Supplementary Table 1. Primer sets used to amplify overlapping DNA fragments of the ACoV genome by RT-PCR and 5'/3' RACE.

Fragment	Genome Location	Method of production	Primer Set
1 [a]	1–550	5' RLM RACE (ABI)	CGC GGA TCC GAA CAC TGC GTT TGC TGG CTT TGA TG ACG AAG CAT AAA GGG ACG GTC AGA
1 [b]	1–375	PCR [a]	CGC GGA TCC GAA CAC TGC GTT TGC TGG CTT TGA TG ACG GCT AGC GCA ATA GTA GAG CAA
2	352–2033	2-step RT-PCR (Epicentre)	TTG CTC TAC TAT TGC GCT AGC CGT TTG GAC TGG CCA TAA GAC GGA AGT
3.28	1967–3593	2-step RT-PCR (Epicentre)	*ACT GTT GTA ATT GGC GAT GTG GCG*[b] *CAG CAG TGT AGC AGC GTT CAA TCA*
3.3	2788–4417	2-step RT-PCR (Epicentre)	*TGC TTA CAT GCC AAT TGC AGA CCC* ACG TTC ATG TTT ACC CTT GCG TGG
3.16	4232–5490	2-step RT-PCR (Epicentre)	AAC CTT GCT CAT GGT GGA GGA CTT *CAC GCA GCA TCA AGA CCT TGT GAA*
3.8	4736–6221	2-step RT-PCR (Epicentre)	*TTG TGT GTC GCT GAT GAC AAA CCC* AAA CAA CAC CCG TCC TTT GTG GTG
3.41	6198–7819	2-step RT-PCR (Epicentre)	CAC CAC AAA GGA CGG GTG TTG TTT *ACA CAC AAG ACC ACA CAG TAG CCA*
3.34	7718–9301	2-step RT-PCR (Epicentre)	*GCT GTC ACG CAA ATA CCT GCA ACT ACC AAG CCA CAA CCC ATT CAA CAC*
3.1	9082–10176	2-step RT-PCR (Epicentre)	*TGA AGC TGA TTA CCG TTG CGC TTG GCC CAG AAC ATG ACA AAG AAG CCA*
3.4	9845–11395	2-step RT-PCR (Epicentre)	TGC ACA TGG TGG CTC AAA GGT GA TGC AGC AGC TTG TTC AGC CAT
3.14	11068–12497	2-step RT-PCR (Epicentre)	*TGA CGA CCC TGA AAC TGC TCA AGA* TCC GGT CAC ATG TAC AGC CAT GAT
4	12293–14347	2-step RT-PCR (Epicentre)	ACA CAG GAT ACA TAT GGT GGC GCT AGT CCC AGC CCA TCA ACT TAG GAT
5	14129–17624	2-step RT-PCR (Epicentre)	*ATG CCA TAT CTG GTA AGG AGC GTG* ACC AGT ACG TCA GAT GAA CCA GCA
6 [c]	17536–20851	2-step RT-PCR (Epicentre)	TTA CGC AAG GGA CAA CCT TGG AGT AGT AAA CCG CGA GCC AGA AAC AGA
7 [c]	23917–25412	2-step RT-PCR (Epicentre)	GTG GGT GTG GTT GTG CAT TTC AGT TGC CTG TTG GAG CTT GTT GAA TGG
8 [c]	26477–27374	3' RLM RACE (ABI)	CCA CAA CTT TGG AAG TGC AGG TGT GCG AGC ACA GAA TTA ATA CGA CT

[a] The template for this set of primers was fragment 1a. [b] Italics represent primers that have mismatches when compared to final ACoV genome sequence due to the fact that the HCoV-229E genomic sequence was used for primer design. [c] These fragments overlap with spike (between fragments 6 and 7) and membrane/nucleocapsid (between fragments 7 and 8) gene sequences that were already available before starting the full-length genome sequencing.