Origin and cross-species transmission of bat coronaviruses in China

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Supplementary Information

Supplementary Note 1

GenBank accession numbers of sequences generated for this study

MN312240-MN312869

China National Genomics Data Center accession numbers of sequences generated for this study

SAMC190658-SAMC191246

GenBank accession numbers of additional sequences included in this study

Bat-CoVs: AY594268, DQ022305, DQ071615, DQ084199-DQ084200, DQ412042-DQ412043, DQ648794-DQ648795, DQ648809, DQ648819, DQ648822-DQ648823, DQ648833-DQ648835, DQ648837, DQ648850, DQ648856-DQ648858, DQ666337-DQ666340, EF065506, EF065513-EF065516, EF203064-EF203067, EU420137-EU420138, FJ588686, GQ153539-GQ153548, HM211098-HM211101, JQ989266-JQ989273, JX993987-JX993988, KC522036-KC522048, KC522075-KC522089, KC881005-KC881006, KF294268-KF294282, KF294373-KF294378, KF294381-KF294383, KF294420-KF294457, KF367457, KF569973-KF569996, KF636752, KJ473795-KJ473804, KJ473806-KJ473816, KJ473820-KJ473822, KP876505-KP876510, KP876512-KP876515, KP876517-KP876528, KP876532-KP876534, KP876536-KP876537, KP876540-KP876542, KP876544-KP876546, KP886808-KP886809, KP895482-KP895494, KP895496, KP895498-KP895525, KT381902-KT381925, KT444582, KU182954-KU182968, KU182970-KU183003, KU343190-KU343196, KU343198, KU343200, KX285115-KX285179, KX285183, KX285185-KX285197, KX285199-KX285220, KX285223, KX442564, KX447544-KX447565, KY009612-KY009634, KY770850-KY770860, KY383882, KY417142-KY417152, KY783855-KY783881, KY783883-KY783903, MF760455, MF760515, MF769447-MF769451, MF769453, MF769466-MF769470, MF769475-MF769478, MF769485, MF769508-MF769511, MF769513, MG021452, MG762654-MG762656, MG762658

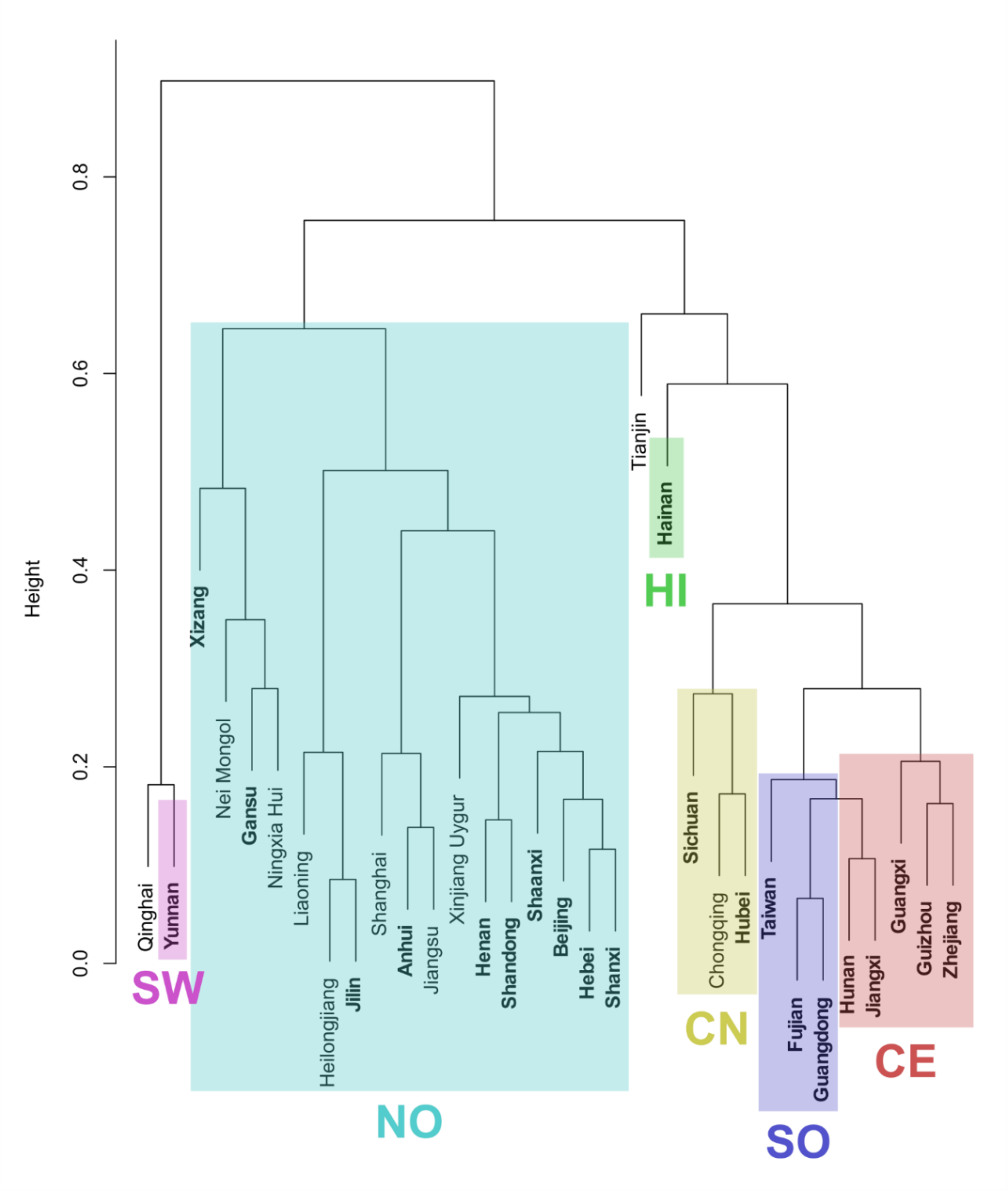
Human CoVs: MN908947, MN975262, NC_004718

GISAID accession numbers of additional sequences included in this study

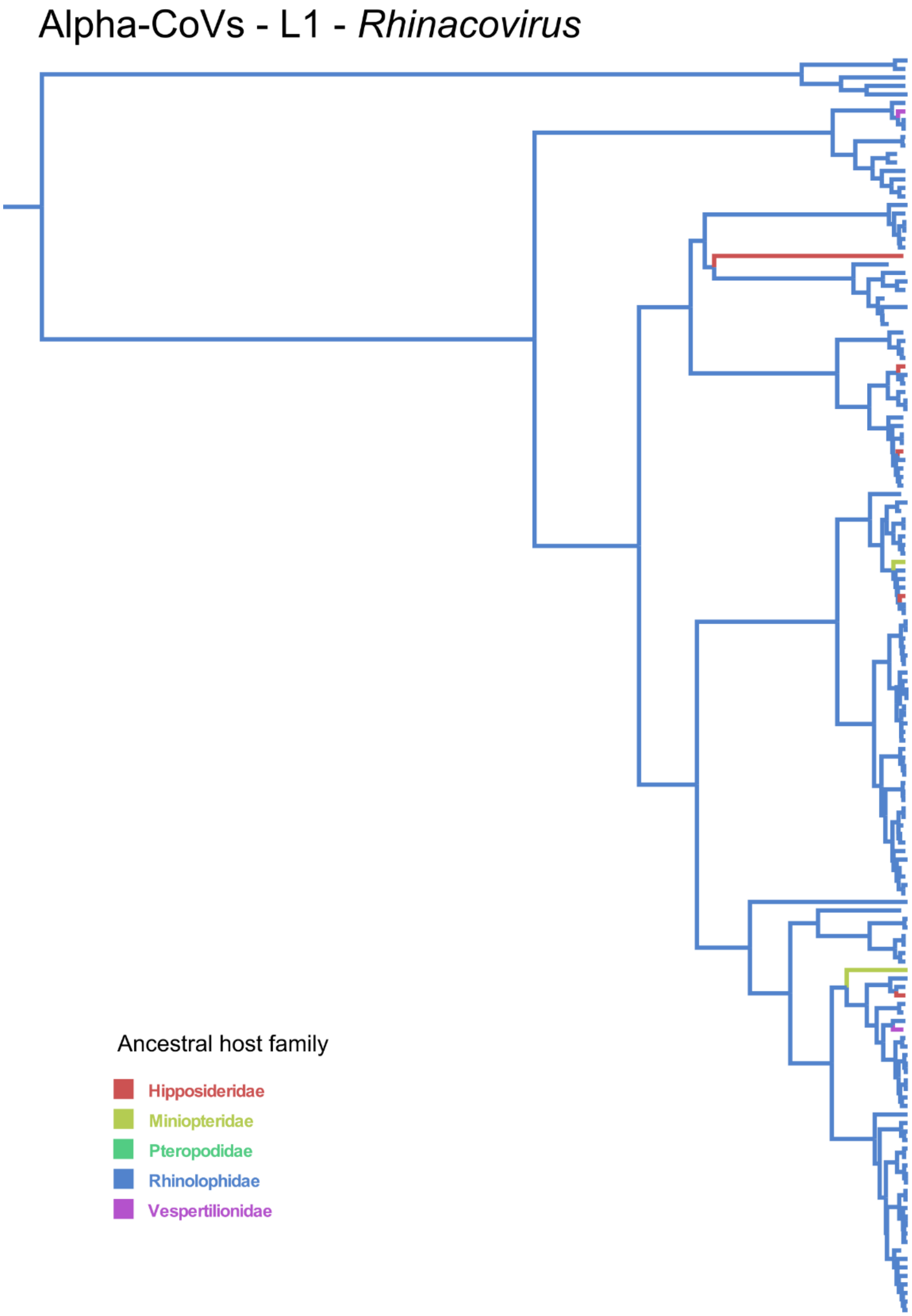
Pangolin CoVs: EPI_ISL_410538-410544, EPI_ISL_410721

Bat-CoV: EPI_ISL_412977

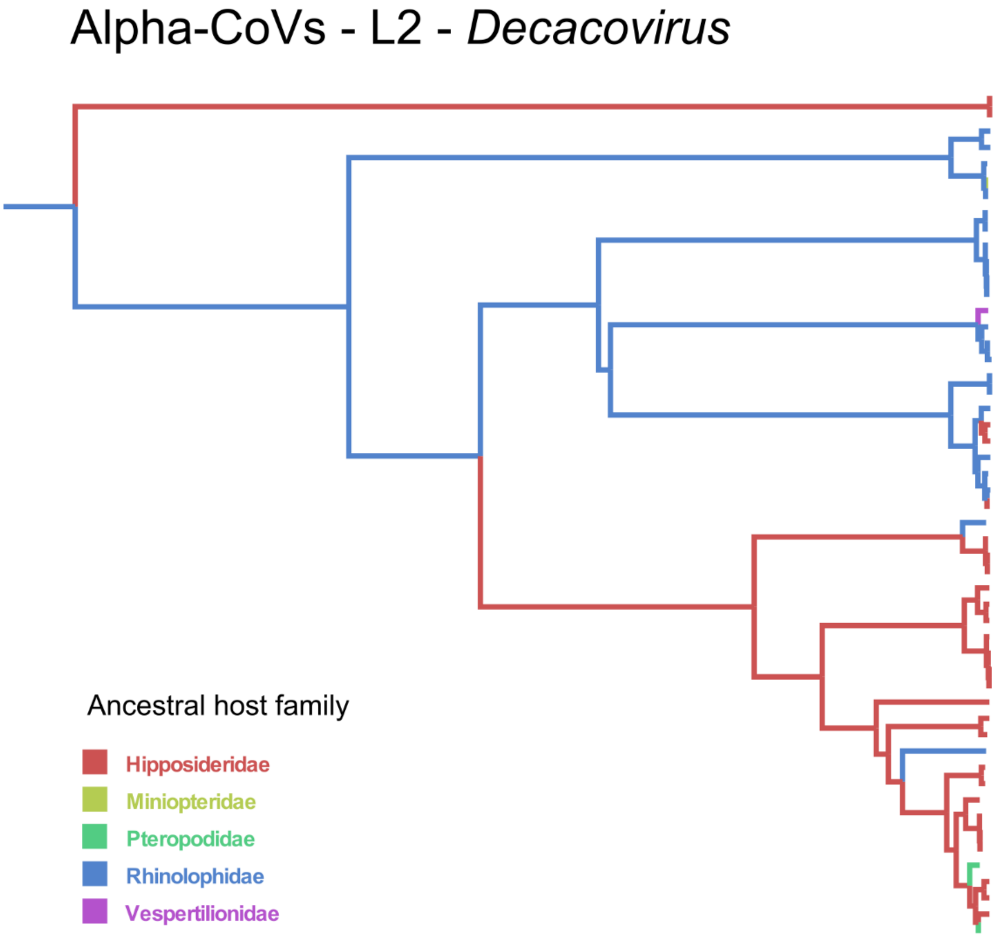
Supplementary Figures



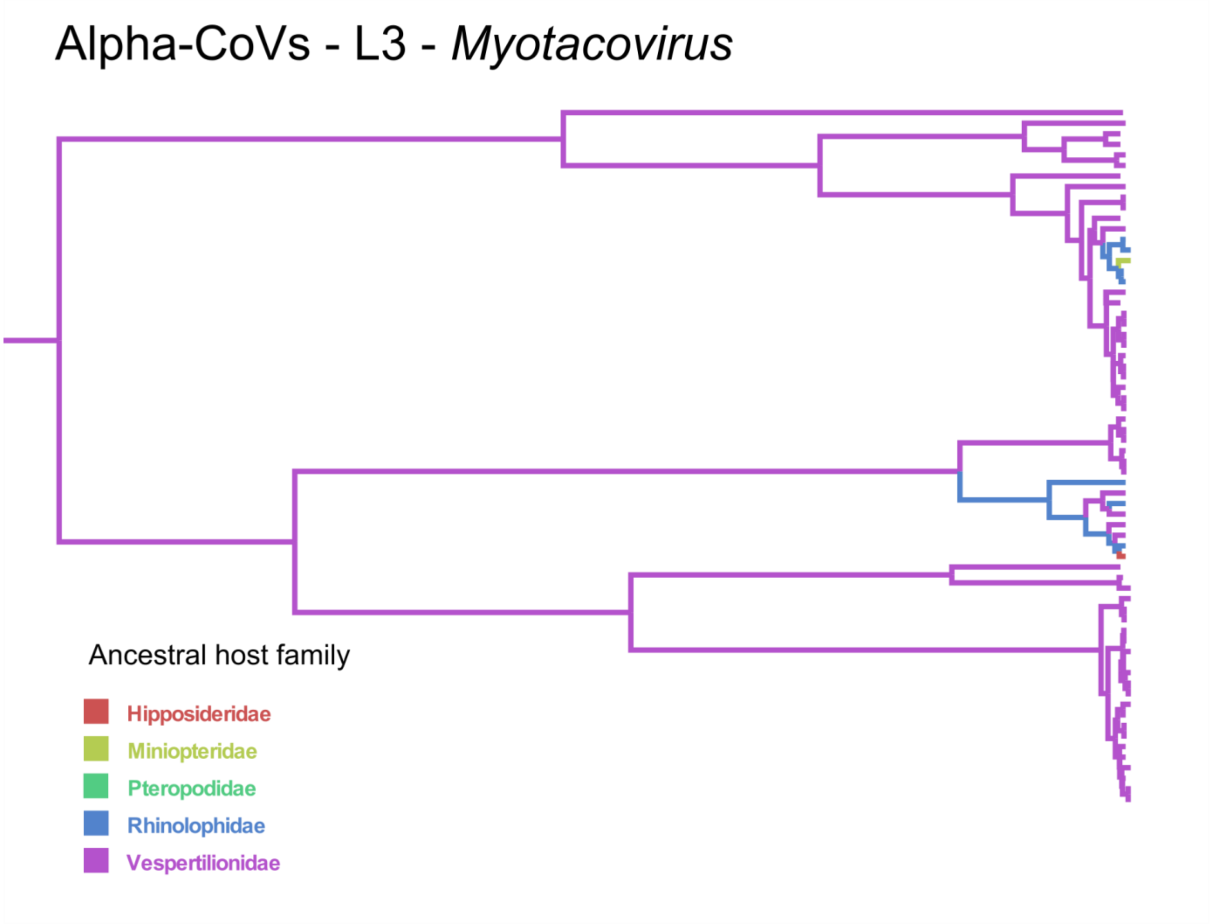
Supplementary Figure 1: Cluster dendrogram of Chinese provinces based on similarities between their mammalian diversity (hierarchical clustering). Provinces with CoV sequences available in this study are highlighted in bold.



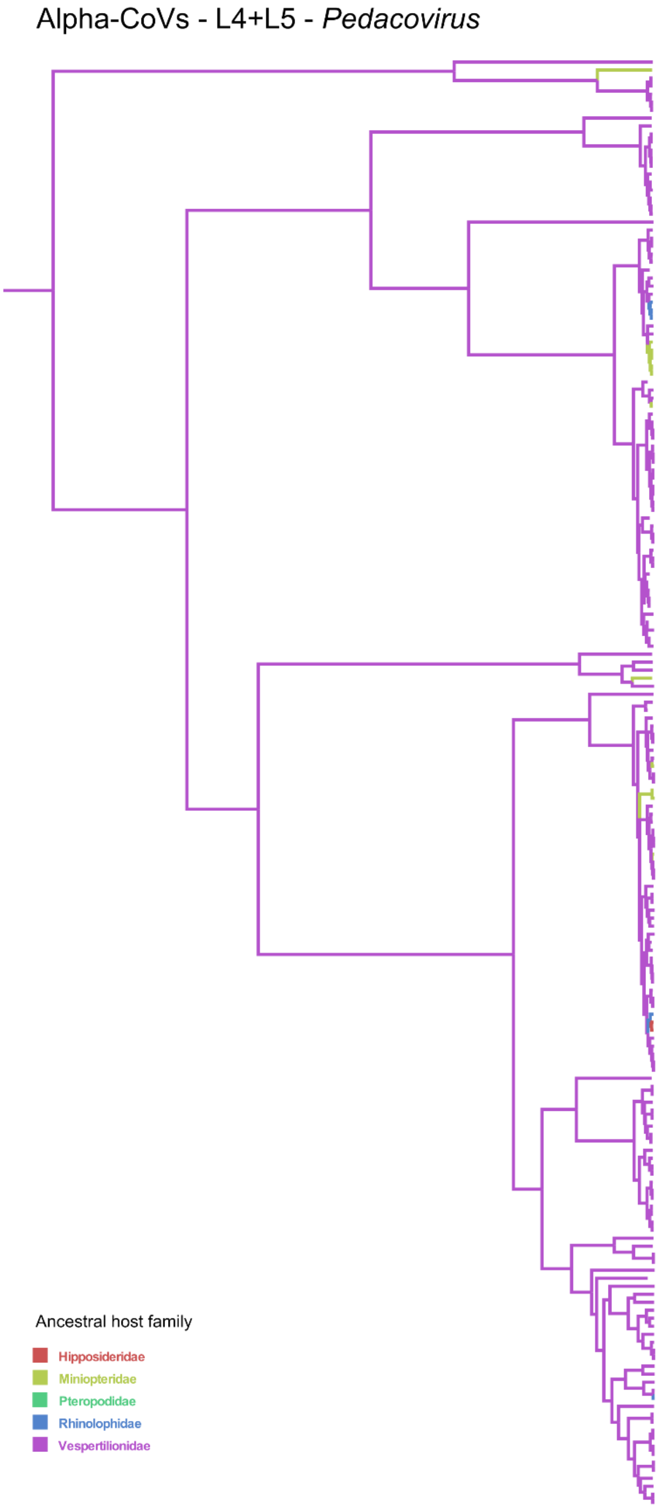
Supplementary Figure 2: Zoomed in alpha-CoV maximum clade credibility annotated tree focusing on Lineage L1 corresponding to *Rhinacovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with the highest probability.



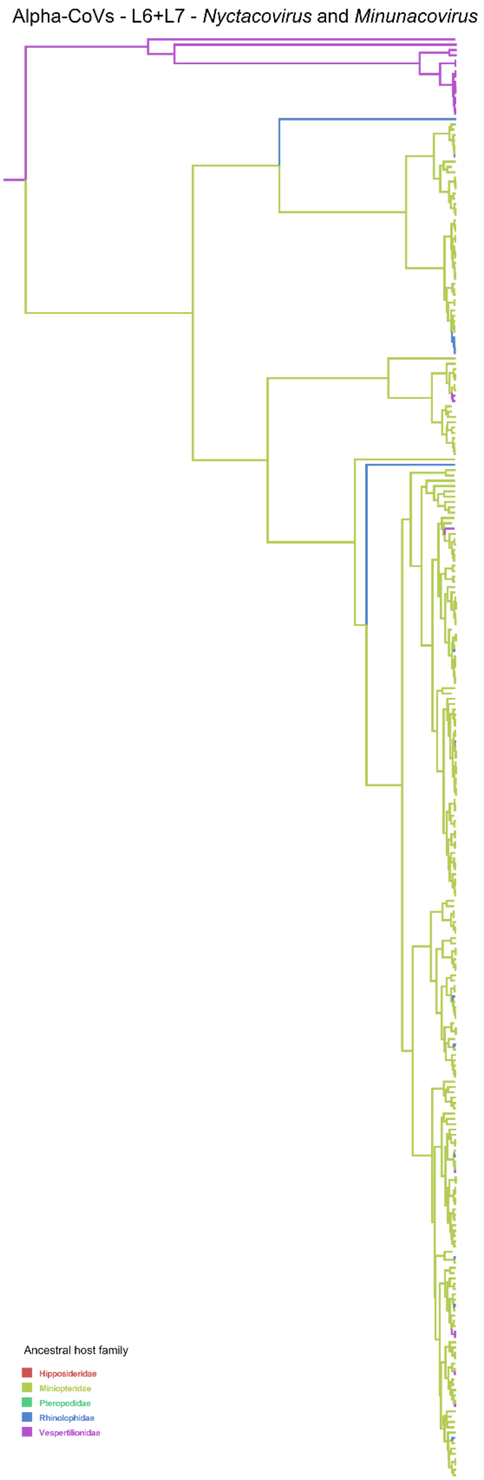
Supplementary Figure 3: Zoomed in alpha-CoV maximum clade credibility annotated tree focusing on Lineage L2 corresponding to *Decacovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with the highest probability.



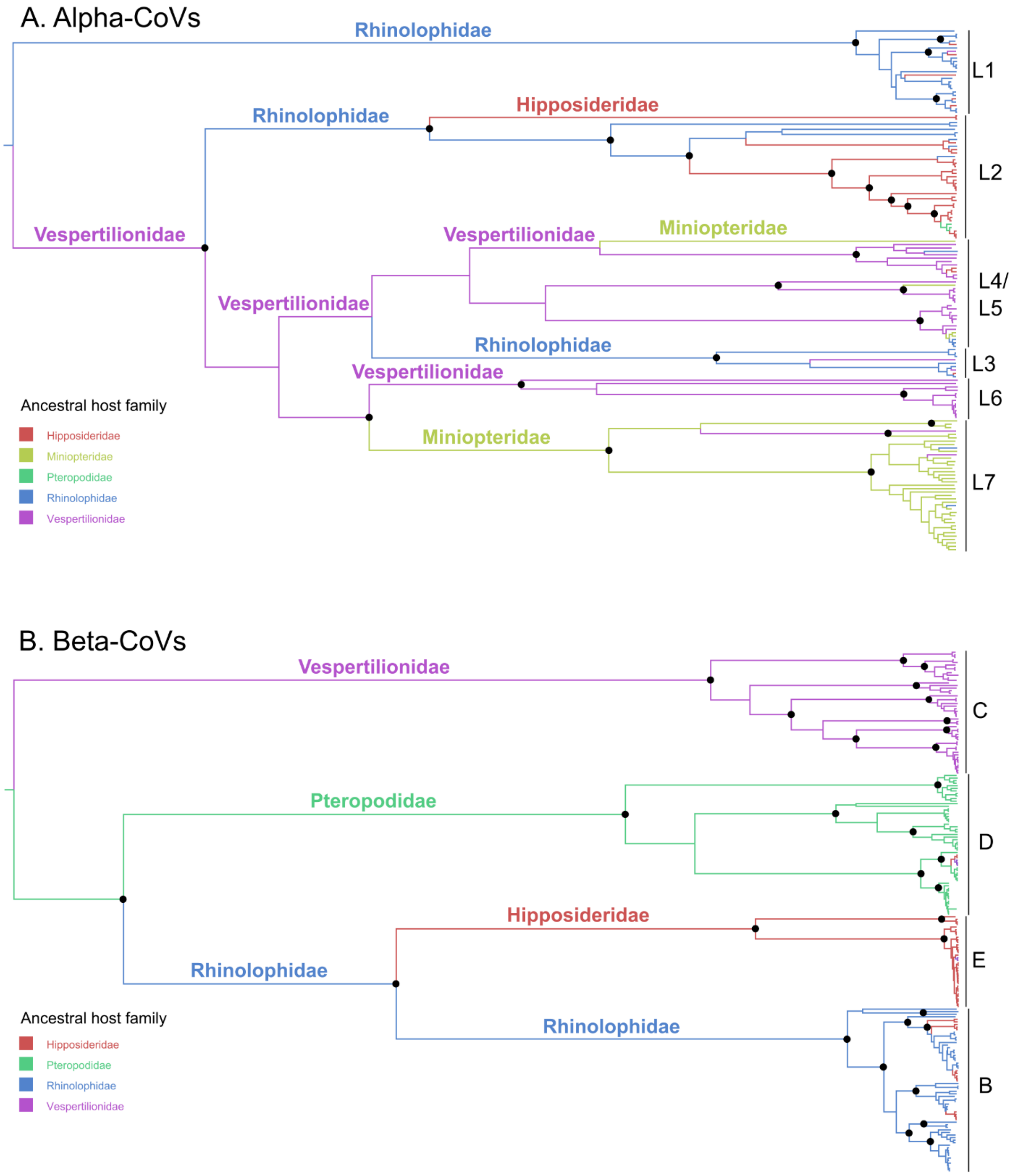
Supplementary Figure 4: Zoomed in alpha-CoV maximum clade credibility annotated tree focusing on Lineage L3 corresponding to *Myotacovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with the highest probability.



Supplementary Figure 5: Zoomed in alpha-CoV maximum clade credibility annotated tree focusing on Lineages L4 and L5 corresponding to *Pedacovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with the highest probability.

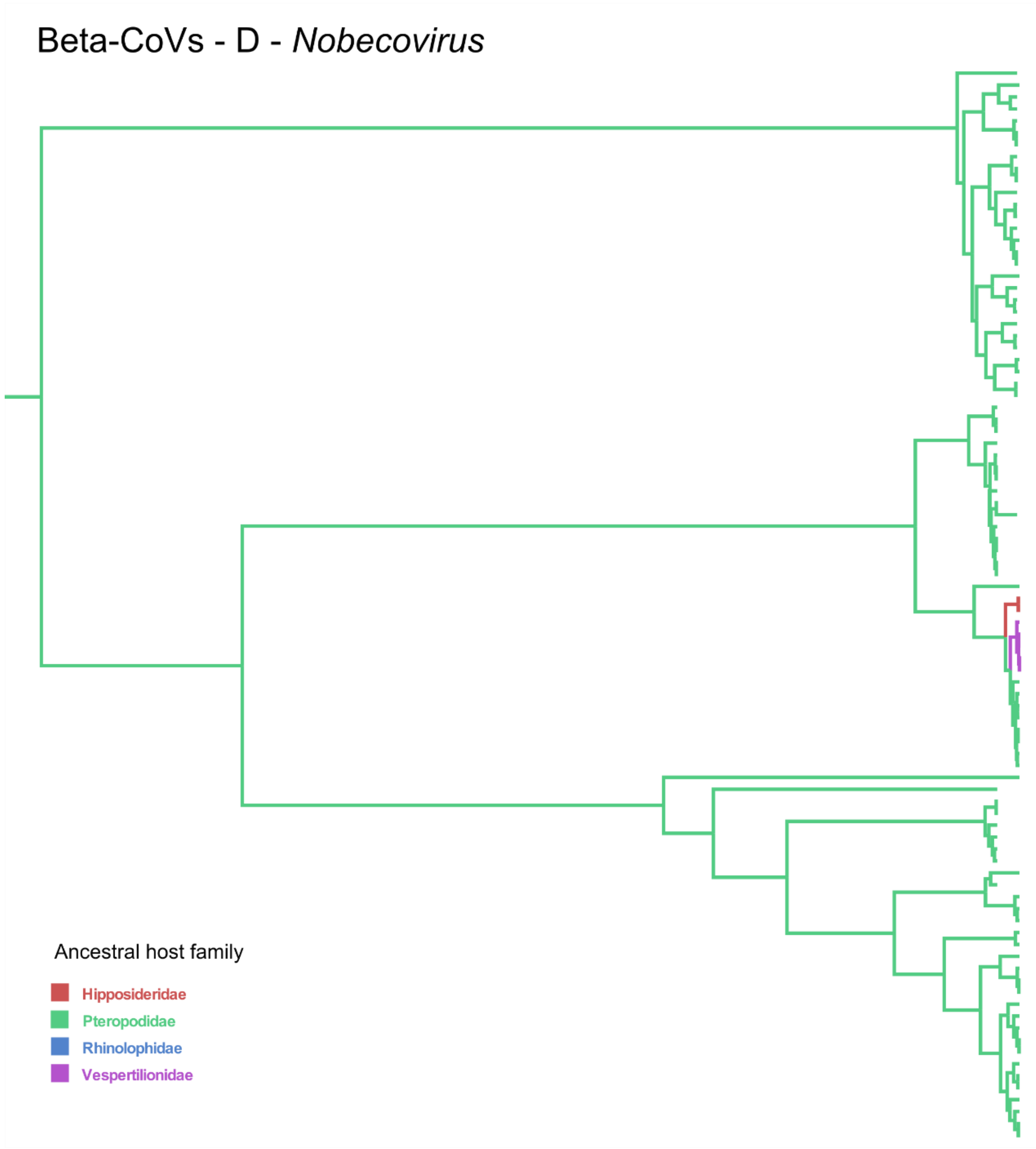


Supplementary Figure 6: Zoomed in alpha-CoV maximum clade credibility annotated tree focusing on Lineages L6 and L7 corresponding to *Nyctacovirus* and *Minunacovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with the highest probability.

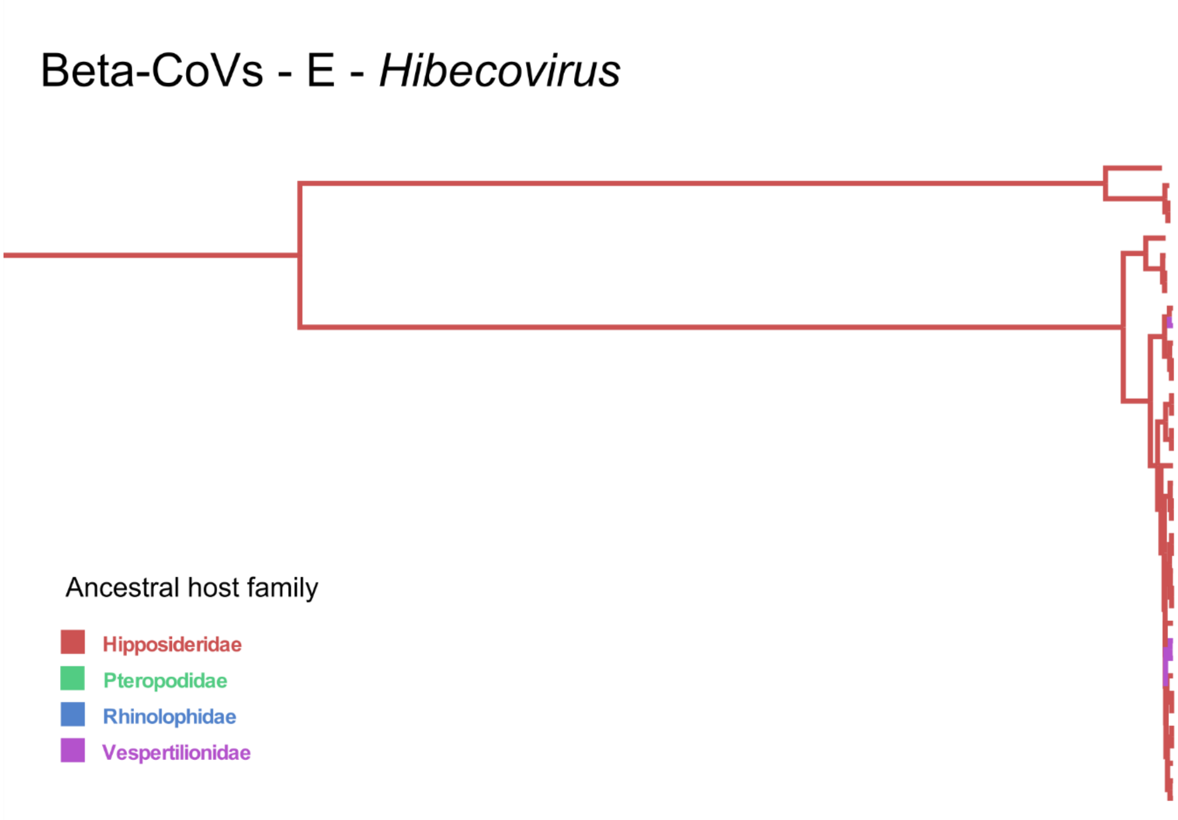


Supplementary Figure 7: Alpha-CoV (A) and beta-CoV (B) maximum clade credibility annotated trees using random subset of RdRp sequences to normalize sampling effort across bat families and bat host family as discrete character state. Branches colors correspond to the inferred ancestral family with the highest probability. Branch lengths are scaled according to time. Well-supported nodes (posterior probability > 0.95) are indicated with a black dot. The ICTV approved CoV subgenera were highlighted: Rhinacovirus (L1), Decacovirus (L2), Myotacovirus (L3), Pedacovirus (L5), Nyctacovirus (L6), Minunacovirus (L7) and an unidentified lineage (L4) for alpha-CoVs; and Merbecovirus (Lineage C), Nobecovirus (lineage D), Hibecovirus (lineage E) and Sarbecovirus (Lineage B) for beta-CoVs.

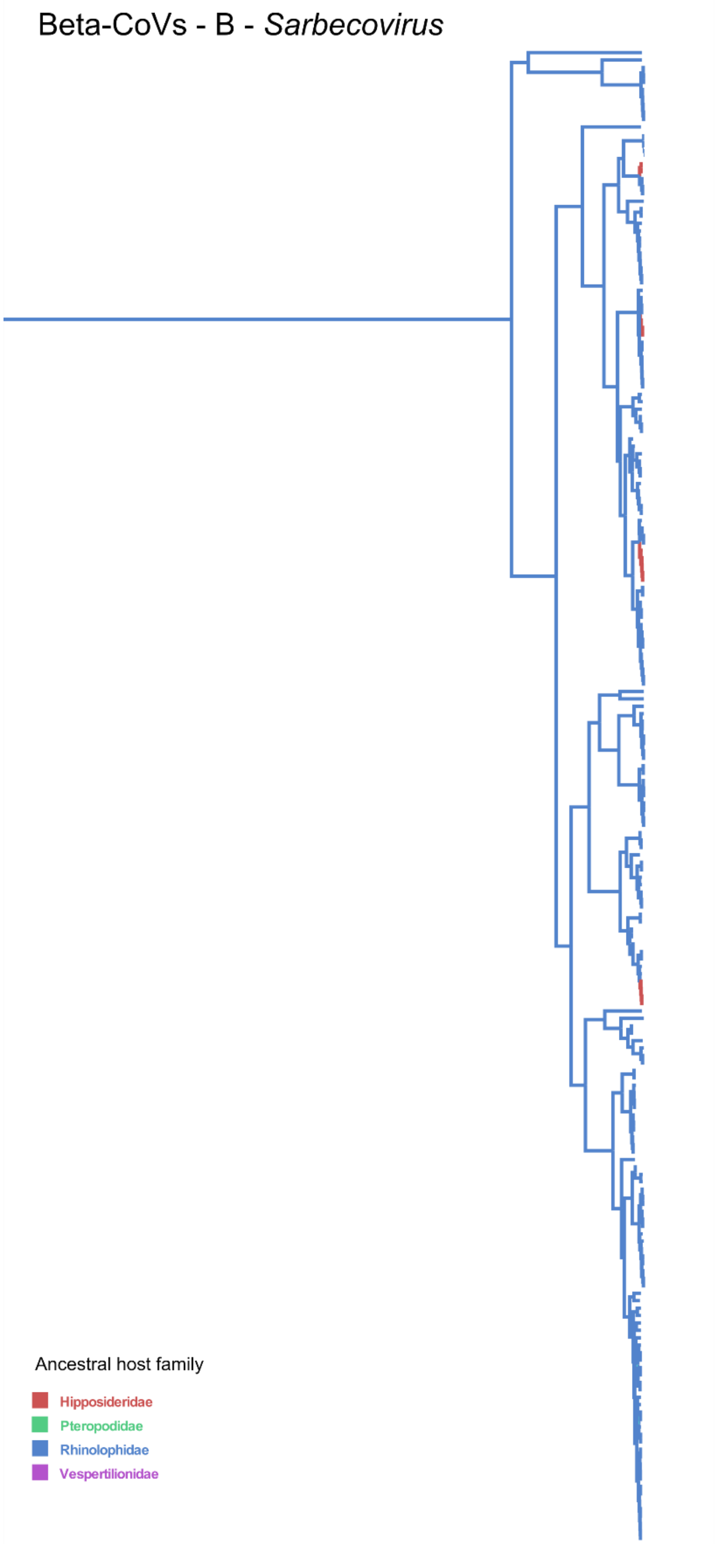
Supplementary Figure 8: Zoomed in beta-CoV maximum clade credibility annotated tree focusing on Lineage C corresponding to *Merbecovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with the highest probability.



Supplementary Figure 9: Zoomed in beta-CoV maximum clade credibility annotated tree focusing on Lineage D corresponding to *Nobecovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with the highest probability.

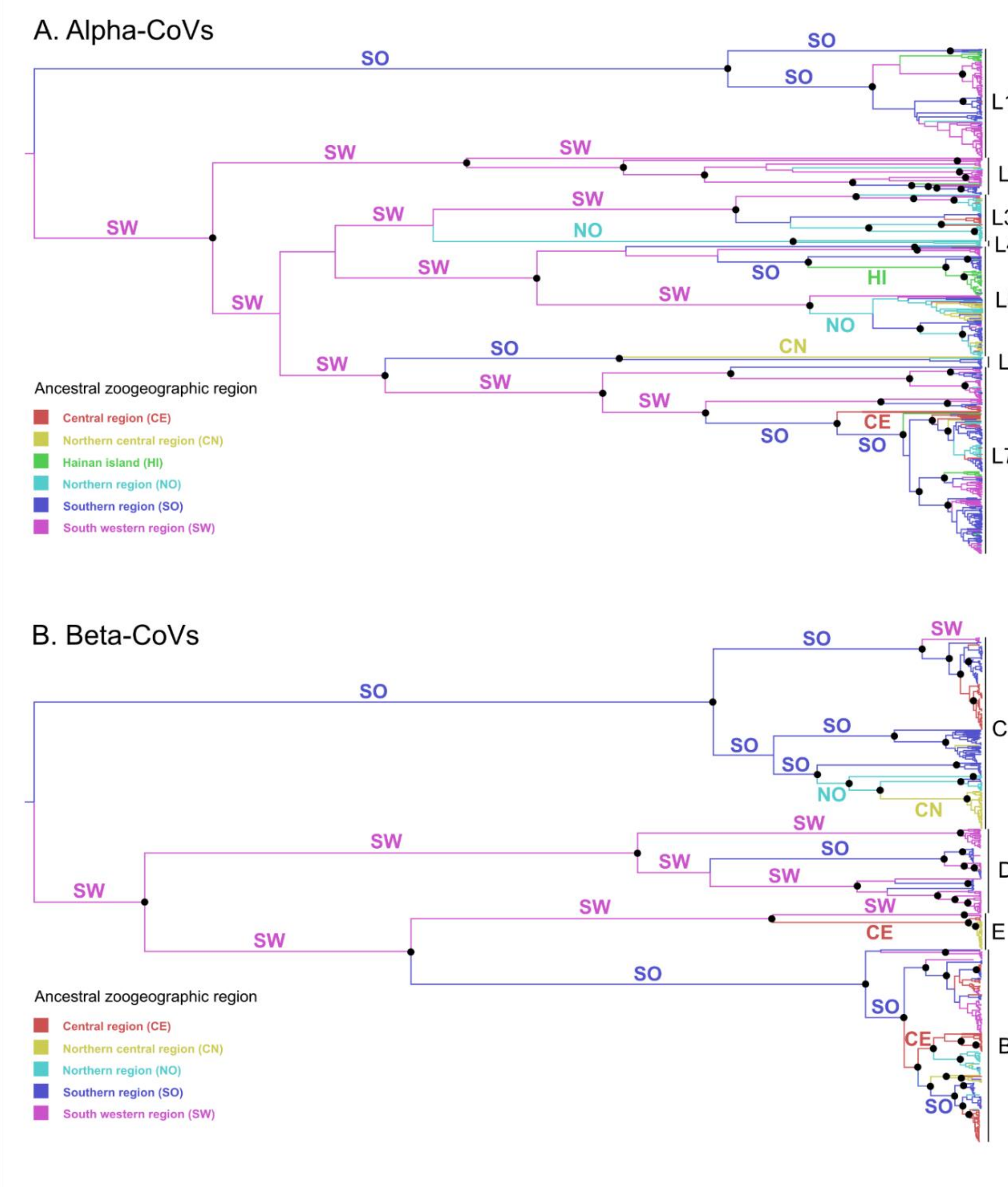


Supplementary Figure 10: Zoomed in beta-CoV maximum clade credibility annotated tree focusing on Lineage E corresponding to *Hibecovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with the highest probability.

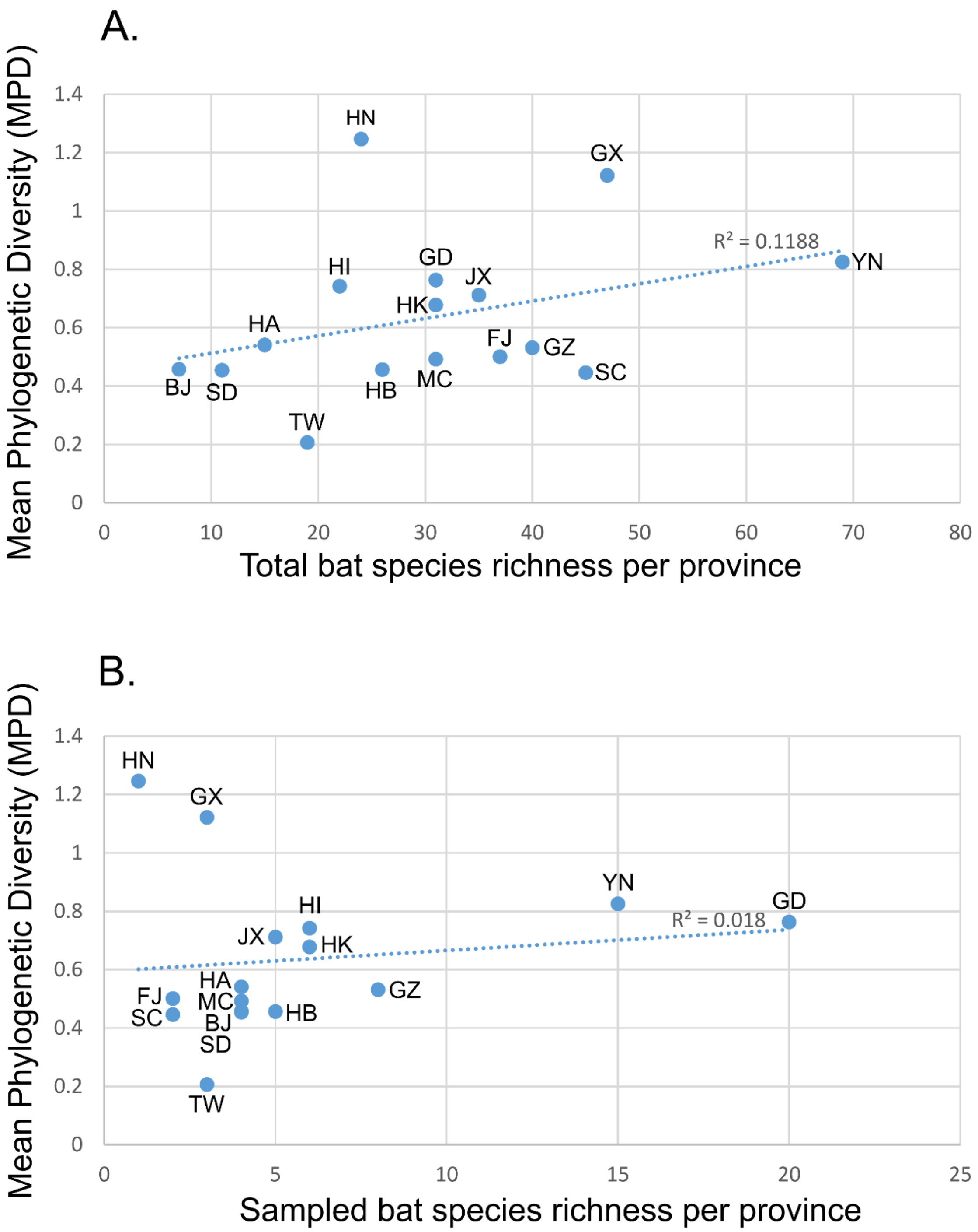


Beta-CoVs - B - *Sarbecovirus*

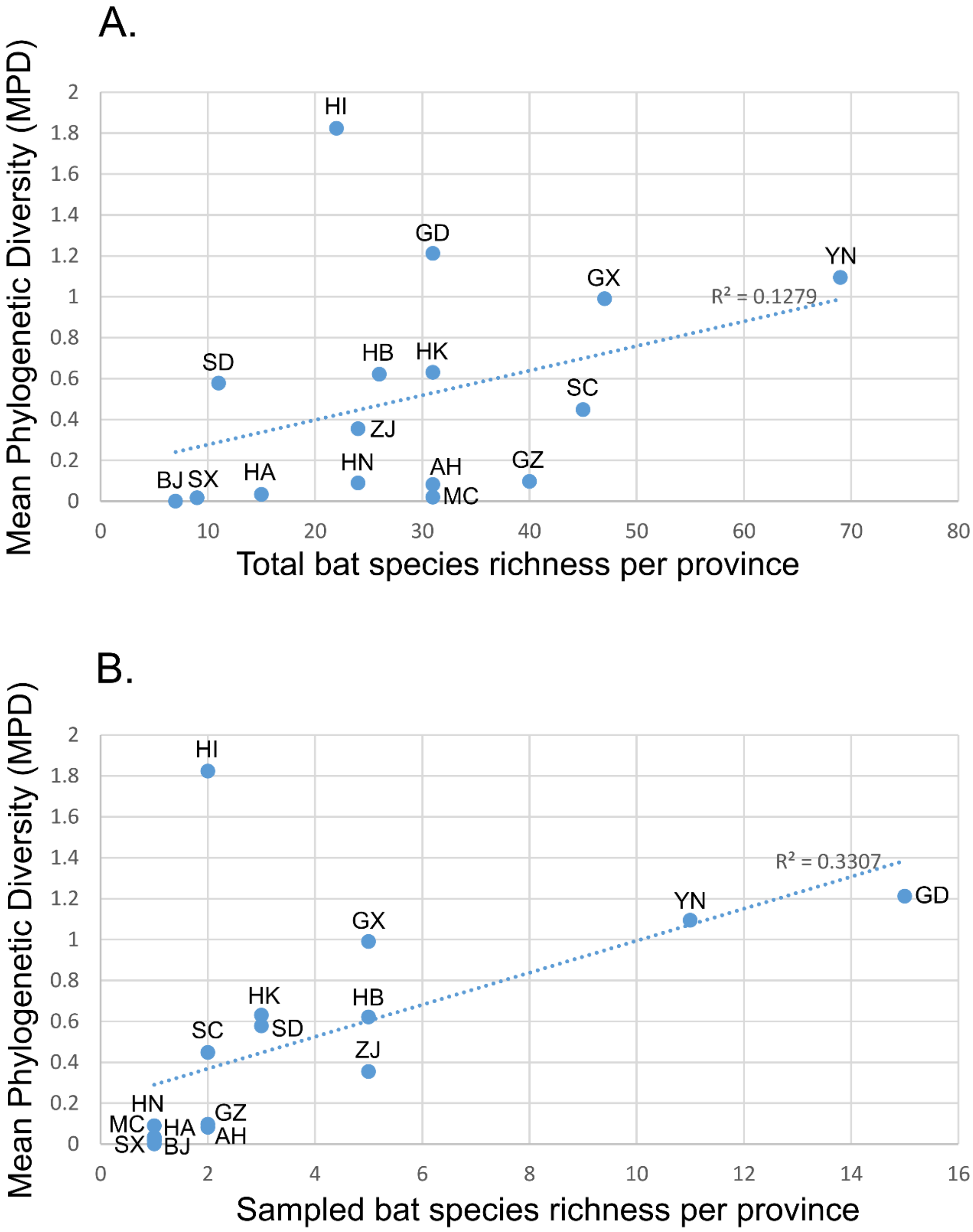
Supplementary Figure 11: Zoomed in beta-CoV maximum clade credibility annotated tree focusing on Lineage C corresponding to *Sarbecovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with the highest probability.



Supplementary Figure 12: Alpha-CoV (A) and beta-CoV (B) maximum clade credibility annotated trees using complete datasets of RdRp sequences and zoogeographic regions as discrete character state. Branches colors correspond to the inferred zoogeographic region with the highest probability. Branch lengths are scaled according to time. Well-supported nodes (posterior probability > 0.95) are indicated with a black dot. The ICTV approved CoV subgenera were highlighted: Rhinacovirus (L1), Decacovirus (L2), Myotacovirus (L3), Pedacovirus (L5), Nyctacovirus (L6), Minunacovirus (L7) and an unidentified lineage (L4) for alpha-CoVs; and Merbecovirus (Lineage C), Nobecovirus (lineage D), Hibecovirus (lineage E) and Sarbecovirus (Lineage B) for beta-CoVs. NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region; HI, Hainan island



Supplementary Figure 13: Scatter plot and linear regression between alpha-CoV phylogenetic diversity (MPD) and total (A) or sampled (B) bat species richness per province using the complete dataset. BJ, Beijing; FJ, Fujian; GD, Guangdong; GX, Guangxi; GZ, Guizhou; HA, Henan; HB, Hubei; HI, Hainan; HK, Hong Kong; HN, Hunan; JX, Jiangxi; MC, Macau; SC, Sichuan; SD, Shandong; TW, Taiwan; YN, Yunnan.



Supplementary Figure 14: Scatter plot and linear regression between beta-CoV phylogenetic diversity (MPD) and total (A) or sampled (B) bat species richness per province using the complete dataset. AH, Anhui; BJ, Beijing; GD, Guangdong; GX, Guangxi; GZ, Guizhou; HA, Henan; HB, Hubei; HI, Hainan; HK, Hong Kong; HN, Hunan; MC, Macau; SC, Sichuan; SD, Shandong; SX, Shanxi; YN, Yunnan; ZJ, Zhejiang.

Supplementary Tables

Supplementary Table 1: Total numbers of RdRp sequences available for all CoV lineages from each bat species included in this study. Numbers in parentheses correspond to the number of sequences retrieved from GenBank.

	Beta-CoVs				Alpha-CoVs						
	B	C	D	E	L1	L2	L3	L4	L5	L6	L7
Pteropodidae											
Cynopterus sphinx			23 (14)								
Eonycteris spelaea			11								
Megaerops sp.			1 (1)								
Rousettus leschenaultii			35 (35)			2 (2)					
Rousettus sp.			13								
Hipposideridae											
Aselliscus stoliczkanus	4 (1)					2			2		
Hipposideros armiger	4 (2)		2	1	2	2	1 (1)				
Hipposideros cineraceus					1 (1)						
Hipposideros pomona	3			4 (1)	1	23 (10)					
Hipposideros pratti	1			29 (1)	1 (1)						
Rhinolophidae											
Rhinolophus affinis	5 (3)				59 (9)	5 (1)					1 (1)
Rhinolophus ferrumequinum	20 (12)				1 (1)	6 (5)					
Rhinolophus hipposideros						1 (1)					
Rhinolophus macrotis	2 (2)				1		1 (1)				
Rhinolophus monoceros									3 (3)		
Rhinolophus pearsonii	2 (2)						1 (1)				1 (1)
Rhinolophus pusillus	37 (28)				6 (4)		1 (1)		1 (1)		2 (2)
Rhinolophus rex	1 (1)				7 (7)						
Rhinolophus sinicus	107 (47)				27 (20)	6 (6)	2 (2)				8 (5)
Rhinolophus					1 (1)						

stheno											
Rhinolophus thomasi	1 (1)										
Rhinolophus sp.	9				37	3			1		1
Miniopteridae											
Miniopterus schreibersii					2		1 (1)	1 (1)	10 (9)		139 (80)
Miniopterus fuscus						1 (1)					11 (2)
Miniopterus magnater											4 (4)
Miniopterus pusillus											34 (2)
Miniopterus sp.									1		38 (14)
Vespertilionidae											
Eptesicus serotinus		9 (9)								2 (2)	
Hypsugo sp.		13 (2)								11 (4)	
Ia io		3 (2)					1 (1)				
Murina leucogaster								6 (6)			
Myotis chinensis							1		6		
Myotis daubentonii		5 (5)			1 (1)		5 (5)		28 (28)		3 (3)
Myotis davidii							10 (10)		10 (10)		1 (1)
Myotis fimbriatus									6 (6)		
Myotis horsfieldii			1								1
Myotis myotis							1 (1)				
Myotis pequinius		3 (3)									
Myotis ricketti		1 (1)			1 (1)		24 (21)		56 (19)		4 (2)
Myotis siligorensis							1 (1)				
Myotis sp.						1 (1)	6 (6)		3 (1)		
Nyctalus plancyi										1 (1)	
Pipistrellus abramus		34 (21)	3								
Pipistrellus pipistrellus		1 (1)									
Pipistrellus sp.			1								
Scotophilus kuhlii		1 (1)							44 (14)		

Tylonycteris pachypus		96 (57)									1
Tylonycteris robustula										1 (1)	
Vespertilio sinensis		39 (2)		3					3		
Total	196	205	90	37	148	52	56	7	174	15	249

Supplementary Table 2: Significant pairwise transitions between bat families for alpha-CoVs and their corresponding Bayes Factor (BF) and posterior probability (PP) using the complete dataset and random subset. Only transitions with BF >10 for at least one dataset are presented.

Donor family	Recipient family	Complete dataset		Random dataset	
		BF	PP	BF	PP
Miniopteridae	Rhinolophidae	23483.1	1	28.9	0.899
Miniopteridae	Vespertilionidae	23483.1	1	3.1	0.468
Rhinolophidae	Hipposideridae	23483.1	1	148.8	0.978
Vespertilionidae	Miniopteridae	23483.1	1	14.2	0.814
Vespertilionidae	Rhinolophidae	23483.1	1	2.9	0.469
Rhinolophidae	Miniopteridae	7825.5	0.999	0.6	0.168
Rhinolophidae	Vespertilionidae	3351.9	0.999	20.3	0.861
Hipposideridae	Pteropodidae	2606.3	0.999	14.5	0.816
Hipposideridae	Rhinolophidae	408.8	0.992	47.3	0.935

Supplementary Table 3: Significant pairwise transitions between bat families for beta-CoVs and their corresponding Bayes Factor (BF) and posterior probability (PP) using the complete dataset and random subset. Only transitions with BF >10 for at least one dataset are presented.

Donor family	Recipient family	Complete dataset		Random dataset	
		BF	PP	BF	PP
Hipposideridae	Vespertilionidae	16194.7	0.999	20243.3	0.999
Rhinolophidae	Hipposideridae	16194.7	1	20243.3	1
Pteropodidae	Hipposideridae	7.7	0.773	25.6	0.919

Supplementary Table 4: Number of state changes (Markov jumps) from/to each bat family (donor/receiver) along the significant inter-family transition rates for alpha-CoVs using the complete dataset and random subset.

Family	Complete dataset			Random dataset		
	Donor	Receiver	Total	Donor	Receiver	Total
Hipposideridae	11	13.5	24.5	28.4	24.6	53
Rhinolophidae	28.4	33.3	61.7	35.2	31.9	67.1
Vespertilionidae	21.8	24.3	46.1	6.6	10.5	7.1
Miniopteridae	31.6	19.3	50.9	8.3	6.6	14.9
Pteropodidae	0	2.4	2.4	0	4.8	4.8

Supplementary Table 5: Number of state changes (Markov jumps) from/to each bat family (donor/receiver) along the significant inter-family transition rates for beta-CoVs using the complete dataset and random subset.

Family	Complete dataset			Random dataset		
	Donor	Receiver	Total	Donor	Receiver	Total
Hipposideridae	3.4	7.9	11.3	2.4	6.9	9.3
Rhinolophidae	6.3	0	6.3	5.3	0	5.3
Vespertilionidae	0	3.4	3.4	0	2.4	2.4
Pteropodidae	1.6	0	1.6	1.6	0	1.6

Supplementary Table 6: Significant pairwise transitions between bat genera for alpha-CoVs and their corresponding Bayes Factor (BF) and posterior probability (PP) using the complete dataset and random subset. Only transitions with BF >10 for at least one dataset are presented.

Donor genus	Recipient genus	Complete dataset		Random dataset	
		BF	PP	BF	PP
Miniopterus	*Myotis*	88497.5	1	1410.2	0.991
Miniopterus	*Rhinolophus*	88497.5	1	440.3	0.973
Rhinolophus	*Hipposideros*	88497.5	1	99559.7	1
Myotis	*Miniopterus*	11051.4	0.999	5844.9	0.998
Scotophilus	*Miniopterus*	2669.8	0.996	21.1	0.632
Rhinolophus	*Myotis*	1540.5	0.993	771.7	0.984
Myotis	*Vespertilio*	1438.7	0.992	167.4	0.932
Rhinolophus	*Miniopterus*	1167.8	0.99	0.4	0.034
Hipposideros	*Aselliscus*	322.9	0.963	1734. 6	0.993
Myotis	*Rhinolophus*	242.1	0.952	11.4	0.481
Hipposideros	*Rousettus*	112.7	0.902	523.1	0.977
Miniopterus	*Tylonycteris*	102.4	0.893	1351.7	0.991
Scotophilus	*Myotis*	45.3	0.787	170.7	0.933
Myotis	*Aselliscus*	22.9	0.651	1.9	0.132
Rhinolophus	*Ia*	21.7	0.639	1.2	0.091
Aselliscus	*Rhinolophus*	17.8	0.591	1.8	0.128
Murina	*Miniopterus*	16.5	0.573	1.4	0.099
Hypsugo	*Eptesicus*	15.4	0.556	15.3	0.555
Hipposideros	*Rhinolophus*	10.7	0.465	134.6	0.916
Eptesicus	*Hypsugo*	10.2	0.455	10.8	0.467
Vespertilio	*Aselliscus*	3.9	0.242	68.8	0.848
Ia	*Hipposideros*	1.4	0.106	10.4	0.459

Supplementary Table 7: Significant pairwise transitions between bat genera for beta-CoVs and their corresponding Bayes Factor (BF) and posterior probability (PP) using the complete dataset and random subset. Only transitions with BF >10 for at least one dataset are presented.

Donor genus	Recipient genus	Complete dataset		Random dataset	
		BF	PP	BF	PP
Rousettus	*Eonycteris*	19130.4	0.999	95425.9	1
Rhinolophus	*Hipposideros*	4544.7	0.997	47706.3	0.999
Hipposideros	*Vespertilio*	2887.3	0.995	10591.1	0.999
Tylonycteris	*Scotophilus*	1354.1	0.990	10591.1	0.999
Eonycteris	*Rousettus*	380.6	0.966	13.4	0.502
Hypsugo	*Myotis*	211.9	0.941	862.3	0.985
Ia	*Pipistrellus*	68.9	0.838	160.5	0.923
Rousettus	*Megaerops*	63.5	0.827	166.8	0.926
Cynopterus	*Myotis*	31.9	0.706	28.8	0.684

Cynopterus	*Rousettus*	31.4	0.703	816.6	0.984
Cynopterus	*Pipistrellus*	22.9	0.633	70.5	0.841
Cynopterus	*Hipposideros*	20.8	0.611	29.3	0.688
Myotis	*Eptesicus*	18.4	0.580	15.1	0.533
Hipposideros	*Aselliscus*	14.3	0.519	5.1	0.279
Rhinolophus	*Aselliscus*	11.3	0.461	37.3	0.737
Eptesicus	*Myotis*	11.2	0.457	12.2	0.479

Supplementary Table 8: Number of state changes (Markov jumps) from/to each bat genus (donor/receiver) along the significant inter-family transition rates for alpha-CoVs using the complete dataset and random subset.

Genus	Complete dataset			Random dataset		
	Donor	Receiver	Total	Donor	Receiver	Total
Aselliscus	1.3	5.6	6.9	0.7	2.7	3.4
Eptesicus	1	1.3	2.3	0.7	0.8	1.5
Hipposideros	10.9	17.9	28.8	6.6	10.5	17.1
Hypsugo	1.3	1	2.3	0.8	0.7	1.5
Ia	0	1.2	1.2	0	1.3	1.3
Miniopterus	37.3	23.4	60.7	5.8	4.2	10
Murina	1.7	0	1.7	1.2	0	1.2
Myotis	25.4	26.6	52	4.4	2.7	7.1
Nyctalus	0	0	0	0	0	0
Rhinolophus	36.8	37.7	74.5	13.8	9	22.8
Rousettus	0	2.3	2.3	0	1.7	1.7
Scotophilus	7.1	0	7.1	2.3	0	2.3
Tylonycteris	0	2	2	0	1.4	1.4
Vespertilio	0	3.9	3.9	0	1.3	1.3

Supplementary Table 9: Number of state changes (Markov jumps) from/to each bat genus (donor/receiver) along the significant inter-family transition rates for beta-CoVs using the complete dataset and random subset.

Genus	Complete dataset			Random dataset		
	Donor	Receiver	Total	Donor	Receiver	Total
Aselliscus	0	2.9	2.9	0	1.4	1.4
Cynopterus	12.3	0	12.3	5.4	0	5.4
Eonycteris	1.2	20.2	21.4	4.1	2.8	6.9
Eptesicus	1.7	1.9	3.6	0.9	0.8	1.7
Hipposideros	5.8	14.5	20.3	1.8	5.3	7.1
Hypsugo	3.1	0	3.1	1.5	0	1.5
Ia	3.4	0	3.4	1.4	0	1.4
Megaerops	0	2.9	2.9	0	0.2	0.2
Myotis	1.9	7.5	9.4	0.8	3.5	4.3
Pipistrellus	0	6.3	6.3	0	2.8	2.8
Rhinolophus	14.2	0	14.2	5.1	0	5.1
Rousettus	23.1	5.1	28.2	3	5.7	8.7
Scotophilus	0	2.9	2.9	0	1.3	1.3
Tylonycteris	2.9	0	2.9	1.3	0	1.3
Vespertilio	0	5.5	5.5	0	1.6	1.6

Supplementary Table 10: Significant pairwise transitions between zoogeographic regions for alpha-CoVs and their corresponding Bayes Factor (BF) and posterior probability (PP) using the complete dataset and random subset. Only transitions with BF >10 for at least one dataset are presented. NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region; HI, Hainan island.

Donor region	Recipient region	Complete dataset		Random dataset	
		BF	PP	BF	PP
CN	SO	30740.3	1	2.3	0.350
HI	SO	30740.3	1	2397.6	0.998
NO	CN	2790.7	0.998	6.2	0.592
SO	CE	649.9	0.993	13.4	0.759
NO	CE	441.3	0.990	122.9	0.966
SW	SO	267.8	0.984	13.3	0.757
SW	NO	136.1	0.969	0.5	0.112
SO	SW	83.6	0.951	19.7	0.822
CE	SW	60.4	0.934	2.4	0.362
SO	HI	58.3	0.932	5.2	0.550
HI	NO	32.1	0.882	0.3	0.063
CN	NO	2.9	0.405	14.2	0.769

Supplementary Table 11: Significant pairwise transitions between zoogeographic regions for beta-CoVs and their corresponding Bayes Factor (BF) and posterior probability (PP) using the complete dataset and random subset. Only transitions with BF >10 for at least one dataset are presented. NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region.

Donor region	Recipient region	Complete dataset		Random dataset	
		BF	PP	BF	PP
SO	CE	835.5	0.996	122.7	0.974
NO	SO	94.2	0.966	0.6	0.157
SW	SO	66.0	0.953	95.2	0.967
CE	SW	45.5	0.933	132.6	0.976
NO	CN	27.7	0.895	197.8	0.984
CE	NO	14.3	0.814	8.8	0.730
SO	SW	10.7	0.766	1.4	0.305
CE	SO	5.8	0.6	22.9	0.875

Supplementary Table 12: Number of state changes (Markov jumps) from/to each zoogeographic region (donor/receiver) along the significant dispersal routes for alpha-CoVs using the complete dataset and random subset. NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region; HI, Hainan island.

Region	Complete dataset			Random dataset		
	Donor	Receiver	Total	Donor	Receiver	Total
CE	19.9	41.2	61.1	0	41.2	41.2
CN	42.9	22.4	65.3	23.6	0	23.6
HI	36.8	9.4	46.2	18.1	0	18.1
NO	46.5	20.1	66.5	25.1	23.6	48.7
SO	52	88.6	140.6	30.6	32.6	63.2
SW	29	45.5	74.5	14.6	14.5	29.1

Supplementary Table 13: Number of state changes (Markov jumps) from/to each zoogeographic region (donor/receiver) along the significant dispersal routes for beta-CoVs using the complete dataset and random subset. NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region.

Region	Complete dataset			Random dataset		
	Donor	Receiver	Total	Donor	Receiver	Total
CE	14.8	9.6	24.2	25.4	12.1	37.5
CN	0	7.5	7.5	0	7.6	7.6
NO	17.4	6.0	23.4	7.6	0	7.6
SO	17.1	17.4	34.5	12.1	21.4	33.5
SW	7.5	16.4	23.9	8.3	12.2	20.5

Supplementary Table 14: Mean Phylogenetic Distance (mpd.obs) and its standardized effect size (mpd.obs.z) within bat families for alpha-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mpd.obs.p) are highlighted in bold.

	Complete dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Hipposideridae	29	0.688	0.857	0.054	11	-3.138	**0.0110**	1000
Miniopteridae	222	0.333	0.853	0.015	1	-34.984	**0.0010**	1000
Pteropodidae	2	0.006	0.869	0.405	1	-2.129	**0.0010**	1000
Rhinolophidae	123	0.713	0.854	0.023	1	-6.167	**0.0010**	1000
Vespertilionidae	174	0.634	0.853	0.018	1	-12.010	**0.0010**	1000
	Random subset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Hipposideridae	29	0.697	0.921	0.037	1	-6.089	**0.0010**	1000
Miniopteridae	39	0.326	0.920	0.029	1	-20.262	**0.0010**	1000
Pteropodidae	2	0.007	0.903	0.383	7	-2.340	**0.0070**	1000
Rhinolophidae	34	0.921	0.919	0.034	464	0.040	0.4640	1000
Vespertilionidae	30	0.755	0.920	0.036	1	-4.515	**0.0010**	1000

Supplementary Table 15: Mean Phylogenetic Distance (mpd.obs) and its standardized effect size (mpd.obs.z) within bat families for beta-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mpd.obs.p) are highlighted in bold.

	Complete dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Hipposideridae	21	0.7053	1.2273	0.0693	1	-7.527	**0.0010**	1000
Pteropodidae	58	0.4290	1.2315	0.0315	1	-25.481	**0.0010**	1000
Rhinolophidae	103	0.1187	1.2306	0.0203	1	-54.789	**0.0010**	1000
Vespertilionidae	117	0.4542	1.2304	0.0184	1	-42.097	**0.0010**	1000
	Random subset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Hipposideridae	21	0.724838	1.261965	0.059781	1	-8.98499	0.000999	1000
Pteropodidae	33	0.438785	1.26173	0.041737	1	-19.7172	0.000999	1000
Rhinolophidae	34	0.123321	1.262034	0.038973	1	-29.2182	0.000999	1000
Vespertilionidae	39	0.545279	1.260986	0.037071	1	-19.3065	0.000999	1000

Supplementary Table 16: Mean Nearest Taxon Distance (mntd.obs) and its standardized effect size (mntd.obs.z) within bat families for alpha-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mntd.obs.p) are highlighted in bold.

	Complete dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Hipposideridae	29	0.0484	0.1205	0.0300	8	-2.4027	**0.0080**	1000
Miniopteridae	222	0.0239	0.0254	0.0036	343	-0.4042	0.3427	1000
Pteropodidae	2	0.0057	0.8612	0.4040	4.5	-2.1177	**0.0045**	1000
Rhinolophidae	123	0.0175	0.0414	0.0067	1	-3.5612	**0.0010**	1000
Vespertilionidae	174	0.0310	0.0312	0.0049	468	-0.0575	0.4675	1000
	Random subset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Hipposideridae	29	0.0474	0.1346	0.0313	2	-2.7889	**0.0020**	1000
Miniopteridae	39	0.0545	0.1065	0.0230	11	-2.2656	**0.0110**	1000
Pteropodidae	2	0.0075	0.9117	0.3732	4	-2.4229	**0.0040**	1000
Rhinolophidae	34	0.0602	0.1183	0.0275	13	-2.1108	**0.0130**	1000
Vespertilionidae	30	0.1483	0.1319	0.0304	711	0.5411	0.7103	1000

Supplementary Table 17: Mean Nearest Taxon Distance (mntd.obs) and its standardized effect size (mntd.obs.z) within bat families for beta-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mntd.obs.p) are highlighted in bold.

	Complete dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Hipposideridae	21	0.0826	0.1145	0.0376	222	-0.847	0.222	1000
Pteropodidae	58	0.0156	0.0424	0.0102	1	-2.610	**0.001**	1000
Rhinolophidae	103	0.0119	0.0262	0.0043	1	-3.344	**0.001**	1000
Vespertilionidae	117	0.0247	0.0233	0.0035	658	0.388	0.657	1000
	Random subset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Hipposideridae	21	0.0922	0.1179	0.0342	255	-0.7498	0.2547	1000
Pteropodidae	33	0.0234	0.0689	0.0175	2	-2.5961	**0.0020**	1000
Rhinolophidae	34	0.0246	0.0666	0.0162	1	-2.5910	**0.0010**	1000
Vespertilionidae	39	0.0599	0.0574	0.0132	604	0.1888	0.6034	1000

Supplementary Table 18: Mean Phylogenetic Distance (mpd.obs) and its standardized effect size (mpd.obs.z) within bat genera for alpha-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mpd.obs.p) are highlighted in bold.

	Complete dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Eptesicus	2	0.0155	0.8360	0.4188	8	-1.9591	**0.0080**	1000
Hipposideros	25	0.6517	0.8556	0.0618	3	-3.2997	**0.0030**	1000
Hypsugo	3	0.0192	0.8580	0.2572	2	-3.2614	**0.0020**	1000
Miniopterus	222	0.3332	0.8534	0.0154	1	-33.8196	**0.0010**	1000
Murina	4	0.1323	0.8527	0.2033	11	-3.5438	**0.0110**	1000
Myotis	130	0.5830	0.8534	0.0222	1	-12.1821	**0.0010**	1000
Rhinolophus	123	0.7127	0.8521	0.0239	1	-5.8310	**0.0010**	1000
Rousettus	2	0.0057	0.8369	0.4131	3	-2.0122	**0.0030**	1000
Scotophilus	29	0.0457	0.8518	0.0550	1	-14.6628	**0.0010**	1000
Vespertilio	3	0.0101	0.8534	0.2666	1	-3.1629	**0.0010**	1000
Aselliscus	4	0.7467	0.8573	0.2034	281	-0.5441	0.2807	1000
Tylonycteris	2	0.8257	0.8670	0.3970	263	-0.1040	0.2627	1000
Nyctalus	1	NA	NaN	NA	NA	NA	NA	1000
Ia	1	NA	NaN	NA	NA	NA	NA	1000
	Random subset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Eptesicus	2	0.0176	0.9298	0.3730	14	-2.4458	**0.0140**	1000
Hipposideros	25	0.6612	0.9194	0.0416	1	-6.2046	**0.0010**	1000
Hypsugo	3	0.0211	0.9064	0.2276	1	-3.8894	**0.0010**	1000
Miniopterus	39	0.3257	0.9198	0.0292	1	-20.3600	**0.0010**	1000
Murina	4	0.1285	0.9252	0.1703	5	-4.6778	**0.0050**	1000
Myotis	8	0.7143	0.9234	0.0927	26	-2.2564	**0.0260**	1000
Rhinolophus	34	0.9206	0.9175	0.0323	482	0.0960	0.4815	1000
Rousettus	2	0.0075	0.9064	0.3793	2	-2.3701	**0.0020**	1000
Scotophilus	6	0.0316	0.9176	0.1175	1	-7.5397	**0.0010**	1000
Vespertilio	3	0.0184	0.9273	0.2322	2	-3.9145	**0.0020**	1000
Aselliscus	4	0.7599	0.9189	0.1710	177	-0.9295	0.1768	1000
Tylonycteris	2	0.8217	0.9508	0.3537	231.5	-0.3651	0.2313	1000
Nyctalus	1	NA	NaN	NA	NA	NA	NA	1000
Ia	1	NA	NaN	NA	NA	NA	NA	1000

Supplementary Table 19: Mean Phylogenetic Distance (mpd.obs) and its standardized effect size (mpd.obs.z) within bat genera for beta-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mpd.obs.p) are highlighted in bold.

	Complete dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Cynopterus	9	0.0387	1.2272	0.1376	1	-8.6357	**0.0010**	1000
Eonycteris	10	0.3887	1.2222	0.1305	1	-6.3859	**0.0010**	1000
Eptesicus	5	0.1658	1.2498	0.2304	6	-4.7052	**0.0060**	1000
Hipposideros	20	0.6994	1.2297	0.0704	1	-7.5356	**0.0010**	1000
Hypsugo	5	0.0422	1.2328	0.2353	1	-5.0602	**0.0010**	1000
Ia	2	0.0415	1.2711	0.6764	39	-1.8179	**0.0390**	1000
Myotis	8	0.7057	1.2244	0.1535	7	-3.3787	**0.0070**	1000
Pipistrellus	33	0.1848	1.2329	0.0446	1	-23.5152	**0.0010**	1000

Rhinolophus	103	0.1187	1.2299	0.0217	1	-51.1789	**0.0010**	1000
Rousettus	42	0.3904	1.2304	0.0401	1	-20.9568	**0.0010**	1000
Tylonycteris	43	0.0393	1.2295	0.0411	1	-28.9869	**0.0010**	1000
Vespertilio	24	0.4223	1.2301	0.0632	1	-12.7811	**0.0010**	1000
Aselliscus	1	NA	NaN	NA	NA	NA	NA	1000
Megaerops	1	NA	NaN	NA	NA	NA	NA	1000
Scotophilus	1	NA	NaN	NA	NA	NA	NA	1000
	Random subset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Cynopterus	7	0.0444	1.2603	0.1643	1	-7.4009	**0.0010**	1000
Eonycteris	10	0.3830	1.2599	0.1084	1	-8.0918	**0.0010**	1000
Eptesicus	5	0.1666	1.2609	0.2150	3	-5.0891	**0.0030**	1000
Hipposideros	20	0.7198	1.2636	0.0644	1	-8.4454	**0.0010**	1000
Hypsugo	5	0.0429	1.2568	0.2157	1	-5.6279	**0.0010**	1000
Ia	2	0.0423	1.2299	0.6504	44.5	-1.8258	**0.0445**	1000
Myotis	7	0.7409	1.2604	0.1551	8	-3.3502	**0.0080**	1000
Pipistrellus	7	0.6448	1.2594	0.1680	10	-3.6586	**0.0100**	1000
Rhinolophus	34	0.1233	1.2603	0.0414	1	-27.4860	**0.0010**	1000
Rousettus	17	0.3935	1.2628	0.0750	1	-11.5884	**0.0010**	1000
Tylonycteris	8	0.0427	1.2642	0.1369	1	-8.9241	**0.0010**	1000
Vespertilio	7	0.7478	1.2580	0.1613	12	-3.1631	**0.0120**	1000
Aselliscus	1	NA	NaN	NA	NA	NA	NA	1000
Megaerops	1	NA	NaN	NA	NA	NA	NA	1000
Scotophilus	1	NA	NaN	NA	NA	NA	NA	1000

Supplementary Table 20: Mean Nearest Taxon Distance (mntd.obs) and its standardized effect size (mntd.obs.z) within bat genera for alpha-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mntd.obs.p) are highlighted in bold.

	Complete dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Eptesicus	2	0.0155	0.8361	0.4293	11	-1.9114	**0.0110**	1000
Hipposideros	25	0.0613	0.1355	0.0356	13	-2.0856	**0.0130**	1000
Hypsugo	3	0.0101	0.6834	0.3046	1	-2.2107	**0.0010**	1000
Miniopterus	222	0.0239	0.0253	0.0036	354	-0.3752	0.3536	1000
Murina	4	0.0675	0.5582	0.2503	29	-1.9598	**0.0290**	1000
Myotis	130	0.0312	0.0393	0.0070	127	-1.1619	0.1269	1000
Rhinolophus	123	0.0175	0.0416	0.0071	1	-3.3978	**0.0010**	1000
Rousettus	2	0.0057	0.8577	0.4033	3	-2.1128	**0.0030**	1000
Scotophilus	29	0.0123	0.1194	0.0307	1	-3.4858	**0.0010**	1000
Vespertilio	3	0.0067	0.6734	0.3079	1	-2.1656	**0.0010**	1000
Aselliscus	4	0.1922	0.5786	0.2391	53	-1.6160	0.0529	1000
Tylonycteris	2	0.8257	0.8529	0.3976	280.5	-0.0683	0.2802	1000
Nyctalus	1	NA	NaN	NA	NA	NA	NA	1000
Ia	1	NA	NaN	NA	NA	NA	NA	1000
	Random subset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Eptesicus	2	0.0176	0.9167	0.3761	12	-2.3905	**0.0120**	1000
Hipposideros	25	0.0627	0.1514	0.0379	8	-2.3394	**0.0080**	1000
Hypsugo	3	0.0113	0.7619	0.2925	1	-2.5657	**0.0010**	1000
Miniopterus	39	0.0545	0.1060	0.0219	13	-2.3561	**0.0130**	1000
Murina	4	0.0660	0.6334	0.2445	12	-2.3205	**0.0120**	1000
Myotis	8	0.4345	0.3939	0.1392	620	0.2914	0.6194	1000
Rhinolophus	34	0.0602	0.1195	0.0278	14	-2.1340	**0.0140**	1000
Rousettus	2	0.0075	0.9389	0.3615	2	-2.5764	**0.0020**	1000
Scotophilus	6	0.0107	0.4958	0.1836	1	-2.6423	**0.0010**	1000
Vespertilio	3	0.0115	0.7442	0.2942	1	-2.4905	**0.0010**	1000
Aselliscus	4	0.1951	0.6353	0.2489	39	-1.7686	**0.0390**	1000
Tylonycteris	2	0.8217	0.9268	0.3632	231	-0.2894	0.2308	1000
Nyctalus	1	NA	NaN	NA	NA	NA	NA	1000
Ia	1	NA	NaN	NA	NA	NA	NA	1000

Supplementary Table 21: Mean Nearest Taxon Distance (mntd.obs) and its standardized effect size (mntd.obs.z) within bat genera for beta-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mntd.obs.p) are highlighted in bold.

	Complete dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Cynopterus	9	0.0068	0.2779	0.1044	1	-2.5964	**0.0010**	1000
Eonycteris	10	0.0201	0.2470	0.0910	1	-2.4935	**0.0010**	1000
Eptesicus	5	0.0066	0.5392	0.2396	1	-2.2232	**0.0010**	1000
Hipposideros	20	0.0883	0.1218	0.0390	209	-0.8599	0.2088	1000
Hypsugo	5	0.0342	0.5407	0.2477	6	-2.0445	**0.0060**	1000
Ia	2	0.0415	1.2035	0.6902	41	-1.6835	**0.0410**	1000
Myotis	8	0.2677	0.3179	0.1275	351	-0.3938	0.3506	1000
Pipistrellus	33	0.0909	0.0723	0.0215	803	0.8643	0.8022	1000

Rhinolophus	103	0.0119	0.0261	0.0042	1	-3.3579	**0.0010**	1000
Rousettus	42	0.0325	0.0565	0.0154	40	-1.5572	**0.0400**	1000
Tylonycteris	43	0.0028	0.0559	0.0153	1	-3.4829	**0.0010**	1000
Vespertilio	24	0.0047	0.1001	0.0321	1	-2.9686	**0.0010**	1000
Aselliscus	1	NA	NaN	NA	NA	NA	NA	1000
Megaerops	1	NA	NaN	NA	NA	NA	NA	1000
Scotophilus	1	NA	NaN	NA	NA	NA	NA	1000
	Random subset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Cynopterus	7	0.0093	0.4256	0.1495	1	-2.7847	**0.0010**	1000
Eonycteris	10	0.0189	0.2808	0.0911	1	-2.8739	**0.0010**	1000
Eptesicus	5	0.0084	0.6073	0.2377	2	-2.5197	**0.0020**	1000
Hipposideros	20	0.0986	0.1244	0.0349	239	-0.7397	0.2388	1000
Hypsugo	5	0.0356	0.6098	0.2502	1	-2.2954	**0.0010**	1000
Ia	2	0.0423	1.3030	0.6178	33	-2.0405	**0.0330**	1000
Myotis	7	0.3056	0.4231	0.1559	243	-0.7536	0.2428	1000
Pipistrellus	7	0.3442	0.4248	0.1514	301	-0.5324	0.3007	1000
Rhinolophus	34	0.0246	0.0669	0.0161	2	-2.6303	**0.0020**	1000
Rousettus	17	0.0674	0.1504	0.0432	19	-1.9231	**0.0190**	1000
Tylonycteris	8	0.0078	0.3623	0.1238	1	-2.8652	**0.0010**	1000
Vespertilio	7	0.0081	0.4180	0.1494	1	-2.7430	**0.0010**	1000
Aselliscus	1	NA	NaN	NA	NA	NA	NA	1000
Megaerops	1	NA	NaN	NA	NA	NA	NA	1000
Scotophilus	1	NA	NaN	NA	NA	NA	NA	1000

Supplementary Table 22: Mean Phylogenetic Distance (mpd.obs) and its standardized effect size (mpd.obs.z) within zoogeographic regions for alpha-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mpd.obs.p) are highlighted in bold. NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region; HI, Hainan island.

	Complete dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
CE	33	0.6571	0.8088	0.0531	13	-2.8550	**0.0130**	1000
CN	26	0.4569	0.8073	0.0602	1	-5.8252	**0.0010**	1000
HI	36	0.7413	0.8063	0.0515	125	-1.2631	0.1249	1000
NO	61	0.7342	0.8051	0.0367	44	-1.9351	**0.0440**	1000
SO	195	0.7418	0.8048	0.0169	1	-3.7391	**0.0010**	1000
SW	161	0.8226	0.8047	0.0201	811	0.8898	0.8102	1000
	Random subset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
CE	33	0.6753	0.8627	0.0444	1	-4.2172	**0.0010**	1000
CN	26	0.4747	0.8603	0.0540	1	-7.1421	**0.0010**	1000
HI	36	0.7807	0.8602	0.0428	38	-1.8555	**0.0380**	1000
NO	42	0.7455	0.8625	0.0374	2	-3.1302	**0.0020**	1000
SO	48	0.7953	0.8612	0.0360	46	-1.8293	**0.0460**	1000
SW	47	0.9428	0.8622	0.0367	1000	2.1976	**0.9990**	1000

Supplementary Table 23: Mean Phylogenetic Distance (mpd.obs) and its standardized effect size (mpd.obs.z) within zoogeographic regions for beta-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mpd.obs.p) are highlighted in bold. NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region.

	Complete dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
CE	53	0.9032	1.2591	0.0372	1	-9.5621	**0.0010**	1000
CN	40	1.0626	1.2571	0.0462	1	-4.2134	**0.0010**	1000
NO	23	0.8428	1.2543	0.0688	1	-5.9774	**0.0010**	1000
SO	103	1.1273	1.2571	0.0223	1	-5.8184	**0.0010**	1000
SW	67	1.0388	1.2577	0.0330	1	-6.6241	**0.0010**	1000
	Random subset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
CE	30	0.6653	1.2250	0.0666	1	-8.4043	**0.0010**	1000
CN	25	0.9666	1.2230	0.0760	5	-3.3733	**0.0050**	1000
NO	23	0.7454	1.2213	0.0794	1	-5.9950	**0.0010**	1000
SO	30	1.0708	1.2238	0.0673	25	-2.2720	**0.0250**	1000
SW	37	1.0042	1.2179	0.0591	3	-3.6137	**0.0030**	1000

Supplementary Table 24: Mean Nearest Taxon Distance (mntd.obs) and its standardized effect size (mntd.obs.z) within zoogeographic regions for alpha-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mntd.obs.p) are highlighted in bold. NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region; HI, Hainan island.

	Complete dataset							
	ntaxa	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
CE	33	0.0583	0.1070	0.0274	19	-1.7747	**0.0190**	1000
CN	26	0.1045	0.1274	0.0342	252	-0.6718	0.2517	1000
HI	36	0.0415	0.1003	0.0246	5	-2.3947	**0.0050**	1000
NO	61	0.0584	0.0691	0.0151	248	-0.7085	0.2478	1000
SO	195	0.0119	0.0300	0.0050	1	-3.6427	**0.0010**	1000
SW	161	0.0200	0.0349	0.0061	5	-2.4495	**0.0050**	1000
	Random subset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
CE	33	0.0601	0.1013	0.0256	43	-1.6079	**0.0430**	1000
CN	26	0.1179	0.1249	0.0322	423	-0.2185	0.4226	1000
HI	36	0.0482	0.0951	0.0225	15	-2.0847	**0.0150**	1000
NO	42	0.0627	0.0843	0.0196	135	-1.0965	0.1349	1000
SO	48	0.0451	0.0769	0.0168	21	-1.8985	**0.0210**	1000
SW	47	0.0679	0.0775	0.0174	311	-0.5539	0.3107	1000

Supplementary Table 25: Mean Nearest Taxon Distance (mntd.obs) and its standardized effect size (mntd.obs.z) within zoogeographic regions for beta-CoVs using the complete dataset and random subset. One-tailed p-values (quantiles) were calculated after randomly reshuffling tip labels 1000 times along the entire phylogeny (=mpd.obs.rank/runs+1). Significant p-value (mntd.obs.p) are highlighted in bold. NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region.

	Complete dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
CE	53	0.0413	0.0460	0.0119	385	-0.3900	0.3846	1000
CN	40	0.0162	0.0615	0.0175	1	-2.5923	**0.0010**	1000
NO	23	0.0097	0.1081	0.0347	1	-2.8372	**0.0010**	1000
SO	103	0.0198	0.0258	0.0041	73	-1.4606	0.0729	1000
SW	67	0.0151	0.0368	0.0083	1	-2.6244	**0.0010**	1000
	Random subset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
CE	30	0.0803	0.0752	0.0239	606	0.2105	0.6054	1000
CN	25	0.0077	0.0899	0.0290	1	-2.8348	**0.0010**	1000
NO	23	0.0094	0.0983	0.0310	1	-2.8703	**0.0010**	1000
SO	30	0.0360	0.0748	0.0229	35	-1.6969	**0.0350**	1000
SW	37	0.0658	0.0592	0.0177	662	0.3720	0.6613	1000

Supplementary Table 26: R square and p-value of linear regression analysis between Alpha-CoV phylogenetic diversity (MPD) and bat species richness (total or sampled) per zoogeographic region or province in China

	Complete dataset	
Linear regression	R square	p-value
Total bat richness per zoogeographic region	0.033	0.728
Sampled bat richness per zoogeographic region	0.199	0.374
Total bat richness per province	0.119	0.191
Sampled bat richness per province	0.018	0.621
	Random subset	
Linear regression	R square	p-value
Total bat richness per zoogeographic region	0.075	0.599
Sampled bat richness per zoogeographic region	0.209	0.362
Total bat richness per province	0.203	0.080
Sampled bat richness per province	0.073	0.311

Supplementary Table 27: R square and p-value of linear regression analysis between Beta-CoV phylogenetic diversity (MPD) and bat species richness (total or sampled) per zoogeographic region or province in China

	Complete dataset	
Linear regression	R square	p-value
Total bat richness per zoogeographic region	0.090	0.624
Sampled bat richness per zoogeographic region	0.440	0.222
Total bat richness per province	0.128	0.174
Sampled bat richness per province	0.331	**0.020**
	Random subset	
Linear regression	R square	p-value
Total bat richness per zoogeographic region	0.011	0.866
Sampled bat richness per zoogeographic region	0.352	0.292
Total bat richness per province	0.101	0.231
Sampled bat richness per province	0.352	**0.015**

Supplementary Table 28: Phylogenetic β-diversity (standardized effect size (SES) of the Mean Phylogenetic Distance (MPD)) among bat families for alpha-CoVs using the complete dataset (below the diagonal) and random subset (above the diagonal).

	Hipposideridae	Rhinolophidae	Vespertilionidae	Miniopteridae	Pteropodidae
Hipposideridae		20.1333	-4.5575	1.1073	4.0884
Rhinolophidae	7.1505		7.8328	10.0433	0.0297
Vespertilionidae	8.4421	7.0519		3.0433	3.6763
Miniopteridae	15.5949	20.3070	13.8885		-3.4863
Pteropodidae	-2.6837	4.4666	4.0478	5.3109	

Supplementary Table 29: Phylogenetic β-diversity (standardized effect size (SES) of the Mean Phylogenetic Distance (MPD)) among bat families for Beta-CoVs using the complete dataset (below the diagonal) and random subset (above the diagonal).

	Hipposideridae	Rhinolophidae	Vespertilionidae	Pteropodidae
Hipposideridae		7.6102	-12.614	3.0319
Rhinolophidae	-11.9738		15.5243	15.8607
Vespertilionidae	5.2859	24.4489		8.8575
Pteropodidae	5.9384	18.2126	27.8056	

Supplementary Table 30: Phylogenetic β-diversity (standardized effect size (SES) of the Mean Phylogenetic Distance (MPD)) among bat genera for alpha-CoVs using the complete dataset (below the diagonal) and random subset (above the diagonal).

	Aselliscus	*Hipposideros*	*Rhinolophus*	*Eptesicus*	*Hypsugo*	*Ia*	*Murina*	*Myotis*	*Nyctalus*	*Scotophilus*	*Tylonycteris*	*Vespertilio*	*Miniopterus*	*Rousettus*
Aselliscus		-2.800	-0.509	0.288	0.948	-0.775	-1.288	-2.951	-0.565	-1.171	0.736	-3.34	4.102	-1.171
Hipposideros	-1.101		1.446	2.755	4.408	-0.044	0.723	1.609	0.526	2.528	3.645	0.634	20.23	-4.814
Rhinolophus	1.638	6.981		0.843	2.235	-1.99	-2.113	-3.783	-0.959	-1.778	1.322	-2.145	10.110	3.036
Eptesicus	0.479	2.554	1.655		-4.702	-0.592	-1.018	-1.041	-1.739	-0.581	-0.4	-0.876	1.185	1.877
Hypsugo	1.046	3.799	2.946	-3.818		-0.418	-0.611	-0.421	-1.784	0.030	-0.027	-0.529	2.872	2.769
Ia	-0.396	0.299	0.062	-0.258	-0.039		-1.765	-2.244	-0.890	-1.63	-0.388	-1.518	-0.268	0.634
Murina	-0.364	2.212	-0.705	-0.238	0.238	-0.623		-3.554	-1.573	-2.870	-0.552	-2.75	-0.145	1.414
Myotis	-2.075	8.289	4.289	0.012	0.99	-1.727	-2.202		-1.857	-3.894	-0.602	-6.332	-0.242	2.339
Nyctalus	-0.296	0.826	-0.009	-1.554	-1.554	-0.603	-0.858	-1.205		-1.401	-0.912	-1.375	-0.910	0.819
Scotophilus	0.957	10.902	7.918	1.590	2.728	0.445	-0.401	-3.158	0.088		-0.020	-3.355	1.144	2.285
Tylonycteris	0.769	2.967	1.724	-0.408	-0.131	-0.099	0.086	0.248	-0.872	2.056		-0.476	-5.056	2.298
Vespertilio	-2.293	1.328	-1.047	-0.593	-0.252	-0.852	-2.276	-6.619	-1.068	-3.216	-0.334		-0.131	1.259
Miniopterus	3.069	15.72	20.662	0.728	1.778	0.43	1.312	7.774	-0.622	10.820	-3.077	0.07		7.978
Rousettus	-0.601	-2.944	4.751	1.869	2.565	0.549	2.215	4.124	0.917	5.396	2.155	1.532	5.732	

Supplementary Table 31: Phylogenetic β-diversity (standardized effect size (SES) of the Mean Phylogenetic Distance (MPD)) among bat genera for beta-CoVs using the complete dataset (below the diagonal) and random subset (above the diagonal).

	Aselliscus	*Hipposideros*	*Rhinolophus*	*Eptesicus*	*Hypsugo*	*Ia*	*Myotis*	*Pipistrellus*	*Scotophilus*	*Tylonycteris*	*Vespertilio*	*Cynopterus*	*Eonycteris*	*Megaerops*	*Rousettus*
Aselliscus		-2.172	-5.361	0.576	0.666	0.254	0.917	1.073	0.868	2.011	0.001	0.851	2.489	1.393	2.371
Hipposideros	-2.064		-11.697	0.524	0.855	-0.001	1.376	1.937	1.792	5.119	-2.577	0.376	5.859	2.969	5.995
Rhinolophus	-4.736	-11.642		1.918	2.334	0.823	3.401	4.119	2.745	8.087	-0.253	2.805	10.023	4.514	11.32
Eptesicus	0.702	1.176	2.491		-5.272	-4.151	-4.692	-4.486	-1.645	-3.921	-4.900	0.993	4.437	2.401	4.356
Hypsugo	0.831	1.588	3.092	-4.464		-3.526	-4.943	-4.795	-1.987	-4.795	-4.552	1.211	4.618	2.488	4.671
Ia	0.401	0.54	1.314	-3.586	-2.922		-3.677	-2.756	-1.109	-2.566	-3.512	0.387	2.622	1.572	2.502
Myotis	1.033	2.206	4.361	-3.906	-4.137	-3.037		-4.043	-1.914	-4.639	-4.041	0.355	4.371	2.506	4.313
Pipistrellus	1.597	5.021	11.489	-5.82	-6.718	-3.602	-5.913		-1.803	-4.393	-3.617	0.754	4.898	2.712	4.860
Scotophilus	0.93	1.966	2.852	-1.372	-1.669	-0.920	-1.744	-2.495		-4.247	-1.064	1.785	3.555	1.836	3.695
Tylonycteris	2.593	9.336	20.573	-5.027	-6.129	-3.055	-7.00	-14.206	-4.906		-2.563	4.477	9.210	4.307	10.176
Vespertilio	-0.364	-3.713	-2.526	-6.447	-5.95	-4.477	-5.889	-9.562	-1.434	-7.181		0.280	4.144	2.386	3.944
Cynopterus	0.378	-0.659	1.227	1.250	1.562	0.631	1.004	3.47	1.821	6.808	-1.505		-4.091	-0.688	-6.017
Eonycteris	1.838	4.353	7.791	4.368	4.646	2.724	4.938	9.092	3.355	13.055	3.582	-3.698		-3.456	-10.8
Megaerops	1.119	2.386	3.624	2.3388	2.431	1.557	2.565	3.991	1.782	5.519	2.201	-0.654	-2.913		-3.464
Rousettus	2.172	6.571	16.731	5.735	6.327	3.449	6.756	15.928	4.298	23.882	5.498	-5.729	-10.765	-3.676	

Supplementary Table 32: Phylogenetic β-diversity (standardized effect size (SES) of the Mean Phylogenetic Distance (MPD)) among zoogeographic regions for Alpha-CoVs using the complete dataset (below the diagonal) and random subset (above the diagonal). NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region; HI, Hainan island.

	CE	CN	NO	SO	SW	HI
CE		-0.4238	2.9153	-4.8786	-2.7423	4.4078
CN	0.9041		-1.2683	-5.5677	-1.4736	0.4568
NO	-1.7163	-2.8428		1.7891	0.943	4.8338
SO	-2.8927	-1.2139	-1.7968		-2.0649	3.5021
SW	0.6287	2.4100	2.0902	0.6691		4.7082
HI	3.7697	1.2204	3.5429	2.6766	6.1801	

Supplementary Table 33: Phylogenetic β-diversity (standardized effect size (SES) of the Mean Phylogenetic Distance (MPD)) among zoogeographic regions for Beta-CoVs using the complete dataset (below the diagonal) and random subset (above the diagonal). NO, Northern region; CN, Central northern region; SW, South western region; CE, Central region; SO, Southern region.

	CE	CN	NO	SO	SW
CE		-2.3751	-9.0517	0.9142	6.3531
CN	-5.2248		-3.6026	-1.3420	6.8906
NO	-6.7161	-5.686		0.0850	6.2733
SO	-1.6547	-5.4274	-1.2255		8.6052
SW	7.0965	3.6185	3.4593	16.3362	

Supplementary Table 34: GenBank accession numbers of Alpha-CoV sequences

	Lineages						
Hosts	L1	L2	L3	L4	L5	L6	L7
Pteropodidae							
Rousettus leschenaultii		JQ989270-271					
Hipposideridae							
Aselliscus stoliczkanus		MN312307 MN312477			MN312268-269		
Hipposideros armiger	MN312240 MN312251	MN312473 MN312475	KY770852				
Hipposideros cineraceus	KU182955						
Hipposideros pomona	MF769513	MN312250 MN312290 MN312308 MN312310-312 MN312314-315 MN312406-408 MN312455 MN312581 JQ989266-269 JQ989272-273 KP895522-523 KU343195-196					
Hipposideros pratti	KX285186						
Rhinolophidae							
Rhinolophus affinis	KX285119-120 MF769453 MF769468-470 MF769485 MN312247 MN312261 MN312267 MN312273 MN312276 MN312289 MN312303 MN312318 MN312320-321 MN312323 MN312325-329 MN312331-334 MN312336 MN312338 MN312341 MN312344-349 MN312351-352 MN312354-355 MN312359 MN312454 MN312456 MN312458 MN312465 MN312476 MN312479 MN312561	MN312356 MN312474 MN312481-482 KP876527					KP876544

	MN312576-580 MN312582-583 MN312587-588 KP876528 KU343198						
Rhinolophus ferrumequinum	KJ473808	MN312417 KF569979-981 KJ473807 KX285155					
Rhinolophus hipposideros		KF569982					
Rhinolophus macrotis	MN312411		KY770854				
Rhinolophus monoceros					KT381913 KT381915-916		
Rhinolophus pearsonii			KY770853				KF294272
Rhinolophus pusillus	MF760455 MF760515 MF769475-476 MN312516 MN312586		KY770855		KY009617		KY783865 KY783896
Rhinolophus rex	KX285187-193						
Rhinolophus sinicus	MF769447-451 MF769466-467 MF769477-478 MF769508-509 MF769511 MN312291 MN312293-294 MN312449-450 MN312478 MN312515 EF203064-067 KP876537 KP876540-541 KU182954	KP876532 KP876536 KU182967-968 KU182970-971	KX285168 KX285169				MN312405 MN312451 MN312590 KP876509 KP876525-526 KP876533 KP876545
Rhinolophus stheno	KP895525						
Rhinolophus sp.	MN312241-242 MN312246 MN312249 MN312252 MN312254 MN312256-257 MN312260 MN312263 MN312265 MN312270-272 MN312274-275 MN312277-278 MN312301 MN312319 MN312322 MN312324 MN312337 MN312339-340 MN312350 MN312357 MN312457 MN312461-462	MN312330 MN312463 MN312472			MN312258		MN312253

	MN312480 MN312243 MN312245 MN312264 MN312292 MN312299 MN312335						
Miniopteridae							
Miniopterus schreibersii	MN312286 MN312466		KX285179	KF294378	KX285171 KX285176 MN312445 KT381919-923 KX285176 KF294383		KX285115-117 KX285121-124 KX285170 KX285172-175 KX285177-178 MN312248 MN312279-280 MN312283-284 MN312287-288 MN312302 MN312372-373 MN312378 MN312380 MN312382-387 MN312389 MN312394 MN312397-400 MN312402 MN312404 MN312421-422 MN312507 MN312592 KY783870-872 KY783874 KY783876-878 KY783880 MN312452-453 MN312483-484 MN312486-487 MN312491 MN312493-498 MN312504 MN312511-512 MN312537 MN312547 MN312550-551 MN312559-560 MN312564-565 KJ473795-804 KP876505-506 KP876512-515 KT381917-918 KU343190 KX285118 KX285171-175 DQ648835 DQ648850 KF294268-271 KF294273-282 KP876507-508 KP876510 KP876517-518 KP876521 KU343191 KU343194 KY783887-888 KY783890-894

							KY783897-901 KY783903
Miniopterus fuscus		KP876534					MN312295-297 MN312300 MN312305 MN312313 MN312566-568 KU343192-193
Miniopterus magnater							DQ666337 DQ666339-340 EU420138
Miniopterus pusillus							MN312365-366 MN312377 MN312379 MN312381 MN312388 MN312390-392 MN312401 MN312403 MN312435-439 MN312485 MN312488-490 MN312492 MN312499-502 MN312505-506 MN312508-510 MN312513 MN312548 DQ666338 EU420137
Miniopterus sp.					MN312446		KX285129-133 MN312262 MN312281-282 MN312285 MN312298 MN312306 MN312317 MN312342-343 MN312353 MN312358 MN312360-362 MN312460 MN312468 MN312470 KY783873 KY783875 KY783879 MN312304 MN312309 MN312467 MN312469 MN312503 MN312562-563 KP876519-520 KP876522-524 KP876542
Vespertilionidae							
Eptesicus serotinus						KY009627 KY009631	
Hypsugo sp.						KX285210-213 MN312569-575	
Ia io			KY770857				
Murina				KF294373-377 KU182966			

leucogaster							
Myotis chinensis			MN312412		MN312375 MN312523-524 MN312530 MN312532-533		
Myotis daubentonii	KP895492		KF569975 KF569995 KP895499 KP895508 KP895510		KF569974 KF569976-978 KF569994 KP895494 KP895496 KP895498 KP895500-507 KP895509 KP895511-521		DQ648855 KP895491 KP895493
Myotis davidii			KX285201-206 KF294381 KF569991 KY770851 KY770856		KF294382 KF569983-988 KF569990 KF569992-993		KF569989
Myotis fimbriatus					KY009612 KY009620 KY009623 KY009629 KY009630 KY009633		
Myotis horsfieldii							MN312433
Myotis myotis			KX285183				
Myotis ricketti	MF769510		KX285137 KX285141-142 KX285126 KX285128 KX285147-149 KX285151-152 KX285154 MN312415 KJ473806 KX285137-140 KX285142-154		KX285215-216 MN312367 MN312370 MN312410 MN312416 KX285127 KX285214 KX285217-218 KY383882 KY783866-869 KY783881 KY783883-885 MN312363 MN312368-369 MN312371 MN312374 MN312376 MN312393 MN312395-396 MN312409 MN312414 MN312418 MN312440 MN312442-444 MN312448 MN312520-522 MN312525-528 MN312531 MN312534-536 MN312543-546 MN312549 DQ648833 KP895490 KY009616 KY009625		KX285143 MN312364 MN312447 KX285141

Myotis siligorensis			KY770850				
Myotis sp.		KJ473810	KX285138-139 KX285144-146 KX285153		KX285194 MN312413 MN312514		
Nyctalus plancyi						KJ473809	
Scotophilus kuhlii					MN312419-420 MN312423-432 MN312434 MN312538-542 MN312552-558 MN312584-585 MN312589 MN312593-594 DQ648822-823 DQ648858 KT381902-912		
Tylonycteris pachypus							MN312591
Tylonycteris robustula						KX447559	
Vespertilio sinensis					MN312517-519		

Supplementary Table 35: GenBank accession numbers of Beta-CoV sequences

	Lineages			
Hosts	B	C	D	E
Pteropodidae				
Cynopterus sphinx			MN312674 MN312827-828 MN312836-841 KU182961-962 KU182992-003	
Eonycteris spelaea			MN312612-613 MN312616 MN312619 MN312622-623 MN312666-670	
Megaerops sp.			KU182986	
Rousettus leschenaultii			MG762654-656 MG762658 EF065513-514 KP895482-489 KP895524 KU182958-960 KU182974-985 KU182987-991	
Rousettus sp.			MN312610 MN312614-615 MN312617-618 MN312620-621 MN312624 MN312627-631	
Hipposideridae				
Aselliscus stoliczkanus	KY417142 MN312601 MN312603 MN312607			
Hipposideros armiger	KX285135-136 MN312598 MN312856		MN312860-861	MN312817
Hipposideros pomona	MN312658-659 MN312661			MN312608-609 MN312625 KU343200
Hipposideros pratti	MN312855			MN312789-813 MN312863-865 KF636752
Rhinolophidae				
Rhinolophus affinis	MN312602 MN312634 KF569973 KF569996 KP876546			
Rhinolophus ferrumequinum	KX285156 MN312832-835 MN312857 MN312867-869 DQ412042 DQ648856 KF294456 KJ473811-813 KP886808-809 KU182964 KY417145 KY770860			

Rhinolophus macrotis	DQ412043 DQ648857			
Rhinolophus pearsonii	KF294442-443			
Rhinolophus pusillus	MN312652 MN312656 MN312660 MN312662-664 MN312742 MN312843-844 JX993987 KF294420 KF294422-424 KF294426-430 KF294434-438 KF294444-454 KF294457 KT381914			
Rhinolophus rex	KF294455			
Rhinolophus sinicus	KX285125 KX285134 KX285220 KY417151-152 MN312595-596 MN312600 MN312604-606 MN312637-645 MN312650 MN312653-654 MN312657 MN312688 MN312691-711 MN312738-741 MN312814-816 MN312818-821 MN312826 MN312829-831 MN312845-846 MN312858-859 DQ022305 DQ071615 DQ084199-200 DQ648795 FJ588686 GQ153539-548 KC881005-006 KF294421 KF294431-433 KF294440-441 KF367457 KJ473814-816 KT444582 KU182963 KX447563-565 KY417143-144 KY417146-152 KY770858-859			
Rhinolophus thomasi	KF294425			
Rhinolophus sp.	MN312632-633 MN312635-636 MN312671-673 MN312651			

	MN312655			
Vespertilionidae				
Eptesicus serotinus		KY009613 KY009618-619 KY009621 KY009624 KY009626 KY009628 KY009632 KY009634		
Hypsugo sp.		KX285208 MN312842 MN312848-849 MN312852-854 KX285207 KX285209 MN312647 MN312850-851 KX442564		
Ia io		KX285195-196 KX285196 MN312847		
Myotis daubentonii		KU182956-957 KU182965 KU182972-973		
Myotis horsfieldii			MN312680	
Myotis pequinius		KY009614-615 KY009622		
Myotis ricketti		KX285219		
Pipistrellus abramus		KX285197 KX285199-200 MG021452 MN312646 MN312648-649 MN312665 MN312678-679 MN312681-683 MN312685-687 MN312866 DQ648809 KC522075-089 KJ473820	MN312675 MN312677 MN312684	
Pipistrellus pipistrellus		DQ648819		
Pipistrellus sp.			MN312676	
Scotophilus kuhlii		KX285160		
Tylonycteris pachypus		KX285157-159 KX285161-167 KY783855-864 KY783886 MN312689-690 MN312712-737 MN312743-748 MN312822-825 MN312862 DQ648794 KC522036-048 KJ473822 KX285160		

		KX447544-558 KX447560-562 KY783889 KY783895 KY783902		
Vespertilio sinensis		KX285223 MN312749-753 MN312753 MN312757-788 KJ473821		MN312754 MN312755 MN312756

Supplementary Table 36: Acknowledgement table of GISAID data used in this study. We gratefully acknowledge the Authors from the Originating laboratories responsible for obtaining the specimens and the Submitting laboratories where genetic sequence data were generated and shared via the GISAID Initiative, on which some of our analysis are based.

Virus name	GISAID Accession No.	Collection date	Originating laboratory	Submitting laboratory	Authors
hCoV-19/pangolin/Guangxi/P4L/2017	EPI_ISL_410538	2017	Beijing Institute of Microbiology and Epidemiology	Beijing Institute of Microbiology and Epidemiology	Wu-Chun Cao; Tommy Tsan-Yuk Lam; Na Jia; Ya-Wei Zhang; Jia-Fu Jiang; Bao-Gui Jiang
hCoV-19/pangolin/Guangxi/P1E/2017	EPI_ISL_410539	2017			
hCoV-19/pangolin/Guangxi/P5L/2017	EPI_ISL_410540	2017			
hCoV-19/pangolin/Guangxi/P5E/2017	EPI_ISL_410541	2017			
hCoV-19/pangolin/Guangxi/P2V/2017	EPI_ISL_410542	2017			
hCoV-19/pangolin/Guangxi/P3B/2017	EPI_ISL_410543	2017			
hCoV-19/pangolin/Guangxi/P2S/2017	EPI_ISL_410544	2017			
hCoV-19/pangolin/Guangdong/1/2019	EPI_ISL_410721	2019	South China Agricultural University	South China Agricultural University	Yongyi Shen, Lihua Xiao, Wu Chen
hCoV-19/bat/Yunnan/RmYN02/2019	EPI_ISL_412977	2019-06-25	Shandong First Medical University & Shandong Academy of Medical Sciences	Institute of Microbiology, Chinese Academy of Sciences	Weifeng Shi, Tao Hu, Hong Zhou, Juan Li, Xing Chen, Alice Catherine Hughes, Yuhai Bi