

S9 Table: Pairwise similarities inferred from distance estimations between betacoronavirus full genomes

Accession	Coronaviruses as comparison	Lineage	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28				
1	NC00657	HCoV HKU1		0.002	0.002	0.002	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.003	0.003	0.003	0.003			
2	NC_003045	Bovine CoV	A	72.7		0.003	0.001	0.002	0.002	0.002	0.003	0.002	0.002	0.002	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.003	0.003	0.002	0.003	0.003		
3	NC_006852	MHV-JHM		72.0	72.3		0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.002	0.003	0.003	0.003	0.003		
4	NC005147	HCoV OC43		72.6	96.6	72.5		0.002	0.002	0.002	0.002	0.003	0.002	0.002	0.003	0.002	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.002	0.003	0.003	0.003		
5	AY714217	HCoV SARS-CoV CDC		45.7	45.2	44.1	45.2		0.000	0.000	0.002	0.001	0.002	0.001	0.002	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.002		
6	GU553365	HCoV SARS-CoV HKU39849		45.6	45.1	43.9	45.1	100.0		0.000	0.002	0.001	0.002	0.001	0.002	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.003		
7	AY572034	Civet SARS-CoV 007		45.6	45.1	43.9	45.1	99.7	99.7		0.002	0.001	0.002	0.001	0.002	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.002		
8	NC_009694	BtCoV <i>Rhinolophus</i> -SARS HKU3	B	45.5	44.8	44.0	44.9	87.8	87.9	87.7		0.002	0.002	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.003	0.003		
9	KF367457	BtCoV <i>Rhinolophus</i> -SARS WIV1		45.4	44.6	43.5	44.9	95.6	95.6	95.4	88.2		0.002	0.001	0.002	0.003	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.002		
10	DQ412043	BtCoV <i>Rhinolophus</i> -SARS Rm1		45.2	44.5	43.7	44.7	88.1	88.1	88.0	90.3	88.5		0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.003		
11	DQ071615	BtCoV <i>Rhinolophus</i> -SARS Rp3		45.6	45.0	44.0	45.0	92.5	92.6	92.4	89.7	93.5	90.5		0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002		
12	NC_009021	BtCoV <i>Rousettus</i> /HKU9-1	D	46.2	45.4	44.0	45.4	51.8	51.8	51.8	51.5	51.6	51.5	51.7		0.002	0.002	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.002	0.003	0.002		
13	EF065516	BtCoV <i>Rousettus</i> /HKU9-4		45.8	44.9	43.8	44.9	51.6	51.5	51.5	51.1	51.3	50.9	51.3	79.6		0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.002	
14	NC_022643	<i>Erinaceus</i> CoV VMC/DEU/2012		47.4	46.4	44.9	46.4	49.2	49.1	49.2	49.1	49.1	49.1	49.2	47.7	47.7		0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.003	0.002	0.002	0.002	0.002	
15	KC164505	HCoV MERS/England1		46.1	45.5	44.4	45.6	49.5	49.3	49.4	49.3	49.3	49.1	49.4	47.6	47.3	69.3		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.002	
16	KM210277	HCoV MERS/England/4/2013		46.1	45.6	44.4	45.6	49.5	49.3	49.4	49.2	49.2	49.1	49.4	47.6	47.3	69.3	99.8		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.002	0.002	0.001
17	KU308549	HCoV MERS/Korea/Seoul/SNU/103		46.1	45.5	44.4	45.6	49.4	49.3	49.4	49.2	49.3	49.1	49.4	47.6	47.3	69.3	99.8	99.7		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.002	0.002	0.001	0.002	
18	KF958702	HCoV MERS/Jeddah/human/1		46.2	45.6	44.4	45.7	49.5	49.4	49.4	49.3	49.4	49.2	49.5	47.7	47.4	69.2	99.9	99.8	99.7		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.002	0.002	0.001	0.002	
19	KF917527	HCoV MERS/Jeddah/Camel/1		46.2	45.6	44.4	45.7	49.5	49.4	49.4	49.3	49.4	49.2	49.5	47.7	47.4	69.2	99.9	99.8	99.7	100.0		0.000	0.000	0.000	0.000	0.000	0.003	0.002	0.002	0.001	0.002		
20	KJ713299	HCoV MERS/KSA/CAMEL/376		46.1	45.6	44.4	45.6	49.5	49.3	49.4	49.3	49.3	49.1	49.4	47.6	47.3	69.3	99.8	99.9	99.7	99.8	99.8		0.000	0.000	0.000	0.000	0.003	0.002	0.002	0.001	0.002		
21	KJ713298	HCoV MERS/KSA/CAMEL/363		46.1	45.6	44.4	45.6	49.5	49.3	49.4	49.2	49.2	49.1	49.4	47.6	47.3	69.3	99.9	99.8	99.7	99.8	99.8	99.8		0.000	0.000	0.000	0.003	0.002	0.002	0.001	0.002		
22	KJ713297	HCoV MERS/KSA/CAMEL/503		46.1	45.6	44.4	45.6	49.5	49.3	49.4	49.2	49.2	49.1	49.4	47.6	47.3	69.3	99.8	99.8	99.7	99.8	99.8	99.8	99.9		0.000	0.003	0.002	0.002	0.001	0.002			
23	KJ477102	HCoV MERS/CAMEL/NRCE-HKU20	C	46.1	45.5	44.4	45.6	49.5	49.4	49.4	49.2	49.3	49.0	49.4	47.6	47.3	69.2	99.5	99.5	99.3	99.4	99.4	99.4	99.5	99.4		0.003	0.002	0.002	0.001	0.001			
24	NC009020	BatCoV <i>Pipistrellus</i> /HKU5		45.1	44.3	43.8	44.4	48.4	48.3	48.3	48.2	48.1	48.0	48.3	46.9	46.6	66.1	70.1	70.0	70.1	69.8	69.8	70.0	70.0	70.0	69.9		0.003	0.002	0.002	0.003			
25	NC009019	BatCoV <i>Tyonycteris</i> /HKU4		47.4	46.3	44.7	46.3	49.6	49.4	49.5	49.2	49.3	49.1	49.6	48.2	47.5	67.1	69.7	69.6	69.7	69.5	69.5	69.7	69.7	69.7	69.5	72.9		0.002	0.003	0.003			
26	KX574227	BtCoV <i>Pipistrellus</i> /PREDICT-PDF2180		46.9	45.8	45.0	45.8	49.4	49.4	49.4	49.2	49.2	49.2	49.4	48.0	47.5	70.0	83.4	83.4	83.4	83.4	83.4	83.4	83.4	83.4	83.4	83.3	69.7	69.3		0.001	0.001		
27	KC869678	BtCoV <i>Neoromicia</i> /PML/RSA/2011		46.9	45.8	44.8	45.9	49.5	49.4	49.4	49.3	49.2	49.1	49.4	48.2	47.8	70.0	85.6	85.5	85.5	85.4	85.4	85.5	85.5	85.6	85.4	69.7	69.4	86.2		0.001			
28	this study	BtCoV <i>Neoromicia</i> 5038/KZN/RSA/2015		47.0	45.8	44.8	45.9	49.5	49.4	49.4	49.3	49.2	49.1	49.4	48.3	47.9	70.1	85.5	85.5	85.5	85.4	85.4	85.5	85.5	85.5	85.4	69.5	69.4	86.3	97.2				