Supplemental Figure S1.

			Isola	ates		G	enor	nes		Ali	gnn	nent									G	ene	: S											1	Sho	wN
	Collection								150	0								1530	0								15	60								
	2019 Hubei:Wuhan	Y	Q	A	G	s	T	P	Z N	Ģ	V	Е	G	F	N	С	Y I	F P	L	Q	s	Y	G	F	Q	P	т	N	G	V	G	Y	Q	P 3	C IF	1
BaTG13	2013 I Yunnan		- 20	•	4	•	к			1	Q	т	•	L	•	17	1 3	γ.	- 2	Y	R	•		•	¥	•	•	D	-		* 1	н				
ZXC21	2015 I Zhejiang															G	VI	RТ	•	s	т		D	•	N	•	N	v	P	L	Е		•	A 1	t .	
ZC45	2017 I Zhejiang															G	V I	RT		s	т	•	D	\sim	N	•	N	v	P	L	Е		• >	A 1	÷ .	
GD01	2003 I Guangdong	F	s	P	D	G	ĸ	÷	. т	5	P	P	Α	L	•	•	- 3	η.	•	N	D		(\mathbf{r})	×	¥	т	×	т	•	I			•	е э	- 24	
WIV16	2013 I Yunnan	P	s	P	D	G	ĸ	• 3	. т	8	P	P	A	¥	÷.	-	2 3	Ν.		N	D	•	÷	3	Y	I	÷	4	•	I	•		•	23	1	1
YN2018B	2016 I Yunnan	F	s	P	D	G	ĸ	• •	. т	8	P	P	A	•		•	• 1	м.		N	D	•		•	F	т	•	•	•	I				•		
- SHC014	2011 Yunnan	10	s	P		G	Q	s	. s		A	v	•	P		•2	. 1	s .	•	R	P		\mathbf{x}_{i}		F	т	•	A	•	•		н	•	e 2		
- Rs9401	2015 I Yunnan	F	s	P	D	G	K	4 S	. т	ŝ	P	P	A		•	•	- 3	κ.	•	N	D	•	•		F	т	٠		•	I	•	•	•	•	- 9	•
YN2013	2013 I Yunnan														•	G	V I	R T	•	s	т		D		N	•	N	v	Р	L	D	•	• 0	A 1	e	
R14092	2012 Yunnan														•	G	V I	R T	•	s	т	•	D	•	N	•	N	v	P	L	D	•	•	A 1		•
SC2018	2016 Sichuan	G														G	v	т т	•	s	т	•	D	•	N	•:	N	v	P	•	A	•	•	A 1		1
HuB2013	2013 Hubei:Wuhan	G													•	G	V 1	т т	•	S	т	•	D	•	N	•	N	v	P	÷	A	•	• <	A	۰ ۱	•
Shaanxi201	2011 I Shaanxi														•	G	v 3	Y T	•	S	т	•	D	•	¥	•	s	v	P	L	D	•	• 23	A 1	e	1
	2013 I Yunnan														•	G	VI	RT	•	s	т	•	D	•	¥	•	•	v	P	I	Е	•	•	A 1	· ·	•
Yunnan2011	2011 I Yunnan															G	V	RT	•	S	т		D	•	¥	•	s	v	P	L	Е		•	A 1	•	•
BtCoV/273/2	2005 2004 I Hubei:Wuhan	E													•	G	3	R T	۰.	S	т	•	D	٠	N	Q	N	v	P	L	Е	•	• > 3	A 1	· .	•
Rs4247	2013 I Yunnan	G													•	G	v s	Y T	•	S	т	•••	D	•	N	•	N	v	P	÷	А		•	A 1	e :	•
- <u>As6526</u>	2014 I Yunnan														•	G	VI	RT	•	S	т	•	D	•	¥	•	•	v	P	I	Е	•	•	A	•	
Em1	2003 I Guangdong														•	G	V 1	ΥT	•	s	т	•	D	٠	¥	•	s	I	P	•	Е		*. C	A 1	•	1
BtCoV/279/2	005 2004 I Hubei:Wuhan															G	V 1	Y T	•	s	т	•	D	٠	¥	•	s	I	P	e	Е	•	• •	A 1	•	
GX2013	2013 I Guangxi	G													•	G	V 3	ΥT	•	S	т	•	D	•	N	•	N	v	P	•	A	•	•	A	•	•
Ц НКИЗ-1	2003 I Guangdong	G													•	G	v	Y T	•	S	т	•	D	٠	N	•	N	v	P	•	A	•	•	A	• •	
HKU3-7	2006 I Guangdong	G													•	G	V 1	т т	•	S	т	•	D	•	N	•	N	v	P	22	A	1	• 3	A 1	•	

Fig S1. Macro-evolutionary browser of coronavirus genomes. This is a companion genome browser of SARS-CoV (SARS) & SARS-CoV-2 (COVID-19) genomes in the evolutionary context of their respective animal-host relatives in China. Here, aligned amino-acid sequences (*right panel*) of the Spike protein – showing part of the highly variable receptor binding domain (RBD) – are arranged according to the sequence phylogeny (*left panel*). All sequences are compared to the Covid-19 strain (WIV02) at the top, with "." representing the same residue, letters representing a difference, and blanks representing alignment gaps. At the bottom, we show nucleotide substitution rates at three codon positions, as a way to show gene sites under positive selection (e.g., 5'-end, where rates at 1st and 2nd codon positions reach to the level at 3rd codon positions). This macro-evolutionary browser is designed after *Borreliabase*, a browser of Lyme disease pathogen genomes we developed and maintain (Di et al. 2014). This browser helps, e.g., the design of vaccines against a specific CoV strain, a group of CoV strains, or all future CoVs spilling over from animal reservoirs.

Reference cited:

Di L, Pagan PE, Packer D, Martin CL, Akther S, Ramrattan G, et al. *BorreliaBase*: a phylogeny-centered browser of *Borrelia* genomes. BMC Bioinformatics. 2014 Jul 3;15(1):233.