

Figure 1 Geography of sampling sites and host taxonomy.

(A) Distribution of sampling location and host species of bat samples. Size of each circle represents the number of samples with distinct host individuals. Color within the circle represents host species according to the legend. Color of circles represents their geographic sites. For clarity, the number of individuals per host genus is summarized for each geographic site.

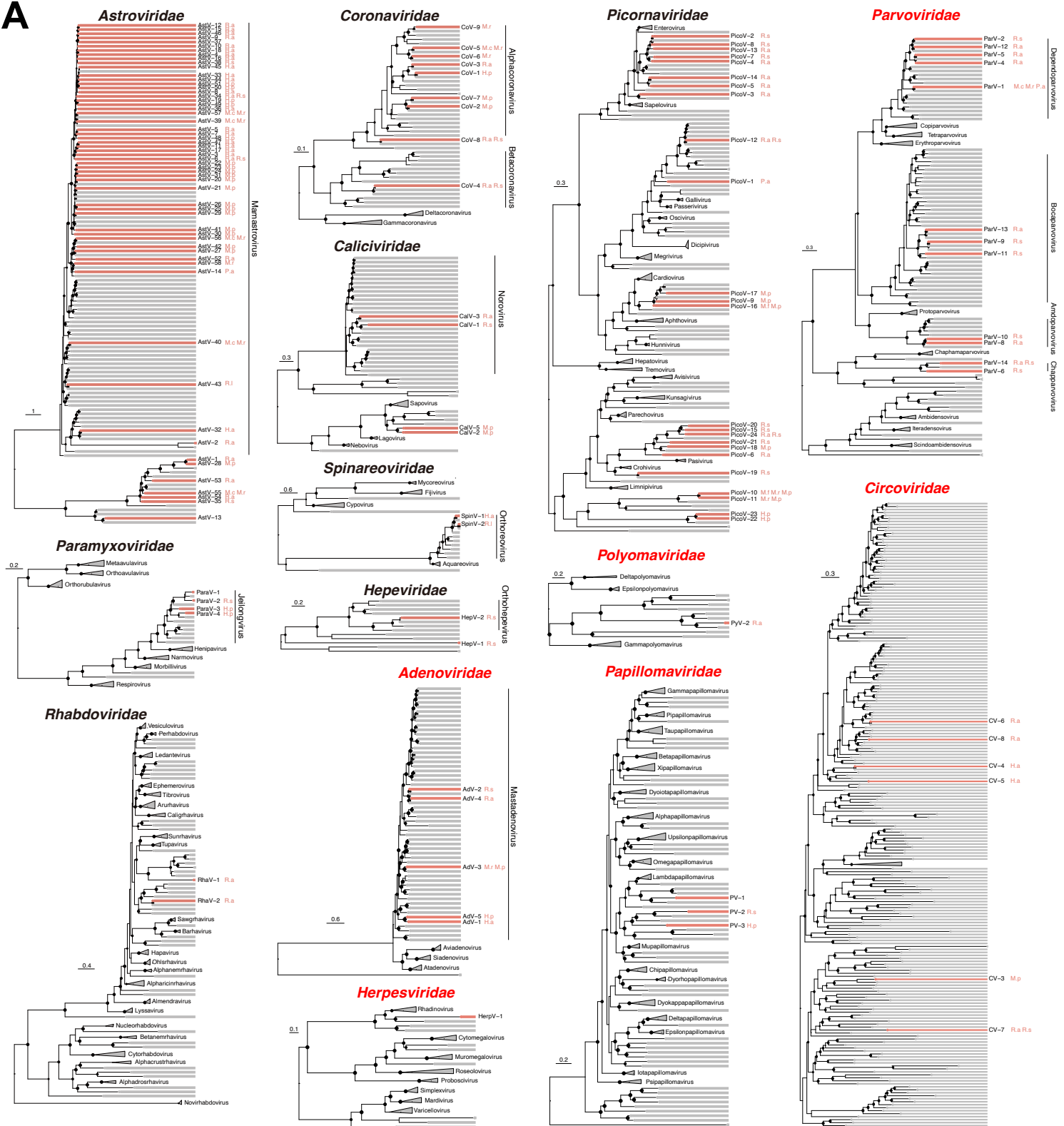
(B) Evolutionary relationship among the sampled bat species (host phylogenies of host species were derived from the public subsets of mammalian phylogeny, <http://vertlife.org/phylosubsets>).

(C) Distribution of bat samples across cities. Color represents city of sampling locations.

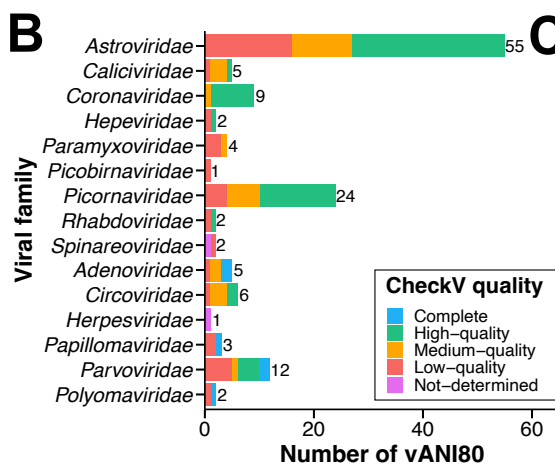
(D) Distribution of bat samples by sampling year. Color represents city of sampling locations.

(E) Sampling distribution of *Rhinolophus* bats in bat roosts with at least 25 samples.

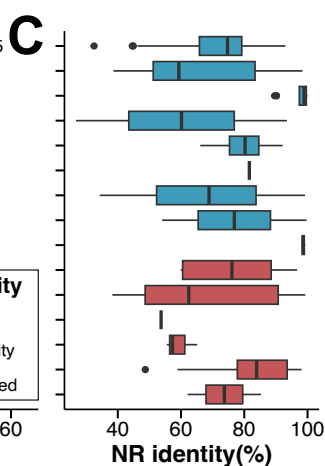
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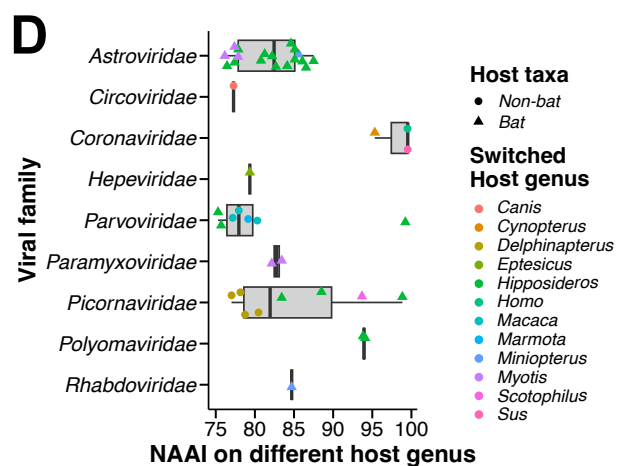


Figure 2 Evolutionary diversity of vertebrate-associated viruses.

(A) Maximum likelihood phylogenetic trees of major viral families on replication-associated proteins (RAPs). The name of the viral family is shown above each tree. The solid black circles on each branch node represents bootstrap value above 50. The tip nodes on each tree represent vANI80 representatives identified in the present study, with host species annotated.

(B) Completeness of representative genomes in each viral family, with the color indicating genome completeness.

(C) Amino acid identity of replication-associated proteins (RAP-AAI) between the identified viruses and the known viruses.

(D) Amino acid identity between vANI80s of Rhinolophus bats and their closest virus with different host genus across viral families.

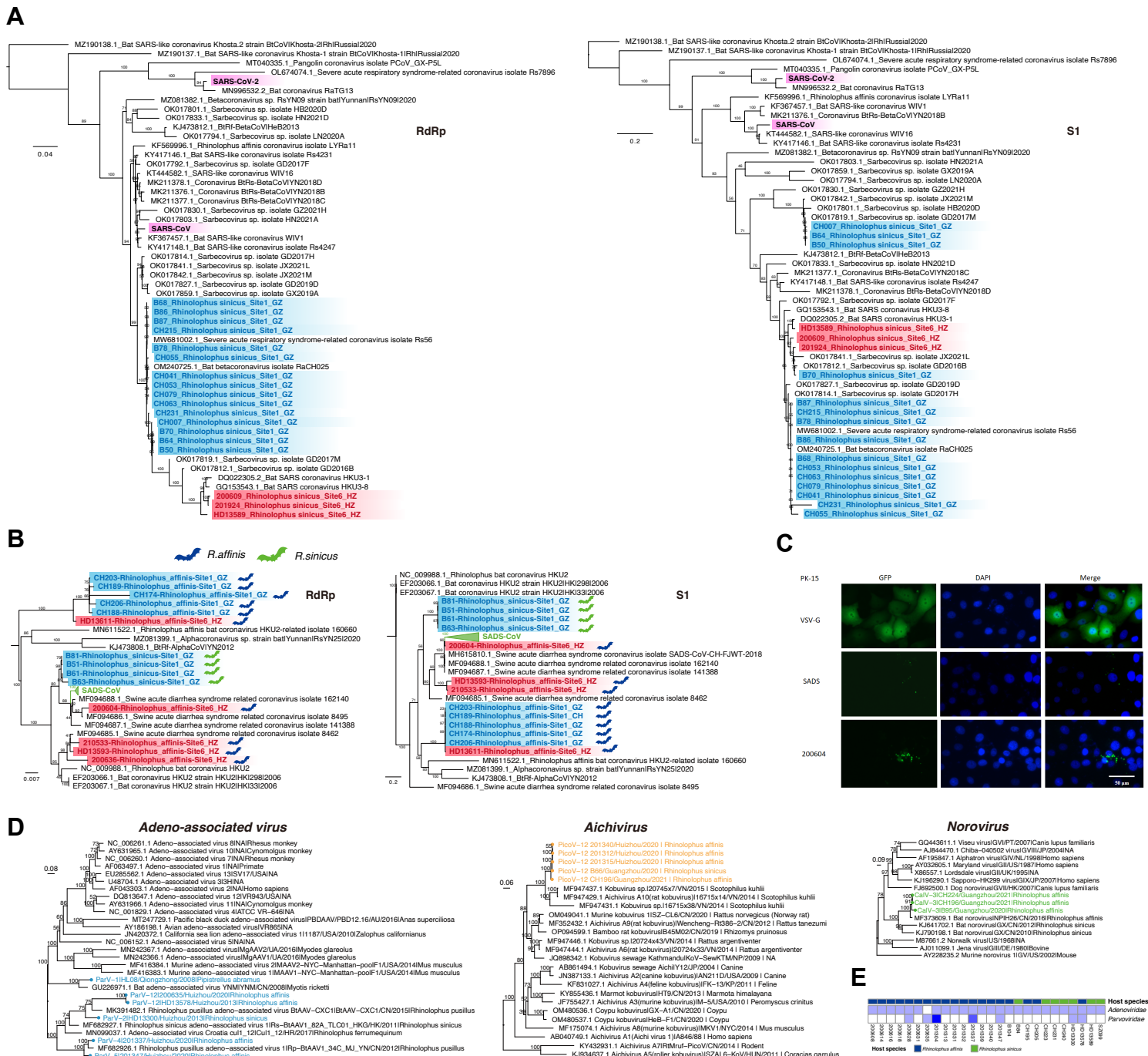


Figure 3 Intra-specific evolution of viruses related to human or livestock infection identified in *Rhinolophus* bats.

(A) Phylogeny of severe acute respiratory syndrome-related coronavirus (SARSr-CoV, CoV-4) in RdRp and S1-gene.

(B) Phylogeny of swine acute diarrhea syndrome-related coronavirus (SADSr-CoV, CoV-8) in RdRp and S1-gene. The phylogenetic tree was estimated using a maximum likelihood method based on the nucleotide of RdRp or S1-gene. The scale bar represents the number of nucleotide substitutions per site. Within each phylogeny, the names in black represented public viral genomes, whereas the viruses newly identified here are colored by geography.

(C) Infection experiment of porcine kidney (PK-15) cells of pseudovirus encoding the S-gene of SADS-CoV/HZ/200604.

(D) Phylogeny of Adeno-associated virus (ParV-2, ParV-12, ParV-5, ParV-4), Aichivirus (PicoV-12) and Norovirus (CalV-3) in RdRp. The trees were midpoint-rooted for clarity only.

(E) Heatmap of Adeno-associated viruses and adenovirus occurrence across *Rhinolophus* samples.

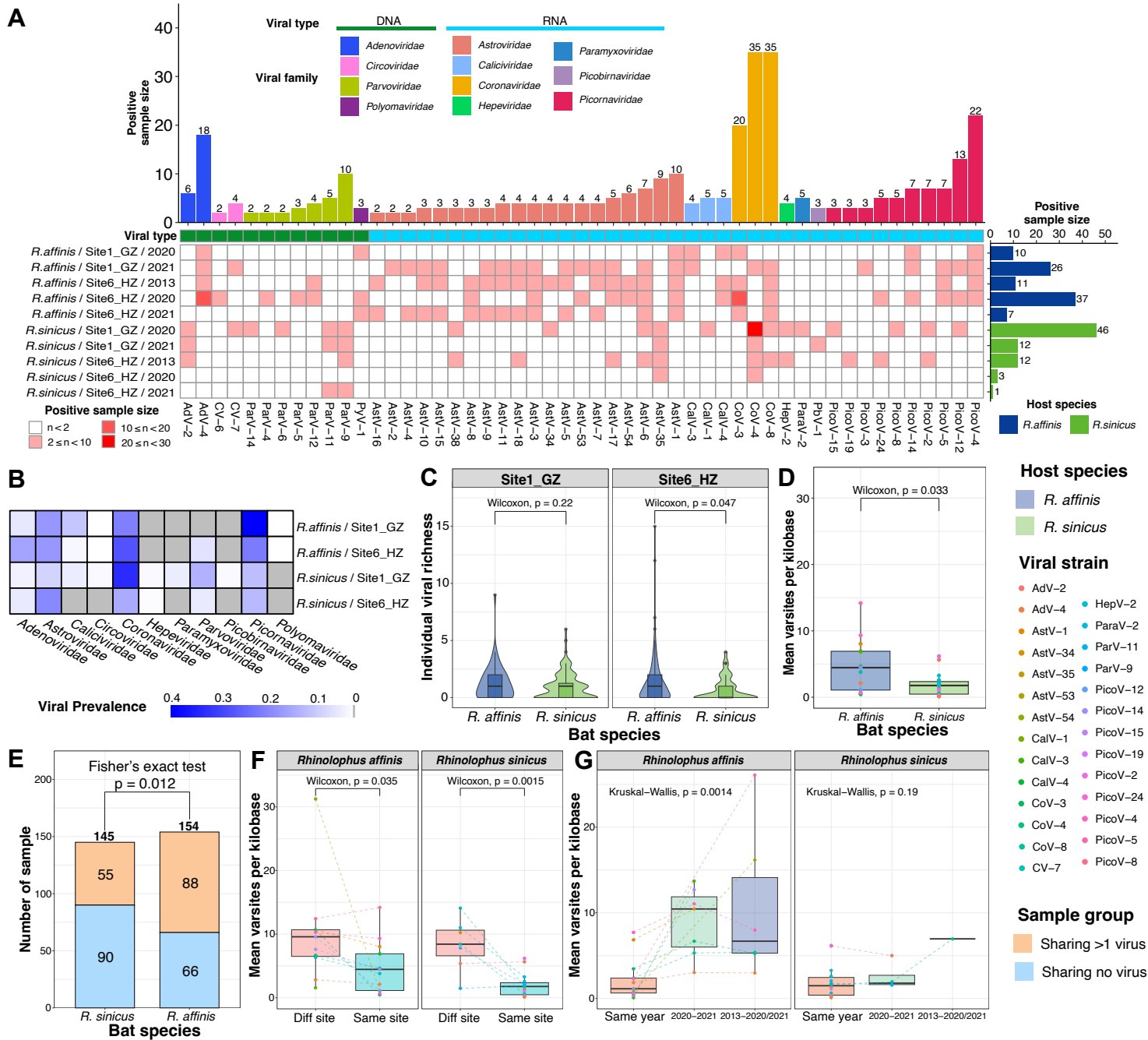


Figure 4 Comparison across viral communities between *Rhinolophus* bats.

- (A) Geographic and host distribution of *Rhinolophus* virome across Site1_GZ and Site6_HZ.
- (B) Viral positive rate of *Rhinolophus* bats across Site1_GZ and Site6_HZ from 2013 to 2021.
- (C) Standard viral richness (viral records per individual) across viral families within *R. affinis* and *R. sinicus*. Nucleotide diversity of vANI80s within geographic site.
- (D) The number of samples carrying core vANI80 clusters shared across Site1_GZ and Site6_HZ.
- (E) Genetic difference of vANI80s between Site1_GZ and Site6_HZ.
- (F) Viral virome and genetic difference across time.

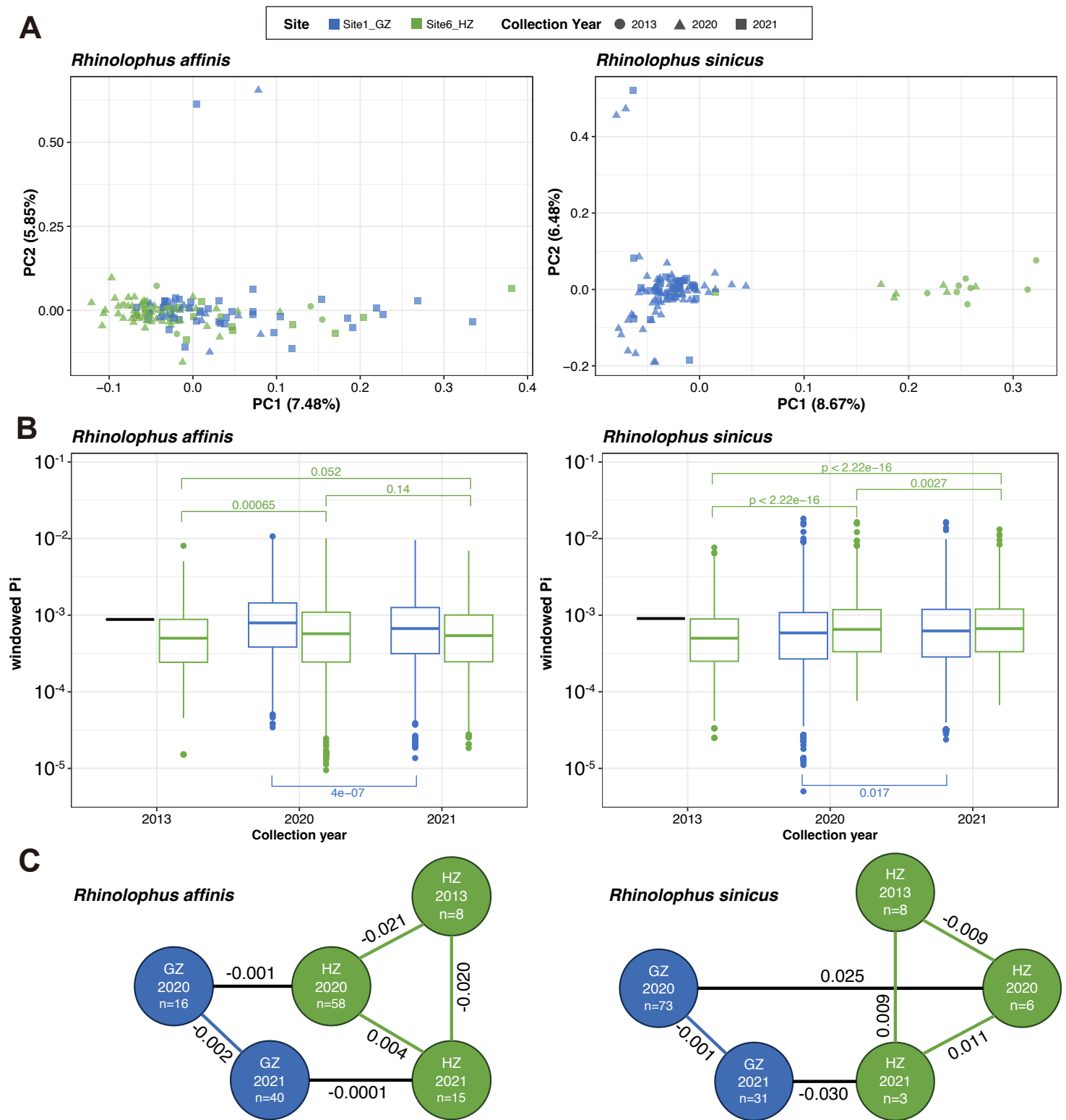


Figure 5. Assessment of genetic variation among *Rhinolophus affinis* and *R. sinicus* samples across different years and bat roosts.

(A) Principal component analysis (PCA) of host population genetics. The population structure within *R. affinis* (left) and *R. sinicus* (right) populations is visualized using PCA. The percentage of variation explained by each component is indicated in parentheses. Points are distinguished by collection site and year by shape and colors, respectively.

(B) Boxplots of within-site genetic diversity. The boxplots represent the genetic diversity within *R. affinis* (left) and *R. sinicus* (right) samples, as measured across collection years 2013, 2020, and 2021. The y-axis shows genetic diversity on a log scale. Statistically significant differences in genetic diversity across years are denoted by p-values.

(C) Fixation index (FST) among viral populations: *R. affinis* (left) and *R. sinicus* (right) are compared pairwise, with the FST values showing on the edge. The axes separate the data by collection site (GZ for Guangzhou, HZ for Huizhou) and year. The sample sizes for population are provided within the circles.

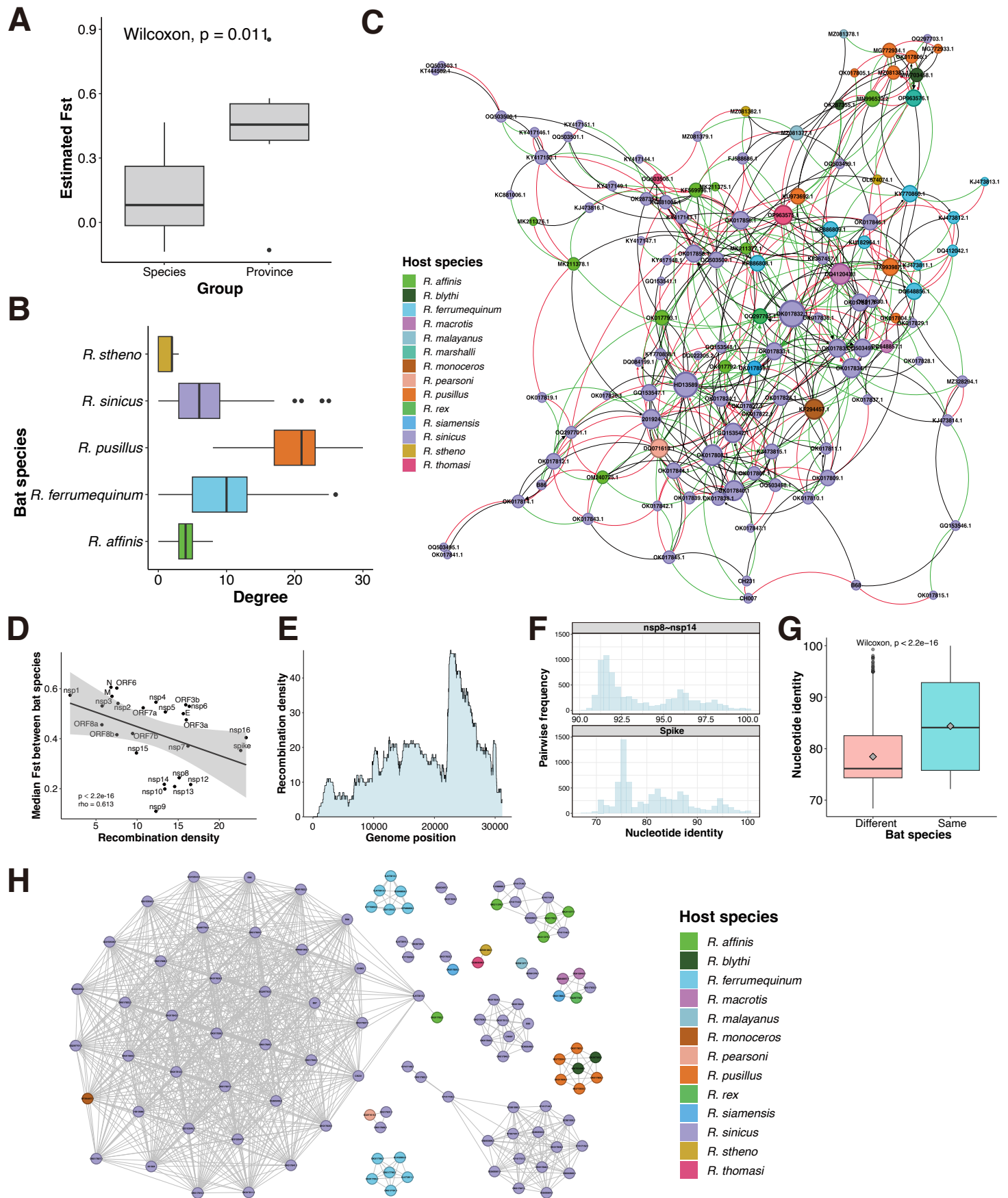
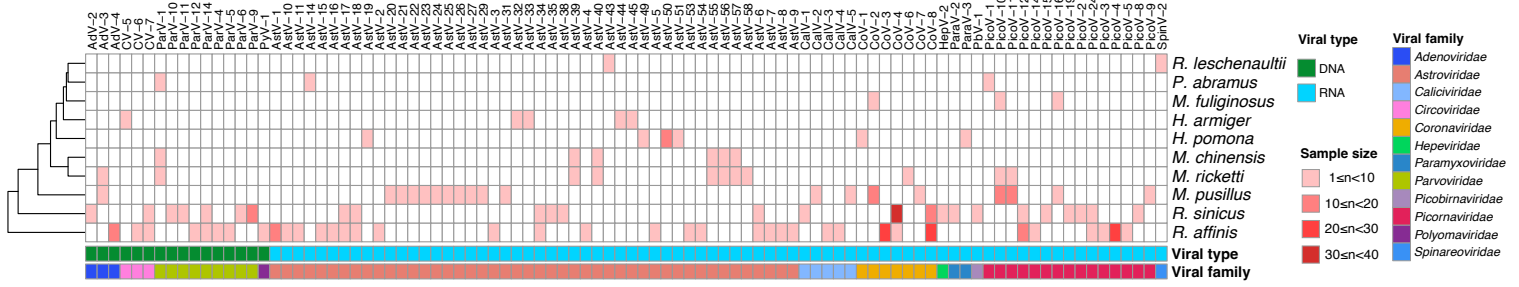


Figure 6. Genome comparison of SARSr-CoVs.

- (A) Mean fixation index among viral populations.
- (B) Boxplot of recombination frequency across host taxa.
- (C) Network of within- and between-host recombination. Node represents viral genome. Edge represents the linkage among parents and recombinant within each recombination event. Colour of nodes represents host species. Size of nodes represents node degree.
- (D) Correlation between recombination density and gene fixation index among host taxa.
- (E) Distribution of recombination density across coronavirus genome.
- (F) Frequency of pairwise nucleotide identity in nsp8-14 and S-gene.
- (G) Nucleotide identity between the S-genes of SARSr-CoV genomes within and between host species after controlling for RdRp identity (ANI>95%).
- (H) S-genes sharing among SARSr-CoV genomes. Node represents viral genome. Edge represents the sharing of S-gene with at least 92% ANI. Colour of nodes represents host species.

A



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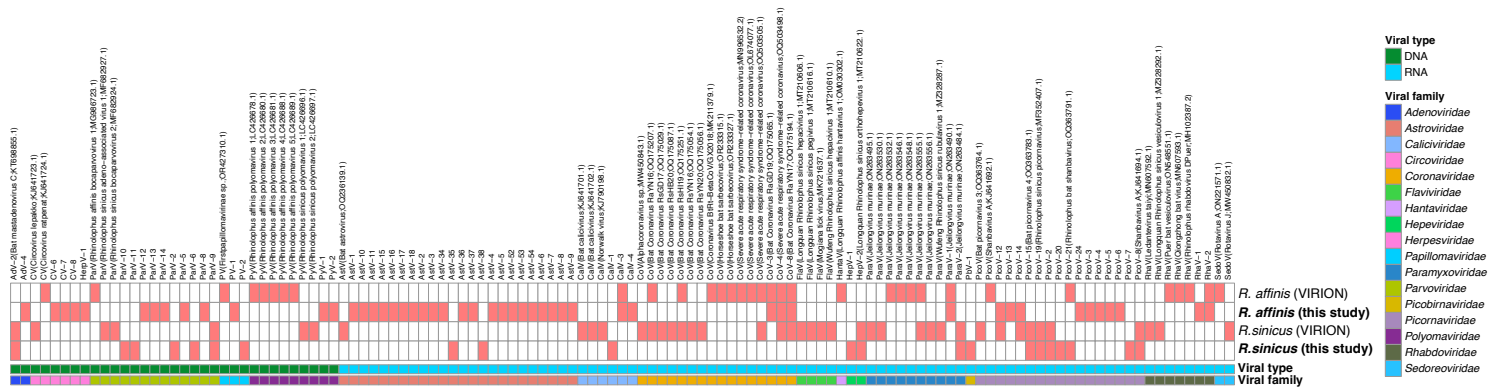
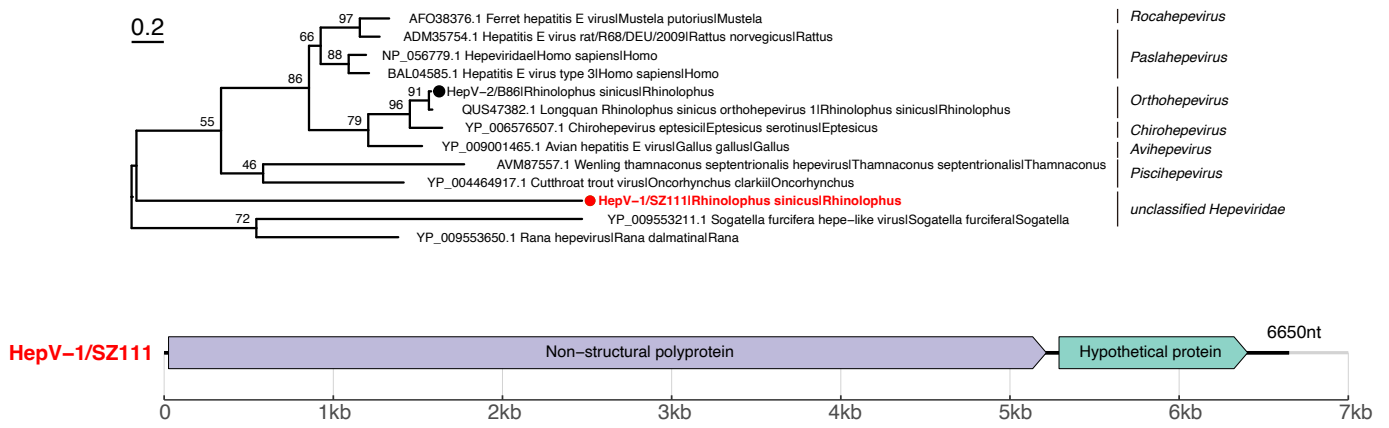


Figure S1. Distribution of vANI80s.

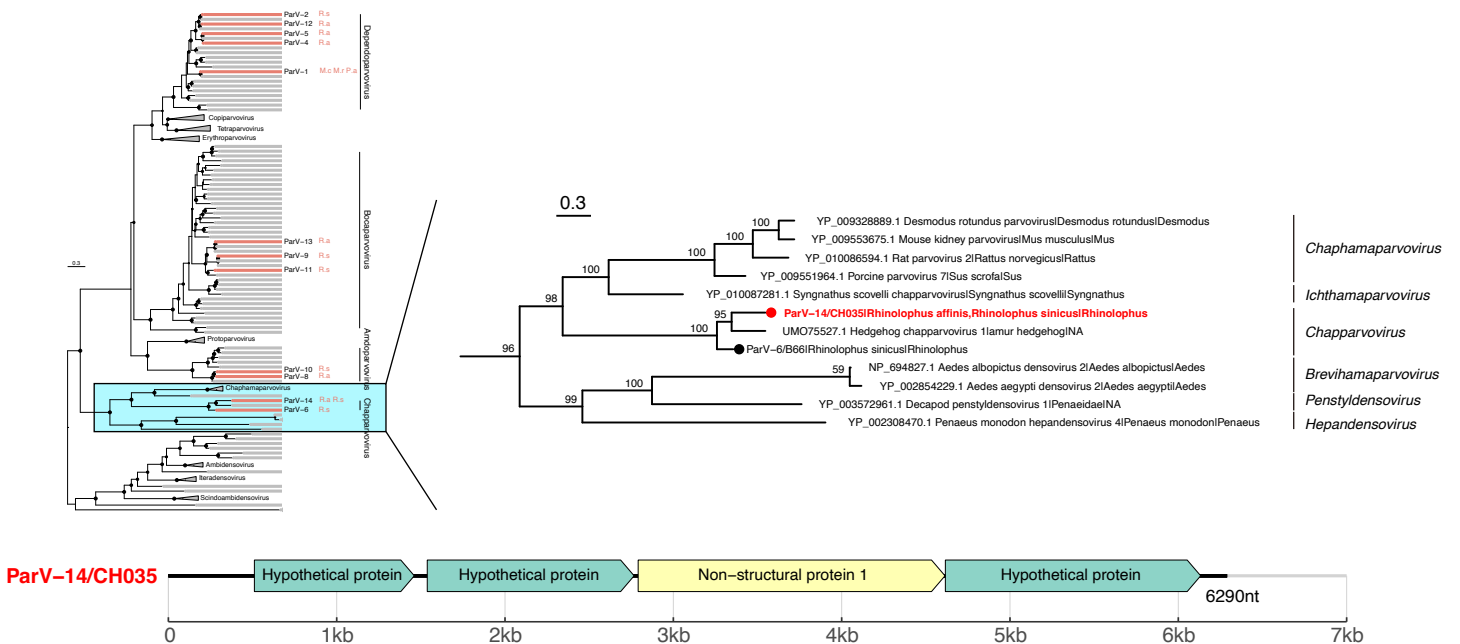
(A) Distribution of vANI80 clusters detected in at least two samples across host species.

(B) Comparison of vANI80s clusters identified in the present study and public database (VIRION).

A

Hepeviridae

B

Parvoviridae**Figure S2. Evolution of HepV-1 of Hepeviridae and ParV-14 of Parvoviridae.**

(A) Phylogenetic position, and genome structure of HepV-1.

(B) Phylogenetic position, and genome structure of ParV-14.

A

		442		472	479	487	491
Human_SARS_CoV_GZ02	NTRNID	ATSTGNY	NYKYR	YLRHGKLRPFERDIS	NVPFSPDGKPCCTPPALN	CYWPLNDYGFYTT	TGIGYQPYR
Civet_SARS_CoV_civet020	NTRNID	ATSTGNY	NYKYR	YLRHGKLRPFERDIS	NVPFSPDGKPCCTPPALN	CYWPLNDYGFYTT	TGIGYQPYR
Human_SARS_CoV_Tor2	NTRNID	ATSTGNY	NYKYR	YLRHGKLRPFERDIS	NVPFSPDGKPCCTPPALN	CYWPLNDYGFYTT	TGIGYQPYR
Human_SARS_CoV_BJ01	NTRNID	ATSTGNY	NYKYR	YLRHGKLRPFERDIS	NVPFSPDGKPCCTPPALN	CYWPLNDYGFYTT	TGIGYQPYR
Civet_SARS_CoV_civet010	NTRNID	ATSTGNY	NYKYR	YLRHGKLRPFERDIS	NVPFSSDGKPCCTPPAPN	CYWPLRGYGFYTT	SIGGYQPYR
Civet_SARS_CoV_SZ3	NTRNID	ATSTGNY	NYKYR	YLRHGKLRPFERDIS	NVPFSPDGKPCCTPPALN	CYWPLNDYGFYTT	SIGGYQPYR
Bat_SARSr_CoV_Rs4874	NTRNID	ATQTGNY	NYKYR	SLRHGKLRPFERDIS	NVPFSPDGKPCCTPPAFN	CYWPLNDYGFYITN	GIGYQPYR
Bat_SARSr_CoV_Rs3367	NTRNID	ATQTGNY	NYKYR	SLRHGKLRPFERDIS	NVPFSPDGKPCCTPPAFN	CYWPLNDYGFYITN	GIGYQPYR
Bat_SARSr_CoV_WIV1	NTRNID	ATQTGNY	NYKYR	SLRHGKLRPFERDIS	NVPFSPDGKPCCTPPAFN	CYWPLNDYGFYITN	GIGYQPYR
Bat_SARSr_CoV_YN2013	NTANQD	---VG---	SYFYR	SHRSTKLKPFERDLS	---SDE---	NGVRTLSTYDFNPNVPLDY	QATR
Bat_SARSr_CoV_Rs672	NTAKQD	---QG---	QYYYS	SRKTKLKPFERDLT	---SDE---	NGVRTLSTYDFYPNPVPIEY	QATR
Bat_SARSr_CoV_GX201	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_HuB20	NTAKQD	---TG---	YYYYS	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_HKU31	NTAKHD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_ZXC21	NTAKQD	---TG---	HYFYR	SHRSTKLKPFERDLS	---SDE---	NGVRTLSTYDFNPNVPLEY	QATR
Bat_SARSr_CoV_ZC45	NTAKQD	---VG---	NFYYS	SHRSTKLKPFERDLS	---SDE---	NGVRTLSTYDFNPNVPLEY	QATR
Bat_SARSr_CoV_GD2019E	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_GD2019D	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_GD2019B	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_GD2019A	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
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Bat_SARSr_CoV_GD2017N	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_GD2017L	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
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Bat_SARSr_CoV_GD2017H	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_GD2017F	NTAKQD	---TG---	NYYYR	SHRKNKLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_GD2016B	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_HKU3-7	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_HKU3-8	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat_SARSr_CoV_GD2017Q	NTAKQD	---KG---	KYYYS	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVAY	QATR
Bat_SARSr_CoV_GD2017P	NTAKQD	---QG---	QYYYS	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVAY	QATR
Bat_SARSr_CoV_GD2017M	NTANLD	---QG---	QYYYS	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
Bat_SARSr_CoV_GD2017G	NTANLD	---QG---	QYYYS	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
Bat_SARSr_CoV_Rs56	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
Bat_SARSr_CoV_Rs67	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
Bat_SARSr_CoV_Rs68	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
Bat_SARSr_CoV_Rs87	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
Bat_SARSr_CoV_Rs200609	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDDG---	NGVYTLSTYDFNPNVPVAY	QATR
Bat-SARSr-CoV-RaCH025	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
Bat-SARSr-CoV-RaCH027	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYSNPVPEY	QATR
Bat-SARSr-CoV-RaCH039	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
CH063	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
B68	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
B86	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
B87	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
CH231	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYSNPVPEY	QATR
201924	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDD---	NGVYTLSTYDFNPNVPVAY	QATR
HD13589	NTAKQD	---TG---	NYYYR	SHRKTTLKPFERDLS	---SDD---	NGVYTLSTYDFNPNVPVAY	QATR
B50	NTANLD	---QG---	QYYYS	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
CH007	NTANLD	---QG---	QYYYS	SHRKTTLKPFERDLS	---SDE---	NGVRTLSTYDFYPNPVPEY	QATR
		5 aa deletion		12-13 aa deletion			

5 aa deletion

12-13 aa deletion

Guangdong

B

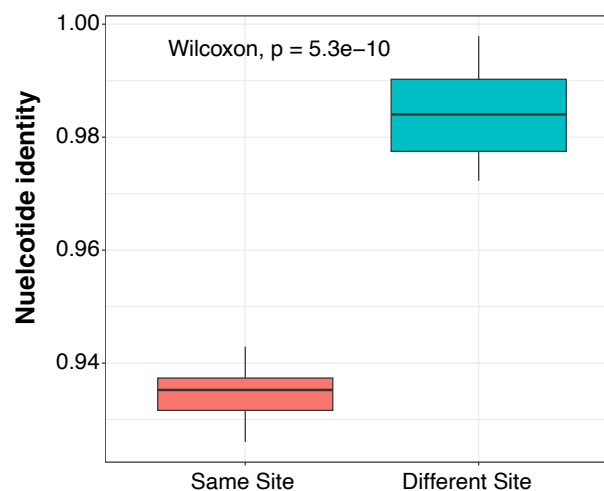


Figure S3. Genetic comparison of SARSr-CoVs.

(A) Alignment in RBD region of severe acute respiratory syndrome-related coronaviruses (SARSr-CoVs).
 (B) Pairwise nucleotide identity between the identified SARSr-CoVs within and between the sampling location.

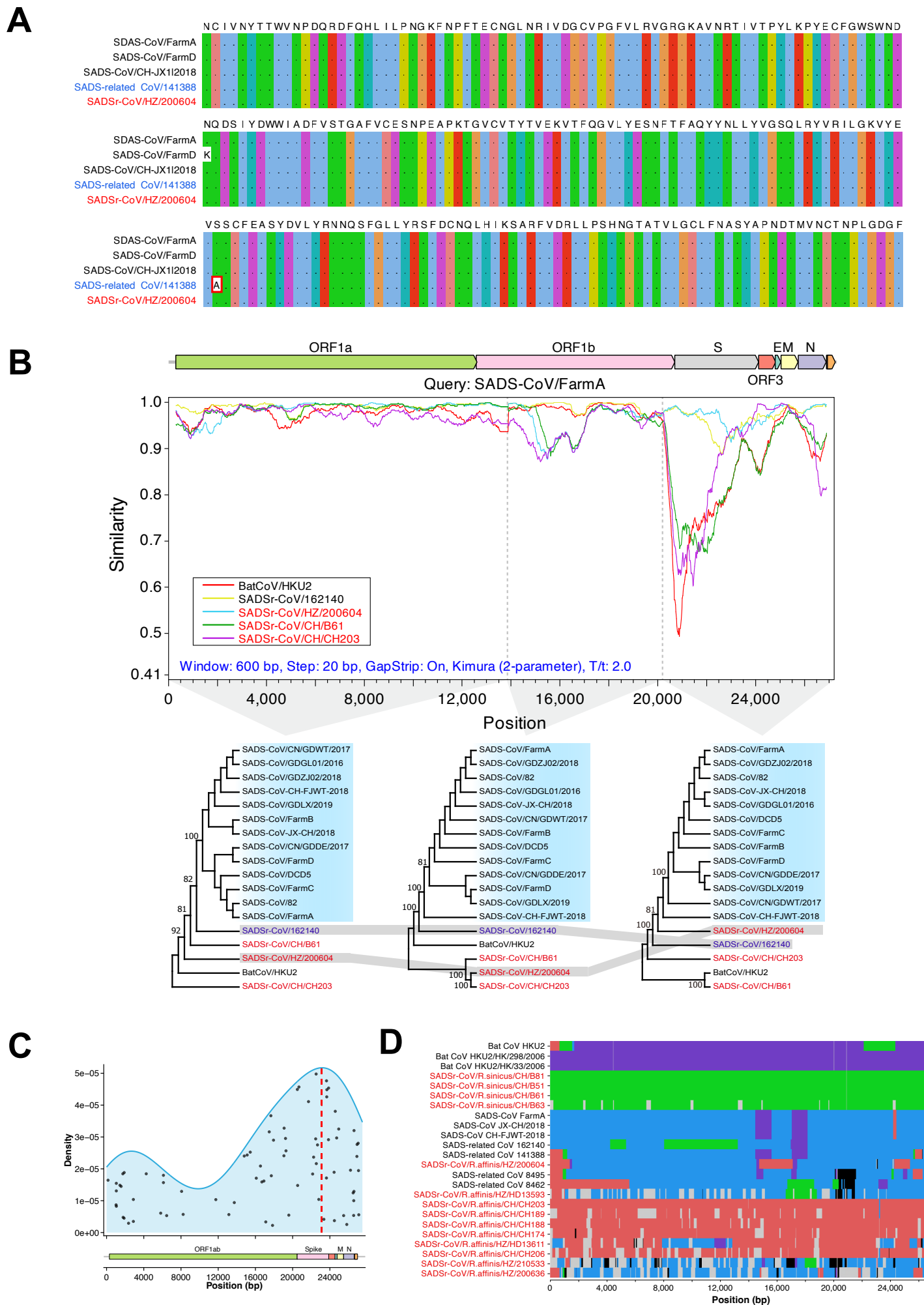


Figure S4. Recombination of SADSr-CoVs.

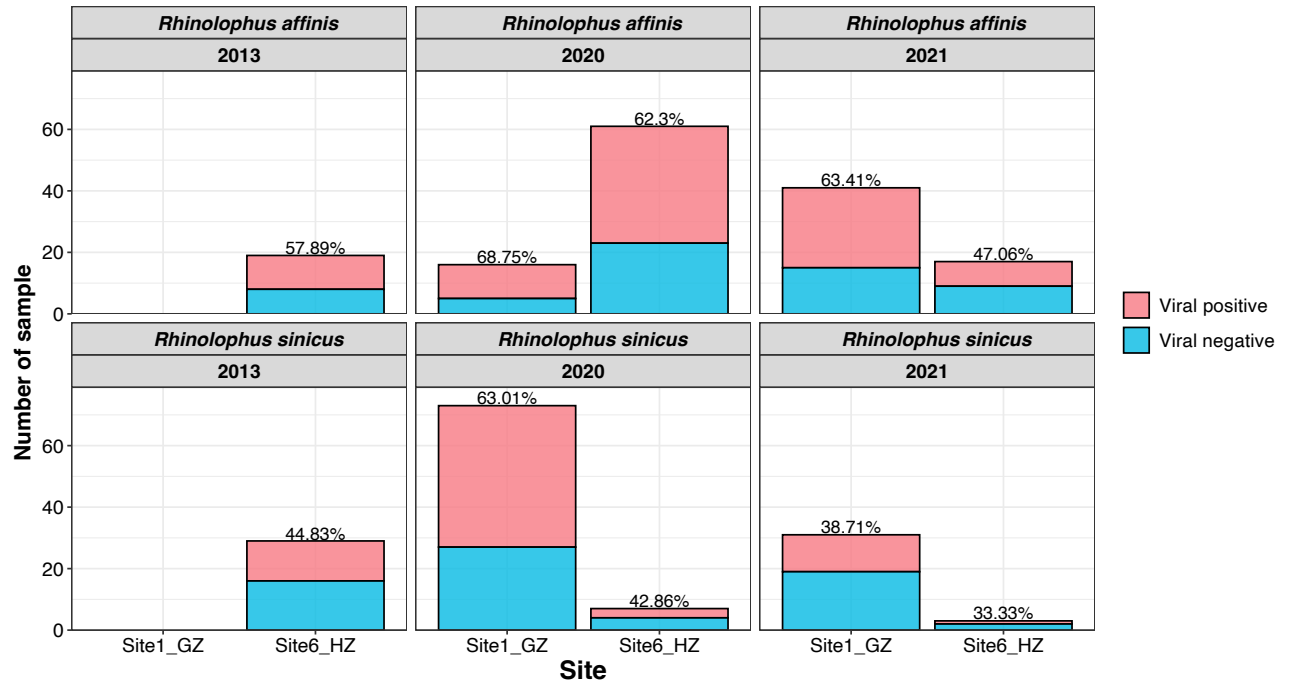
(A) Alignment in CTD region;

(B) Recombination of SADSr-CoVs.

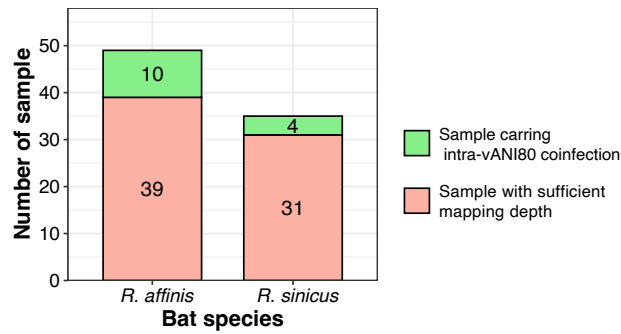
(C) Distribution of recombination segments across genome.

(D) Cluster of SADSr-CoVs using fastGEAR. Color represents the lineage of the genomic segment.

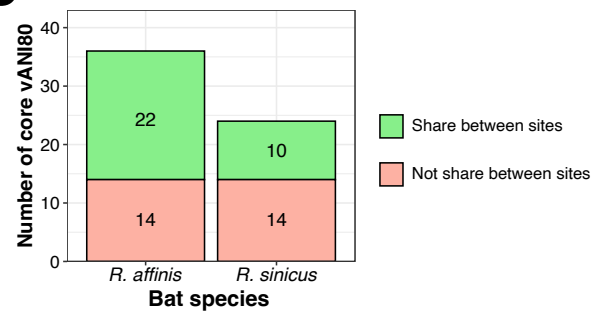
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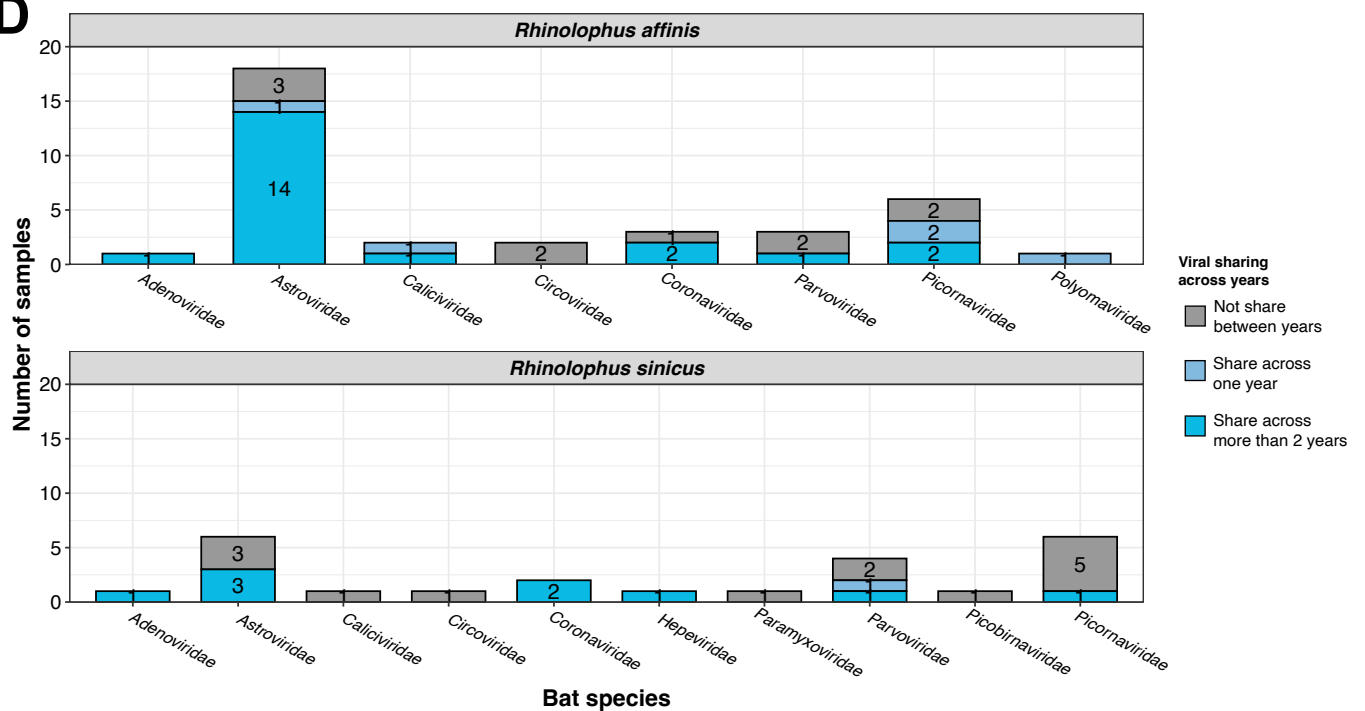


Figure S5. Distribution of core vANI80s in *Rhinolophus* bats.

(A) Viral positive rate of *Rhinolophus* bats across Site1_GZ and Site6_HZ from 2013 to 2021, with the numbers indicating viral positive rate.

(B) Samples with intra-vANI80 coinfection.

(C) Viral sharing count between Guangzhou and Huizhou among *Rhinolophus* bats.

(D) The proportion of vANI80s shared across years among viral families.

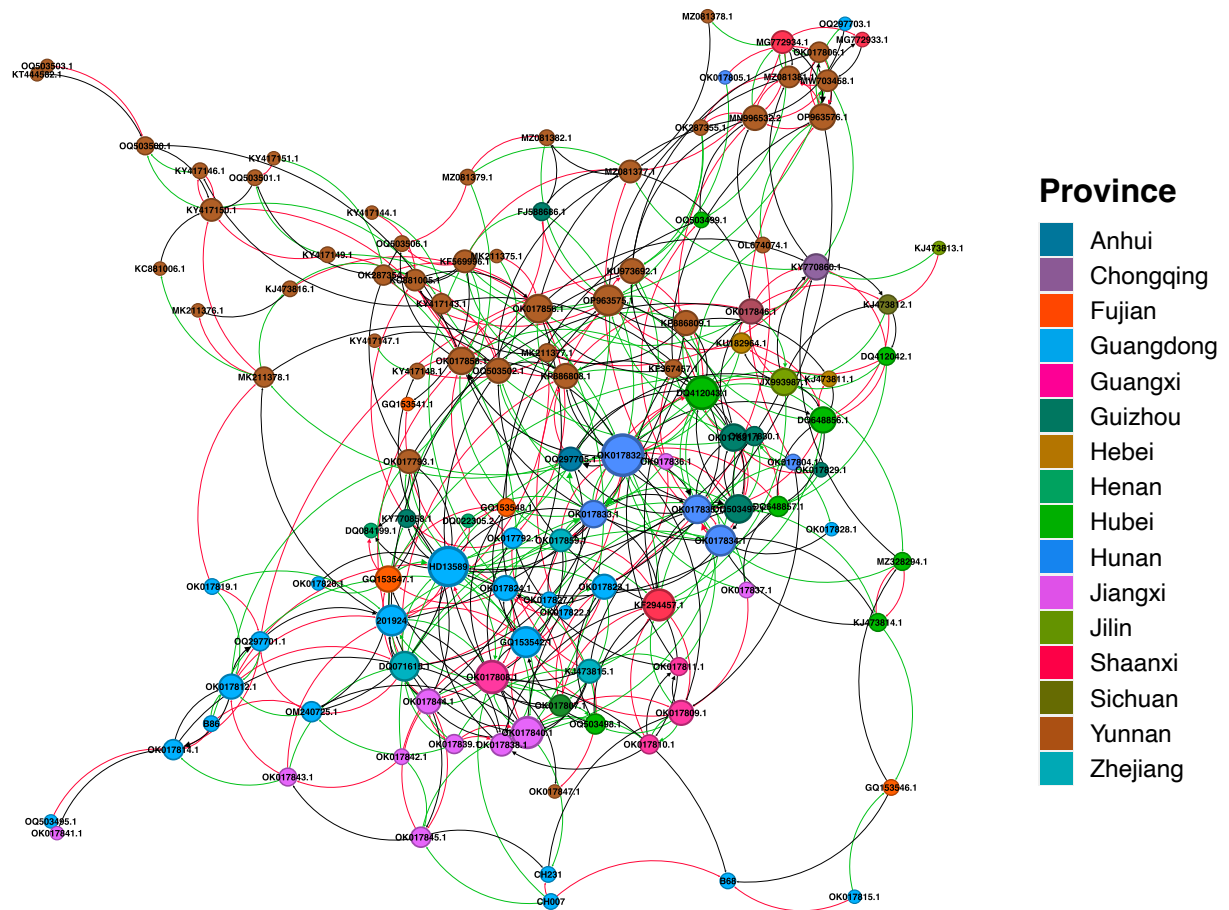


Figure S6. Recombination across provinces. Network of inter- and intra-province recombination frequency. Node represents viral genome. Edge represents the linkage among parents and recombinant within each recombination event. Colour of nodes represents province. Size of nodes represents node degree.

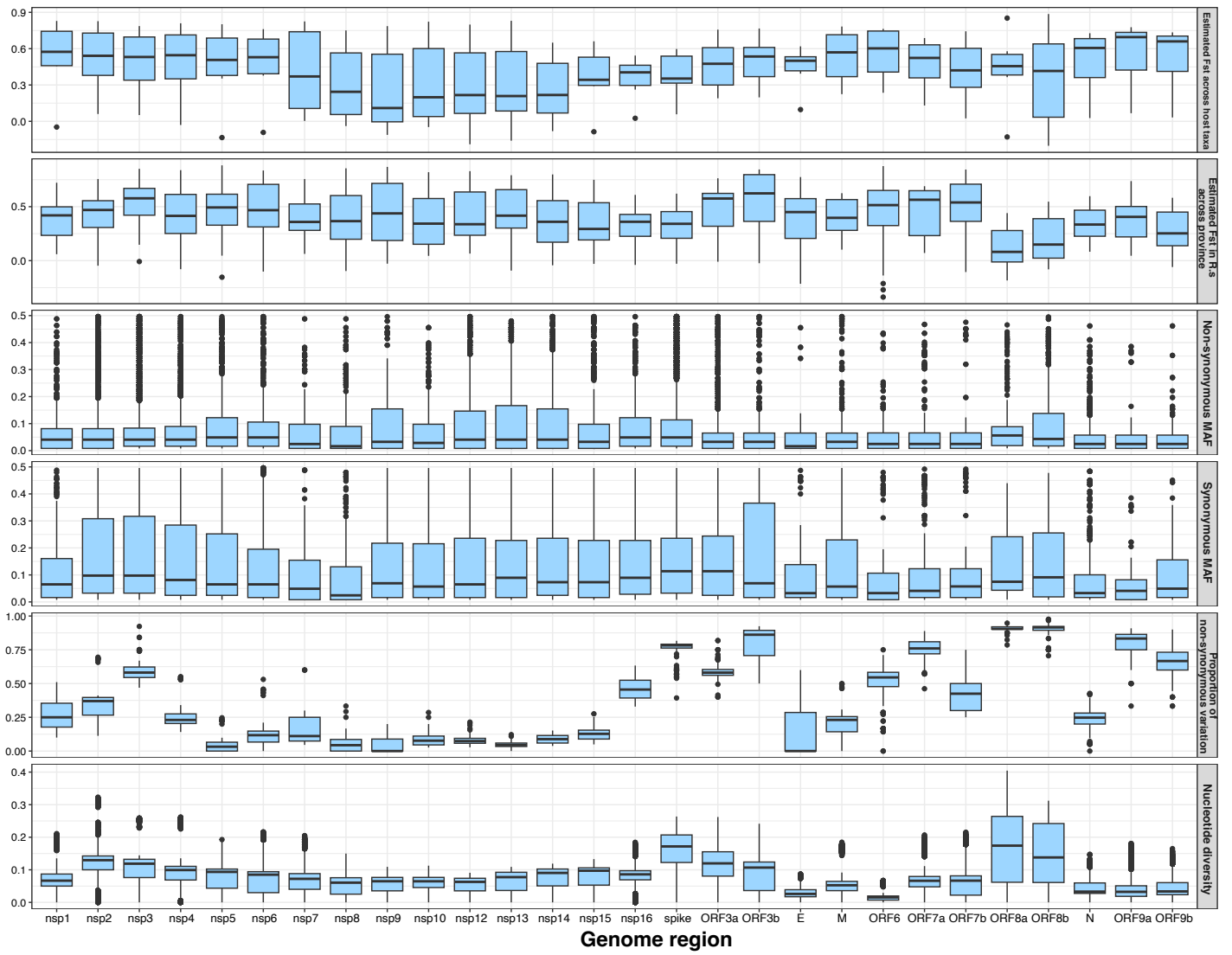


Figure S7. Modular evolution of SARSr-CoVs. Population statistics of SARSr-CoVs across genetic components, including fixation index of genetic components across host taxa, fixation index of genetic components across provinces within *R. sinicus*, minor allele frequency (MAF) of nonsynonymous mutations, MAF of synonymous mutations, proportion of nonsynonymous mutations and nucleotide diversity.