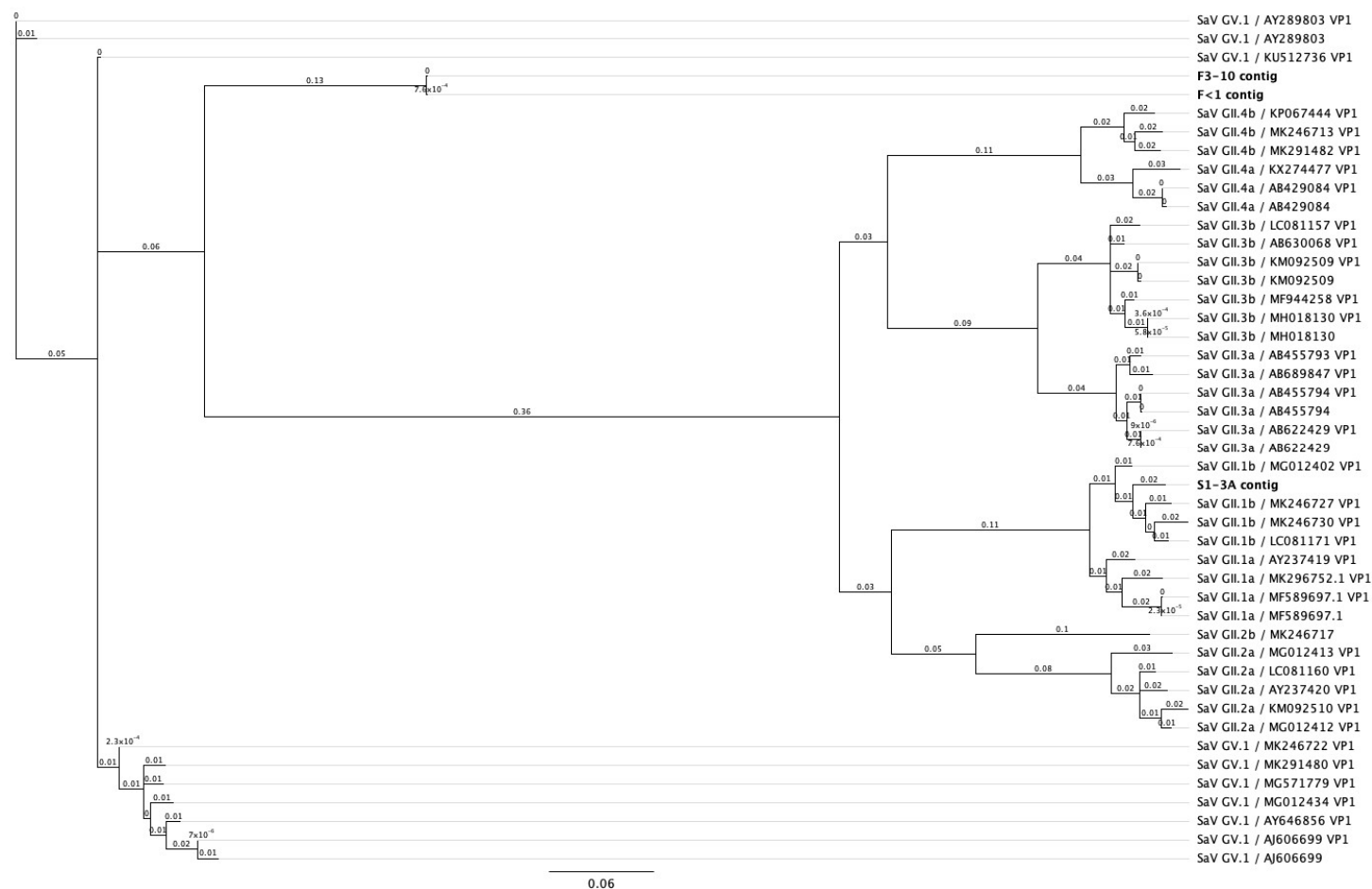


Supplementary material 1. Metagenomic sequencing summary statistics obtained with genome detective.

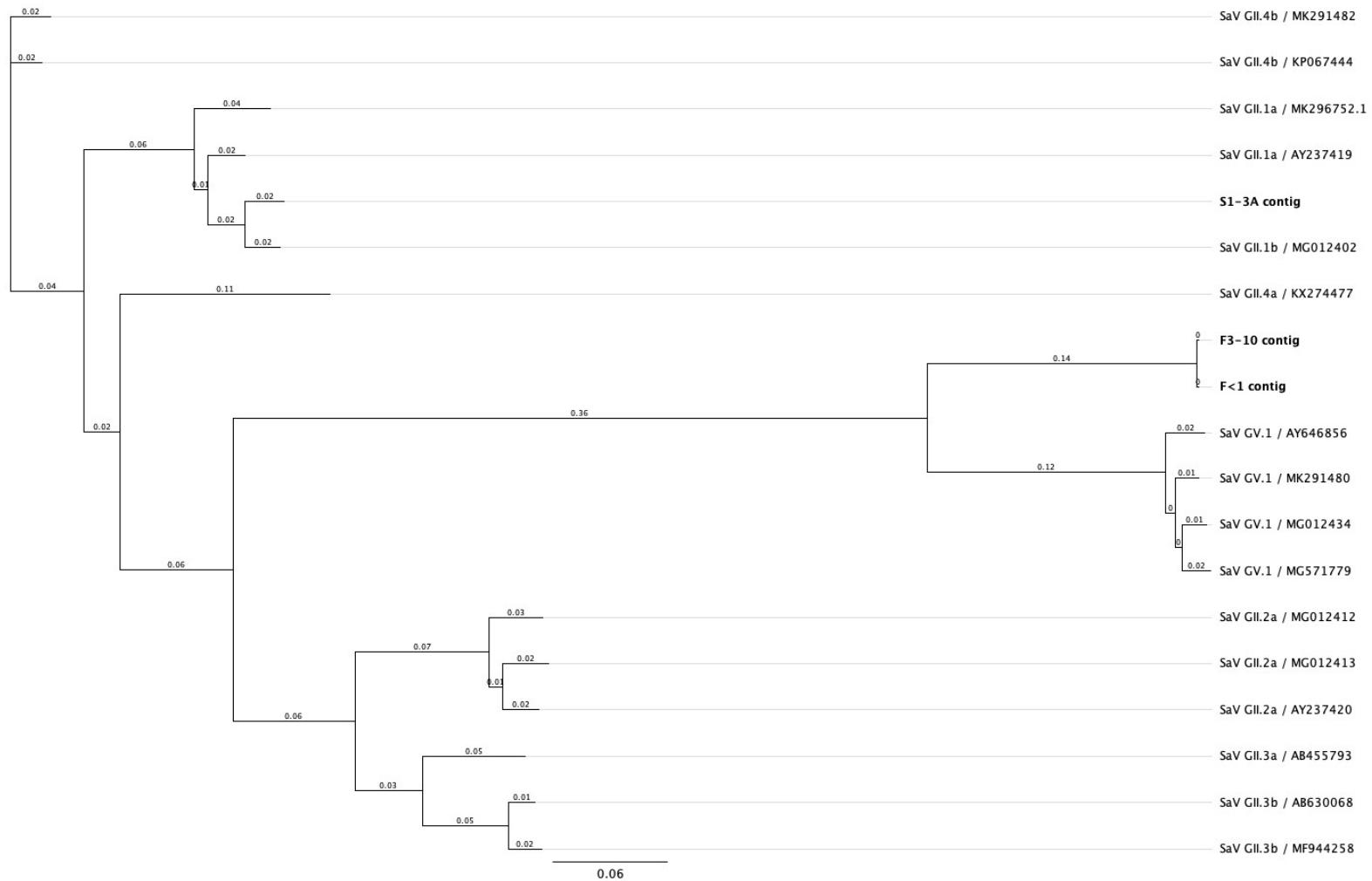
Sample	Initial paired end reads	Removed reads after quality (percentage)	Used reads	Non-viral reads (percentage)	reads used for assembly	Mapped reads into contigs
F<1	6,095,990	468,766 (7%)	5,627,224	2,867,732 (50%)	2,759,492	2,364,300
F1-3A	5,613,532	220,524 (3%)	5,393,008	4,161,306 (77%)	1,231,702	487,708
F3-10	9,237,546	513,822 (5%)	8,723,724	1,049,524 (12%)	7,674,200	7,463,778
F>10	12,265,116	655,736 (5%)	11,609,380	4036,566 (34%)	7,572,814	7,414,041
S<1A	1,982,130	119,564 (6%)	1,862,566	1,049,222 (56%)	813,344	873,829
S<1B	1,258,278	69,804(5%)	1,188,474	850,264 (71%)	338,210	199,647
S1-3A	1,549,150	60,662 (3%)	1,488,488	819,480 (55%)	669,008	514,749
S1-3B	1,037,992	41,840 (4%)	996,152	725,326 (72%)	270,826	85,046
S1-3C	881,740	37,730 (4%)	844,010	379,784 (44%)	464,226	17,425
S3-10	2,419,026	70,822 (2%)	2,348,204	1,387,786 (59%)	960,418	578,919

Supplementary material 3. Phylogenetic trees of sapovirus contigs. Trees were constructed by using tree view software within Geneious (software version 11.0 (<https://www.geneious.com>) maximum-likelihood (Tamura-Nei model, Bootstrap of 1,000 replicates) analysis. Phylogenetic trees with the full sapovirus types (a), full length VP1 (b), complete genomes are presented. The labels on the branch indicate the number of substitutions per site.

a.

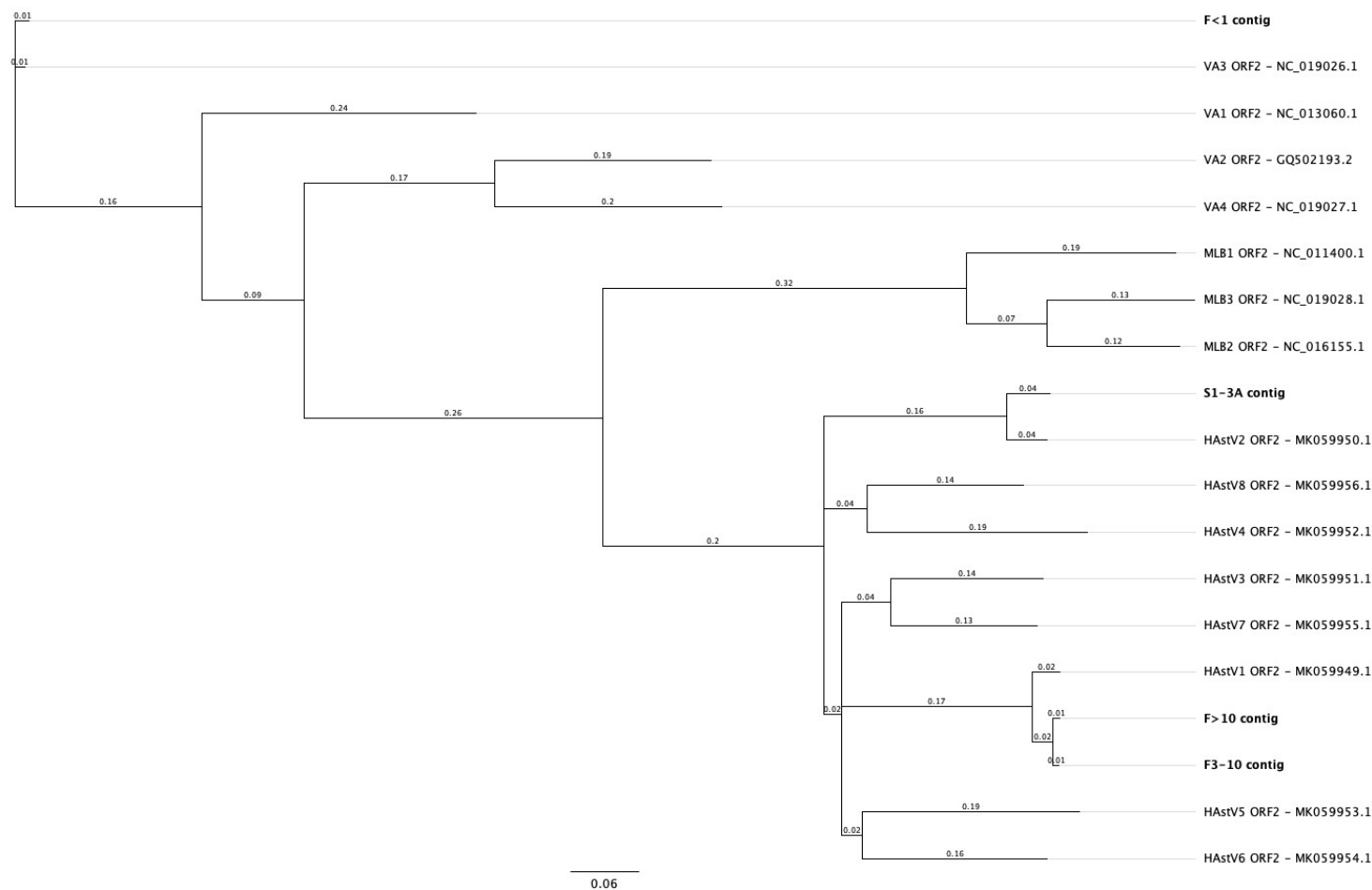


b.

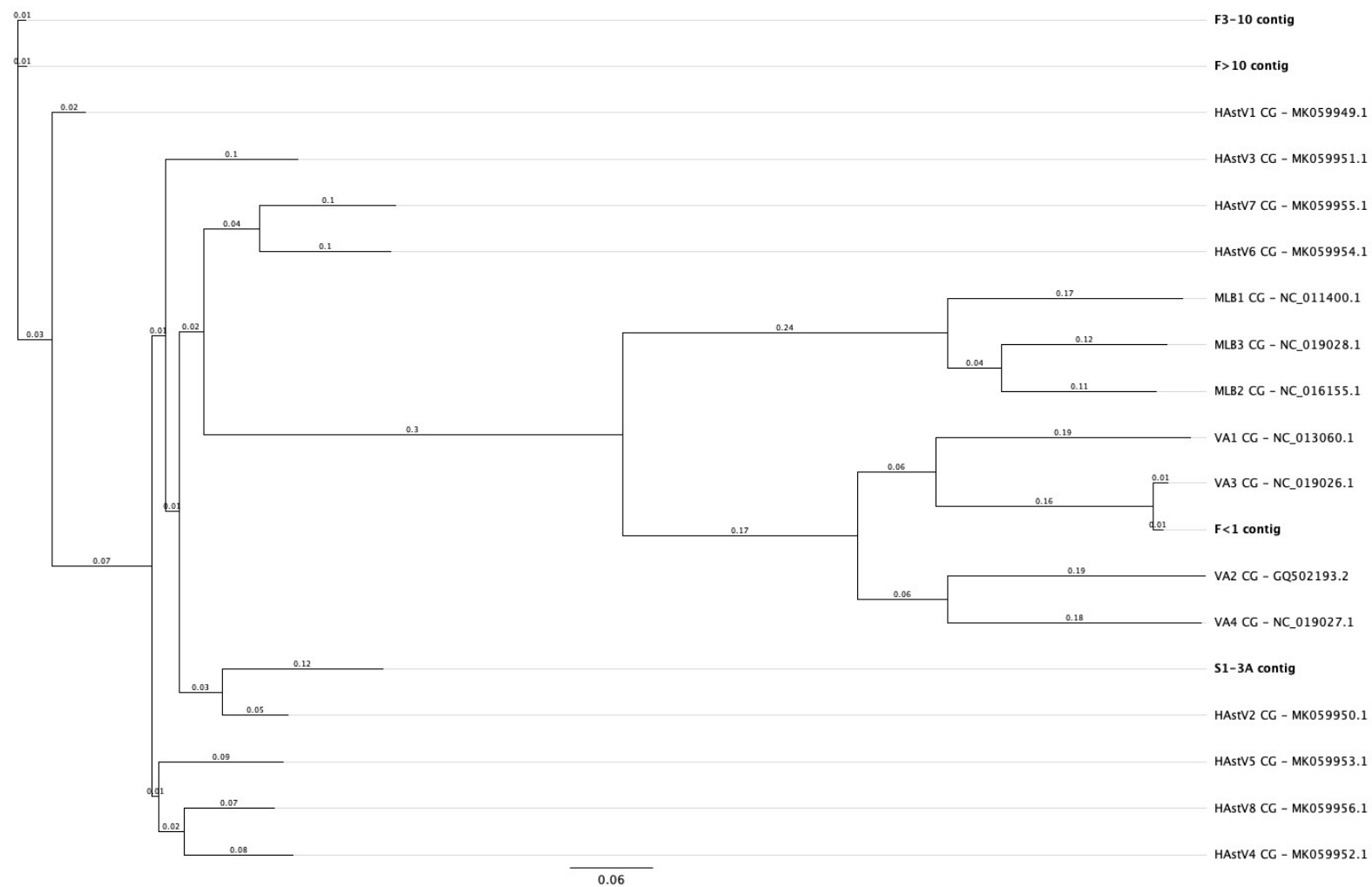


Supplementary material 4. Phylogenetic trees of mamastrovirus contigs. Trees were constructed by using tree view software within Geneious (software version 11.0 (<https://www.geneious.com>) maximum-likelihood (Tamura-Nei model, Bootstrap of 1,000 replicates) analysis. Phylogenetic trees with the full mamastrovirus types (a), full length ORF2 (b), complete genomes are presented. The labels on the branch indicate the number of substitutions per site.

a.



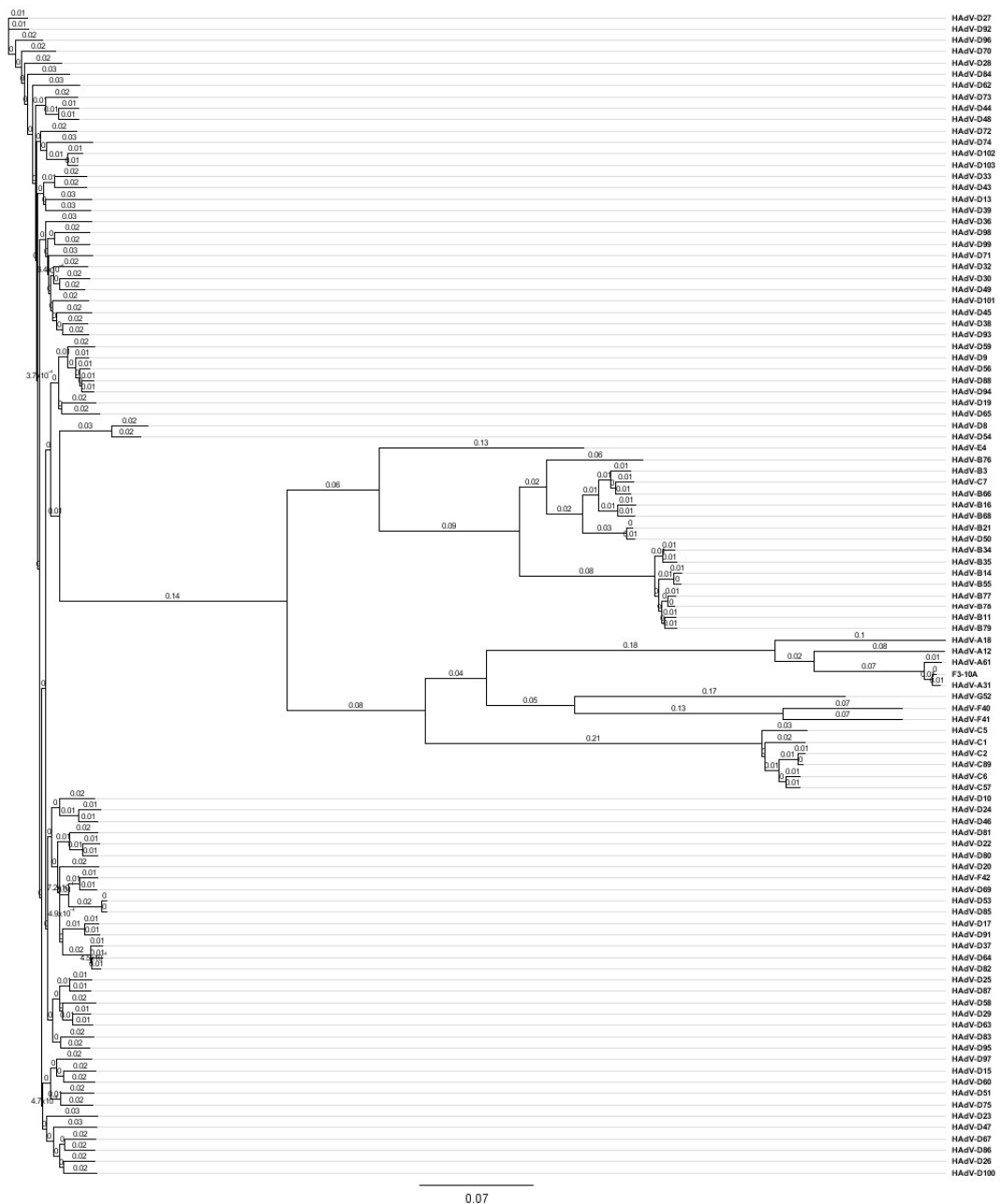
b.



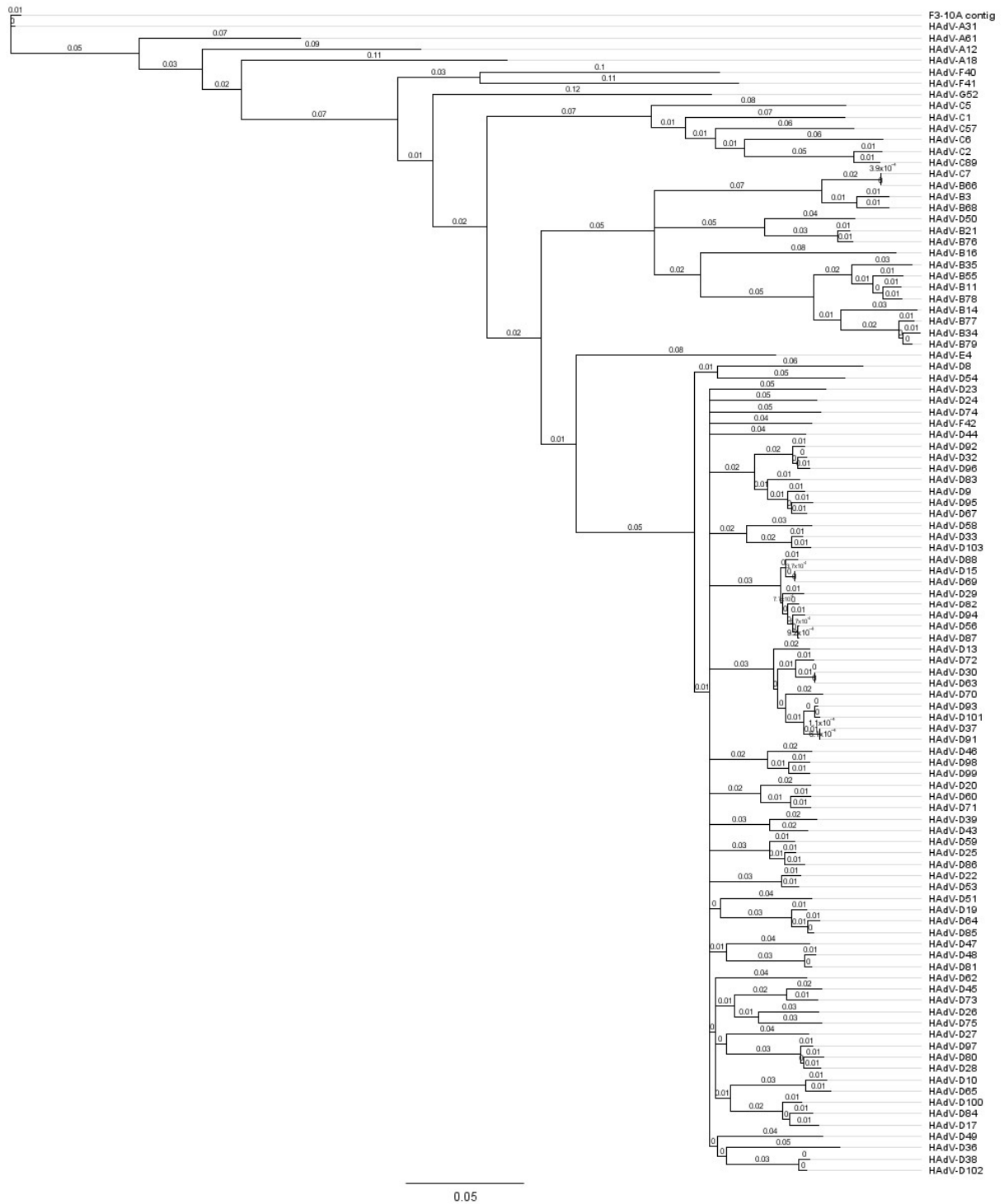
Supplementary material 5

Accession numbers of reference adenovirus types were retrieved from the Human Adenovirus Working Group (<http://hadvwg.gmu.edu/>). Full adenovirus genomes or the annotated regions corresponding to the hexon, penton and fiber were extracted and aligned with MUSCLE. Phylogenetic tree were constructed by using tree view software within Geneious (software version 11.0 (<https://www.geneious.com>) maximum-likelihood (Tamura-Nei model, Bootstrap of 1,000 replicates) analysis. Phylogenetic trees with the full adenovirus reference types (a), using the hexon (b), penton (c) and fiber (d) are presented. The labels on the branch indicate the number of substitutions per site.

a)



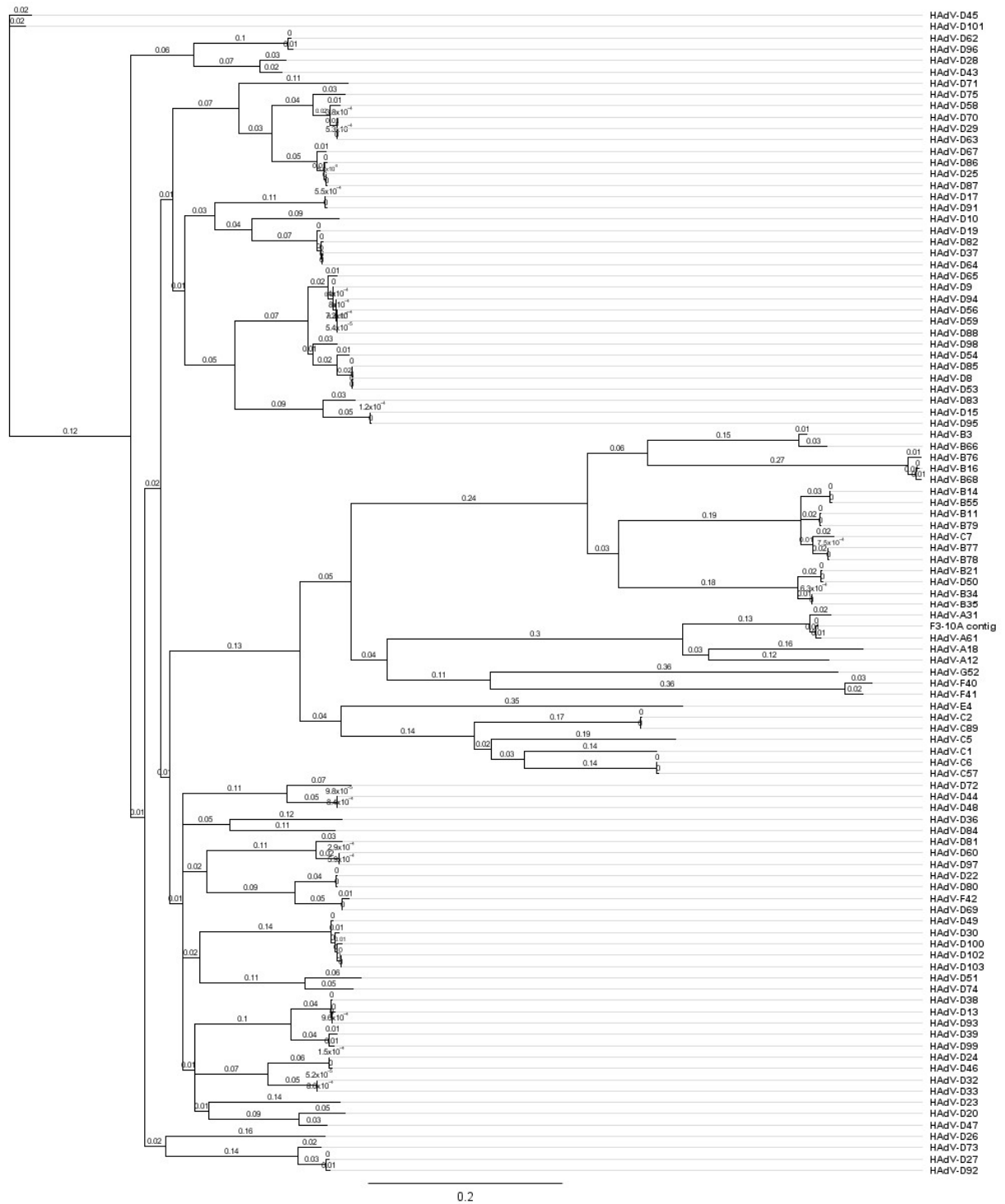
b)



c)



d)



Supplementary material 6. Characterization of enterovirus (a) and rhinovirus (b) contigs detected in the gastroenteritis pools using the enterovirus typing tool by RIVM (v.0.1).

(a)

Sample	Contig length	BLAST score	Genotype	VP1 Serotype, Sub-Genogroup	Classification
F1-3A	7,400	80.481865	CV-A10	CV-A10	Picornaviridae Enterovirus A
	7,193	83.12013	E-6	E-6	Picornaviridae Enterovirus B
	7,011	95.69187	CV-A6	CV-A6	Picornaviridae Enterovirus A
	2,696	83.11688	CV-B5	CV-B5	Picornaviridae Enterovirus B
	471	83.6518	-	-	Picornaviridae Enterovirus B
	1,248	86.3124	-	-	Picornaviridae Enterovirus B
F3-10	680	91.87592	-	-	Picornaviridae Enterovirus B
	817	83.190186	-	-	Picornaviridae Enterovirus B
	722	84.02778	E-6	E-6	Picornaviridae Enterovirus B
	965	81.12033	E-6	E-6	Picornaviridae Enterovirus B
	2,835	85.472496	-	-	Picornaviridae Enterovirus B
S<1A	7,213	83.90564	CV-B5	CV-B5	Picornaviridae Enterovirus B
S<1B	2,737	93.78882	E-13	E-13	Picornaviridae Enterovirus B
	2,068	92.30769			
	1,367	91.93899			
S1-3A	6,865	80.99679	E-9	E-9	Picornaviridae Enterovirus B
	7,085	85.63747	E-3	E-3	Picornaviridae Enterovirus B
	6,650	89.35338	CV-A6	CV-A6	Picornaviridae Enterovirus A
	6,902	80.17743	CV-A10	CV-A10	Picornaviridae Enterovirus A
	2,608	93.66603	E-13	E-13	Picornaviridae Enterovirus B
	365	90.95891			Picornaviridae Enterovirus B

	1,363				Picornaviridae Enterovirus B
S1-3B	7,158	95.96199	CV-A16	CV-A16 , B1a	Picornaviridae Enterovirus A
	6,284	78.27817	CV-B1	CV-B1	Picornaviridae Enterovirus B
	436	87.006966	CV-A4	CV-A4	Picornaviridae Enterovirus A
	458	86.18421	CV-A4		Picornaviridae Enterovirus A
	1,105	85.791855	CV-A4	CV-A4	Picornaviridae Enterovirus A
	2,122	83.577156	CV-A8		Picornaviridae Enterovirus A
	564	83.27402	EV-A71		
S1-3C	1,224	84.72222	E-9	E-9	Picornaviridae Enterovirus B
	635	86.456696			Picornaviridae Enterovirus B
	614	83.68679			Picornaviridae Enterovirus B
	794	86.901764			Picornaviridae Enterovirus B
S1-3B (unassigned)	1,454	82.09366	E-16	E-16	Picornaviridae Enterovirus B
	741	80.13514	E-16	E-16	Picornaviridae Enterovirus B
	358	92.20056	NTP	NTP	Picornaviridae Enterovirus B

(b)

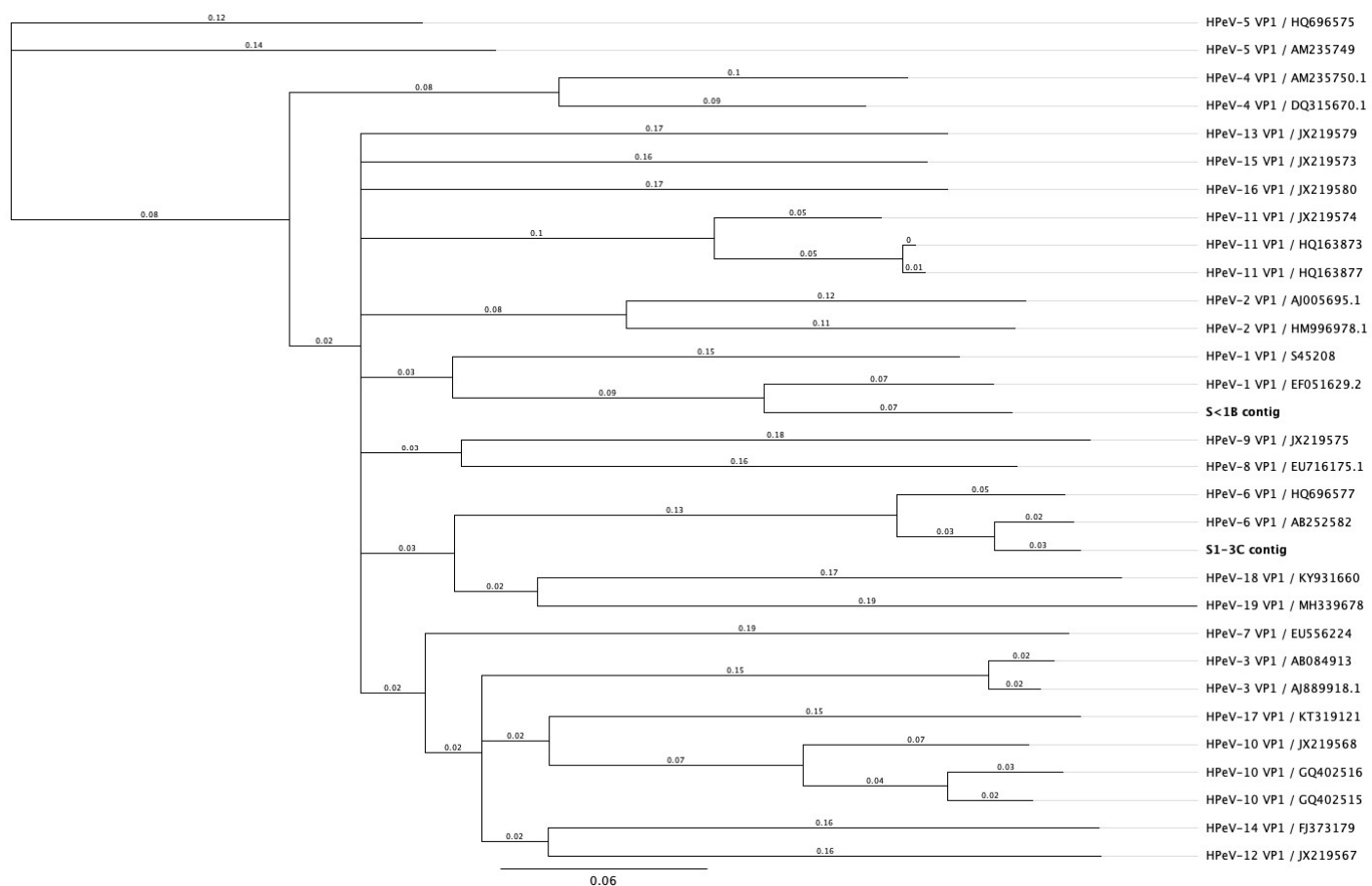
Sample	Contig length	BLAST score	Genotype	VP1 Serotype, Sub-Genogroup	Classification
F3	597	90.60403	HRV-A60		Picornaviridae Rhinovirus A
	483	90.47619	HRV-A60		Picornaviridae Rhinovirus A
	592	88.983055	NTP		Picornaviridae Rhinovirus A
S1	459	94.77124	HRV-B52		Picornaviridae Rhinovirus B
	574	91.78322	HRV-B52		Picornaviridae Rhinovirus B
	1,155	92.03463	HRV-B52		Picornaviridae Rhinovirus B
	766	92.81985	HRV-B52		Picornaviridae Rhinovirus B
	626	93.29073	NTP		Picornaviridae Rhinovirus B
	413	91.26214	NTP		Picornaviridae Rhinovirus B
	451	93.11111	NTP		Picornaviridae Rhinovirus B
	409	93.887535	NTP		Picornaviridae Rhinovirus B
S2	6,499	86.74773	HRV-A78		Picornaviridae Rhinovirus A

Supplementary material 7. Characterization of non-enterovirus Picornaviridae contigs detected on the fecal pools analyzed, including parechovirus and cardiovirus.

Pool	Contig length	Classification	VP1 Genotype	% VP1 Identity	% VP1 Coverage	% Genome Identity	% Genome Coverage
S<1B	7,248	Parechovirus A	HPeV-1	87.8	100	87.8	98.5
S1-3B	796	Parechovirus A	-	-	-	95.6	10.8
	471	Parechovirus A	-	92.0	7.1	95.8	6.4
	1,695	Parechovirus A	-	-	-	95.4	23.1
	343	Parechovirus A	-	-	-	95.0	4.7
	6,949	Parechovirus A	HPeV-6	95.4	100	95.9	94.6
S3-10	7,942	Cardiovirus B	SAFV-2	94.7	100	90.7	98.7

Supplementary material 8. Phylogenetic trees of retrieved parechovirus contigs. Trees were constructed by using tree view software within Geneious (software version 11.0 (<https://www.geneious.com>) maximum-likelihood (Tamura-Nei model, Bootstrap of 1,000 replicates) analysis. Phylogenetic trees were constructed using the (a), full length of the VP1 genomic sequence (b), full human parechovirus complete genomes. The labels on the branch indicate the number of substitutions per site.

a.



b.

