Supplementary Information: Origin and cross-species transmission of bat coronaviruses in China

Latinne *et al.*

<u>Supplementary Note 1</u>

GenBank accession numbers of sequences generated for this study

MN312240- MN312303, MN312316-MN312607, MN312632-MN312665, MN312671-MN312869

GenBank accession numbers of additional sequences included in this study

Bat-CoVs: AY864196*, DQ022305, DQ071615, DQ084199, DQ084200, DQ249224*, DQ249226*, DQ249228*, DQ412042, DQ412043, DQ648794, DQ648795, DQ648809, DQ648819, DQ648822, DQ648823, DQ648833, DQ648835, DQ648837, DQ648850, DQ648856, DQ648857, DQ648858, DQ666337, DQ666338, DQ666339, DQ666340, EF065506*, EF065513, EF065514, EF065515*, EF065516*, EF203064, EF203065, EF203066, EF203067, EU420137, EU420138, FJ588686, GQ153539, GQ153540, GQ153541, GQ153542, GQ153543, GQ153544, GQ153545, GQ153546, GQ153547, GQ153548, HM211098, HM211099, HM211100, HM211101, JQ989266, JQ989267, JQ989268, JQ989269, JQ989270, JQ989271, JQ989272, JQ989273, JX993987, KC522036, KC522037, KC522038, KC522039, KC522040, KC522041, KC522042, KC522043, KC522044, KC522045, KC522046, KC522047, KC522048, KC522075, KC522076, KC522077, KC522078, KC522079, KC522080, KC522081, KC522082, KC522083, KC522084, KC522085, KC522086, KC522087, KC522088, KC522089, KC881005, KC881006, KF294268, KF294269, KF294270, KF294271, KF294272, KF294273, KF294274, KF294275, KF294276, KF294277, KF294278, KF294279, KF294280, KF294281, KF294282, KF294373, KF294374, KF294375, KF294376, KF294377, KF294378, KF294381, KF294382, KF294383, KF294420, KF294421, KF294422, KF294423, KF294424, KF294425, KF294426, KF294427, KF294428, KF294429, KF294430, KF294431, KF294432, KF294433, KF294434, KF294435, KF294436, KF294437, KF294438, KF294440, KF294441, KF294442, KF294443, KF294444, KF294445, KF294446, KF294447, KF294448, KF294449, KF294450, KF294451, KF294452, KF294453, KF294454, KF294455, KF294456, KF294457, KF367457, KF569973, KF569974, KF569975, KF569976, KF569977, KF569978, KF569979, KF569980, KF569981, KF569982, KF569983, KF569984, KF569985, KF569986, KF569987, KF569988, KF569989, KF569990, KF569991, KF569992, KF569993, KF569994, KF569995, KF569996, KF636752, KJ473795, KJ473796, KJ473797, KJ473798, KJ473799, KJ473800, KJ473801, KJ473802, KJ473803, KJ473804, KJ473806, KJ473807, KJ473808, KJ473809, KJ473810, KJ473811, KJ473812, KJ473813, KJ473814, KJ473815, KJ473816, KJ473820, KJ473821, KJ473822, KP876505, KP876506, KP876507, KP876508, KP876509, KP876510, KP876512, KP876513, KP876514, KP876515, KP876517, KP876518, KP876519, KP876520, KP876521, KP876522, KP876523, KP876524, KP876525, KP876526, KP876527, KP876528, KP876532, KP876533, KP876534, KP876536, KP876537, KP876540, KP876541, KP876542, KP876544, KP876545, KP876546, KP886808, KP886809, KP895482, KP895483, KP895484, KP895485, KP895486, KP895487, KP895488, KP895489, KP895490, KP895491, KP895492, KP895493, KP895494, KP895496, KP895498, KP895499, KP895500, KP895501, KP895502, KP895503, KP895504, KP895505, KP895506, KP895507, KP895508, KP895509, KP895510, KP895511, KP895512, KP895513, KP895514, KP895515, KP895516, KP895517, KP895518, KP895519, KP895520, KP895521, KP895522, KP895523, KP895524, KP895525, KT381902, KT381903, KT381904, KT381905, KT381906, KT381907, KT381908, KT381909, KT381910, KT381911, KT381912, KT381913, KT381914, KT381915, KT381916, KT381917, KT381918, KT381919, KT381920, KT381921, KT381922, KT381923, KT444582, KU182954, KU182955, KU182956, KU182957, KU182958, KU182959, KU182960, KU182961, KU182962, KU182963, KU182964, KU182965, KU182966, KU182967, KU182968, KU182970, KU182971, KU182972, KU182973, KU182974, KU182975, KU182976, KU182977, KU182978, KU182979, KU182980, KU182981, KU182982, KU182983, KU182984, KU182985, KU182986,

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*Undated sequences included in phylogenetic diversity and Mantel test analyses only.

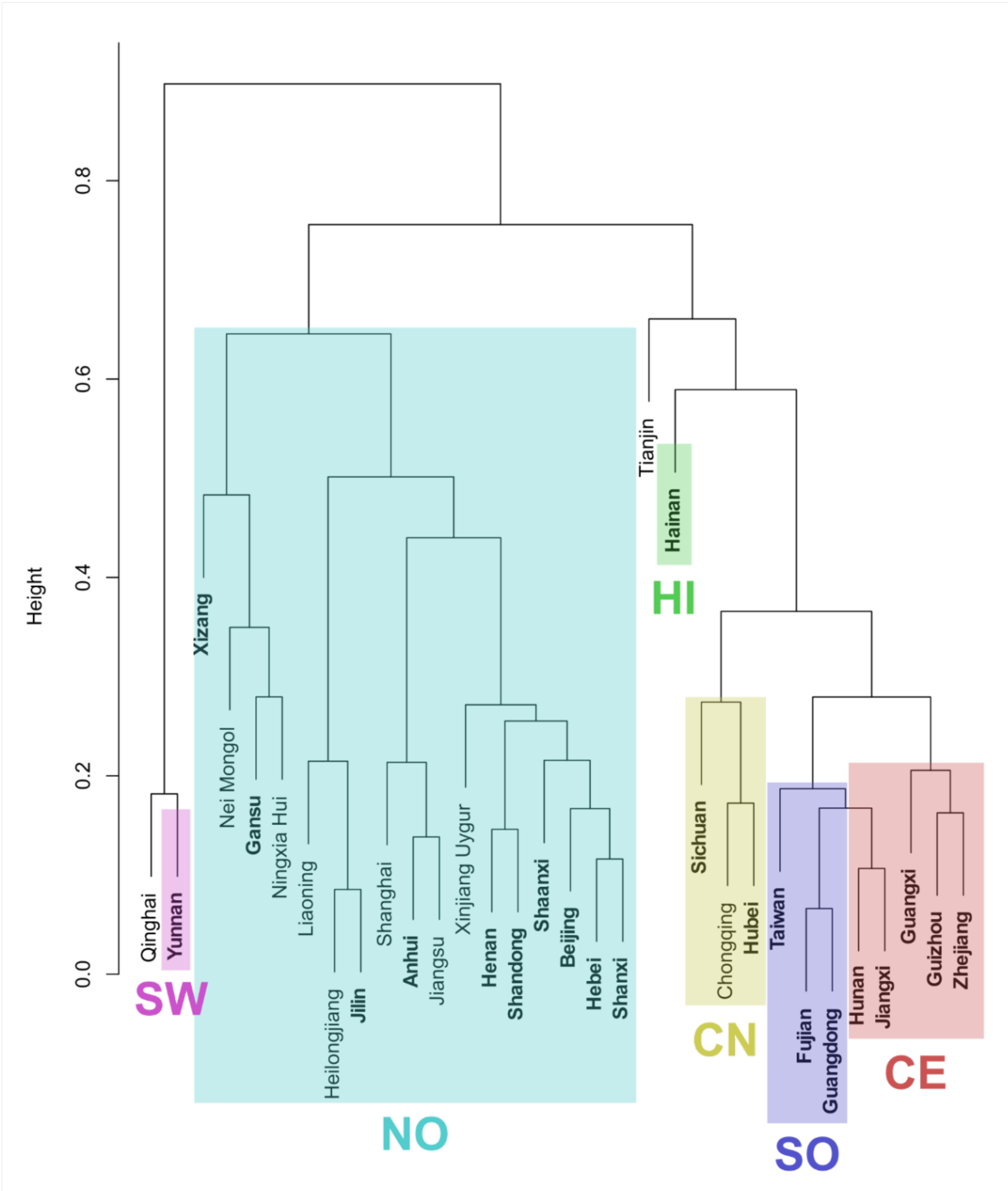
Accession numbers of additional sequences included only in the phylogenetic analysis and median-joining network of SARS-CoV-2 and other CoVs from the Sarbecovirus subgenus (Fig. 3):

Human CoVs: GenBank MN908947, MN975262, NC_004718

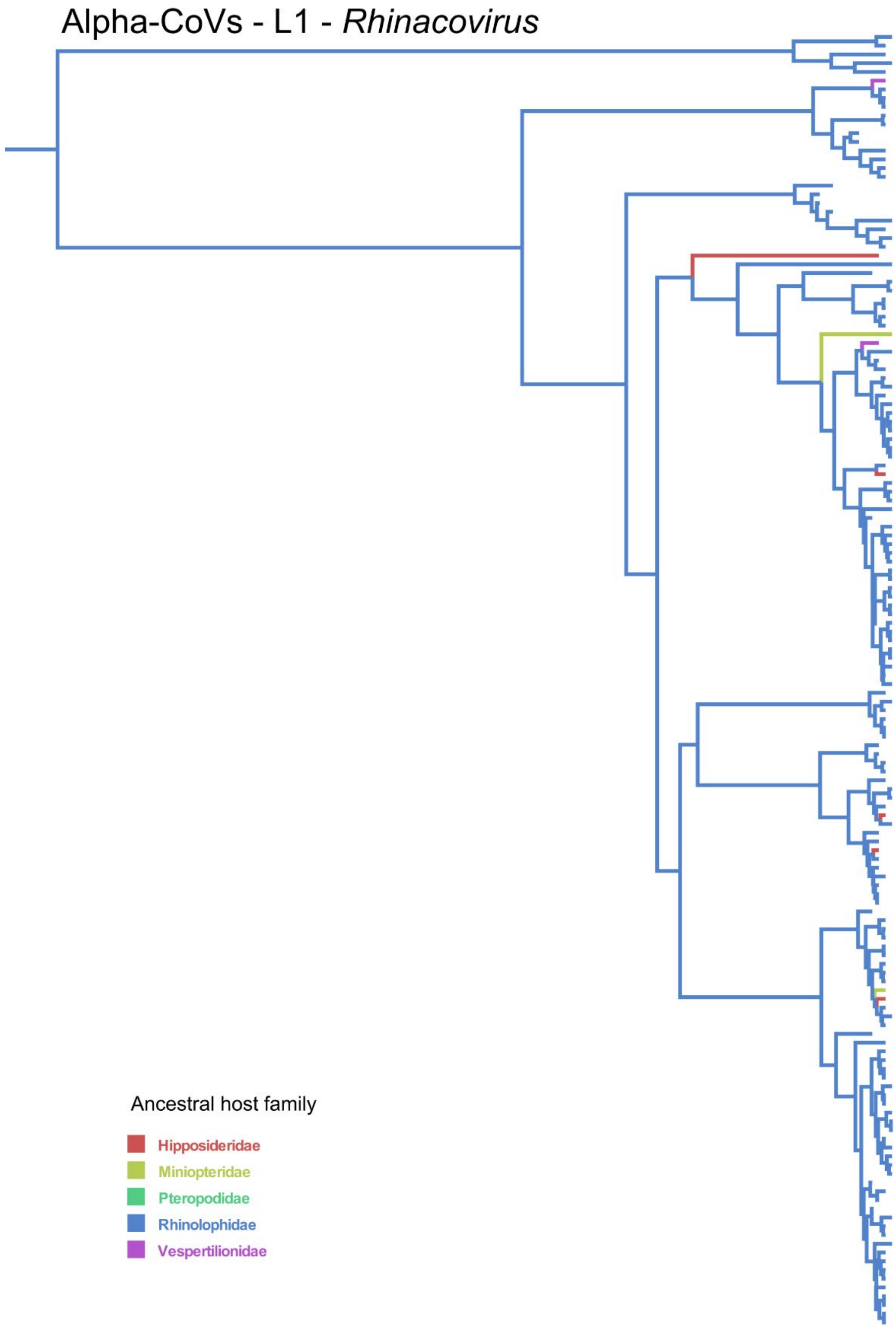
Pangolin CoVs: GISAID EPI_ISL_410538-410544, EPI_ISL_410721

Bat-CoV: GISAID EPI_ISL_412977

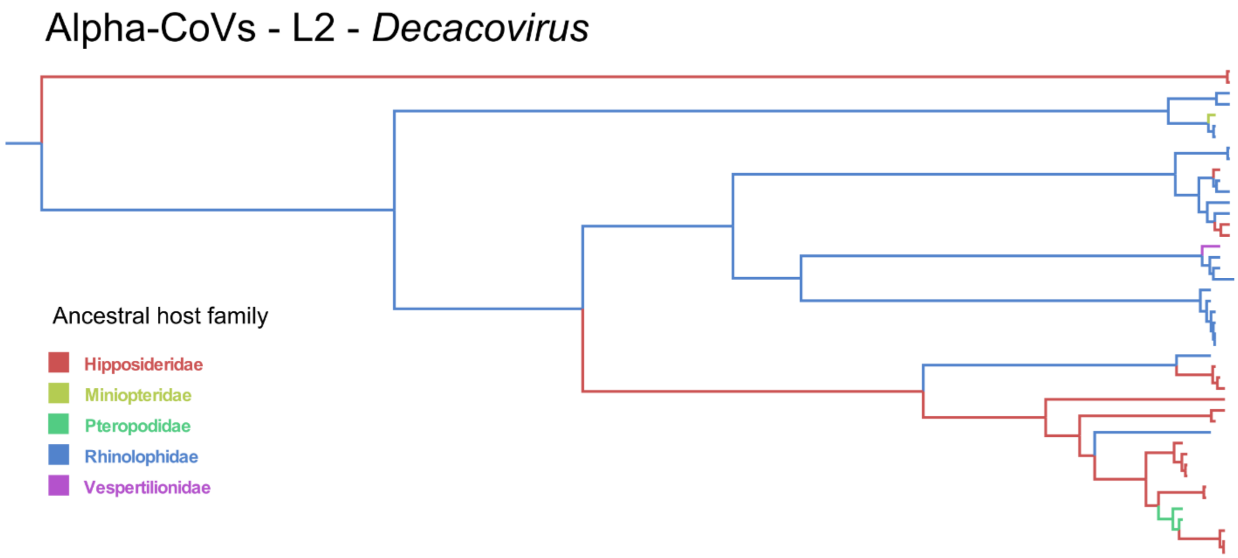
Supplementary Figures



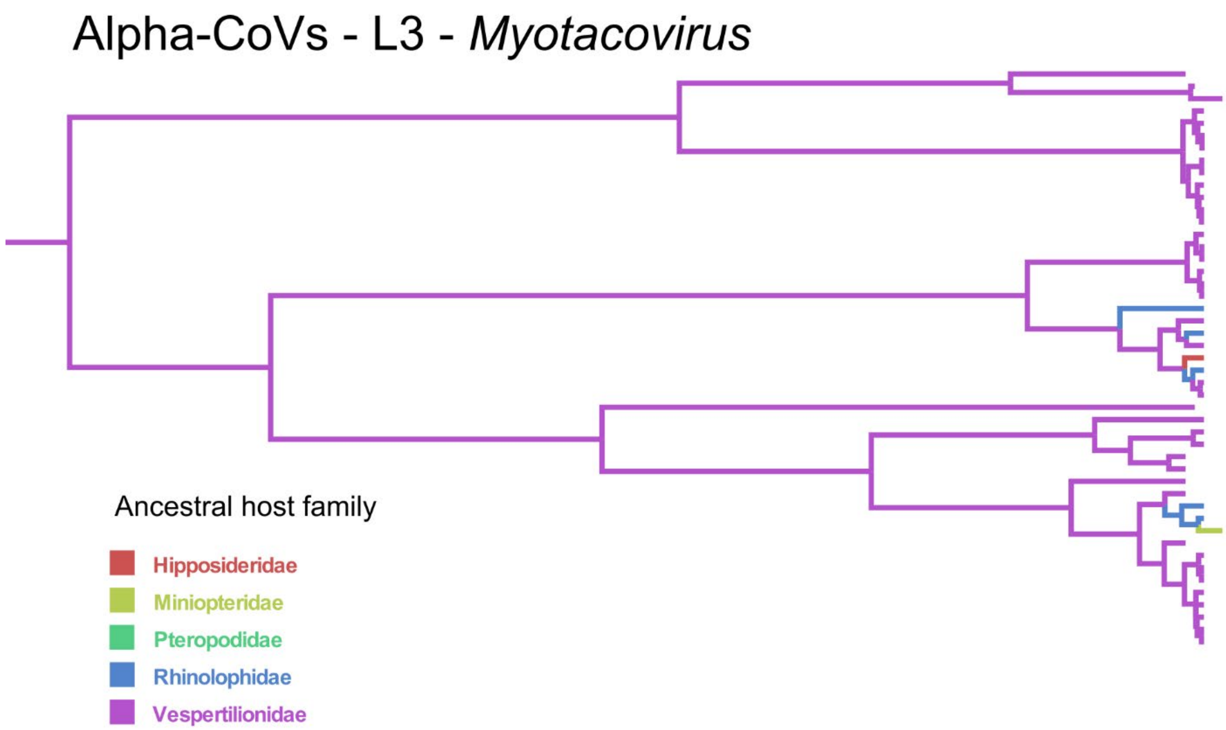
Supplementary Figure 1: Cluster dendrogram of Chinese provinces based on similarities between their mammalian diversity (hierarchical clustering). Provinces with CoV sequences available in this study are highlighted in bold.



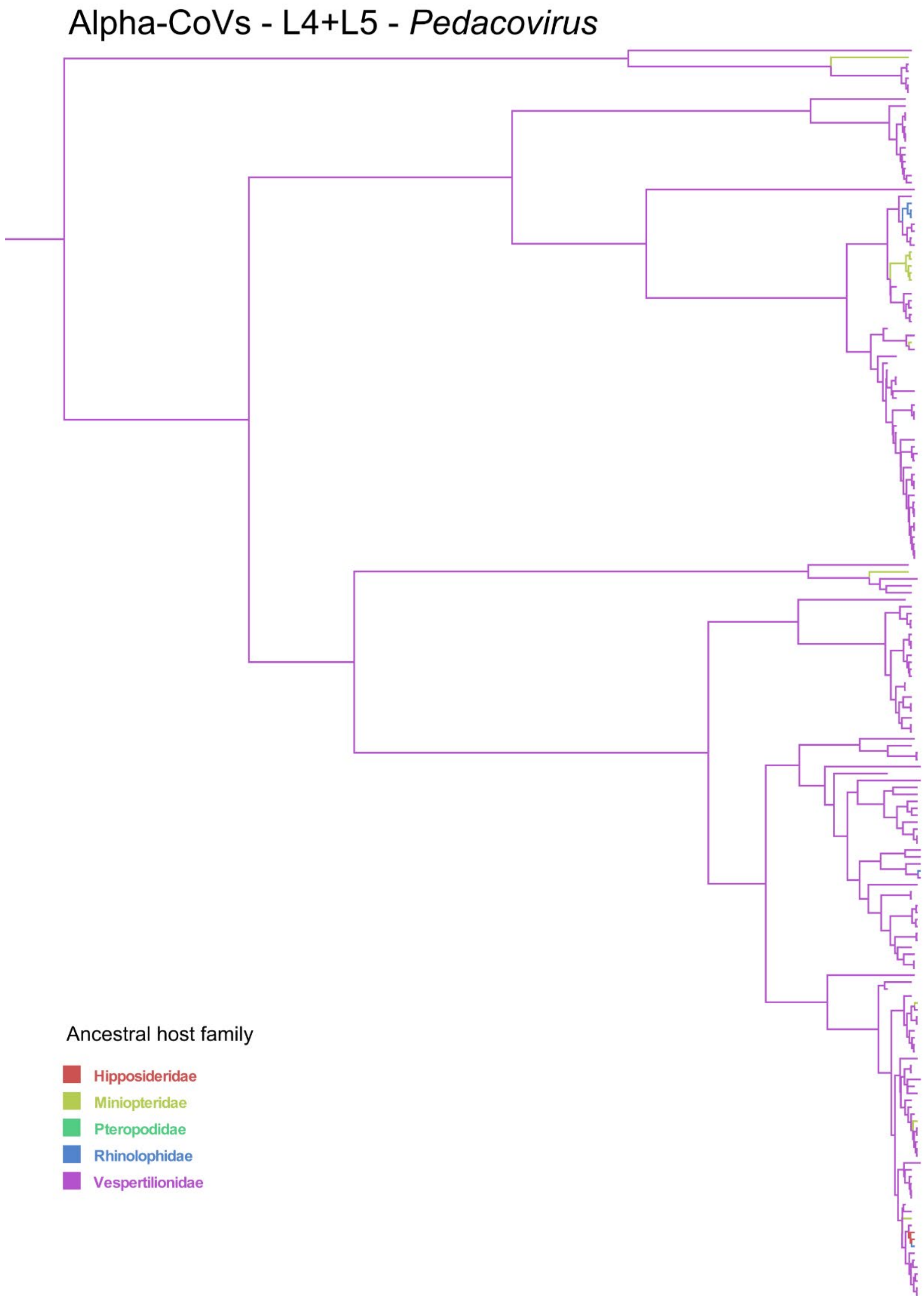
Supplementary Figure 2: Zoomed in alpha-CoV maximum clade credibility annotated tree focusing on Lineage L1 corresponding to *Rhinacovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family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



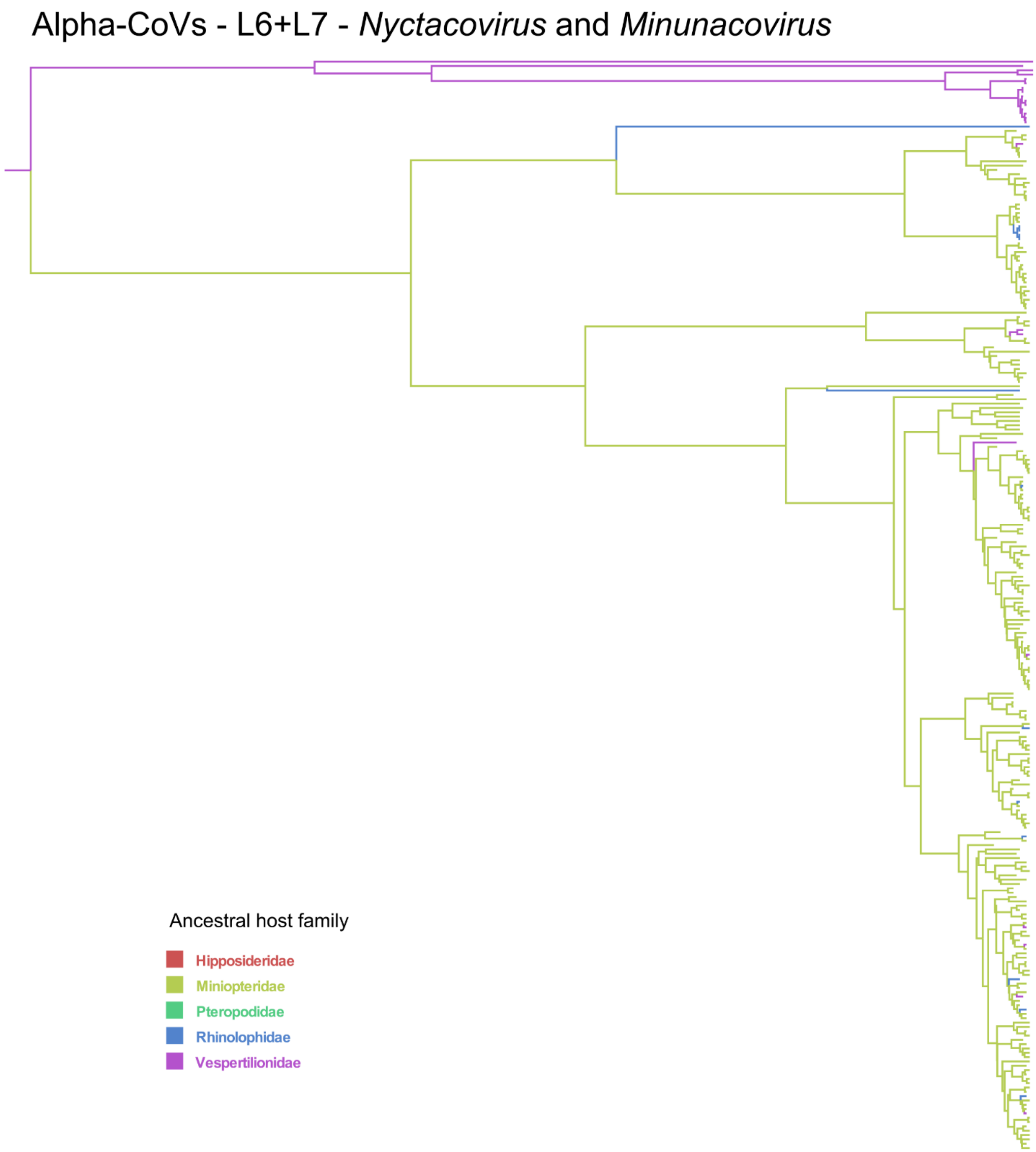
Supplementary Figure 3: Zoomed in alpha-CoV maximum clade credibility annotated tree focusing on Lineage L2 corresponding to *Decacovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with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



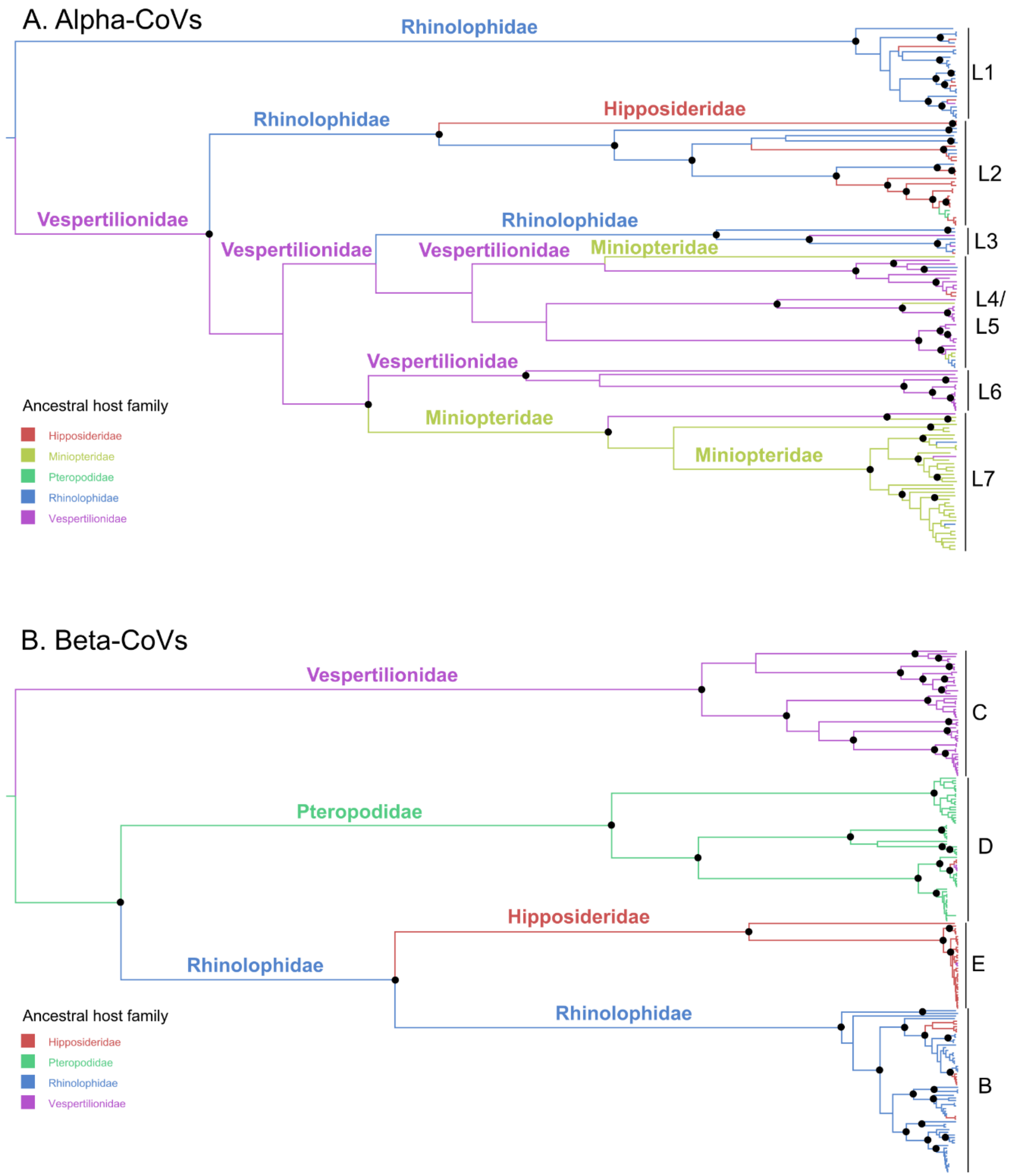
Supplementary Figure 4: Zoomed in alpha-CoV maximum clade credibility annotated tree focusing on Lineage L3 corresponding to *Myotacovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family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



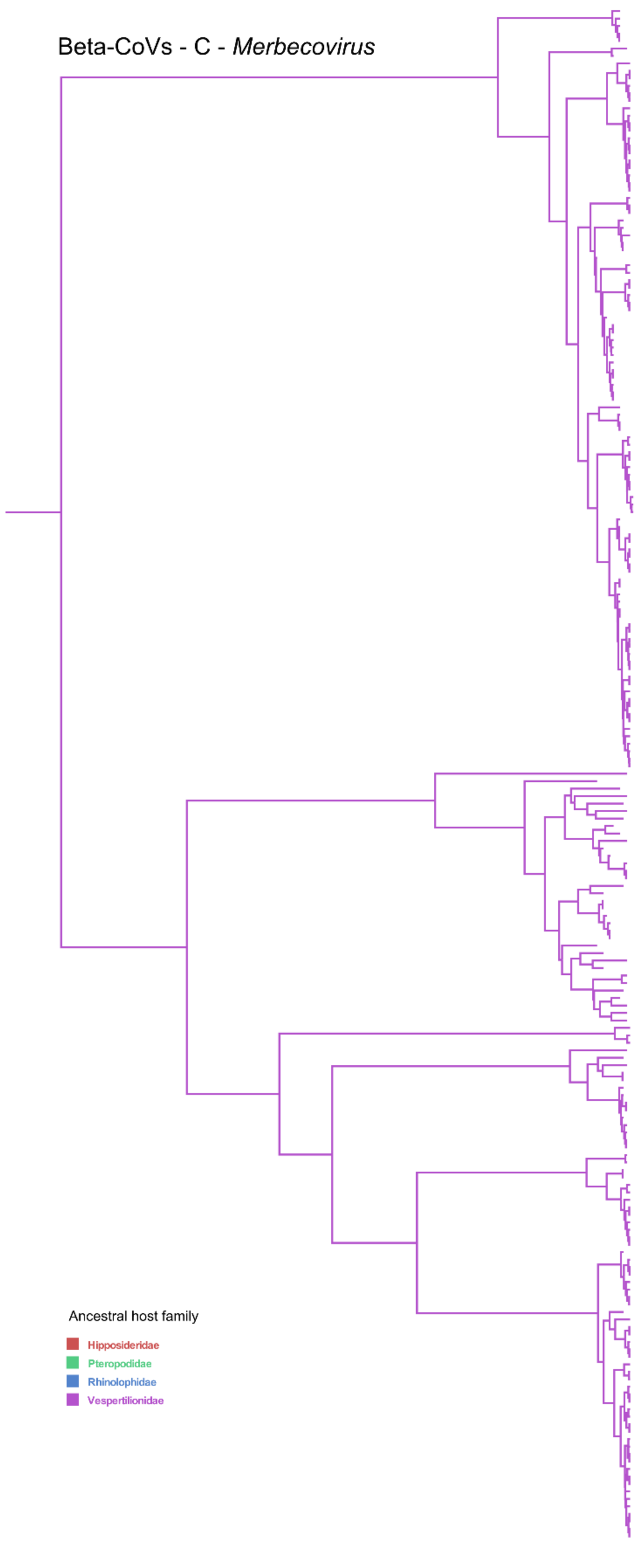
Supplementary Figure 5: Zoomed in alpha-CoV maximum clade credibility annotated tree focusing on Lineages L4 and L5 corresponding to *Pedacovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral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



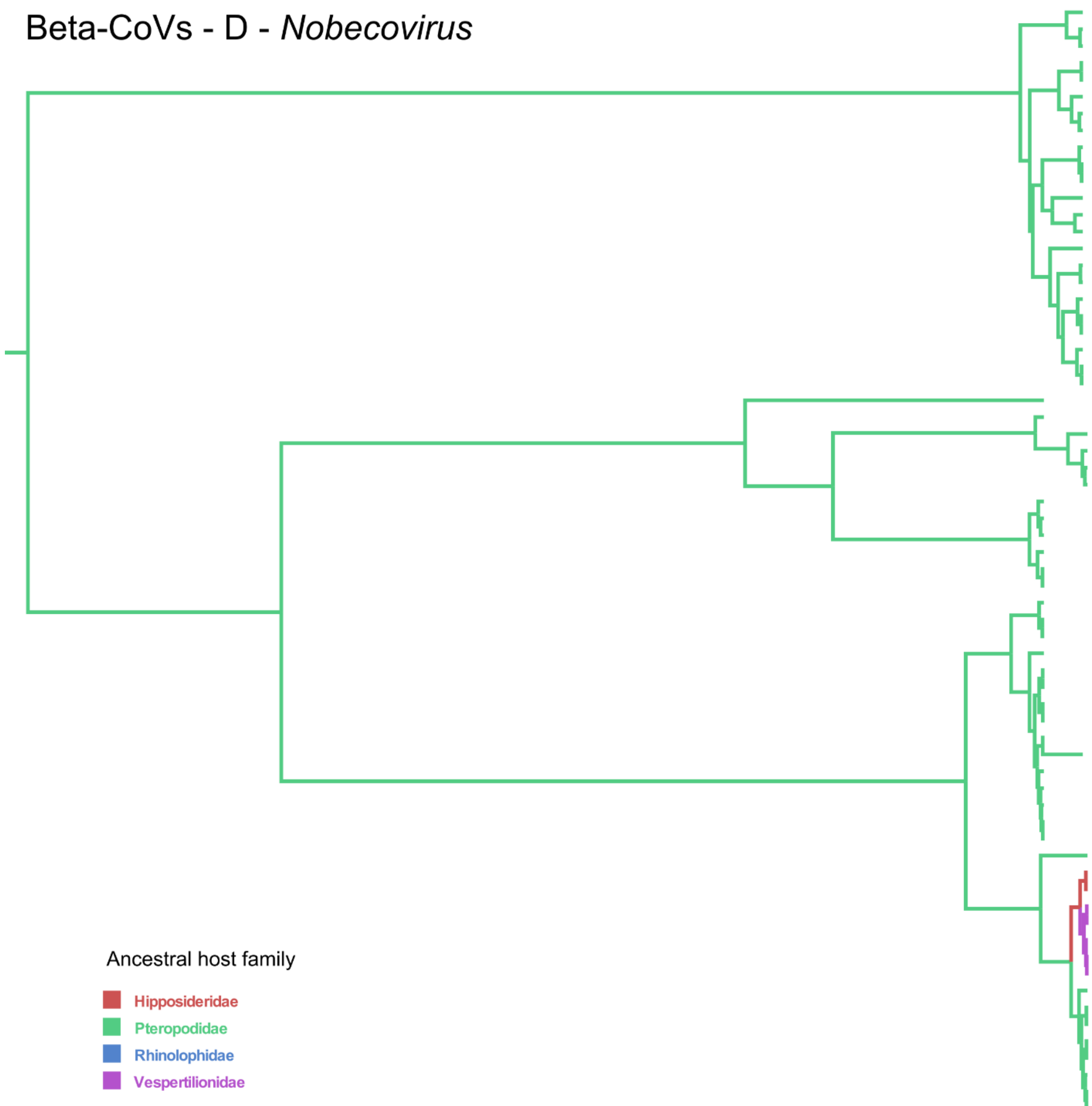
Supplementary Figure 6: Zoomed in alpha-CoV maximum clade credibility annotated tree focusing on Lineages L6 and L7 corresponding to *Nyctacovirus* and *Minunacovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the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



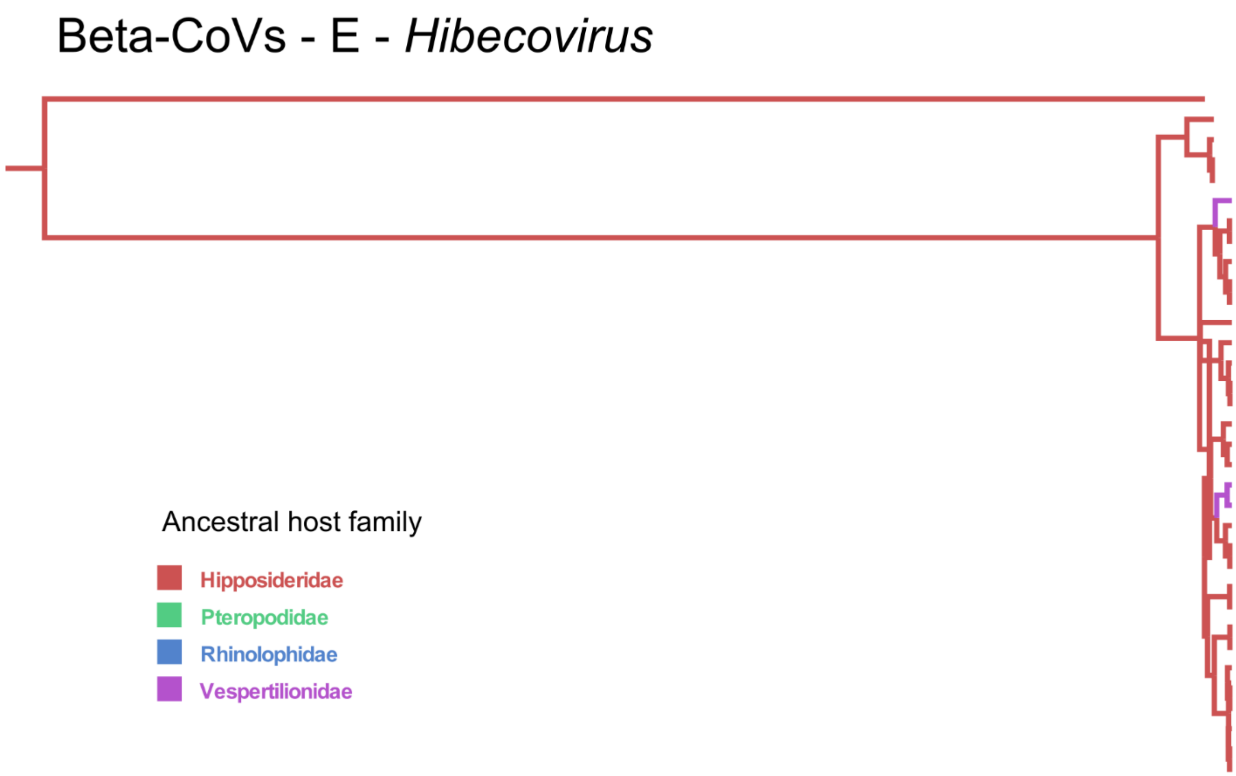
Supplementary Figure 7: Alpha-CoV (A) and beta-CoV (B) maximum clade credibility annotated trees using random subset of RdRp sequences to normalize sampling effort across bat families and bat host family as discrete character state. Branches colors correspond to the inferred ancestral family with the 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.



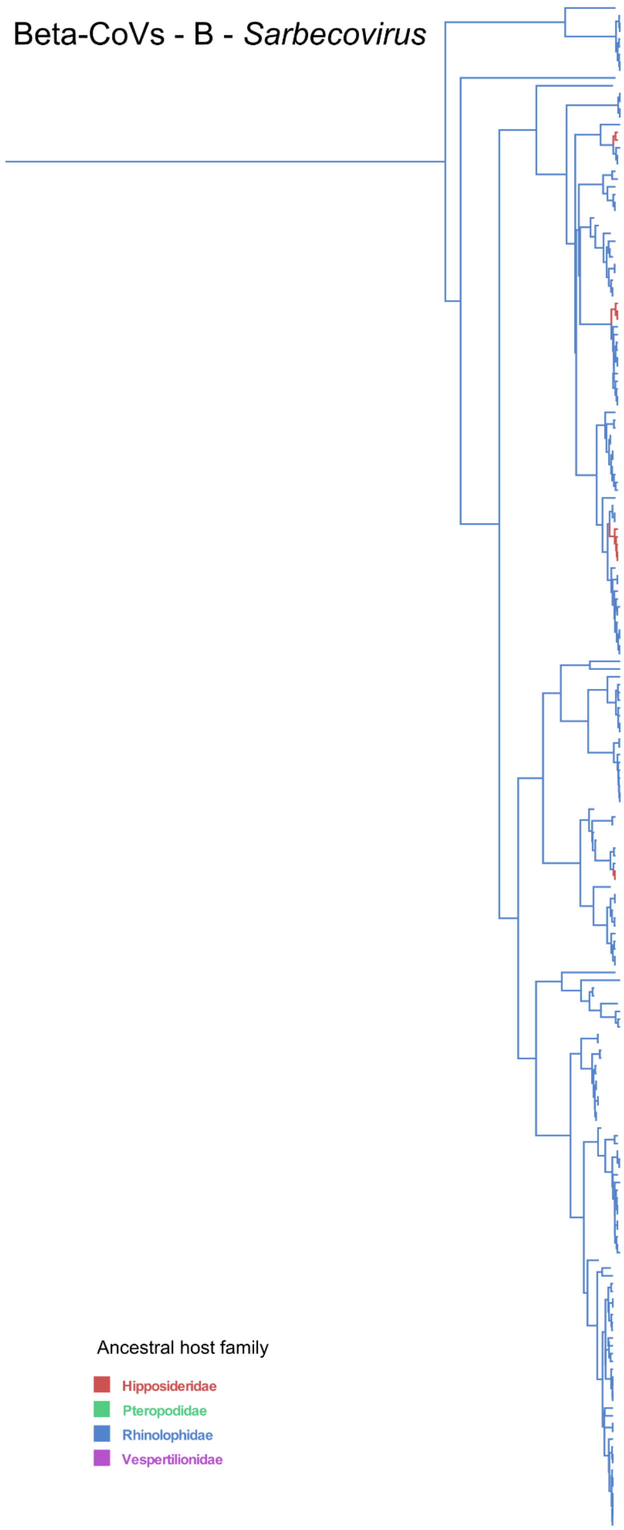
Supplementary Figure 8: Zoomed in beta-CoV maximum clade credibility annotated tree focusing on Lineage C corresponding to *Merbecovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with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



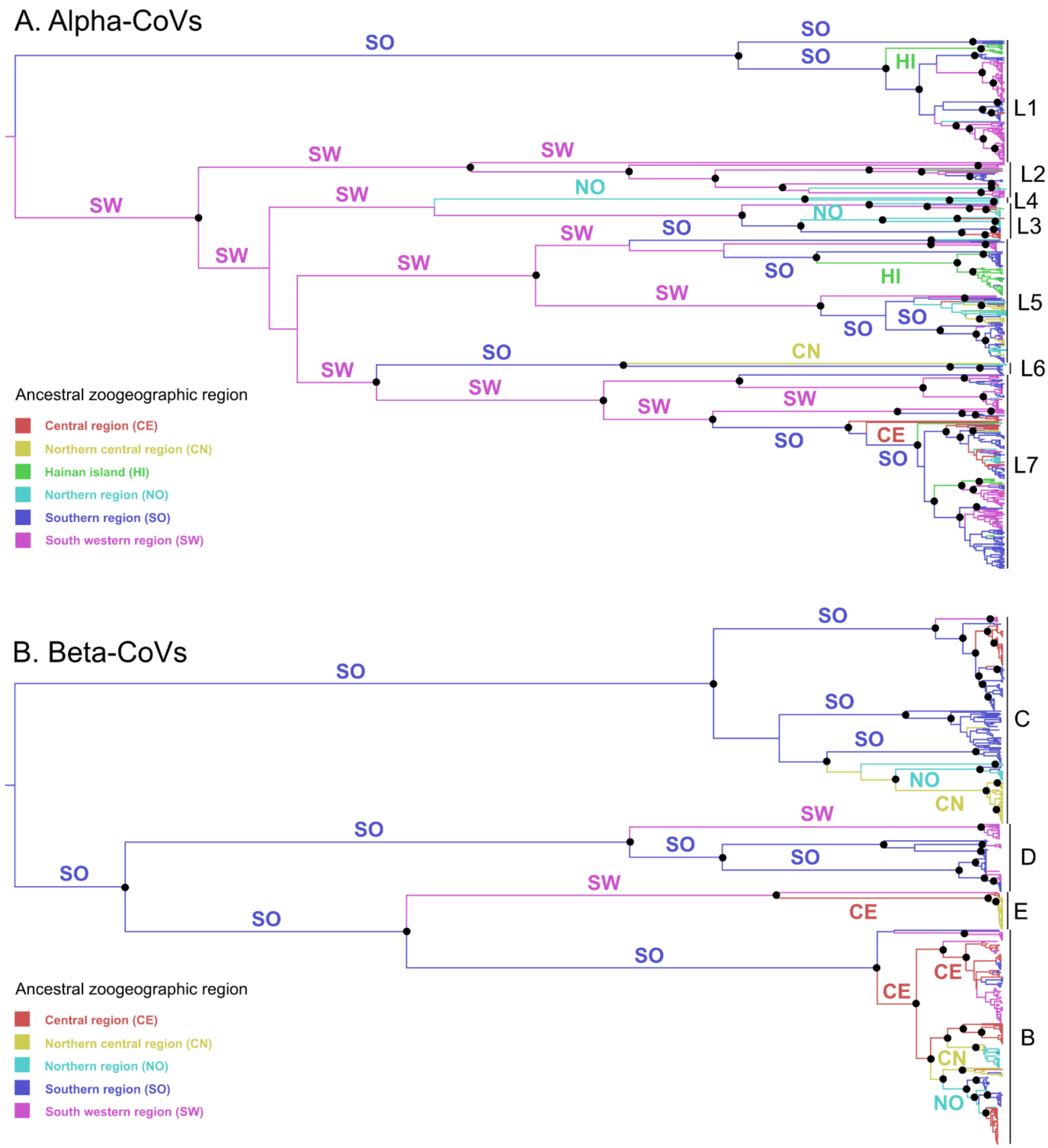
Supplementary Figure 9: Zoomed in beta-CoV maximum clade credibility annotated tree focusing on Lineage D corresponding to *Nobecovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with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



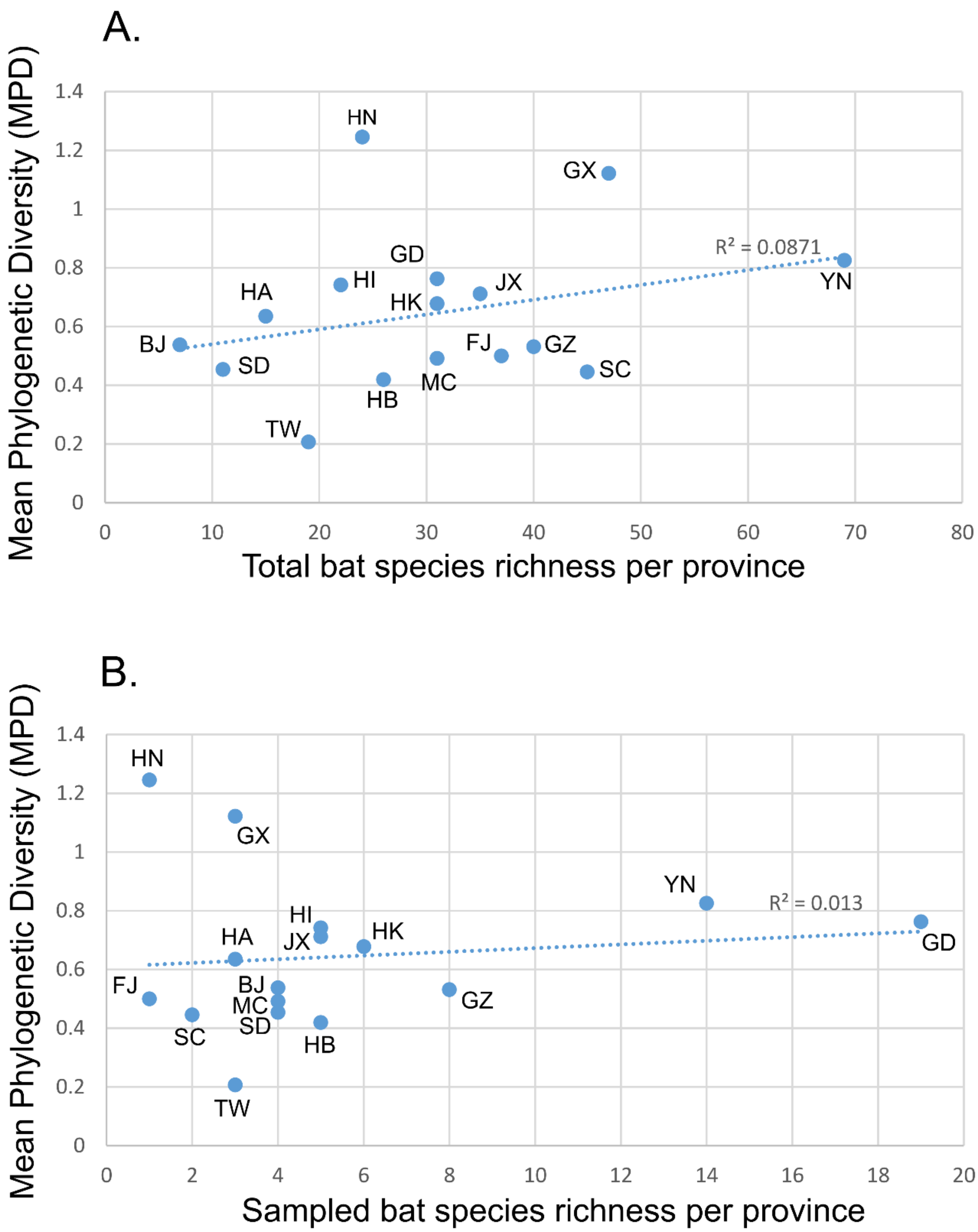
Supplementary Figure 10: Zoomed in beta-CoV maximum clade credibility annotated tree focusing on Lineage E corresponding to *Hibecovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with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



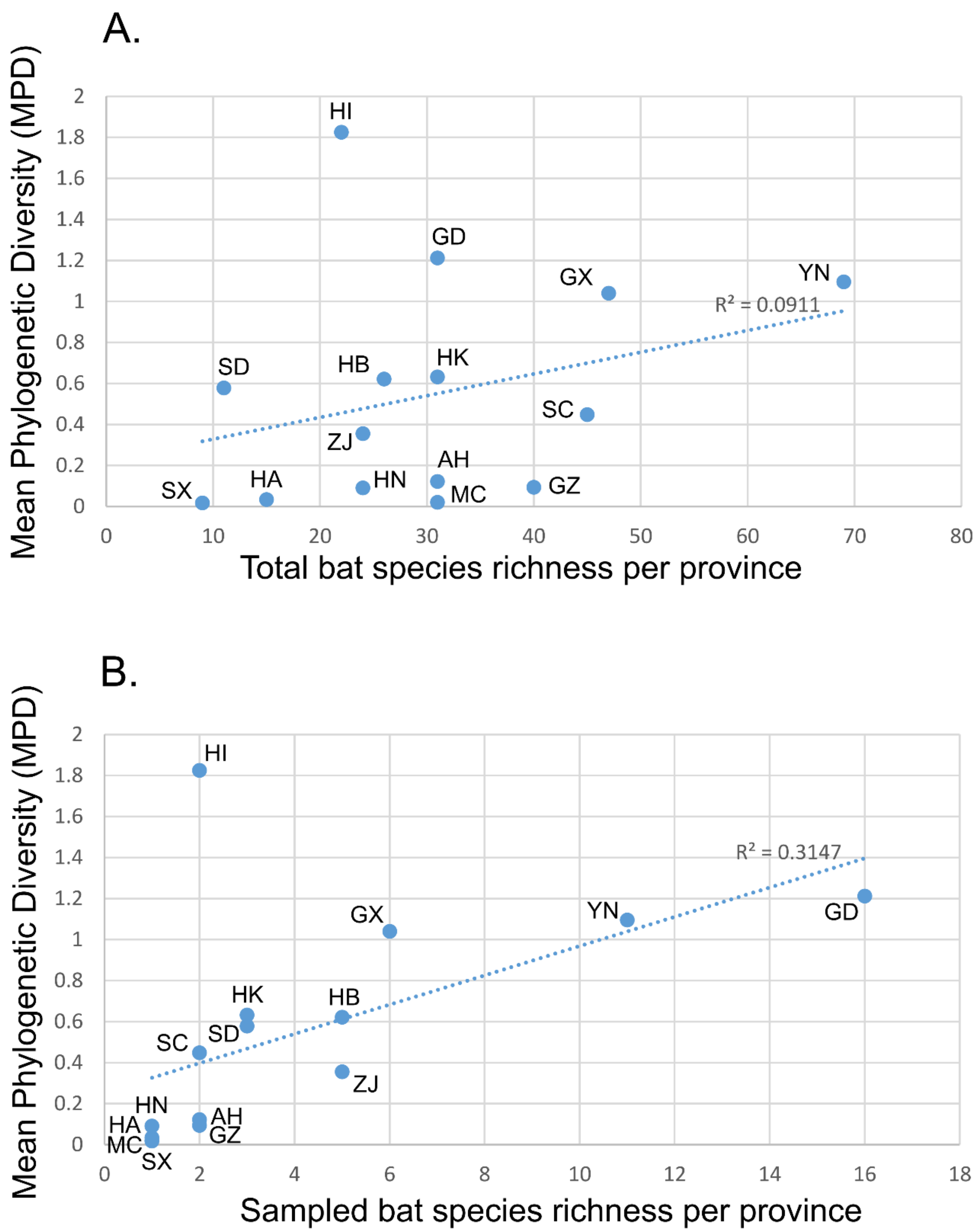
Supplementary Figure 11: Zoomed in beta-CoV maximum clade credibility annotated tree focusing on Lineage C corresponding to *Sarbecovirus* and obtained using complete dataset of RdRp sequences and bat host family as discrete character state. Branch colors correspond to the inferred ancestral family with 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 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)								
Megaerops sp.			1 (1)								
Rousettus leschenaultii			37 (37)			2 (2)					
Hipposideridae											
Aselliscus stoliczkanus	4 (1)					1			2		
Hipposideros armiger	4 (2)		2	1	2	2	1 (1)				
Hipposideros cineraceus					1 (1)						
Hipposideros pomona	3			1 (1)	1 (1)	17 (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 stheno					1 (1)						
Rhinolophus thomasi	1 (1)										
Rhinolophus sp.	9				37	3			1		1
Miniopteridae											

Miniopterus schreibersii					2		1 (1)	1 (1)	9 (8)		133 (79)
Miniopterus fuscus						1 (1)					9 (2)
Miniopterus magnater									1 (1)		4 (4)
Miniopterus pusillus											36 (4)
Miniopterus sp.									1		35 (14)
Vespertilionidae											
Eptesicus serotinus		9 (9)								2 (2)	
Hypsugo sp.		13 (4)								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)		15 (14)		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	68	34	148	45	47	7	174	15	240

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	23483.0	1	17.8	0.845
Miniopteridae	Vespertilionidae	23483.0	1	2.1	0.388
Rhinolophidae	Hipposideridae	23483.0	1	90.2	0.965
Vespertilionidae	Miniopteridae	23483.0	1	8.3	0.717
Vespertilionidae	Rhinolophidae	3911.1	0.999	2.2	0.404
Rhinolophidae	Miniopteridae	583.9	0.994	0.7	0.178
Rhinolophidae	Vespertilionidae	439.9	0.993	9.4	0.743
Hipposideridae	Pteropodidae	273.0	0.988	9.6	0.747
Hipposideridae	Rhinolophidae	73.0	0.957	50.6	0.939

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	20243.4	1	2528.4	0.999
Rhinolophidae	Hipposideridae	20243.4	1	20243.3	1
Pteropodidae	Hipposideridae	29.2	0.929	25	0.917

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	18.1	16.2	34.3	30.6	24.1	54.7
Rhinolophidae	34.6	40	74.6	33.6	32.2	65.8
Vespertilionidae	22.4	26.9	49.3	5.3	9.5	14.8
Miniopteridae	33.5	20.4	53.9	7.5	5.3	12.8
Pteropodidae	0	5.3	5.3	0	5.9	5.9

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	3.7	8.1	11.8	2.5	7.1	9.6
Rhinolophidae	6.4	0	6.4	5.4	0	5.4
Vespertilionidae	0	3.7	3.7	0	2.5	2.5
Pteropodidae	1.7	0	1.7	1.7	0	1.7

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*	86690.7	1	0.4	0.028
Miniopterus	*Rhinolophus*	86690.7	1	24.6	0.667
Rhinolophus	*Hipposideros*	86690.7	1	335.6	0.965
Myotis	*Miniopterus*	9621.4	0.999	0.6	0.050
Scotophilus	*Miniopterus*	1914.4	0.994	65.6	0.842
Rhinolophus	*Myotis*	1757.2	0.993	2.2	0.152
Myotis	*Vespertilio*	1508.8	0.992	6.8	0.355
Myotis	*Rhinolophus*	659.8	0.982	4.7	0.275
Rhinolophus	*Miniopterus*	533.0	0.977	0.1	0.011
Hipposideros	*Rousettus*	165.7	0.931	11.6	0.485
Miniopterus	*Tylonycteris*	68.3	0.847	23.8	0.660
Scotophilus	*Myotis*	54.5	0.816	0.6	0.049
Hipposideros	*Rhinolophus*	20.7	0.627	27.1	0.688
Murina	*Miniopterus*	19.2	0.610	5.9	0.325
Rhinolophus	*Ia*	17.7	0.590	10.9	0.469
Hypsugo	*Eptesicus*	17.3	0.584	10.7	0.466
Rhinolophus	*Aselliscus*	16.4	0.571	1.3	0.096
Rousettus	*Hipposideros*	11.3	0.479	26.9	0.686
Aselliscus	*Vespertilio*	1.06	0.079	13.7	0.526
Vespertilio	*Aselliscus*	3.93	0.242	13.4	0.521

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
Rhinolophus	*Hipposideros*	18426.7	0.999	22.3	0.645
Hipposideros	*Vespertilio*	7890.1	0.998	419.9	0.971
Rousettus	*Megaerops*	4797.9	0.997	351.6	0.966
Tylonycteris	*Scotophilus*	1928.7	0.994	107.3	0.897
Hypsugo	*Myotis*	361.5	0.967	184.57	0.937
Ia	*Pipistrellus*	106.7	0.897	29.6	0.707
Cynopterus	*Rousettus*	52.1	0.809	56.5	0.821
Cynopterus	*Pipistrellus*	47.2	0.793	19.5	0.614
Cynopterus	*Myotis*	36	0.746	21.8	0.640
Cynopterus	*Hipposideros*	28.4	0.698	16.7	0.576
Rhinolophus	*Aselliscus*	17.2	0.583	28.9	0.701

Eptesicus	*Myotis*	15.2	0.552	11.7	0.488
Megaerops	*Cynopterus*	13.3	0.519	10.1	0.451
Myotis	*Eptesicus*	12.5	0.503	14.7	0.545
Ia	*Eptesicus*	11.3	0.479	7.7	0.384
Aselliscus	*Hipposideros*	1.9	0.137	10.7	0.465

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	0	1.4	1.4	0.5	1.3	1.8
Eptesicus	0	0.8	0.8	0	0.8	0.8
Hipposideros	7	17.3	24.3	4.3	11.5	15.8
Hypsugo	0.8	0	0.8	0.8	0	0.8
Ia	0	0.8	0.8	0	1.3	1.3
Miniopterus	34.1	27.6	61.7	5	1.8	6.8
Murina	1.6	0	1.6	0	0	0
Myotis	25.2	27.1	52.3	0	0	0
Nyctalus	0	0	0	0	0	0
Rhinolophus	38.3	35.5	73.8	12	6.2	18.2
Rousettus	1.4	1.6	3	0.9	1.7	2.3
Scotophilus	8	0	8	1.8	0	1.8
Tylonycteris	0	1.5	1.5	0	1.4	1.4
Vespertilio	0	2.8	2.8	1.3	0.5	1.8

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	1.1	1.1	0.4	1.1	1.5
Cynopterus	4.6	0.2	4.8	5.3	0.3	5.6
Eptesicus	0.8	1.6	2.4	0.9	0.8	1.7
Hipposideros	2.3	6.1	8.4	1.5	5.6	7.1
Hypsugo	1.3	0	1.3	1.4	0	1.4
Ia	2.3	0	2.3	1.4	0	1.4
Megaerops	0.2	1.2	1.4	0.3	1.2	1.5
Myotis	0.7	2.9	3.6	0.8	3.5	4.3
Pipistrellus	0	2.6	2.6	0	2.7	2.7
Rhinolophus	6	0	6	5	0	5
Rousettus	1.2	1.3	2.5	1.2	1.5	2.7
Scotophilus	0	1.2	1.2	0	1.3	1.3
Tylonycteris	1.2	0	1.2	1.3	0	1.3
Vespertilio	0	2.3	2.3	0	1.5	1.5

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
HI	SO	30740.4	1	2951.9	0.999
CN	SO	15368	1	2	0.324
SO	CE	5119.8	0.999	26.9	0.863
NO	CN	3411.8	0.999	376.2	0.989
SW	SO	710.7	0.994	55.4	0.928
SW	NO	150.2	0.972	2.2	0.339
NO	CE	93.6	0.956	137	0.970
CE	SW	68.9	0.942	64.1	0.937
SO	SW	41.8	0.907	3	0.414
CE	NO	28.7	0.870	1.4	0.253
HI	NO	23.7	0.848	0.3	0.056
SO	HI	23.6	0.847	3.8	0.472
SO	NO	1.3	0.235	66.8	0.940

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
NO	SO	212.6	0.985	0.6	0.164
SO	CE	168.4	0.981	9.5	0.745
CE	SW	54	0.943	17.6	0.843
SO	SW	23.4	0.878	3.7	0.532
CN	NO	11.2	0.774	0.9	0.218
SW	SO	5.7	0.635	11.5	0.780
NO	CN	2.8	0.460	82.6	0.962
CE	NO	2.8	0.463	11	0.771
CE	SO	9.7	0.748	24.7	0.883

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	36	41.6	77.6	15	43.1	58.1
CN	44.7	24.4	69.1	0	20.9	20.9
HI	36.8	9.4	46.2	18.6	0	18.6
NO	47.9	39.4	87.3	45.4	20.6	66
SO	53.5	91.5	145	39.2	33.7	72.9
SW	30.2	42.8	73	15.1	15	30.1

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	8.9	8.6	17.5	30.6	15.5	46.1
CN	3.3	0	3.3	7.2	7.1	14.3
NO	11	3.3	14.3	7.1	6.4	13.5
SO	16.4	11	27.4	14.4	19.7	34.1
SW	0	16.7	16.7	7.3	18.1	25.4

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	24	0.765	0.855	0.062	89	-1.458	0.0889	1000
Miniopteridae	207	0.336	0.856	0.015	1	-34.060	**0.0010**	1000
Pteropodidae	2	0.006	0.866	0.407	1	-2.115	**0.0010**	1000
Rhinolophidae	121	0.698	0.856	0.023	1	-6.782	**0.0010**	1000
Vespertilionidae	168	0.624	0.855	0.019	1	-12.412	**0.0010**	1000
	Random dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Hipposideridae	24	0.5509	0.6604	0.0282	2	-3.8871	**0.0020**	1000
Miniopteridae	39	0.2764	0.6643	0.0167	0	-23.25	**0.0000**	1000
Pteropodidae	2	0.0128	0.6551	0.2644	3	-2.4289	**0.0030**	1000
Rhinolophidae	34	0.56	0.6577	0.0213	0	-4.5845	**0.0000**	1000
Vespertilionidae	30	0.4827	0.6624	0.0217	0	-8.273	**0.0000**	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	19	0.696	1.197	0.079	1	-6.281	**0.0010**	1000
Pteropodidae	38	0.438	1.196	0.05	1	-15.034	**0.0010**	1000
Rhinolophidae	102	0.119	1.196	0.024	1	-45.447	**0.0010**	1000
Vespertilionidae	113	0.459	1.1961	0.022	1	-32.876	**0.0010**	1000
	Random dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Hipposideridae	19	0.419	0.8199	0.0561	0	-7.1458	**0**	1000
Pteropodidae	32	0.3262	0.808	0.0412	0	-11.6874	**0**	1000
Rhinolophidae	34	0.1111	0.8184	0.0367	0	-19.2965	**0**	1000
Vespertilionidae	39	0.3885	0.8169	0.0312	0	-13.7186	**0**	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	24	0.0574	0.1413	0.0387	12	-2.1650	**0.0120**	1000
Miniopteridae	207	0.0259	0.0269	0.0039	407	-0.2584	0.4066	1000
Pteropodidae	2	0.0057	0.8392	0.4089	3	-2.0385	**0.0030**	1000
Rhinolophidae	121	0.0179	0.0420	0.0071	1	-3.3853	**0.0010**	1000
Vespertilionidae	168	0.0322	0.0321	0.0050	503	0.0186	0.5025	1000
	Random dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Hipposideridae	24	0.0414	0.1194	0.0264	0	-2.9499	**0.0000**	1000
Miniopteridae	39	0.0441	0.0792	0.0152	5	-2.3162	**0.0050**	1000
Pteropodidae	2	0.0128	0.6551	0.2644	3	-2.4289	**0.0030**	1000
Rhinolophidae	34	0.0452	0.0875	0.0175	9	-2.427	**0.0090**	1000
Vespertilionidae	30	0.0984	0.0971	0.0202	522	0.0652	0.5215	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	19	0.1174	0.1315	0.0453	381	-0.3126	0.3806	1000
Pteropodidae	38	0.0144	0.0650	0.0183	1	-2.7667	**0.0010**	1000
Rhinolophidae	102	0.0121	0.0247	0.0040	1	-3.1199	**0.0010**	1000
Vespertilionidae	113	0.0259	0.0226	0.0035	824	0.9623	0.8232	1000
	Random dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Hipposideridae	19	0.0685	0.0958	0.0239	121	-1.1422	0.1209	1000
Pteropodidae	32	0.0136	0.056	0.0121	0	-3.495	**0.0000**	1000
Rhinolophidae	34	0.022	0.051	0.0106	2	-2.742	**0.0020**	1000
Vespertilionidae	39	0.0352	0.0437	0.0086	166	-0.9884	0.1658	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	0.8554	0.4008	4	-2.0957	**0.0040**	1000
Hipposideros	21	0.7186	0.8589	0.0610	27	-2.2997	**0.0270**	1000
Hypsugo	3	0.0192	0.8537	0.2706	1	-3.0842	**0.0010**	1000
Miniopterus	207	0.3358	0.8567	0.0154	1	-33.7337	**0.0010**	1000
Murina	4	0.1323	0.8457	0.2204	21	-3.2366	**0.0210**	1000
Myotis	124	0.5679	0.8544	0.0228	1	-12.5797	**0.0010**	1000
Rhinolophus	121	0.6983	0.8565	0.0225	1	-7.0243	**0.0010**	1000
Rousettus	2	0.0057	0.8486	0.4113	5	-2.0496	**0.0050**	1000
Scotophilus	29	0.0457	0.8568	0.0553	1	-14.6620	**0.0010**	1000
Vespertilio	3	0.0101	0.8480	0.2653	1	-3.1578	**0.0010**	1000
Aselliscus	3	0.6838	0.8547	0.2632	232	-0.6492	0.2318	1000
Tylonycteris	2	0.8257	0.8593	0.4115	284	-0.0817	0.2842	1000
Nyctalus	1	NA	NaN	NA	NA	NA	NA	1000
Ia	1	NA	NaN	NA	NA	NA	NA	1000
	Random dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Eptesicus	2	0.0159	0.6676	0.2789	6	-2.3364	**0.006**	1000
Hipposideros	21	0.5313	0.6629	0.031	2	-4.2367	**0.002**	1000
Hypsugo	3	0.0246	0.6654	0.1643	0	-3.9011	**0**	1000
Miniopterus	39	0.2764	0.6622	0.0169	0	-22.8574	**0**	1000
Murina	4	0.1116	0.657	0.1262	7	-4.3209	**0.007**	1000
Myotis	8	0.3791	0.6567	0.0635	0	-4.3686	**0**	1000
Rhinolophus	34	0.56	0.6621	0.0196	0	-5.2027	**0**	1000
Rousettus	2	0.0128	0.6402	0.2892	4	-2.169	**0.004**	1000
Scotophilus	6	0.0369	0.6627	0.084	0	-7.4492	**0**	1000
Vespertilio	3	0.0192	0.6565	0.1647	0	-3.8698	**0**	1000
Aselliscus	3	0.4767	0.6576	0.184	108	-0.9837	0.1079	1000
Tylonycteris	2	0.6749	0.6644	0.2844	409	0.0369	0.4086	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	1.1881	0.1511	1	-7.6046	**0.0010**	1000
Eptesicus	5	0.1658	1.2010	0.2333	5	-4.4372	**0.0050**	1000
Hipposideros	18	0.6869	1.1943	0.0844	1	-6.0141	**0.0010**	1000
Hypsugo	5	0.0422	1.1855	0.2568	1	-4.4522	**0.0010**	1000
Ia	2	0.0415	1.2074	0.7084	35	-1.6458	**0.0350**	1000
Myotis	8	0.7057	1.1964	0.1677	16	-2.9257	**0.0160**	1000
Pipistrellus	33	0.1848	1.1965	0.0538	1	-18.8059	**0.0010**	1000
Rhinolophus	102	0.1187	1.1959	0.0242	1	-44.5611	**0.0010**	1000

Rousettus	30	0.3752	1.1925	0.0639	1	-12.7959	**0.0010**	1000
Tylonycteris	39	0.0398	1.2003	0.0472	1	-24.5878	**0.0010**	1000
Vespertilio	24	0.4223	1.1921	0.0715	1	-10.7651	**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 dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
Cynopterus	7	0.0398	0.8192	0.1239	0	-6.2905	**0**	1000
Eptesicus	5	0.1691	0.8192	0.1585	3	-4.1012	**0.0030**	1000
Hipposideros	18	0.414	0.8117	0.0591	0	-6.7261	**0**	1000
Hypsugo	5	0.0363	0.8097	0.1605	0	-4.8173	**0**	1000
Ia	2	0.0496	0.7943	0.4273	63	-1.7426	0.0629	1000
Myotis	7	0.4873	0.8114	0.1238	19	-2.6164	**0.0190**	1000
Pipistrellus	7	0.4001	0.8086	0.1212	5	-3.3707	**0.0050**	1000
Rhinolophus	34	0.1111	0.8155	0.0366	0	-19.2248	**0**	1000
Rousettus	25	0.2443	0.8206	0.044	0	-13.0853	**0**	1000
Tylonycteris	8	0.0445	0.817	0.1027	0	-7.5232	**0**	1000
Vespertilio	7	0.3577	0.8148	0.118	4	-3.8752	**0.0040**	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	0.8641	0.4087	11	-2.0763	**0.0110**	1000
Hipposideros	21	0.0723	0.1547	0.0451	30	-1.8284	**0.0300**	1000
Hypsugo	3	0.0101	0.6607	0.2967	2	-2.1924	**0.0020**	1000
Miniopterus	207	0.0259	0.0269	0.0039	412	-0.2590	0.4116	1000
Murina	4	0.0675	0.5603	0.2434	28	-2.0246	**0.0280**	1000
Myotis	124	0.0329	0.0411	0.0069	109	-1.1957	0.1089	1000
Rhinolophus	121	0.0179	0.0418	0.0073	1	-3.2816	**0.0010**	1000
Rousettus	2	0.0057	0.8757	0.3973	3	-2.1897	**0.0030**	1000
Scotophilus	29	0.0123	0.1253	0.0309	1	-3.6514	**0.0010**	1000
Vespertilio	3	0.0067	0.6761	0.3002	1	-2.2299	**0.0010**	1000
Aselliscus	3	0.3437	0.6618	0.2990	149	-1.0637	0.1489	1000
Tylonycteris	2	0.8257	0.8456	0.4140	290	-0.0479	0.2902	1000
Nyctalus	1	NA	NaN	NA	NA	NA	NA	1000
Ia	1	NA	NaN	NA	NA	NA	NA	1000
	Random dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Eptesicus	2	0.0159	0.6676	0.2789	6	-2.3364	**0.006**	1000
Hipposideros	21	0.047	0.1304	0.0292	0	-2.8549	**0**	1000
Hypsugo	3	0.014	0.529	0.1999	0	-2.576	**0**	1000
Miniopterus	39	0.0441	0.0801	0.0151	6	-2.3887	**0.006**	1000
Murina	4	0.0578	0.4376	0.1578	15	-2.4066	**0.015**	1000
Myotis	8	0.2165	0.2698	0.0835	260	-0.6384	0.2597	1000
Rhinolophus	34	0.0452	0.0871	0.0173	5	-2.4235	**0.005**	1000
Rousettus	2	0.0128	0.6402	0.2892	4	-2.169	**0.004**	1000
Scotophilus	6	0.0106	0.3337	0.1116	0	-2.896	**0**	1000
Vespertilio	3	0.0133	0.5173	0.2009	0	-2.5085	**0**	1000
Aselliscus	3	0.243	0.5177	0.2141	82	-1.2829	0.0819	1000
Tylonycteris	2	0.6749	0.6644	0.2844	409	0.0369	0.4086	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	0.2726	0.1087	1	-2.4447	**0.0010**	1000
Eptesicus	5	0.0066	0.4926	0.2525	1	-1.9252	**0.0010**	1000
Hipposideros	18	0.1255	0.1414	0.0468	372	-0.3386	0.3716	1000
Hypsugo	5	0.0342	0.5017	0.2415	4	-1.9358	**0.0040**	1000
Ia	2	0.0415	1.1980	0.7073	49	-1.6351	**0.0490**	1000
Myotis	8	0.2677	0.3080	0.1335	385	-0.3021	0.3846	1000
Pipistrellus	33	0.0909	0.0752	0.0226	743	0.6968	0.7423	1000
Rhinolophus	102	0.0121	0.0246	0.0041	1	-3.0422	**0.0010**	1000

Rousettus	30	0.0338	0.0820	0.0254	12	-1.9007	**0.0120**	1000
Tylonycteris	39	0.0042	0.0622	0.0178	1	-3.2606	**0.0010**	1000
Vespertilio	24	0.0047	0.1050	0.0340	1	-2.9477	**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 dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
Cynopterus	7	0.0115	0.2622	0.0925	0	-2.7099	**0**	1000
Eptesicus	5	0.0097	0.3843	0.1465	0	-2.5575	**0**	1000
Hipposideros	18	0.0745	0.1032	0.0269	154	-1.0656	0.1538	1000
Hypsugo	5	0.0269	0.3752	0.1468	0	-2.373	**0**	1000
Ia	2	0.0496	0.7943	0.4273	63	-1.7426	0.0629	1000
Myotis	7	0.1744	0.272	0.092	156	-1.061	0.1558	1000
Pipistrellus	7	0.2016	0.2728	0.0912	227	-0.781	0.2268	1000
Rhinolophus	34	0.022	0.0508	0.0105	1	-2.7313	**0.0010**	1000
Rousettus	25	0.025	0.072	0.0168	0	-2.8037	**0**	1000
Tylonycteris	8	0.0099	0.2398	0.0768	0	-2.9931	**0**	1000
Vespertilio	7	0.0094	0.2794	0.0898	0	-3.0072	**0**	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	0.8081	0.0502	12	-3.0101	**0.0120**	1000
CN	25	0.4252	0.8058	0.0612	1	-6.2207	**0.0010**	1000
HI	36	0.7413	0.8070	0.0498	102	-1.3190	0.1019	1000
NO	50	0.7562	0.8088	0.0401	113	-1.3121	0.1129	1000
SO	195	0.7418	0.8069	0.0164	1	-3.9685	**0.0010**	1000
SW	151	0.8248	0.8079	0.0201	798	0.8402	0.7972	1000
	Random dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
CE	33	0.452	0.5466	0.0288	5	-3.2815	**0.005**	1000
CN	25	0.236	0.5486	0.032	0	-9.7572	**0**	1000
HI	36	0.5348	0.5524	0.0268	257	-0.6556	0.2567	1000
NO	45	0.4635	0.5498	0.0216	0	-3.9882	**0**	1000
SO	48	0.5364	0.5591	0.0204	139	-1.1118	0.1389	1000
SW	48	0.6095	0.5597	0.0202	990	2.4621	**0.9890**	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	49	0.8217	1.2124	0.0446	1	-8.7540	**0.0010**	1000
CN	40	1.0626	1.2107	0.0534	10	-2.7732	**0.0100**	1000
NO	22	0.8652	1.2104	0.0824	3	-4.1869	**0.0030**	1000
SO	103	1.1273	1.2113	0.0249	1	-3.3676	**0.0010**	1000
SW	45	1.0942	1.2127	0.0470	18	-2.5203	**0.0180**	1000
	Random dataset							
	n	mpd.obs	mpd.rand.mean	mpd.rand.sd	mpd.obs.rank	mpd.obs.z	mpd.obs.p	runs
CE	30	0.4079	0.6673	0.0524	0	-4.9504	**0.0000**	1000
CN	25	0.4921	0.6717	0.0563	3	-3.1899	**0.0030**	1000
NO	22	0.4295	0.6827	0.0563	0	-4.4948	**0.0000**	1000
SO	30	0.6281	0.6906	0.0427	74	-1.4654	**0.0739**	1000
SW	32	0.7362	0.6841	0.0437	892	1.1915	0.8911	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	0.1099	0.0272	27	-1.9004	**0.0270**	1000
CN	25	0.1089	0.1333	0.0364	266	-0.6710	0.2657	1000
HI	36	0.0415	0.1003	0.0246	4	-2.3914	**0.0040**	1000
NO	50	0.0724	0.0814	0.0191	354	-0.4701	0.3536	1000
SO	195	0.0119	0.0300	0.0049	1	-3.7067	**0.0010**	1000
SW	151	0.0211	0.0367	0.0065	3	-2.3829	**0.0030**	1000
	Random dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
CE	33	0.0394	0.0753	0.0152	10	-2.3665	**0.0100**	1000
CN	25	0.068	0.0936	0.0202	117	-1.2659	0.1169	1000
HI	36	0.036	0.0711	0.0138	4	-2.5394	**0.0040**	1000
NO	45	0.0332	0.0594	0.0105	4	-2.4935	**0.0040**	1000
SO	48	0.0314	0.0563	0.0101	5	-2.4758	**0.0050**	1000
SW	48	0.0371	0.0569	0.0102	31	-1.9392	**0.0310**	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	49	0.0460	0.0512	0.0137	370	-0.3790	0.3696	1000
CN	40	0.0162	0.0646	0.0190	1	-2.5487	**0.0010**	1000
NO	22	0.0102	0.1206	0.0394	1	-2.7994	**0.0010**	1000
SO	103	0.0198	0.0241	0.0040	160	-1.0745	0.1598	1000
SW	45	0.0376	0.0561	0.0151	107	-1.2254	0.1069	1000
	Random dataset							
	n	mntd.obs	mntd.rand.mean	mntd.rand.sd	mntd.obs.rank	mntd.obs.z	mntd.obs.p	runs
CE	30	0.0418	0.0566	0.0144	152	-1.0265	0.1518	1000
CN	25	0.009	0.0682	0.0181	0	-3.2694	**0.0000**	1000
NO	22	0.0103	0.0781	0.0216	0	-3.1441	**0.0000**	1000
SO	30	0.0342	0.0557	0.014	63	-1.5313	0.0629	1000
SW	32	0.0378	0.0523	0.0131	144	-1.1089	0.1439	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	0.032	0.733
Sampled bat richness per zoogeographic region	0.153	0.442
Total bat richness per province	0.087	0.267
Sampled bat richness per province	0.013	0.675
	Random subset	
Linear regression	R square	p-value
Total bat richness per zoogeographic region	0.027	0.754
Sampled bat richness per zoogeographic region	0.181	0.4
Total bat richness per province	0.074	0.307
Sampled bat richness per province	0.059	0.364

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	0.01	0.875
Sampled bat richness per zoogeographic region	0.306	0.334
Total bat richness per province	0.091	0.274
Sampled bat richness per province	0.315	**0.029**
	Random subset	
Linear regression	R square	p-value
Total bat richness per zoogeographic region	0.213	0.434
Sampled bat richness per zoogeographic region	0.335	0.307
Total bat richness per province	0.159	0.141
Sampled bat richness per province	0.459	**0.005**

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		-0.2927	2.7739	16.986	-3.7298
Rhinolophidae	5.4639		-3.0047	12.2691	2.967
Vespertilionidae	7.2078	7.6970		2.3133	3.8506
Miniopteridae	13.7614	21.5305	14.0215		7.7518
Pteropodidae	-2.0322	4.9362	4.6024	5.8692	

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		-12.6312	2.6577	7.84
Rhinolophidae	-9.1759		8.6105	15.7475
Vespertilionidae	5.2845	27.3887		16.4852
Pteropodidae	5.7187	14.6651	21.5237	

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		-0.813	-1.154	0.046	0.511	-0.665	-1.615	-3.663	-0.678	-1.882	0.281	-4.143	2.611	0.04
Hipposideros	0.048		-0.017	2.358	4.054	-0.063	0.816	1.261	0.183	2.57	3.03	0.674	17.916	-4.398
Rhinolophus	0.438	5.609		1.111	2.501	-1.462	-1.97	-3.7	-0.92	-1.766	1.408	-2.134	12.12	2.935
Eptesicus	0.087	2.610	1.863		-4.935	-0.524	-0.579	-0.648	-1.746	-0.098	-0.488	-0.517	1.295	1.629
Hypsugo	0.492	3.895	3.201	-3.919		-0.391	-0.116	-0.014	-1.964	0.495	-0.193	-0.134	2.852	2.459
Ia	-0.541	0.231	0.145	-0.245	0.010		-1.269	-1.691	-0.796	-1.054	-0.415	-1.156	0.166	0.61
Murina	-1.101	1.955	-0.653	-0.109	0.306	-0.578		-3.324	-1.254	-2.937	-0.181	-2.7	1.283	1.569
Myotis	-3.873	7.392	4.906	0.112	1.109	-1.620	-2.183		-1.601	-3.978	-0.35	-6.444	1.066	2.267
Nyctalus	-0.641	0.744	0.049	-1.539	-1.481	-0.645	-0.871	-1.173		-1.022	-0.97	-1.137	-0.93	0.586
Scotophilus	-0.709	10.055	8.288	1.742	2.951	0.440	-0.370	-3.537	0.108		0.364	-3.493	2.908	2.398
Tylonycteris	0.255	2.900	1.816	-0.416	-0.153	-0.134	0.123	0.266	-0.841	2.160		-0.223	-5.115	1.861
Vespertilio	-3.320	1.209	-1.059	-0.614	-0.238	-0.892	-2.318	-6.851	-1.083	-3.382	-0.312		1.018	1.274
Miniopterus	1.716	14.467	20.953	0.866	1.918	0.444	1.364	8.020	-0.585	10.986	-3.182	0.104		7.67
Rousettus	0.429	-2.293	5.010	2.001	2.603	0.602	2.289	4.246	0.972	5.681	2.234	1.654	5.916	

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*	*Megaerops*	*Rousettus*
Aselliscus		-2.322	-5.094	0.612	0.542	0.294	0.82	1.011	0.774	1.833	0.055	0.839	1.274	2.853
Hipposideros	-1.656		-11.42	0.304	0.537	0.156	1.243	1.685	1.745	4.679	-2.525	0.191	2.732	8.098
Rhinolophus	-4.225	-9.123		1.63	2.018	1.084	3.225	3.83	2.487	7.508	0.08	2.773	4.225	16.368
Eptesicus	0.811	1.297	2.612		-5.111	-4.09	-4.481	-4.551	-1.725	-3.976	-4.695	1.039	2.121	5.464
Hypsugo	0.936	1.828	3.311	-3.716		-3.292	-4.945	-4.713	-1.981	-4.82	-4.321	1.145	2.237	5.861
Ia	0.518	0.745	1.531	-3.124	-2.459		-3.58	-2.621	-1.013	-2.398	-3.55	0.635	1.549	3.65
Myotis	1.175	2.414	4.690	-3.187	-3.501	-2.652		-3.903	-1.873	-4.77	-4.005	0.475	2.278	5.859
Pipistrellus	1.673	5.047	12.501	-4.922	-5.667	-3.033	-4.967		-1.828	-4.449	-3.509	0.766	2.439	6.416
Scotophilus	0.983	1.890	2.707	-1.194	-1.402	-0.788	-1.493	-2.023		-4.311	-1.074	1.706	1.659	4.269
Tylonycteris	2.531	8.779	19.412	-3.988	-4.989	-2.467	-5.633	-11.715	-4.080		-2.488	4.321	3.952	12.2
Vespertilio	-0.143	-2.665	-1.305	-5.333	-4.996	-3.991	-5.005	-8.079	-1.105	-5.647		0.558	2.28	5.8
Cynopterus	0.533	-0.205	1.592	1.415	1.746	0.753	1.230	3.555	1.767	6.423	-0.888		-0.867	-5.434
Megaerops	1.169	2.349	3.745	2.446	2.482	1.668	2.624	4.045	1.831	5.431	2.341	-0.455		-4.823
Rousettus	2.429	7.048	16.083	5.897	6.244	3.778	7.053	15.553	4.037	21.289	6.530	-3.681	-3.541	

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		-1.3893	-3.1108	-2.5439	4.2327	3.6352
CN	1.0935		-7.3	-2.3602	-0.8375	-0.5136
NO	-0.6702	-3.2064		-1.5174	2.3109	2.7341
SO	-2.7410	-1.2735	-0.6752		4.3695	1.5969
SW	0.5813	2.1005	2.2254	0.1476		6.0280
HI	4.0280	1.2450	3.4984	3.0956	6.1927	

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		-0.5803	-6.2277	1.5807	1.8840
CN	-3.4725		-2.1538	-0.4781	5.0472
NO	-5.4907	-4.2837		0.6521	2.6132
SO	1.4596	-3.2015	0.2793		6.4788
SW	2.0986	2.6351	1.3541	11.8179	

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		MN312477			MN312268-269		
Hipposideros armiger	MN312240 MN312251	MN312473 MN312475	KY770852				
Hipposideros cineraceus	KU182955						
Hipposideros pomona	MF769513	MN312250 MN312290 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 MN312576-580 MN312582-583 MN312587-588	MN312356 MN312474 MN312481-482 KP876527					KP876544

	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	MF769455 MF769515 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 MN312480 MN312243 MN312245	MN312330 MN312463 MN312472			MN312258		MN312253

	MN312264 MN312292 MN312299 MN312335						
Miniopteridae							
Miniopterus schreibersii	MN312286 MN312466		KX285179	KF294378	KX285171 KX285176 MN312445 KT381919-923 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 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 MN312566-568 KU343192-193
Miniopterus magnater					DQ249224*		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 AY864196* DQ249228*
Miniopterus sp.					MN312446		KX285129-133 MN312262 MN312281-282 MN312285 MN312298 MN312317 MN312342-343 MN312353 MN312358 MN312360-362 MN312460 MN312468 MN312470 KY783873 KY783875 KY783879 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 leucogaster				KF294373-377 KU182966			
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		KP895490-491 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 KX285140142 KX285126 KX285128 KX285147-152 KX285154 MN312415 KJ473806		KX285215-216 MN312367 MN312370 MN312410 MN312416 KX285127 KX285214 KX285217-218 KY783866-869 KY783881-885 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 DQ648837 KY009616 KY009625		KX285143 MN312364 MN312447 DQ249226*
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		

*Undated sequences included in phylogenetic diversity and Mantel test analyses only.

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 KU182992-999 KU183000-003	
Megaerops sp.			KU182986	
Rousettus leschenaultii			MG762654-656 MG762658 EF065513-51 EF065515*-516* KP895482-489 KP895524 KU182958-960 KU182974-985 KU182987-991	
Hipposideridae				
Aselliscus stoliczkanus	KY417142 MN312601 MN312603 MN312607			
Hipposideros armiger	KX285135-136 MN312598 MN312856		MN312860-861	MN312817
Hipposideros pomona	MN312658-659 MN312661			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 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 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 KX447544-558 KX447560-562 KY783889 KY783895 KY783902		
Vespertilio sinensis		KX285223 MN312749-753 MN312757-788 KJ473821		MN312754-756

*Undated sequences included in phylogenetic diversity and Mantel test analyses only.

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