYN04*</b>	EPI_ISL_1699444 <sup>2</sup>	<i>Rhinolophus stheno</i> <sup>T4</sup>	Yunnan (China)	Zhou et al. (2021)
<b>Rc-o319</b>	LC556375 <sup>1</sup>	<i>Rhinolophus cornutus</i>	Japan	Murakami et al. (2020)
<b>RbBM48-31*</b>	NC_014470 <sup>1</sup>	<i>Rhinolophus blasii</i>	Bulgaria	Drexler et al. (2010)
<b>RspKY72*</b>	KY352407 <sup>1</sup>	<i>Rhinolophus</i> sp.	Kenya	Tao and Tong (2019)

\*original name slightly modified to be consistent with other names and to facilitate interpretations; 1: NCBI; 2: GISAID; 3: NGDC

Taxonomic issues (Burgin et al., 2020) = T1: currently *Rhinolophus nippon*; T2: currently *Rhinolophus episcopus*; T3 = the taxonomic assignment should be regarded as dubious because *Rhinolophus monoceros* is supposed to be endemic of Taiwan; T4: currently *Rhinolophus microglobosus*.

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