Supplemental Tables

TABLE S1 Real time RT-PCR primers and probes. Numbering is based on a consensus alignment of the Allston/08, Allston/09, Bari/07, Geel/08 and CU-246 genomes

Test	Name	Sequence
A	3461-F	AGAATGGACATCTCTGTGGATGAA
	3553-R	CCAGGAACGAAACTGGATTGA
	Probe-3486-F	TCTTGATGCTCAAACATCGTGCTGCC
B	3443-F	GACTTCAAGATGGACAAGAGAATGG
	3553-R	see above
	Probe-3486-F	see above
C	5750-F	GATTGCGAGGTTCAGATGCTAA
	5823-R	GCCATTGCTCAGTTCTCAAACA
	Probe-5773-F	CAGTGACGCTCCCAATGCTCACGA

TABLE S2 Amplification and sequencing primers used for sequencing the CU-246 genome and the VP1 genes of CU-47, CU-103, LSU/96-6931 and strain 143

Primary sequencing primers	
Name[a,b]	Sequence
38-F	CAMTCGAGCTCWACCGCTCACAAAA
334-R	GGAGTTGTCGGGTACACAAGCAGA
661-F	CCACAAGATTGCCTCTGGAATTGT
775-R	CGAGTTGGTTCCGAGGGCTTTCT
1404-F	CCAACCTGAACATTCTGAAAGCTGAAT
1582-R	CTGTATTGCGGTAATTCCAGCGA
1976-F	AACATTGACCACCACGATGCCTACA
2106-R	CAATTTAGGAGCATGGGGTTGGTATT
2351-F	GCGTTCTCCAAAACCAGGGTCATT
2830-F	CATTCGTGGCAAACACATCCAA
2853-R	TCTTGGATGTGTTTGCCACGAAT
3514-R	CAAGGCAGCACGATGTTTGAGCAT
3560-F	GCCAGGCAAATGAGACAGGACACT
3803-F	CACATTGGCCATGGTGTGTGCAT
4065-F	CGACGAAAACCCAACCTGGAGATT
4204-R	GTTCATCTTGACTTTCACAACAGGAAT
4404-R	GGATTTCGTGGATCTTCAGCTCCAA
4696-F	CGAACAAGGCCTTGCAATACCACAT
4970-F[c]	GATTACTCCAAGTGGGACTCCAC
5072-R	CAGCAGAATCAACGATAGGTGACTTGT
5135-F[d]	GGTTTGCCATCTGGCATGCCGCTA
5219-R	TTGATTGGATGAGTGCACACCCAA
5300-R[c]	TGACAATGTAATCATCACCATA
5532-F	CAATGAATTGGACTGAACCACCAA
5750-F	GATTGCGAGGTTCAGATGCTAA
5824-R[d]	AGCCATVGCTCARTTCTCAAACAC
6270-R	GCTGTTCGGTCTGCGACCTGAA
6359-F	GGCACTCAACCTTCTGCTCCAGCTAT
6754-F	GTTGTGGCATGACATGCACGACA
6869-F	GAAACACGCGGCGGTACTGATT
6922-R	TCTTGCTGGGGGCTTGAGAAGAT
7432-F	CTTCACCCAACAAGGGAACATAATTGTT
7529-R	TCTTAACCTTGTCTTCATCTTCACCAA
7804-F	TCAATTTCCTCTTGAAGCCAGCTA
7858-F	GCAACATAATATTGCTGGCACATCAGT
7971-R	GGCATTTGCAATTGACCCAATCAA
8018-R	GCACCAAGAGCTGTTCCTTGGAGTT
8254-F	GCTGCCGAGCGAAGGTT
8460-R	TTCCAATTGTTTTGCCAAATAGTTCAA

Specific primers for VP1 hypervariable regions of different strains	
6080-F	ATCGTTCTRAAGCACCAATTGGAGTC
6105-F	GTTACACTGAATGGGAAGATGGCACTT
6685-R	AAACTGTAAGAGGCTTGTGCCTCCT
6726-R	ATAACTGGTTCTGTTTGCCTGGCAT
7110-R	AATTTAACTCCACGGTGYTCAGGAGTTG
7228-R	GTAGTAGTCAGGCCACCCGTC
7252-R	GTTGTTTGCCACGATTATGTTGTCGTA
7366-F	AACCGCTCAAAACTCGACGGTGAA
7547-F	CAAGCCCAAACGACTGGTGGTAACTA
7688-F	CCTGAAGCCTTGGCAGTCTT
7938-R	GGCGCTTGTTGCGCTAGCT

[a] Name reflects numbering based on Allston/09.

[b] Primers designed for this study unless otherwise indicated.

[c] Previously described: Jiang X, Huang PW, Zhong WM, Farkas T, Cubitt DW, Matson DO. 1999. Design and evaluation of a primer pair that detects both Norwalk- and Sapporo-like caliciviruses by RT-PCR. J. Virol. Methods 83:145-154. http://dx.doi.org/10.1016/S0166-0934(99)00114-7.

[d] Previously described: Martella V, Pinto P, Lorusso E, Di Martino B, Wang Q, Larocca V, Cavalli A, Comero M, Decaro N, Banyai K, Saif L, Buonavoglia C. 2015. Detection and full-length genome characterization of novel canine vesiviruses. Emerg. Infect. Dis. 21:1433-1436. http://dx.doi.org/10.3201/eid2108.140900.

TABLE S3 Conserved ORF1 regions used in combination for the design of Z probes (ACD)

3290-3633[a] (344 bp)
ATTGTGCTTACTGCCCTCCTGCTGTACATGAAAAGGTACAAGCCAAGGAGTGAAG
CCAAGGGCAAGACAAAGGGAGGACGTGGAGCCATCCGCCATGGAGGGAAGGGGG
TGGTCCTCGCCGATGATGAGTACGATGAATGGAGAGACTTCAAGATGGACAAGAG
AATGGACATCTCTGTGGATGAATTCTTGATGCTCAAACATCGTGCTGCCTTGGGTT
CCGATGACCGGGACTCAATCCAGTTTCGTTCCTGGTGGTCCGCCAGGCAAATGAG
ACAGGACACTGGCCTTGATCATGAAGACGTCACCGTAATTGGCAAAGGAAAGGTG
AGTCACGAAGTGCA

3881-4260 (380 bp)
TTCAATGGTGAATTGGCATATTTCCAAATTAACACGTACCCAAATTCAGCTGCCCC
AGTTGGGTATGACTCAAAGCCCGTGCGTGATCCGTGGGGCCGCCCAGTTTCGACT
GAGTGGAAACACGAGGTCTACAACACTTCCGCAGGGAAGATGTGTGGATCAATCG
CATGGACTGCGACGAAGACTCAACCTGGAGATTGCGGTTTGCCCTACGTTGACGA
TAGGGGGAGAATCGTCGGGCTTCACGCTGGGTCTGGTGGTGATGCGTCCCCAGGA
CGCAAAATCATCATTCCTGTTGTGAAAGTCAAGATGAACTCCAACGGGGTCTTTGC
TAAAGCATTTTGGCAAGAAGATCGCCGAACCATCAAATACAAAGGGCT

5740-6026 (287 bp)
CGATTGCGAGGTTCAGATGCTAAGCAGTGACGCTCCCAATGCTCACGAAATAGTG
TTTGAGAACTGAGCAATGGCTCGCTCAAGCGAATACAGTTCACAAAACTCTCTGG
ATGAGGTGTACGACTACGACACCTACGATCCTTTTCCAAATTTTGAAAGAAATCTG
GCTAGCTATTACTCCACAGACTTCTGTCCTCAAATCAATCTTGAAGACTTCTTTCTT
GACCCTGAAGACTTTGATTTCTGTGACCACCCATTTGAATGCTGCTTTCCAGATTA
CTTGGATT

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[a] Nucleotide numbering is based on the consensus of an alignment of the 2117-like strains.