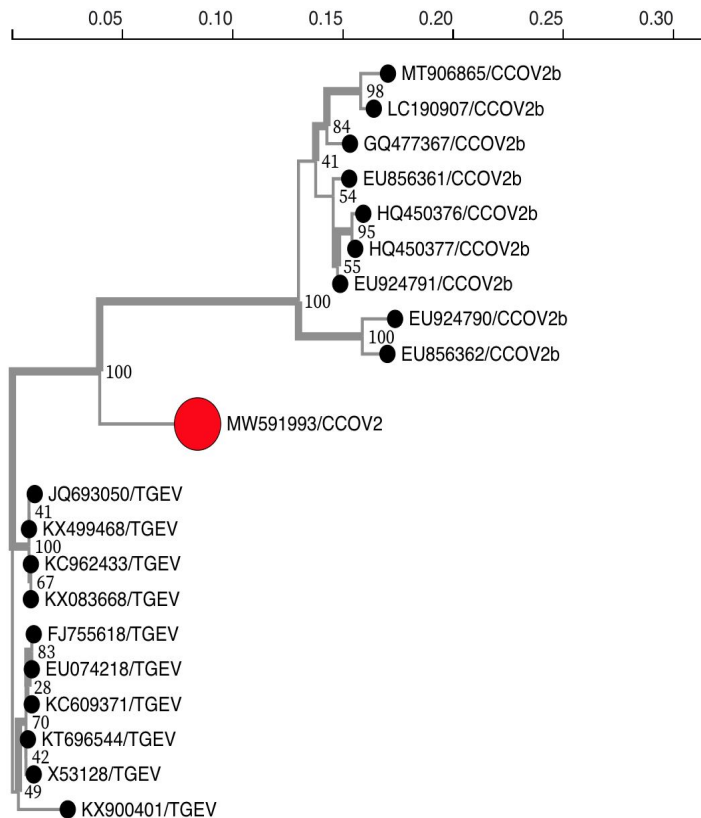


Table S1: Isolate details and sequence accessions for the included CoVs.

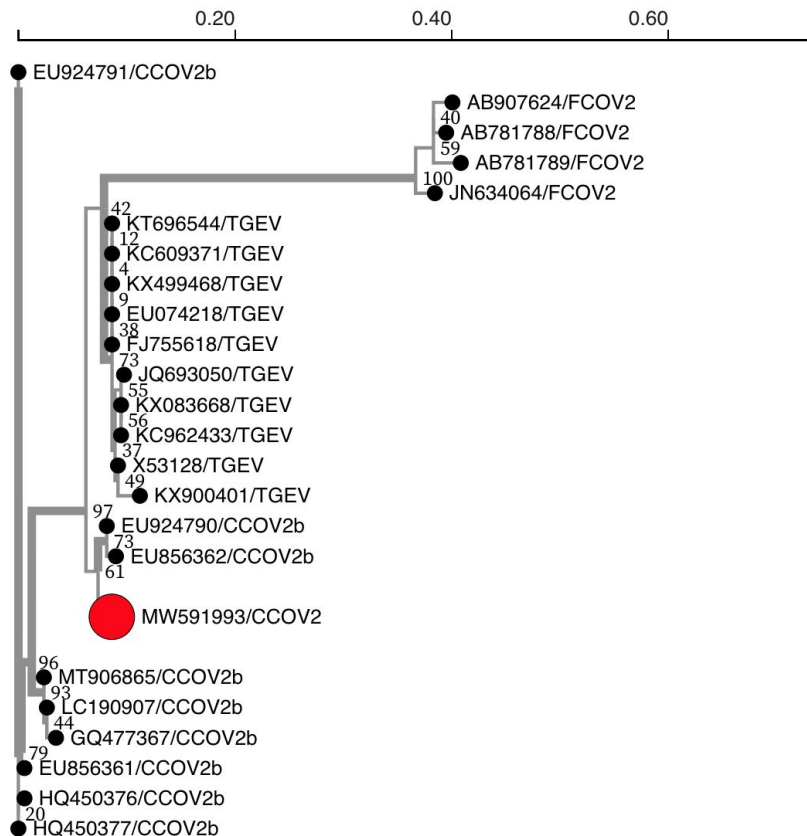
Alignment set	Accession number	Alpha-1 Type	Strain Name	Collection date	Location
1 & 2	MW591993.1	CCoV-HuPN-2018	CCoV-HuPN-2018	2017	Malaysia
1 & 2	EU856361.1	CCoV2b	341/05	Dec 2005	Italy
1 & 2	EU924791.1	CCoV2b	119-08	Mar 2008	Italy
1 & 2	HQ450377.1	CCoV2b	68-09	2009	Greece
1 & 2	HQ450376.1	CCoV2b	66-09	2009	Greece
1 & 2	EU924790.1	CCoV2b	430-07	Oct 2007	Italy
1 & 2	EU856362.1	CCoV2b	174-06	Mar 2006	Italy
1 & 2	MT906865.1	CCoV2b	2020-7	2020	United Kingdom
1 & 2	GQ477367.1	CCoV2b	CCOV-NTU336-2008	Nov 2008	Taiwan
1 & 2	LC190907.1	CCoV2b	CCOV-Dog-HCM47-2015	June 2015	Vietnam
1 & 2	KX900401.1	TGEV	TGEV/USA/Tennessee144/2008	15 Apr 2008	USA - Tennessee
1 & 2	KC609371.1	TGEV	NA	21 May 2013	China
1 & 2	FJ755618.2	TGEV	H16	1973	China
1 & 2	KT696544.1	TGEV	JS2012	2012	China
1 & 2	EU074218.2	TGEV	Attenuated H	NA	China
1 & 2	X53128.1	TGEV	TGEV FD772-70	NA	China
1 & 2	KX499468.1	TGEV	TGEV AHHF	22 Dec 2015	China
1 & 2	KC962433.1	TGEV	TGEV HX	5 May 2012	China
1 & 2	JQ693050.1	TGEV	NA	NA	South Korea
1 & 2	KX083668.1	TGEV	NA	2015	China
2	AB781789.1	FCOV2	KUK-H-L	NA	Japan
2	AB781788.1	FCOV2	M91-267	NA	Japan
2	AB907624.1	FCOV2	Tokyo/cat/130627	NA	Tokyo, Japan
2	JN634064.1	FCOV2	WSU-79-1683	1979	USA - Washington

Figure S1

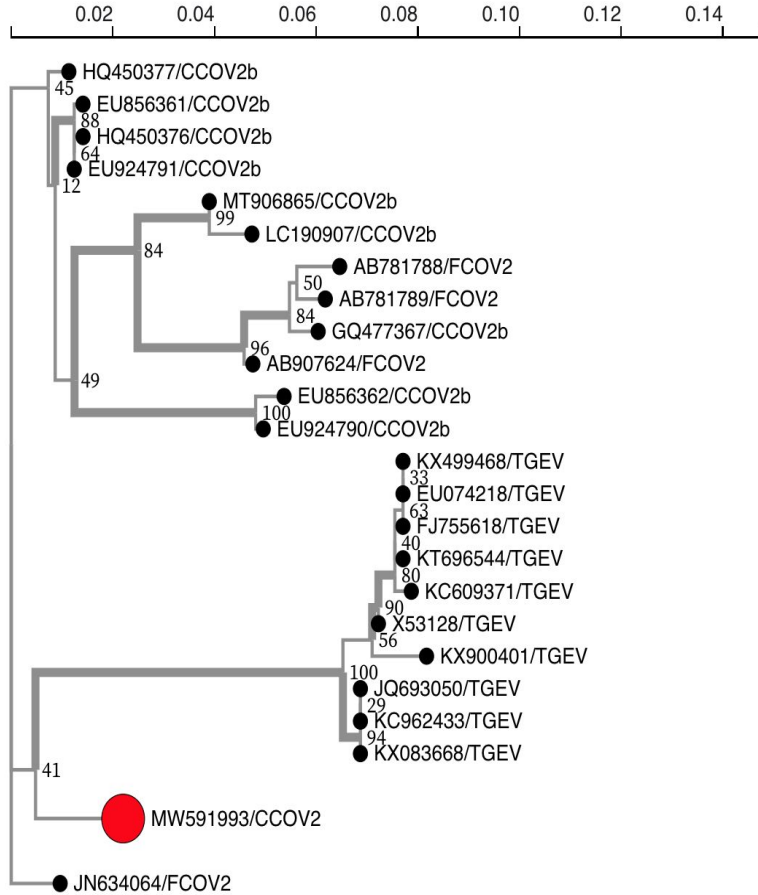
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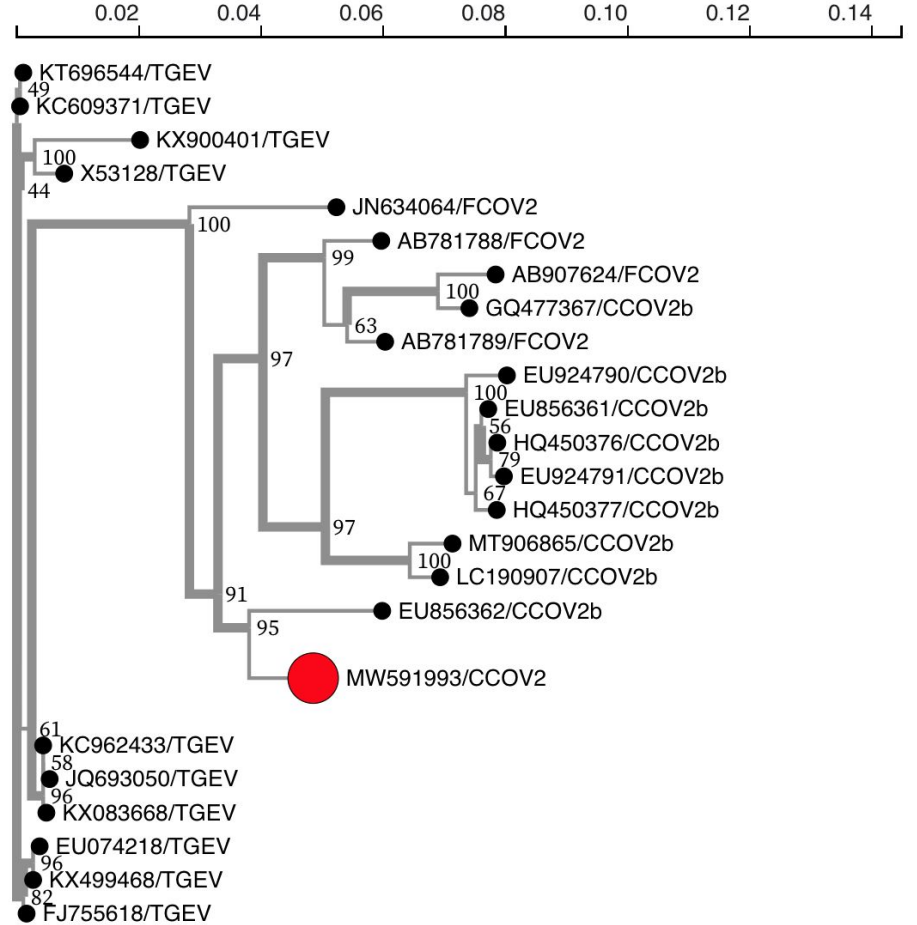
2.



3.



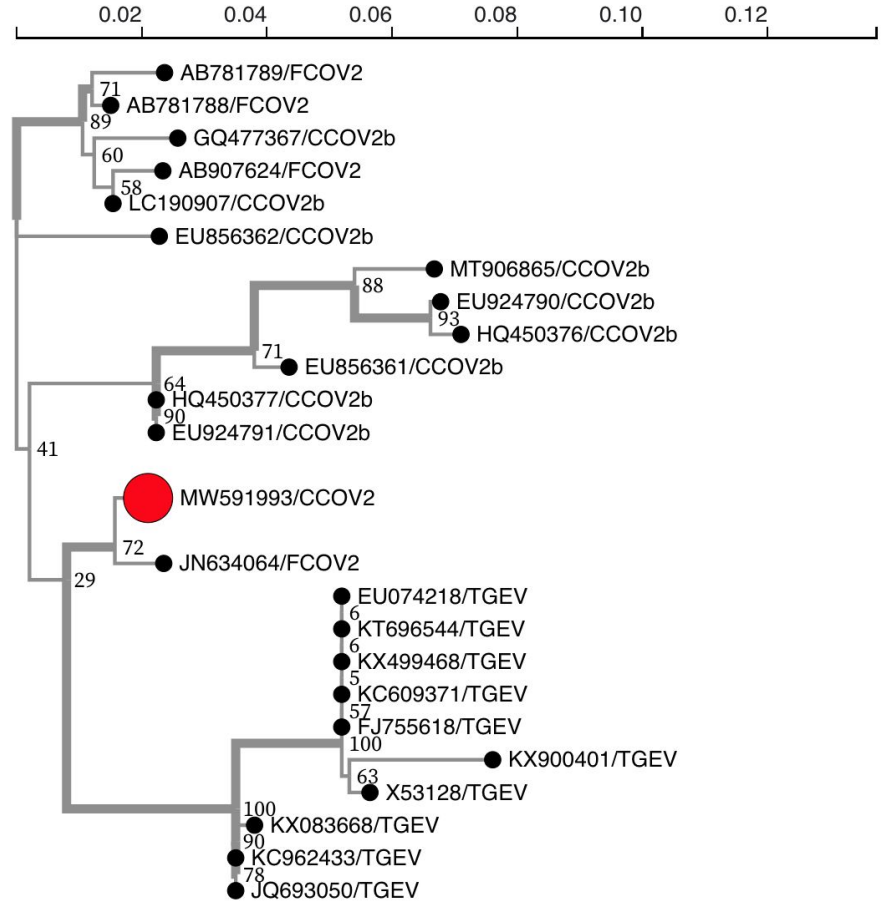
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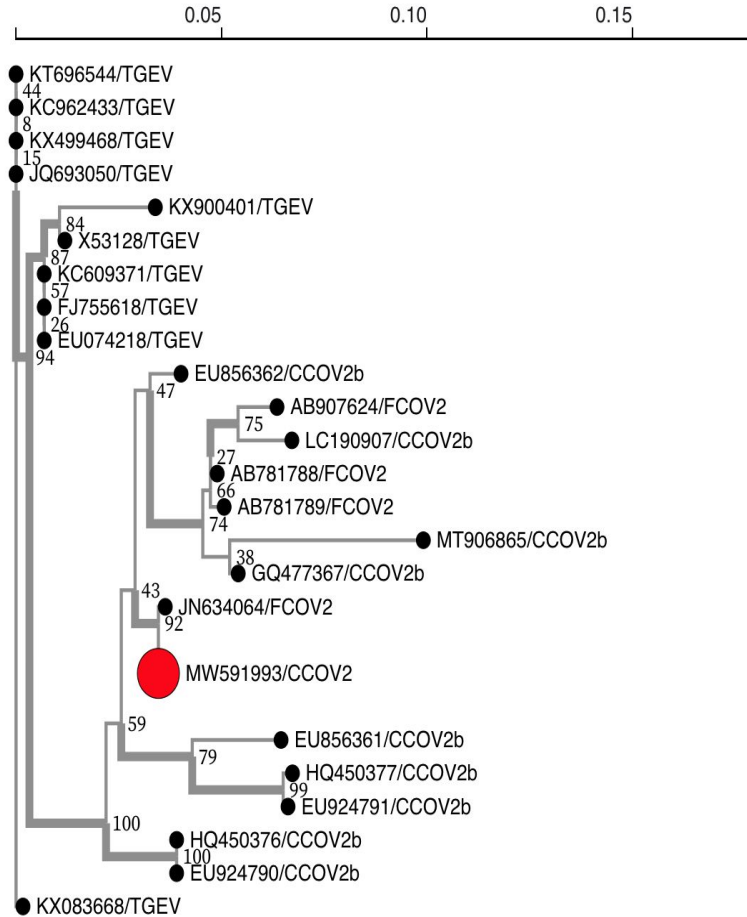
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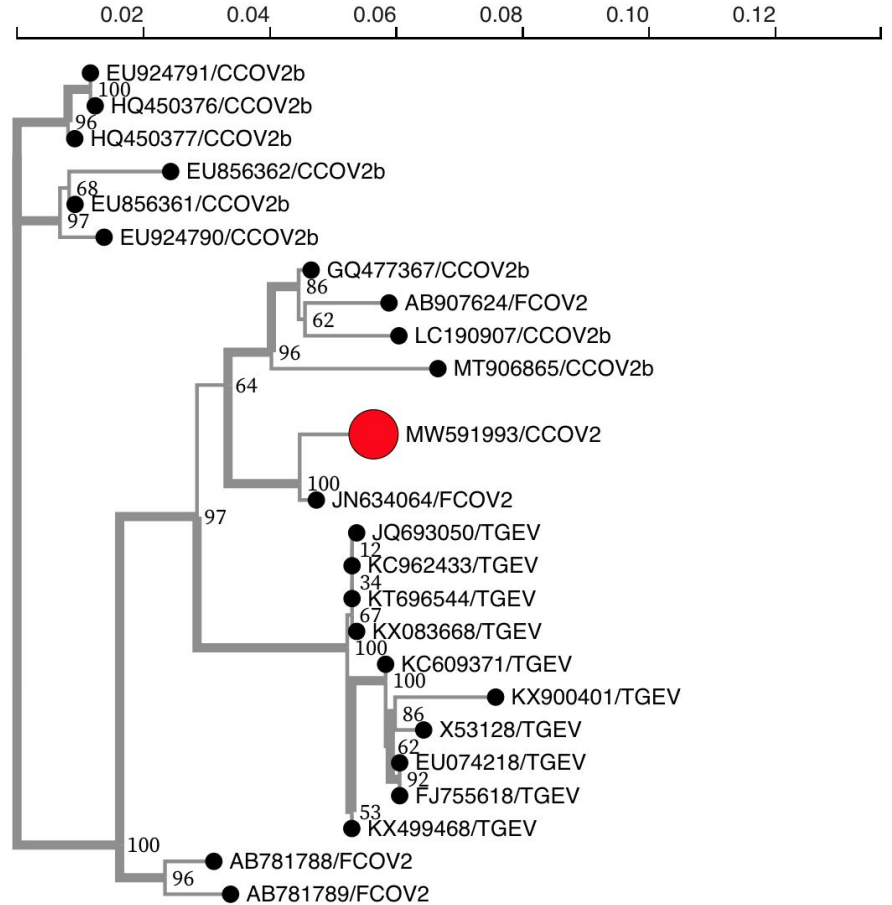
6.



7.



8.



9.

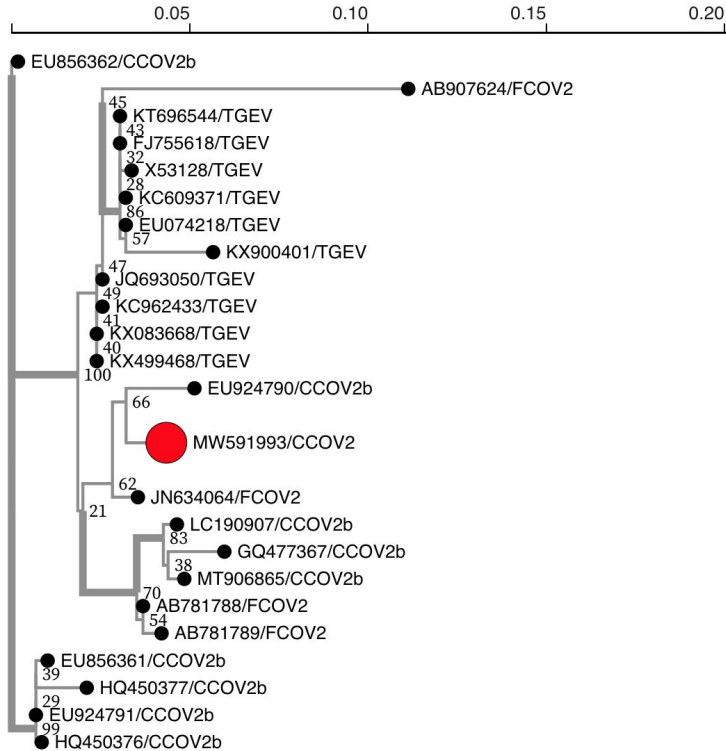


Figure S1. Phylogenetic trees for each GARD fragment inferred using RaxML. 1. Is the first non-recombinant fragment from alignment set I and the further trees correspond to non-recombinant fragments from alignment set II. Tree 2 corresponds to non-recombinant fragment 2 as depicted in the Fig. 1 gene map; tree 3 corresponds to non-recombinant fragment 3, and so on. These trees represent the phylogenetic incongruencies between the different non-recombinant fragments.

Table S2: Positive selection statistics from MEME and FEL

HuPN-2018 sites	FIPV mapped sites	MEME Non-synonymous substitution rate	MEME Synonymous substitution rate	FEL Non-synonymous substitution rate	FEL Synonymous substitution rate	MEME p-value	FEL p-value
13	13	3.58	0	NA	NA	0.04	NA
110	130	30.94	0	29.432	0	0.02	0.02
124	144	3.87	0	NA	NA	0.02	NA
246	262	2.9	0	2.784	0	0.02	0.04
367	384	4.8	0	4.817	0	0.04	0.05
575	603	11.17	0	NA	NA	0.02	NA
529	549	9.23	0	9.46	0	NA	0.05
608	715	11.26	0	NA	NA	0.05	NA
619	637	12.48	0	12.47	0	0.03	0.02
589	619	10.84	0	NA	NA	0.04	NA
1227	1246	27.49	0	NA	NA	0.04	NA
1296	1311	38.37	0	37.386	0	0.01	0.01
1233	1252	3.3	0	3.281	0	0.04	0.04

Figure S2

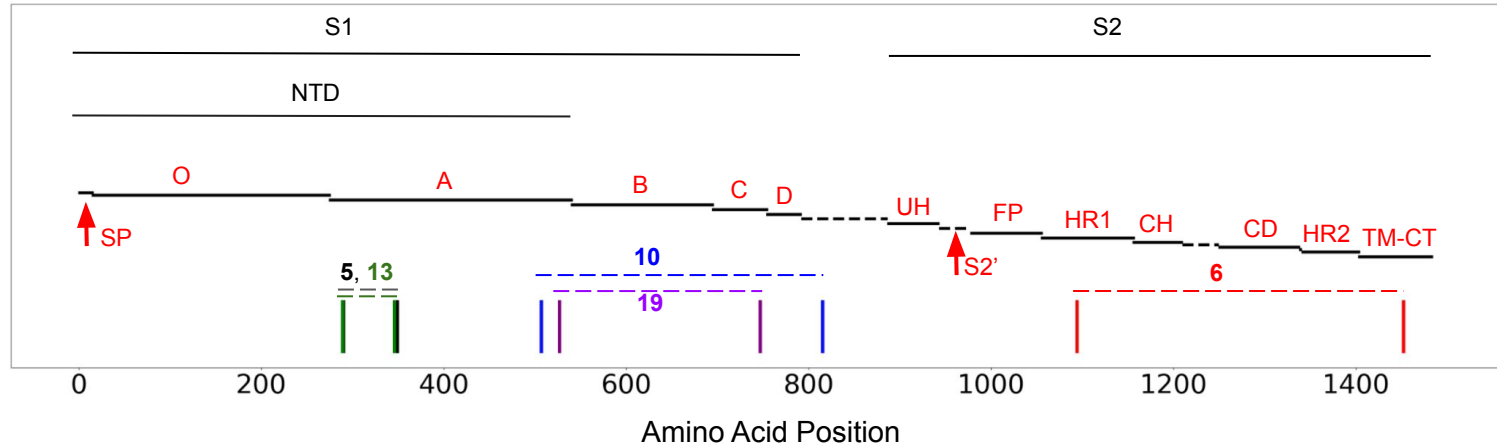


Figure S2. RDP5 results with supported recombination events (event boundaries outlined) that implicate CCoV-HuPn-2018, positioned along a spike gene map. A complete, enumerated list of the RDP5 recombination events, involving all sequences, can be found in Table S3. Event 5 (black) involves a proposed FCoV2 recombinant, with genetic donors: CCoV-HuPn-2018 and a different FCoV2. Event 13 (green) extensively overlaps with 5, as well as with GARD fragment 2 (Fig. 1), where CCoV-HuPn-2018 is a proposed recombinant, with genetic donors: FCoV2 from event 13, as well as a TGEV. Event 10 (cyan) proposes the same FCoV2 sequence from 5 and 13 as the recombinant, with genetic donors: CCoV-HuPn-2018 and a TGEV. Event 19 (purple) falls within 10, with CCoV-HuPn-2018 as the proposed recombinant and the genetic donors: a CCoV2b and a TGEV. Event 6 (red) proposes a CCoV2b as the recombinant, with genetic donors: CCoV-HuPn-2018 and another CCoV2b.

Table S3: RDP5 Recombination Results

<p>⚠ It is possible that this apparent recombination signal could have been caused by an evolutionary process other than recombination.</p> <p>⚠ The additional recombination junction in combination of was most likely either compensated by a subsequent recombination event or off the edge of the analyzed sequence fragments.</p> <p>⚠ The recombination assessment may have been misclassified (one of the identified parents might be the recombinant).</p> <p>Major Parent = Parent contributing the major fraction of sequence.</p> <p>Minor Parent = Parent contributing the minor fraction of sequence.</p> <p>Unknown = Only one parent and a recombination event led to the alignment for a recombination event to be detected. The sequence listed as a reference was used to fix the confidence of a missing parental sequence.</p> <p>NS = No significant P-value was recorded for this recombination event using the particular method in question.</p>		<p>Recombination Event Number</p>		<p>Dissemination Probability</p>		<p>In Recombination Sequence</p>		<p>Reference to recombination junction</p>	
Location ID	Parent File	Major	Minor	Major	Minor	Major	Minor	Major	Minor
1	1	1791	2366	1791	2366	933		1805	1805
2	2	0	0	0	0	0	0	0	0
3	3	0	0	0	0	0	0	0	0
4	4	1474	3198	1474	3198	1474	3198	1474	3198
5	5	580	1590	580	1590	680		1590	1590
6	6	0	0	0	0	0	0	0	0
7	7	2420	3007	2420	3007	2420	3007	2420	3007
8	8	3038	400	3038	400	3038	400	3038	400
9	9	3380	3380	3380	3380	3380	3380	3380	3380
10	10	860	1540	860	1540	860	1540	860	1540
11	11	31	240	31	240	31	240	31	240
12	12	21	1797	21	1797	21	1797	21	1797
13	13	8	184	8	184	8	184	8	184
14	14	2040	2040	2040	2040	2040	2040	2040	2040
15	15	2874	3007	2874	3007	2874	3007	2874	3007
16	16	2480	2874	2480	2874	2480	2874	2480	2874
17	17	212	212	212	212	212	212	212	212
18	18	200	400	200	400	200	400	200	400
19	19	730	1590	730	1590	730	1590	730	1590

Figure S3

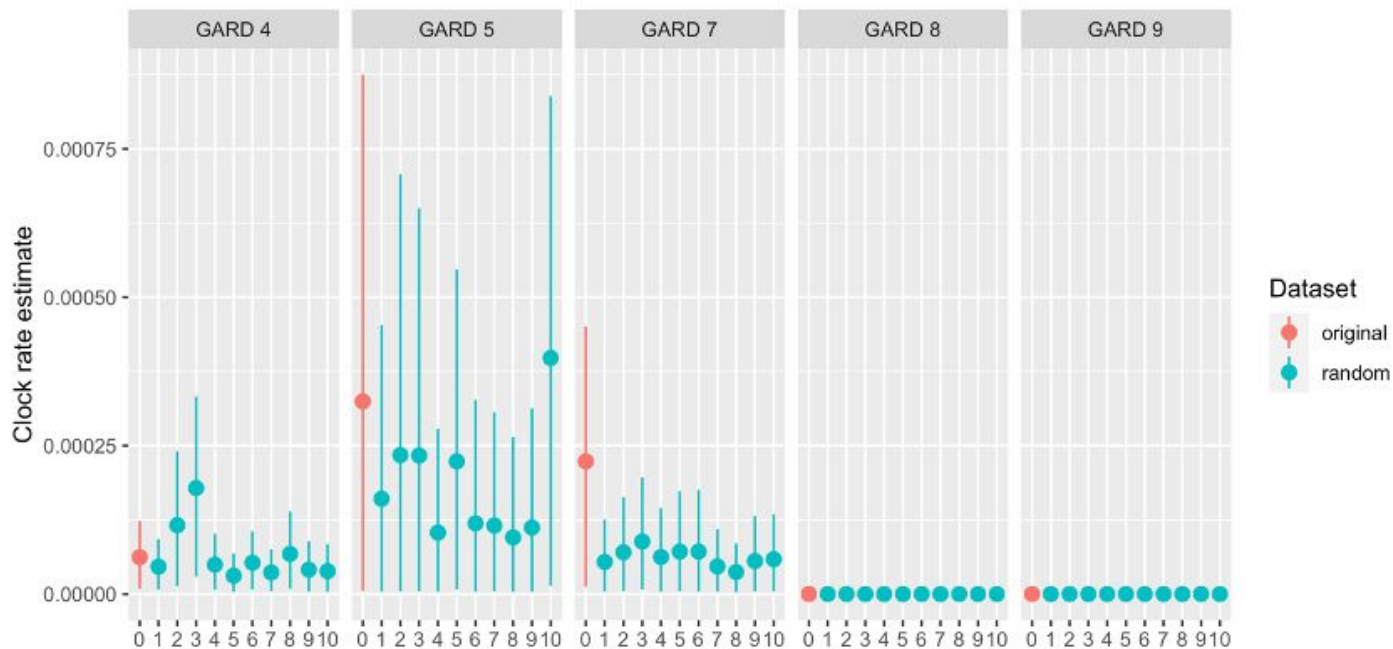


Figure S3. Mean and 95% HPD clock rate estimates for the original dataset and ten datasets with random dates are shown for the five GARD fragments with evidence of temporal signal on the root-tip regression analysis. Only GARD 7 had a mean clock rate estimate above the 95% HPD of the randomized datasets, indicating the presence of a temporal signal.

Table S4: Root-tip-regression results for each GARD Partition

GARD partition	Correlation coefficient	R ²
1	0.083	0.0070
2	-0.046	0.0021
3	-0.11	0.013
4	0.20	0.040
5	0.20	0.039
6	0.088	0.0077
7	0.36	0.13
8	0.30	0.089
9	0.21	0.046

Figure S4



Figure S4. Ancestral host reconstruction and divergence time estimates. Branches are colored by inferred host species. The branch width is proportional to the posterior probability of host assignment (also labeled on branches). Internal nodes are labeled with the divergence time 95% HPD in years from the most recent sample date, 2017. CCoV-HuPn-2018 diverged from FCoV2 JN634064 between 40 and 170 years ago, with a median date estimate of 1957.

Figure S5

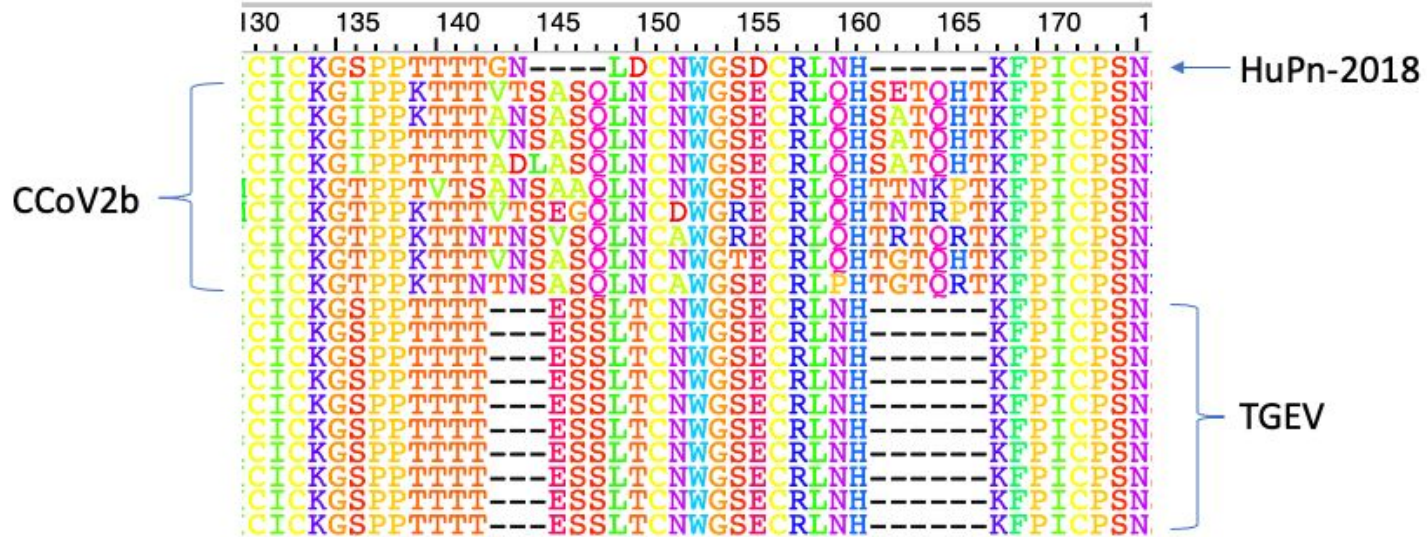


Figure S5. Set I sequence alignment highlighting the region involved in the proposed sialic acid binding, identified in the Krempf et al. (1997) mutation experiments.