

S8 Table: Genome annotation of BtCoVNeo5038 with similarities to compared lineage C betacoronaviruses

Genome description of BtCoVNeo5038			Percentage identities to lineage C coronaviruses																
Open reading frames	Coding region position	No. of amino acids	<i>Neoromicia</i> NeoCoV PML/PHE1		<i>Pipistrellus</i> PREDICT-PDF2180		<i>Tylonycteris</i> BtCoV-HKU4		<i>Pipistrellus</i> BtCoV-HKU5		Human MERS EMC 2012		Human MERS Jeddah		Camel MERS Jeddah		Camel MERS NRCE HKU205		
			nt%	aa%	nt%	aa%	nt%	aa%	nt%	aa%	nt%	aa%	nt%	aa%	nt%	aa%	nt%	aa%	
Nonstructural genes																			
ORF1a	268-13227	4319	96.9	98.1	85.4	89.4	66.9	64.5	66.9	66.0	86.2	89.9	89.8	89.8	86.1	89.8	86.2	89.8	
ORF1ab	268..13440, 13440..21524	7085	97.2	98.6	87.3	86.2	72.0	73.4	72.0	75.5	88.5	92.8	88.4	92.8	88.4	92.8	88.4	92.7	
Coronavirus structural genes																			
Spike	21466-25500	1344	96.0	98.7	85.5	93.5	62.5	60.2	61.8	60.9	67.9	64.0	68.0	63.9	68.0	63.9	67.8	63.7	
Envelope	27573-27821	82	98.0	98.8	91.2	92.7	75.1	74.4	76.3	73.2	92.4	90.2	92.4	90.2	92.4	90.2	92.4	90.2	
Membrane	27836-28495	219	97.7	99.1	85.8	94.5	74.9	82.2	71.9	82.2	87.9	94.5	87.7	94.1	87.7	94.1	87.9	94.5	
Nucleoprotein	28553-29797	414	98.3	99.5	87.4	90.6	72.2	75.4	72.6	74.3	87.4	92.0	87.4	92.0	87.4	92.0	87.2	91.5	
Accessory proteins (hypothetical) of lineage C betacoronaviruses																			
ORF3	25515-25826	103	97.8	97.3	76.5	74.3	49.6	30.1	57.5	26.3	80.4	85.0	80.8	85.0	80.8	85.0	81.1	84.5	
ORF4a	25835-26164	109	98.2	99.1	78.2	75.2	54.7	38.9	54.0	43.0	86.4	87.2	87.0	87.2	87.0	87.2	87.3	87.2	
ORF4b	26040-26816	258	97.2	97.3	72.7	70.9	47.2	30.1	45.7	26.3	83.9	85.0	83.9	85.0	83.9	85.0	83.8	84.5	
ORF5	26823-27497	224	97.2	97.3	75.4	73.7	59.3	45.5	61.9	56.3	84.8	88.4	84.7	88.4	84.7	88.4	84.1	87.1	
ORF8b	28599-29198	199	98.0	94.0	87.7	72.4	74.5	52.3	77.0	53.2	92.6	82.1	92.9	82.1	92.9	82.1	-	-	
Overall genome	30009 bp	-	97.2	98.5	86.2	91.0	69.4	69.4	69.5	71	85.5	88.2	85.4	88.2	85.4	88.1	85.4	88.1	