

TABLE S1 Model selection results for the RdRp gene of coronaviruses through comparison of marginal likelihoods and \log_{10} Bayes factors for each pair of models

Model combination ^a	Ln P (model/data) ^b	S.E. ^c	Model combination			
			Strict_CST	Strict_BSP	Uclد_CST	Uclد_BSP
Strict_CST	-56035.764	+/- 0.098	-	-0.161	-19.808	-19.824
Strict_BSP	-56035.394	+/- 0.094	0.161	-	-19.648	-19.664
Uclد_CST	-55990.153	+/- 0.127	19.808	19.648	-	-0.016
Uclد_BSP	-55990.117	+/- 0.125	19.824	19.664	0.016	-

^aTwo molecular clock models, a strict clock and a relaxed clock assuming uncorrelated lognormal distribution (Uclد) of substitution rates, were compared in combination with models of demographic history, constant size (CST) and Bayesian skyline (BSP). The adopted model was highlighted.

^bMarginal likelihood estimated using the program Tracer 1.5. A \log_{10} Bayes factor was calculated for each pair of model combinations (model 1 in row versus model 2 in column).

^cStandard error for the marginal likelihood.

TABLE S2 Bird species screened and associated CoVs in the present surveillance study

Family	Scientific name	Common name	No. of bird specimens tested	No. (%) of birds positive for CoV	CoV	
<i>Accipitridae</i>	<i>Accipiter gentilis</i>	Northern goshawk	1	0(0)	-	
	<i>Accipiter gularis</i>	Japanese sparrowhawk	1	0(0)	-	
	<i>Accipiter virgatus</i>	Besra	2	0(0)	-	
	<i>Accipiter soloensis</i>	Chinese goshawk	2	0(0)	-	
	<i>Accipiter trivirgatus</i>	Crested goshawk	6	0(0)	-	
	<i>Buteo buteo</i>	Common buzzard	4	0(0)	-	
	<i>Milvus migrans</i>	Black kite	4	0(0)	-	
	<i>Mirafra javanica</i>	Eastern bushlark	1	0(0)	-	
	<i>Alcedinidae</i>	<i>Alcedo atthis</i>	Common kingfisher	15	0(0)	-
<i>Anatidae</i>	<i>Anas acuta</i>	Northern pintail	1	0(0)	-	
	<i>Anas crecca</i>	Common teal	1	0(0)	-	
	<i>Anas penelope</i>	Eurasian wigeon	5	1(20.0)	WiCoV HKU20	
	<i>Aythya fuligula</i>	Tufted duck	3	0(0)	-	
<i>Apodidae</i>	<i>Apus nipalensis</i>	House swift	18	0(0)	-	
<i>Ardeidae</i>	<i>Ardea alba</i>	Great egret	2	0(0)	-	
	<i>Ardeola bacchus</i>	Chinese pond heron	16	0(0)	-	
	<i>Ardea cinerea</i>	Grey heron	7	0(0)	-	
	<i>Botaurus stellaris</i>	Great bittern	1	0(0)	-	
	<i>Butorides striata</i>	Striated heron	1	0(0)	-	
	<i>Egretta eulophotes</i>	Swinhoe's egret	1	0(0)	-	
	<i>Egretta garzetta</i>	Little egret	15	0(0)	-	
	<i>Ixobrychus sinensis</i>	Yellow bittern	1	0(0)	-	
	<i>Nycticorax nycticorax</i>	Black-crowned night heron	15	5(33.3)	NHCoV HKU19	
	<i>Cacatuidae</i>	<i>Cacatua sulphurea</i>	Yellow-crested cockatoo	2	0(0)	-
		<i>Nymphicus hollandicus</i>	Cockatiel	3	0(0)	-
<i>Campephagidae</i>	<i>Pericrocotus cantonensis</i>	Swinhoe's minivet	1	0(0)	-	
	<i>Pericrocotus flammeus</i>	Scarlet minivet	1	0(0)	-	
<i>Columbidae</i>	<i>Chalcophaps indica</i>	Emerald dove	50	0(0)	-	
	<i>Columba livia domestica</i>	Feral pigeon	285	0(0)	-	
	<i>Streptopelia chinensis</i>	Spotted dove	956	0(0)	-	
	<i>Streptopelia orientalis</i>	Oriental turtle dove	4	0(0)	-	
	<i>Streptopelia tranquebarica</i>	Red turtle dove	23	0(0)	-	
<i>Corvidae</i>	<i>Corvus torquatus</i>	Collared crow	2	0(0)	-	
	<i>Corvus splendens</i>	House crow	50	0(0)	-	
	<i>Pica pica</i>	Common magpie	4	0(0)	-	
	<i>Urocissa erythrorhyncha</i>	Blue magpie	2	0(0)	-	
	<i>Cuculidae</i>	<i>Cacomantis merulinus</i>	Plaintive cuckoo	7	0(0)	-
<i>Centropus bengalensis</i>		Lesser coucal	5	0(0)	-	
<i>Centropus sinensis</i>		Greater coucal	6	0(0)	-	
<i>Clamator coromandus</i>		Chestnut-winged cuckoo	2	0(0)	-	
<i>Cuculus canorus</i>		Common cuckoo	2	0(0)	-	
<i>Cuculus sparverioides</i>		Large hawk cuckoo	2	0(0)	-	
<i>Cuculus saturatus</i>		Oriental cuckoo	10	0(0)	-	
<i>Eudynamys scolopacea</i>		Common koel	20	0(0)	-	
<i>Dicaeidae</i>	<i>Dicaeum cruentatum</i>	Scarlet-backed flowerpecker	1	0(0)	-	
<i>Dicruridae</i>	<i>Dicrurus aeneus</i>	Bronzed drongo	1	0(0)	-	
	<i>Dicrurus annectans</i>	Crow-billed drongo	1	0(0)	-	
	<i>Dicrurus hottentottus</i>	Hair-crested drongo	3	0(0)	-	
	<i>Dicrurus macrocercus</i>	Black drongo	2	0(0)	-	
	-	<i>Terpsiphone atrocaudata</i>	Japanese paradise flycatcher	30	0(0)	-
<i>Estrildidae</i>	<i>Erythrura gouldiae</i>	Gouldian finch	1	0(0)	-	
	<i>Lonchura atricapilla</i>	Chestnut munia	32	1(3.1)	MunCoV HKU13	
	<i>Lonchura punctulata</i>	Scaly-breasted munia	31	0(0)	-	
	<i>Lonchura striata</i>	White-rumped munia	100	5(5.0)	MunCoV HKU13	
<i>Falconidae</i>	<i>Falco peregrinus</i>	Peregrine falcon	1	0(0)	-	
<i>Fringillidae</i>	<i>Serinus canaria</i>	Canary	2	0(0)	-	
	<i>Serinus mozambicus</i>	Yellow-fronted canary	1	0(0)	-	
<i>Halcyonidae</i>	<i>Halcyon pileata</i>	Black-capped kingfisher	1	0(0)	-	
	<i>Halcyon smyrnensis</i>	White-throated kingfisher	2	0(0)	-	
<i>Hirundinidae</i>	<i>Hirundo rustica</i>	Barn swallow	8	0(0)	-	
<i>Laniidae</i>	<i>Lanius schach</i>	Long-tailed shrike	6	0(0)	-	
<i>Megalaimidae</i>	<i>Megalaima oorti</i>	Black-browed barbet	1	0(0)	-	

<i>Motacillidae</i>	<i>Anthus richardi</i>	Richard's pipit	1	0(0)	-
	<i>Motacilla alba</i>	White wagtail	2	0(0)	-
<i>Muscicapidae</i>	<i>Copsychus saularis</i>	Oriental magpie robin	108	1(0.9)	MRCoV HKU18
	<i>Ficedula mugimaki</i>	Mugimaki flycatcher	1	0(0)	-
	<i>Ficedula parva</i>	Red-breasted flycatcher	2	0(0)	-
	<i>Luscinia calliope</i>	Siberian rubythroat	2	0(0)	-
	<i>Niltava macgrigoriae</i>	Small niltava	1	0(0)	-
	<i>Oenanthe pleschanka</i>	Pied wheatear	1	0(0)	-
	<i>Phoenicurus aureoreus</i>	Duarian redstart	1	0(0)	-
	<i>Rhyacornis fuliginosa</i>	Plumbeous redstart	1	0(0)	-
<i>Nectariniidae</i>	<i>Aethopyga christinae</i>	Fork-tailed sunbird	3	0(0)	-
	<i>Nectarinia jugularis</i>	Olive-backed sunbird	7	0(0)	-
<i>Paridae</i>	<i>Parus major</i>	Great tit	2	0(0)	-
	<i>Parus monticolus</i>	Green-backed tit	1	0(0)	-
<i>Passeridae</i>	<i>Passer montanus</i>	Tree sparrow	335	7(2.1)	SpCoV HKU17
<i>Phalacrocoracidae</i>	<i>Phalacrocorax carbo</i>	Great cormorant	3	0(0)	-
<i>Phasianidae</i>	<i>Bambusicola thoracicus</i>	Chinese bamboo partidge	1	0(0)	-
	<i>Chrysolophus amherstiae</i>	Lady amherst's pheasant	1	0(0)	-
	<i>Chrysolophus pictus</i>	Golden pheasant	3	0(0)	-
	<i>Coturnix japonica</i>	Japanese quail	9	0(0)	-
	<i>Gallus gallus</i>	Chicken	2	0(0)	-
	<i>Phasianus colchicus</i>	Common pheasant	6	0(0)	-
	<i>Symaticus reevesii</i>	Reeves's pheasant	1	0(0)	-
	<i>Tragopan caboti</i>	Cabot's tragopan	1	0(0)	-
<i>Phylloscopidae</i>	<i>Phylloscopus fuscatus</i>	Dusky warbler	75	0(0)	-
<i>Podicipedidae</i>	<i>Tachybaptus ruficollis</i>	Little grebe	1	0(0)	-
<i>Psittacidae</i>	<i>Agapornis fischeri</i>	Fischer's lovebird	4	0(0)	-
	<i>Melopsittacus undulatus</i>	Budgerigar	5	0(0)	-
	<i>Psittacula alexandri</i>	Red-breasted parakeet	1	0(0)	-
	<i>Psittacus erithacus</i>	African grey parrot	2	0(0)	-
<i>Pycnonotidae</i>	<i>Hemixos castanonotus</i>	Chestnut bulbul	16	0(0)	-
	<i>Pycnonotus aurigaster</i>	Sooty-headed bulbul	111	5(4.5)	BuCoV HKU11
	<i>Pycnonotus jocosus</i>	Red-whiskered bulbul	112	2(1.8)	BuCoV HKU11
	<i>Pycnonotus sinensis</i>	Chinese bulbul	132	3(2.3)	BuCoV HKU11
<i>Rallidae</i>	<i>Amaurornis phoenicurus</i>	White-breasted waterhen	23	0(0)	-
	<i>Gallinula chloropus</i>	Common moorhen	13	1(7.7)	CMCoV HKU21
	<i>Gallirallus striatus</i>	Slaty-breasted rail	6	0(0)	-
	<i>Porzana fusca</i>	Ruddy-breasted crane	8	0(0)	-
	<i>Porzana paykullii</i>	Band-bellied crane	2	0(0)	-
	<i>Rallus aquaticus</i>	Water rail	2	0(0)	-
	<i>Rallina eurizonoides</i>	Slaty-legged crane	1	0(0)	-
<i>Scolopacidae</i>	<i>Calidris ferruginea</i>	Curlew sandpiper	1	0(0)	-
	<i>Lymnocyrtus minimus</i>	Jack snipe	1	0(0)	-
	<i>Scolopax rusticola</i>	Eurasian woodcock	10	0(0)	-
<i>Strigidae</i>	<i>Bubo bubo</i>	Eurasian eagle owl	1	0(0)	-
	<i>Glaucidium brodiei</i>	Collared owl	2	0(0)	-
	<i>Glaucidium cuculoides</i>	Asian barred owl	1	0(0)	-
	<i>Ninox scutulata</i>	Brown hawk owl	3	0(0)	-
<i>Sturnidae</i>	<i>Acridotheres cristatellus</i>	Crested myna	20	0(0)	-
	<i>Acridotheres tristis</i>	Common myna	2	0(0)	-
	<i>Gracula religiosa</i>	Hill myna	4	0(0)	-
	<i>Sturnus contra</i>	Asian pied starling	1	0(0)	-
	<i>Sturnus nigricollis</i>	Black-collared starling	33	0(0)	-
	<i>Sturnus philippensis</i>	Chestnut-cheeked starling	3	0(0)	-
	<i>Sturnus sericeus</i>	Red-billed starling	19	0(0)	-
<i>Timaliidae</i>	<i>Garrulax affinis</i>	Black-faced laughingthrush	1	0(0)	-
	<i>Garrulax canorus</i>	Hwamei	14	0(0)	-
	<i>Garrulax maesi</i>	Grey laughingthrush	1	0(0)	-
	<i>Garrulax perspicillatus</i>	Masked laughingthrush	12	0(0)	-
	<i>Leiothrix argentea</i>	Silver-eared mesia	3	0(0)	-
	<i>Leiothrix lutea</i>	Red-billed leiothrix	3	0(0)	-
<i>Turdidae</i>	<i>Myiophonus caeruleus</i>	Blue-whistling thrush	14	0(0)	-
	<i>Turdus cardis</i>	Japanese thrush	19	0(0)	-
	<i>Turdus chrysolaus</i>	Brown-headed thrush	1	0(0)	-
	<i>Turdus hortulorum</i>	Grey-backed thrush	136	1(0.7)	ThCoV HKU12
	<i>Turdus merula</i>	Blackbird	41	0(0)	-
	<i>Turdus pallidus</i>	Pale thrush	8	0(0)	-
	<i>Turdus rubrocanus</i>	Chestnut thrush	1	0(0)	-
	<i>Zoothera citrina</i>	Orange-headed thrush	4	0(0)	-

<i>Turnicidae</i>	<i>Zoothera dauma</i>	Scaly thrush	8	0(0)	-
	<i>Turnix sylvatica</i>	Small button quail	3	0(0)	-
<i>Zosteropidae</i>	<i>Zosterops japonicus</i>	Japanese white eye	143	3(2.1)	WECov HKU16

TABLE S3 Putative cleavage sites at the junctions between non-structural proteins in the genomes of PorCoV HKU15, WECov HKU16, SpCoV HKU17, MRCoV HKU18, NHCov HKU19, WiCoV HKU20, and CMCoV HKU21

nsp	Putative cleavage site						
	PorCoV HKU15	WECov HKU16	SpCoV HKU17	MRCoV HKU18	NHCov HKU19	WiCoV HKU20	CMCoV HKU21
nsp2/nsp3	AG/SD	AG/SD	AG/SD	AG/AD	VG/GL	DG/VY	AG/VS
nsp3/nsp4	AG/AP	AG/AR	AG/AP	AG/AM	TG/GN	GG/SK	AG/KF
nsp4/nsp5	LQ/AG	LQ/AG	LQ/AG	LQ/AG	VQ/AG	VQ/SG	LQ/AG
nsp5/nsp6	LQ/SG	LQ/SN	LQ/SG	LQ/SG	LQ/GT	LQ/AN	LQ/AS
nsp6/nsp7	VQ/NK	VQ/NK	VQ/NK	VQ/NK	VQ/NK	VQ/NR	VQ/NR
nsp7/nsp8	VQ/AV	LQ/AV	VQ/AV	VQ/AV	LQ/VV	LQ/VV	LQ/AV
nsp8/nsp9	LQ/NN	IQ/NN	LQ/NN	LQ/NN	LQ/NN	CQ/NN	IQ/NN
nsp9/nsp10	LQ/AS	LQ/AN	LQ/AN	LQ/AN	LQ/SS	LQ/AN	LQ/AT
nsp10/nsp11	LQ/NS	LQ/GS	LQ/NS	LQ/NS	LQ/LG	LQ/SN	LQ/NT
nsp12/nsp13	LQ/AS	LQ/AS	LQ/AS	LQ/AS	LQ/AT	LQ/AT	LQ/AS
nsp13/nsp14	LQ/SS	LQ/SS	LQ/SS	LQ/AG	VQ/SL	VQ/AE	VQ/CS
nsp14/nsp15	LQ/NL	LQ/NL	LQ/NL	LQ/NL	LQ/TL	LQ/TL	LQ/TI
nsp15/nsp16	LQ/SL	VQ/SL	LQ/SL	LQ/SL	VQ/AL	LQ/SL	VQ/SL

TABLE S4 Putative accessory proteins downstream to N gene predicted to contain transmembrane helices by TMHMM and TMpred in the genomes of SpCoV HKU17, MRCoV HKU18, NHCov HKU19, WiCoV HKU20 and CMCoV HKU21

CoV	Protein	Location of transmembrane helix predicted by TMHMM	Location of transmembrane helix predicted by TMpred
SpCoV HKU17	NS7b	1 to 22 and 27 to 49	1 to 22 and 31 to 49
MRCoV HKU18	NS7c	43 to 65	41 to 65
NHCov HKU19	NS7b	23 to 45	26 to 42
WiCoV HKU20	NS7d	35 to 54	37 to 53
	NS7c	22 to 44 and 65 to 87	24 to 41 and 67 to 87
CMCoV HKU21	NS7a	42 to 64	45 to 65

TABLE S5 Comparison of amino acid identities of the seven conserved replicase domains for species demarcation [ADRP, nsp5 (3CL^{pro}), nsp12 (RdRp), nsp13 (Hel), nsp14 (ExoN), nsp15 (NendoU) and nsp16 (O-MT)] among the 10 deltacoronaviruses

CoV	Domains	BuCoV HKU11	ThCoV HKU12	MunCoV HKU13	PorCoV HKU15	WECov HKU16	SpCoV HKU17	MRCov HKU18	NHCov HKU19	WiCoV HKU20	CMCoV HKU21
BuCoV HKU11	ADRP	-	90	75	73	79	72	74	61.9	67	61
	3CL ^{pro}	-	87.6	79.2	81.1	82.4	80.8	79.5	57	58.3	77.5
	RdRp	-	92.4	88.2	88.2	90.9	88.2	88.3	72.3	70.8	84.8
	Hel	-	96.5	90	89.4	96	89.6	90.4	76.8	75.4	91
	ExoN	-	96.5	90	89.4	96	89.6	90.4	76.8	75.4	91
	NendoU	-	89.3	76.6	80.1	80.7	80.4	79.2	55.3	50.9	69.4
	O-MT	-	88.2	86	86.4	88.2	86.4	87.1	66.8	67	81.4
ThCoV HKU12	ADRP	-	72	77	82	76	75	59	67	57.1	
	3CL ^{pro}	-	80.5	82.1	83.1	81.8	81.4	57.3	57.7	78.2	
	RdRp	-	86.9	88.2	89.5	88.2	86.8	71.9	71.3	84.4	
	Hel	-	89.6	89.7	94.7	89.9	89.9	76.4	74.5	90.5	
	ExoN	-	89.6	89.7	94.7	89.9	89.9	76.4	74.5	90.5	
	NendoU	-	77.2	79.2	81.3	80.7	79.2	55.6	50.3	69.7	
	O-MT	-	84.9	86.4	85.3	86.7	84.2	66.1	66.3	79.6	
MunCoV HKU13	ADRP	-	82	82	76	83	89	62.9	75	61	
	3CL ^{pro}	-	82.7	76.5	82.7	76.5	83.4	94.5	53.1	55.4	72
	RdRp	-	90.1	87.9	90.1	94.6	72.9	71.7	84.7		
	Hel	-	95.8	89.1	96	98	78	75.7	85.4		
	ExoN	-	95.8	89.1	96	98	78	75.7	85.4		
	NendoU	-	81.5	74.2	83	88.1	57.9	50.3	72		
	O-MT	-	91	83.9	91	91.8	64.6	62.4	82.1		
PorCoV HKU15	ADRP	-	80	97	81	61	74	61			
	3CL ^{pro}	-	76.9	97	84.3	54	57.7	73.6			
	RdRp	-	88.1	97.8	90.6	72.5	71	84.5			
	Hel	-	88.4	99.2	96.1	78.2	74.9	84.6			
	ExoN	-	88.4	99.2	96.1	78.2	74.9	84.6			
	NendoU	-	76.5	96	83.5	58.7	50.5	70.6			
	O-MT	-	84.6	96.8	89.2	65.7	63.4	82.8			
WECov HKU16	ADRP	-	80	76	60	70	61				
	3CL ^{pro}	-	77.2	77.2	55	59.6	76.9				
	RdRp	-	88.3	87.3	71.7	71.5	84.8				
	Hel	-	88.6	89.1	76.6	74.3	90.5				
	ExoN	-	88.6	89.1	76.6	74.3	90.5				
	NendoU	-	75.5	75.8	53.8	50.9	65.1				
	O-MT	-	84.9	84.6	63.6	63.4	80.3				
SpCoV HKU17	ADRP	-	81	61	75	61					
	3CL ^{pro}	-	84.9	52.8	58	73					
	RdRp	-	91	72.3	71	84.7					
	Hel	-	96.3	78.4	75.1	84.9					
	ExoN	-	96.3	78.4	75.1	84.9					
	NendoU	-	84.1	58.4	51.1	71.6					
	O-MT	-	89.6	65	64.2	82.4					
MRCov HKU18	ADRP	-	60	72	59						
	3CL ^{pro}	-	54	56.4	73.3						
	RdRp	-	72.5	71.2	85.1						
	Hel	-	77.7	75.1	84.8						
	ExoN	-	77.7	75.1	84.8						
	NendoU	-	58.2	50.5	73.4						
	O-MT	-	64.3	63.4	83.2						
NHCov HKU19	ADRP	-	57.1	60							
	3CL ^{pro}	-	58.3	55.5							
	RdRp	-	69.3	71.9							
	Hel	-	75.4	77.6							
	ExoN	-	75.4	77.6							
	NendoU	-	53.5	55							
	O-MT	-	61.6	66.1							
WiCoV HKU20	ADRP	-	57.1								
	3CL ^{pro}	-	58.3								
	RdRp	-	70.8								
	Hel	-	76.4								
	ExoN	-	76.4								
	NendoU	-	48.9								
	O-MT	-	64.5								
CMCoV HKU21	ADRP	-									
	3CL ^{pro}	-									
	RdRp	-									
	Hel	-									
	ExoN	-									
	NendoU	-									
	O-MT	-									

Amino acid sequences share more than 90% identity are highlighted in gray