

Supplementary Materials: Molecular Epidemiology of Human Rhinoviruses and Enteroviruses Highlights Their Diversity in Sub-Saharan Africa

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Table S1. Generic primer used for initial screening.

Target	Primer ID	Gene:	Name	Sequence	Position *	Sense	Reference
all HRV/all HEV	11	5'UTR	HRVfor	GCACTTCTGTTTCCCC	164	F	[1]
all HRV/all HEV	23	5'UTR	RevA_B 550Rhino	GAAACACGGACACCCAAAGTAGT	554	R	[1]
all HRV/all HEV	46	5'UTR	F484	CGGCCCCCTGAATGYGGCTAA	484	F	[2]
all HRV	P1.2	VP2	VP2Fwd1049-deg	TGGTGSTGGAARYTRCCWGATGC	~1049	F	[1]
all HRV	P1.204	VP2	R1126	ATCHGGHARYTTCCAMCACCA	1126	R	[2]
all HEV	Ent_P1.39	VP2	R1126ENT	GGDAAYTTCCACCACCAHCC	1126	R	This study
all HEV	Ent_P1.16	VP3	224	GCIATGYTIGGIACICAYRT	1977–1996PV1	F	[3]
all HEV	Ent_P1.15	VP1	222	CICCI GGIGGIAYRWACAT	2969–2951PV1	R	[4]
all HEV	Ent_P1.17	VP1	AN89	CCAGCACTGACAGCAGYNGARAYNGG	2602–2627	F	[3]
all HEV	Ent_P1.18	VP1	AN88	TACTGGACCACCTGGNGGNAYRWACAT	2977–2951	R	[3]

* Postitions are indicated relative to HRV-A2 (NCBI GenBank entry: X02316).

Table S2. Primers used to sequence selected specimens.

Target Sample	N°oligos	Gene	Name	Sequence	Position *	R/F
671/918/949/976/984	1.54	VP2	VP2fwd 1334 HRV A	TGGCTHAATTKTGATGGHAC	1334 to 1353	F
HRV-C	P1.223	VP2	VP2Fwd HRVC	GATAGGCTMAARCAAATCACTAT	848 to 870	F
HRV-C	P1.224	VP2	VP2Fwd HRVCn	GCWTATGGDGAATGGCC	917 to 933	F
671T-984T-949T	P1.233	VP2	VP2Fwd HRVA	GGWGTGGCCACAATATC	924 to 941	F
671T-984T-949T	P1.234	VP2	VP2Fwd HRVAn	GATGCTGATGCMAATGC	947 to 963	F
344T-671T	P1.237	VP2	VP2Fwd HRVA	ATATGGAGTCTGGCCACA	919 to 936	F
344T-671T	P1.238	VP2	VP2Fwd HRVAn	CTATAGATAAACCATCACACCC	1186 to 1207	F
529T	P1.252	VP2	VP2Fwd529T-1525	CCCACTAAACTCATACACATCCC	1668 to 1710	F
344T	P1.256	VP2	VP2Fwd344T_71p1044-1319	GCACACTCATCCAGGTGAAAC	1252 to 1272	F
344T	P1.257	VP2	VP2Fwd344T71_p1044-1377	GACAGGGCAGCCGACAG	1310 to 1325	F
344T	P1.258	VP2	VP2Rev344T71_p1044-1480	CATAGGGTAGAATGAGTGTGGCTG	1436 to 1413	R
344T	P1.259	VP2	VP2Rev344T71_p1044-1564	CAGCTGTAAAGGGGAGATGG	1511 to 1496	R
543T	P1.263	VP2	VP2Rev543T-1088	GATCCGGCTCCTATATAAGCC	1233 to 1217	R
639T-1379	P1.268	VP2	VP2Fwd639T-1379	CTCCACAGTGTCAATAACCG	1530 to 1547	F
701T-1450	P1.270	VP2	VP2Fwd701T-1450	GTCAACCGATGGATAACATGC	1695 to 1715	F
918T	P1.276	VP2	VP2-1054-918T_Fwd	GGAGAGCAAGACTGGAGTGC	1015 to 1035	F
122T	P1.280	VP2	VP2-1113-122T Fwd	CACTATCTTCCTCACCAAATATAACC	1369 to1397	F
610T	P1.285	VP2	VP2-1398-610T Fwd	CCTATAAGTCTGAATCTCTGGCGC	1546 to 1584	F
882T	P1.288	VP2	VP2-850-882T Fwd	GATAGGCTCAAGCAAATACTAT	848 to 868	F
all HEV	Ent_P1.63	VP2	VP2 Fwd HEV	CCATCACCCTCAAGARGC	882 to 900	F

Table S2. *Cont.*

Target Sample	N°oligos	Gene	Name	Sequence	Position *	R/F
all HEV	Ent_P1.64	VP2	VP2 Fwd HEVn	CCGTGGACAARCCWAC	963 to 978	F
288/639/671/918	P1.15	VP3	Primer HRVA C1	ACNTGBTGGTAYCARAC	2165 to 2181	F
529T	P1.253	VP3	Vp3Rev529T-1902	GATGATGCAGGCCTAGATCC	2090 to 2065	R
543T-1747	P1.264	VP3	VP3Fwd543T-1747	GCATACCCCTCCAGATGG	1858 to 1876	F
701T-C17_C28_N4T-2265	P1.271	VP3	Vp3Rev701T-C17_C28_N4-2265	AACATCTRACDGABARATCWGG	2270 to 2248	R
987T-1718	P1.272	VP3	Vp3Fwd987T-1718	CCTGAGTATAGTCCTACAAAGGAG	1677 to 1697	F
918T	P1.277	VP3	P1.277 Vp3-2363-918T Rev	CTGGGTTGGGTAATGGG	2318 to 2300	R
976T	P1.278	VP3	P1.278 VP3-2345-976T Fwd	GCTCTGTTGTATCTGCATGMAA	2226 to 2247	F
976T	P1.279	VP3	P1.279 VP3-3249-976T Rev	AGATTCCCACATGCACAT	3205 to 3187	R
882T	P1.290	VP3	P1.290 VP3-1606-882T Fwd	CAGGGAATCCCAGTGCGC	1600 to 1615	F
590/648/948	P1.9	VP1	Primerhovi_PRPP	TGGTGYCCIMGISCICCMGTGC	~3044 to 3066	F
671/918	1.19	VP1	HRVA Primer 2	YCCWCCACARTCWCCWGGTTC	3484 to 3464	R
288/639	P1.20	VP1	HRVA Primer 3	HATRCCWATVACWCCATG	3517 to 3500	R
265	1.64	VP1	Vp1 rev 2412-A	GTRTGYCCTGTYTCAGCAGCATCYA	2436 to 2412	R
HRV-C	P1.160	VP1	HRVC VP1-1922 Fwd	TRGCMTACACMCCHCCAGG	1992 to 2010	F
HRV-C	P1.161	VP1	HRVC VP1-2190 Fwdn	GCATGHTRCGTGAYACACCMATGAT	2262 to 2286	F
529T-539T-543T-566T-624T-813T-882T-987T	P1.225	VP1	VP1RevHRVCextr1	GWCGDGGRATCCATGC	3056 to 3041	R
529T-539T-543T-566T-624T-813T-882T-987T	P1.226	VP1	VP1RevHRVCextr1n	GTYCCCATGTCATTGT	1089 to 1074	R
122T-288T-383T-386T-610T-638T-701T	P1.228	VP1	VP1RevHRVCextr2 m	ACAWACATGATYTGATAA	2748 to 2730	R
671T-984T-949T	P1.236	VP1	VP1Rev HRVAn	TGCCAAAAGACTGATGC	2826 to 2810	R

Table S2. Cont.

Target Sample	N°oligos	Gene	Name	Sequence	Position *	R/F
344T-671T	P1.239	VP1	VP1Rev HRVA	CATCATAGAACATGTAATATGCTGA	2900 to 2876	R
344T-671T	P1.240	VP1	VP1Rev HRVAn	AAAAGACTGAWGCATAGTCC	1786 to 1763	R
671T	P1.241	VP1	671_VP1Rev	CCTGGTATAAAATATYTCTTG TG	1995 to 1974	R
383T_387T	P1.244	VP1	383_387VP1Rev	ATCYTCAGTGGTCATAAAAYTG TG	1936 to 1914	R
529T_624T_566T_543T_987T_813T	P1.246	VP1	529_624_566_543_987_813VP1Rev	CCWGGRGGKGTGTATGCTA	2010 to 1992	R
539T	P1.248	VP1	539_VP1Rev	GGCCTGTGTGTGACCG	2599 to 2584	R
529T	P1.254	VP1	Vp1Fwd529T-2431	CAGGAGCAAGCACAAATCAG	2615 to 2634	F
529T	P1.255	VP1	Vp1Rev529TsubC35-3117	CAACCCTCCATGCAATCAC	3294 to 3276	R
344T	P1.260	VP1	Vp1Rev344T71_p1044-2527	CATGCTGGGTGGATATTG	2373 to 2354	R
344T	P1.261	VP1	Vp1Rev344T71_p1044-2458	GGGTCTGTCAATGTGACTG	2306 to 2285	R
122T	P1.262	VP1	VP1Rev122T-2336	CAGAAGCTTGAGACCAGGTG	2771 to 2751	R
T543TC02_p1009T-2717	P1.265	VP1	VP1Rev543TC02_p1009-2717	GTAGTATGCTGAACCTAGGCCAG	2806 to 2828	R
T639T-2323	P1.269	VP1	VP1Rev639T-2323	ATGTGTGCCTGTCCTGGAAG	2600 to 2580	R
Vp987T-C02_LZ508T-2468	P1.273	VP1	VpRev987T-C02_LZ508-2468	GCMCCAATTCCATMGCA	2424 to 2407	R
344T	P1.274	VP1	P1.274 VP1-2215_344T_Fwd	GACAAACTTGTGGTCCCCC	2169 to 2189	F
344T	P1.275	VP1	P1.275 VP1-3403_344T_Rev	TGCAATCACAAGTGGGGATG	3323 to 3304	R
610T	P1.286	VP1	P1.286 Vp1-2444-610T Fwd	CCTAGGAAGGTCAGCCTGTG	2514 to 2534	F
610T	P1.287	VP1	P1.287 Vp1-3350-610T Rev	CCCACAATCCCCTGGCTC	3481 to 3464	R
882T	P1.289	VP1	P1.289 Vp2-1743-882T Rev	GAGTCCACCCGTGCCATG	1752 to 1735	R
882T	P1.291	VP1	P1.291 Vp1-2907-882T Rev	GTGCTCTAATACATAGGTGGCCC	2950 to 2928	R

Table S2. *Cont.*

Target Sample	N°oligos	Gene	Name	Sequence	Position *	R/F
all HEV	Ent_P1.65	VP1	VP1 Rev HEV	TAMCCRTCRTAGAACCACTG	2908 to 2885	R
all HEV	Ent_P1.66	VP1	VP1 Rev HEVn	GGGTGKTNGCWGTYTGCCA	2728 to 2710	R
590/648/948	EntP2.11	2C	COXA 19 4450 rev	TCAATRCGGTGTGTTGCTTGAAGT	4846 to 4821	R
383	P2.64	2A	QPM-3098-REV	GGTATGTTGTCWGGSCCWGG	3309 to 3290	R

* Postitions are indicated relative to HRV-A2 (NCBI GenBank entry: X02316).

Table S3. HRV-A genotyping according to sequenced genome regions.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
129	37.93	HRV-A NT	HRV-A NT		
508	35.13	HRV-A NT	HRV-A NT		
929	33.59	HRV-A NT	HRV-A NT		
485	37.27	HRV-A2	HRV-A2 ^a	HRV-A2	
455	25.99	HRV-A7	HRV-A7	HRV-A7	
497	26.69	HRV-A9	HRV-A9	HRV-A9 ^b	
26	29.55	HRV-A12		HRV-A12	
49	35.36	HRV-A12	HRV-A12	HRV-A12	
62	35.04	HRV-A12	HRV-A12	HRV-A12	
81	29.23	HRV-A12	HRV-A12	HRV-A12	
85	29.76	HRV-A12	HRV-A12		
89	30.65	HRV-A12	HRV-A12	HRV-A12	

Table S3. *Cont.*

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
148	37.88	HRV-A12	HRV-A12		
188	29.02	HRV-A12	HRV-A12	HRV-A12	
208	34.9	HRV-A12	HRV-A12	HRV-A12	
269	29.59	HRV-A12		HRV-A12	
306	25.54	HRV-A12	HRV-A12	HRV-A12	
369	27.18	HRV-A12	HRV-A12		
393	22.81	HRV-A12	HRV-A12		
400	31.03	HRV-A12	HRV-A12		
451	39.32	HRV-A12	HRV-A12		
476	32.97	HRV-A12	HRV-A12		
495	34.21	HRV-A12	HRV-A12	HRV-A12	
517	26.1	HRV-A12	HRV-A12		
532	31.78	HRV-A12	HRV-A12		
536	24.69	HRV-A12	HRV-A12		
541	26.7	HRV-A12	HRV-A12		
544	31.97	HRV-A12	HRV-A12		
561	31.81	HRV-A12	HRV-A12		
564	29.62	HRV-A12	HRV-A12		
578	30.59	HRV-A12	HRV-A12		

Table 3. *Cont.*

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
661	34.15	HRV-A12	HRV-A12	HRVA-12	
791	30.45	HRV-A12	HRV-A12		
795	38.51	HRV-A12	HRV-A12		
802	29.14	HRV-A12	HRV-A12 ^c		
91	28.86	HRV-A12/67Access nr: KT751299	HRV-A12	HRV-A67	
963	35.86	HRV-A13	HRV-A13	HRV-A13	
187	25.62	HRV-A21	NT	HRV-A21	
980	28.16	HRV-A21	NT	HRV-A21	
999	32.72	HRV-A21	HRV-A21	HRV-A21	
937	31.56	HRV-A24	HRV-A104	HRV-A24	
752	30.63	HRV-A25-62	HRV-A25-62	HRV-A25-62	
983	34.6	HRV-A25-62	HRV-A25-62	HRV-A25-62	
348	34.07	HRV-A28	HRV-A28	HRV-A28	
531	30.43	HRV-A28	HRV-A28	HRV-A28	
918	23.96	HRV-A36/67Access nr: KT751301	HRV-A36	HRV-A67	VP1: HRV-A67
976	33.99	HRV-A36/67Access nr: KT751300	HRV-A36	HRV-A67	VP1: HRV-A67
82	35.92	HRV-A46	HRV-A46	HRV-A46	
93	29.83	HRV-A46	HRV-A46		
318	33	HRV-A46	HRV-A46		

Table 3. *Cont.*

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
538	32.96	HRV-A46	HRV-A46		
551	29.8	HRV-A46	HRV-A46		
97	31.74	HRV-A65	HRV-A65-A102 ^d	HRV-A65	
123	32.07	HRV-A65	HRV-A65-A102 ^d	HRV-A65	
212	31.95	HRV-A65	HRV-A65-A102 ^d	HRV-A65	
239	33.71	HRV-A65	HRV-A65-A102 ^d	HRV-A65	
304	34.24	HRV-A65	HRV-A65-A102 ^d	HRV-A65	
327	30.84	HRV-A65	HRV-A65-A102 ^d	HRV-A65	
968	35.87	HRV-A65 ^e	HRV-A65-A102 ^d	HRV-A65	
272	32.37	HRV-A65		HRV-A65	
335	27.19	HRV-A65 ^e	HRV-A65-A102 ^d		
376	31.25	HRV-A65 ^e	HRV-A65-A102 ^d		
403	31.51	HRV-A65 ^e	HRV-A65-A102 ^d		
693	32.06	HRV-A65 ^e	HRV-A65-A102 ^d		
719	37.43	HRV-A65 ^e	HRV-A65-A102 ^d		
785	24.7	HRV-A65 ^e	HRV-A65-A102 ^d		
789	29.19	HRV-A65 ^e	HRV-A65-A102 ^d		
798	29.09	HRV-A65 ^e	HRV-A65-A102 ^d		
801	30.76	HRV-A65 ^e	HRV-A65-A102 ^d		

Table 3. Cont.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
850	28.86	HRV-A65 ^e	HRV-A65-A102 ^d		
859	30.89	HRV-A65 ^e	HRV-A65-A102 ^d		
879	36.45	HRV-A65 ^e	HRV-A65-A102 ^d		
917	31.61	HRV-A65 ^e	HRV-A65 ^f		
974	30.98	HRV-A65 ^e	HRV-A65-A102 ^d		
998	29.27	HRV-A65 ^e	HRV-A65-A102 ^d		
1001	25.06	HRV-A65 ^e	HRV-A65-A102 ^d		
446	26.82	HRV-A67	HRV-A67		
546	25.33	HRV-A67 ^g		HRV-A67	
559	32.99	HRV-A67	HRV-A67	HRV-A67	
670	29.55	HRV-A67	HRV-A67		
727	38.67	HRV-A67	HRV-A67		
773	33.8	HRV-A67	HRV-A67		
844	29.38	HRV-A67	HRV-A67		
919	27.17	HRV-A67	HRV-A67		
646	34.54	HRV-A71	HRV-A71	HRV-A71	
654	39.24	HRV-A71	HRV-A71		
671	34.58	HRV-A71	HRV-A71	HRV-A71	
436	37.29	HRV-A73	HRV-A73		

Table 3. Cont.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
808	39.86	HRV-A73	HRV-A73		
911	24.7	HRV-A73	HRV-A73		
995	23.92	HRV-A73	HRV-A73		
103	31.16	HRV-A75	HRV-A75	HRV-A75	
144	39.58	HRV-A75	HRV-A75		
250	32.4	HRV-A75	HRV-A75	HRV-A75	
429	37.49	HRV-A78	HRV-A78	HRV-A78	
899	40.33	HRV-A78	HRV-A78	HRV-A78	
962	33.08	HRV-A80	HRV-A80	HRV-A80	
255	28.55	HRV-A81	HRV-A81		
345	34.54	HRV-A81	HRV-A81	HRV-A81	
365	27.72	HRV-A81	HRV-A81		
411	31.06	HRV-A81	HRV-A81		
456	27.21	HRV-A81	HRV-A81		
461	29.7	HRV-A81	HRV-A81		
562	32.15	HRV-A81	HRV-A81	HRV-A81	
655	28.75	HRV-A81		HRV-A81	
708	30.06	HRV-A81		HRV-A81	
740	27.5	HRV-A81	HRV-A81		

Table 3. *Cont.*

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
782	33.22	HRV-A81	HRV-A81		
829	25.31	HRV-A81	HRV-A81		
840	30.68	HRV-A81	HRV-A81		
849	21.94	HRV-A81	HRV-A81	HRV-A81	
861	31.82	HRV-A81	HRV-A81		
864	33.95	HRV-A81	HRV-A81		
900	25.57	HRV-A81	HRV-A81		
921	31.31	HRV-A81	HRV-A81		
925	30.06	HRV-A81	HRV-A81		
988	25.31	HRV-A81	HRV-A81		
116	35.37	HRV-A88	NT	HRV-A88	
598	30.25	HRV-A90	HRV-A90	HRV-A90	
989	38.09	HRV-A90	HRV-A90		
265	22.96	HRV-A96/A61Access nr: KT751298	HRV-A96	HRV-A61	
320	29.71	HRV-A103	HRV-A103		
949	35.89	HRV-A103	HRV-A103	HRV-A103	
984	34.49	HRV-A103	HRV-A103	HRV-A103	
344	30.36	HRV-A106	HRV-A106	HRV-A106	VP1: HRV-A106
713	34.09	HRV-A106	HRV-A106		

CT value, mean $\pm$ SD 31.1 $\pm$ 4.1

NT: Not typable; ^a NCBI Genbank entry: KC414927.1; ^b NCBI Genbank entry: FJ445115.1; ^c NCBI Genbank entry: JX129436.1; ^d 5'UTR difficult to discriminate between HRV-A65 and HRV-A102. Finally typed as HRV-A65 based on VP4/VP2; ^e considered as HRV-A65 because it clusters with ID 97T, 123T, 212T, 239T, 304T, 327T and 968T on 5'UTR; ^f NCBI GenBank entry: JF781504.1; ^g Co-infection with EV-99.

Table S4. HRV-B genotyping according to sequenced genome regions.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	Other
554	31.72	HRV-B NT	HRV-B NT		
786	34.85	HRV-B NT	HRV-B NT		
39	31.59	HRV-B69	HRV-B69	HRV-B69	
111	31.75	HRV-B69	HRV-B69		
355	23.94	HRV-B69	HRV-B69		
447	34.48	HRV-B69	HRV-B69		
666	28.3	HRV-B69	HRV-B69		
754	26.97	HRV-B69	HRV-B69		
757	30.97	HRV-B69	HRV-B69		
765	37.23	HRV-B69	HRV-B69		
766	33.57	HRV-B69	HRV-B69 ^a		
778	39.95	HRV-B69	HRV-B69		
779	40.49	HRV-B69	HRV-B69		
781	31.05	HRV-B69		HRV-B69	
792	25.61	HRV-B69	HRV-B69		
806	30.51	HRV-B69	HRV-B69		
848	25.8	HRV-B69	HRV-B69		
901	32.53	HRV-B69	HRV-B69		
902	37.15	HRV-B69	HRV-B69	HRV-B69	
930	36.63	HRV-B69	HRV-B69		

Table S4. *Cont.*

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	Other
940	39.9	HRV-B69	HRV B69		
956	27.31	HRV-B69	HRV-B69	HRV-B69	
1003	29.71	HRV-B69	HRV-B69	HRV-B69	
24	31.19	HRV-B72	NT	HRV-B72	
238	26.97	HRV-B72	NT	HRV-B72	
586	28.5	HRV-B72	HRV-B72 ^b		
629	29.09	HRV-B72	HRV-B72 ^b		
56	34.72	HRV-B79	HRV-B79	HRV-B79	
760	39.05	HRV-B79	HRV-B79 ^c		
108	32.42	HRV-B84	HRV-B84	HRV-B84	
157	38.61	HRV-B84	HRV-B84	HRV-B84	
243	33.86	HRV-B84	HRV-B84		
509	28.41	HRV-B84	HRV-B84		
511	37.72	HRV-B84	HRV-B84		
522	34.57	HRV-B84	HRV-B84		
526	29.53	HRV-B84	HRV-B84		
665	32.3	HRV-B84	HRV-B84	HRV-B84	
17	37.52	HRV-B86	HRV-B86	HRV-B86	
28	38.55	HRV-B86	HRV-B86		
95	36.9	HRV-B86	HRV-B86	HRV-B86	

Table S4. Cont.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	Other
427	31.58	HRV-B93	HRV-B93	HRV-B93	
736	32	HRV-B_Pat09	HRV-B72 Access nr: KR997889 87% with JN798562.2	HRV-B27 Access nr: KR997886 85% with FJ445186.1	VP2/VP3: HRV-B84 Access nr: KR997887 78% with JQ837723.1
CT value, mean $\pm$ SD		32.8 $\pm$ 4.4			

NT: Not typable; ^aNCBI GenBank entry: JQ245970.1; ^b NCBI GenBank entry: JN798562.2; ^c NCBI GenBank entry: EU096066.1.

Table S5. HRV-C genotyping according to sequenced genome regions.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
76	33.84	HRV-C NT			
328	32.64	HRV-C NT			
696	34.87	HRV-C NT			
398	25.53	HRV-C1	HRV-C1	HRV-C1	
261	27.31	HRV-C2	HRV-C2	HRV-C2	
383	23.03	HRV-C2	HRV-C2	HRV-C2	
392	28.69	HRV-C2	HRV-C2	HRV-C2	
413	35.31	HRV-C2	HRV-C2	HRV-C2	
424	35.04	HRV-C2	HRV-C2	HRV-C2	
499	31.94	HRV-C2	HRV-C2	HRV-C2	
569	NA	HRV-C2	HRV-C2	HRV-C2	
579	28.72	HRV-C2	HRV-C2		
628	30.07	HRV-C2	HRV-C2	HRV-C2	

Table S5. *Cont.*

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
635	26.59	HRV-C2	HRV-C2	HRV-C2	
5	32.79	HRV-C6	HRV-C6	HRV-C6	
55	25.99	HRV-C6	HRV-C6	HRV-C6	
814	39.81	HRV-C6	HRV-C6	HRV-C6	
484	38.41	HRV-C7	HRV-C7		
507	31.16	HRV-C7	HRV-C7	HRV-C7	
739	27.69	HRV-C7	HRV-C7	HRV-C7	
838	23.04	HRV-C7	HRV-C7	HRV-C7	
882	32.68	HRV-C13	HRV-C13 ^a Access nr: KR997890	HRV-C13	
886	25.97	HRV-C13	HRV-C13 ^a	HRV-C13	
950	33.67	HRV-C13	HRV-C13 ^a	HRV-C13	
1000	27.27	HRV-C13	HRV-C13 ^a	HRV-C13	
688	34.84	HRV-C15	HRV-C15		
122	30.23	HRV-C16	HRV-C16 ^a	HRV-C16	VP1: HRV-C16
639	32.49	HRV-C16	HRV-C16 ^a Access nr: KR997882	HRV-C16	VP1: HRV-C16
330	25.58	HRV-C17	HRV-C17		
334	37.3	HRV-C17	HRV-C17		
610	33.6	HRV-C17	HRV-C17	HRV-C17	VP1: HRV-C17
701	28.84	HRV-C18	HRV-C18 ^a Access nr: KR997891	HRV-C18	
769	25.6	HRV-C18	HRV-C18 ^a	HRV-C18	

Table S5. *Cont.*

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
851	35.58	HRV-C18	HRV-C18 ^a	HRV-C18	
938	36.37	HRV-C18	HRV-C18 ^a	HRV-C18	
982	27.8	HRV-C18	HRV-C18 ^a	HRV-C18	
749	31.84	HRV-C18	HRV-C18 ^{a, b}		
804	28.6	HRV-C18	HRV-C18 ^{a, b}		
836	26.21	HRV-C18	HRV-C18 ^{a, b}		
638	29.2	HRV-C18	HRV-C18 ^c	HRV-C18	
539	32.2	HRV-C19	HRV-C19 ^a Access nr: KR997892	HRV-C19	
530	37.41	HRV-C19	HRV-C19 ^{a, d}		
568	35.72	HRV-C19	HRV-C19 ^{a, d}		
237	24.06	HRV-C22	NT	HRV-C22	
248	28.09	HRV-C22	NT	HRV-C22	
368	29.55	HRV-C22	NT	HRV-C22	
489	33.46	HRV-C22	NT	HRV-C22	
622	21.68	HRV-C22	NT	HRV-C22	
653	33.51	HRV-C22	NT	HRV-C22	
288	20.83	HRV-C23	HRV-C23 ^a Access nr: KR997881	HRV-C23	VP3: HRV-C23 ^e Access nr: KR997881
615	26.71	HRV-C23	HRV-C23 ^{a, f}		
119	35.97	HRV-C27	HRV-C27 ^a Access nr: KR997893	HRV-C27	
387	30.35	HRV-C27	HRV-C27 ^a	HRV-C27	

Table S5. *Cont.*

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
558	21.84	HRV-C27	HRV-C27 ^a	HRV-C27	
342	36.4	HRV-C27	HRV-C27 ^{a, g}		
566	39.54	HRV-C33	HRV-C33 ^a Access nr: KR997894	HRV-C33	
606	38.74	HRV-C33	HRV-C33 ^{a, h}		
390	21.23	HRV-C40		HRV-C40	
466	34.47	HRV-C40	HRV-C40	HRV-C40	
839	31.92	HRV-C40	HRV-C40	HRV-C40	
841	24.16	HRV-C40	HRV-C40		
322	32.91	HRV-C42	HRV-C42	HRV-C42	
401	26.91	HRV-C42	HRV-C42	HRV-C42	
987	31.56	HRV-C46	HRV-C46 ^a Access nr: KR997880	HRV-C46	
543	39.66	HRV-C50	HRV-C50	HRV-C50	
464	28.72	HRV-C51		HRV-C51	
529	36.59	HRV-C55	HRV-C35 92% with JF436925.1	HRV-C35 80% with EU081790.1	5'UTR/2A: HRV-C35 Access nr: KR997885 81% with JF436925.1
583	27.93	HRV-C55	HRV-C35 92% with JF436925.1	HRV-C35 80% with EU081790.1	
584	38.83	HRV-C55	HRV-C35 92% with JF436925.1		
626	39.67	HRV-C55	HRV-C35 92% with JF436925.1	HRV-C35 80% with EU081790.1	
668	38.61	HRV-C55	HRV-C35 92% with JF436925.1		
624	38.4	HRV-C_Pat22 ⁱ	HRV-C54 Access nr: KR997884 81% with KP282614.1	HRV-C48 Access nr: KR997884 85% with JF519763	VP2/VP3: HRV-C28 Access nr: KR997888 74% with JN798569.1

Table S5. *Cont.*

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	other
617	32.19	HRV-C_Pat22 ⁱ	HRV-C54 81% with KP282614.1	HRV-C48 85% with JF519763	
644	38.57	HRV-C_Pat22 ⁱ	HRV-C54 81% with KP282614.1	HRV-C48 85% with JF519763	
710	31.6	HRV-C_Pat22 ⁱ	HRV-C54 81% with KP282614.1		
813	39.65	HRV-C_Pat21 ^j	HRV-C36 91% with KF499421.1	HRV-C36 85% with KF688657.1	5'UTR/VP3: HRV-C36 Access nr: KR997883 84% with JN541267.1

CT value, mean $\pm$ SD 31.9 $\pm$ 5.2

NA: Not available; NT: Not typable;^a New 5'UTR sequences provided for these serotypes; ^b Considered as HRV-C18 because it clusters with ID 701T, 769T, 851T, 938T and 982T on 5'UTR; ^c NCBI GenBank entry: KF499468.1; ^d Considered as HRV-C19 because it clusters with ID 539T on 5'UTR; ^e New VP3 sequence provided for HRV-C23; ^f Considered as HRV-C23 because it clusters with ID 288T on 5'UTR; ^g Considered as HRV-C27 because it clusters with ID 119T, 387T and 558T on 5'UTR; ^h Considered as HRV-C33 because it clusters with ID 566T on 5'UTR; ⁱ NCBI GenBank entry: FJ615745; ^j NCBI GenBank entry: FJ615737.

Table S6. HEV-A genotyping according to sequenced genome regions.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	VP1
893	33.49	CV-A2	NT	CV-A2	
416	36.4	CV-A4	NT	CV-A4	
672	32.16	CV-A4	NT	CV-A4	
842	28.1	CV-A4	NT	CV-A4	
399	37.56	CV-A6	NT	CV-A6	CV-A6
3	39.12	CV-A8	NT	CV-A8	
431	35.92	CV-A10	NT	CV-A10	CV-A10
48	40.68	CV-A10/A8	CV-A10	CV-A8	
477	36.01	CV-A10/A8	CV-A10	CV-A8	

Table S6. Cont.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	VP1
922	30.08	HEV-A71	CV-A8	HEV-A71	HEV-A71
996	37.13	HEV-A71	CV-A8	HEV-A71	HEV-A71
CT value, mean $\pm$ SD	35.2 $\pm$ 3.8				
NT: Not typable.					

Table S7. HEV-B genotyping according to sequenced genome regions.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	VP1
857	34.72	CV-A9	NT	CV-A9	
909	37.53	CV-B1	NT	NT	CV-B1 ^a
862	32.23	CV-B1 ^b	NT	NT	
952	40.62	CV-B1 ^b	NT	NT	
955	35.49	CV-B1 ^b	NT	NT	
822	35.67	CV-B2	NT	CV-B2	
888	32.37	CV-B2	HEV-B106	CV-B2	CV-B2
894	36.75	CV-B2	HEV-B106	CV-B2	CV-B2
895	36.96	CV-B2	HEV-B106	CV-B2	CV-B2
941	40.8	CV-B2	NT	CV-B2	
777	37.11	CV-B5	NT	NT	CV-B5
860	31.94	CV-B5	NT	NT	CV-B5
871	35.62	CV-B5	NT	NT	CV-B5

Table S7. *Cont.*

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	VP1
904	40.8	CV-B5	NT	NT	CV-B5
961	30.73	CV-B5	NT	NT	CV-B5
977	37.28	CV-B5	NT	NT	CV-B5
1005	30.68	CV-B5	NT	NT	CV-B5
1007	29.58	CV-B5	NT	NT	CV-B5
887	35.97	CV-B5 ^c	NT	NT	
932	32.49	CV-B5 ^c	NT	NT	
313	40.18	E-6	NT	NT	E-6
162	40.9	E-7	NT	NT	E-7
951	26.56	E-9	NT	NT	E-9
407	37.92	E-9 ^d	NT	NT	
807	34.33	E-9 ^d	NT	NT	
825	27.37	E-9 ^d	NT	NT	
866	32.11	E-9 ^d	NT	NT	
994	25.93	E-9 ^d	NT	NT	
863	37.75	E-11	NT	NT	E-11
CT value, mean $\pm$ SD		34.8 $\pm$ 4.3			

NT: Not Typable; ^a NCBI GenBank entry: KJ472841.1; ^b Considered as CV-B1 because it clusters with 909T on 5'UTR and VP4/VP2; ^c Considered as CV-B5 because it clusters with 777T, 860T, 871T, 904T, 932T, 961T, 977T, 1005T and 1007T on 5'UTR and VP4/VP2; ^d Considered as E-9 because it clusters with 951T on 5'UTR and VP4/VP2.

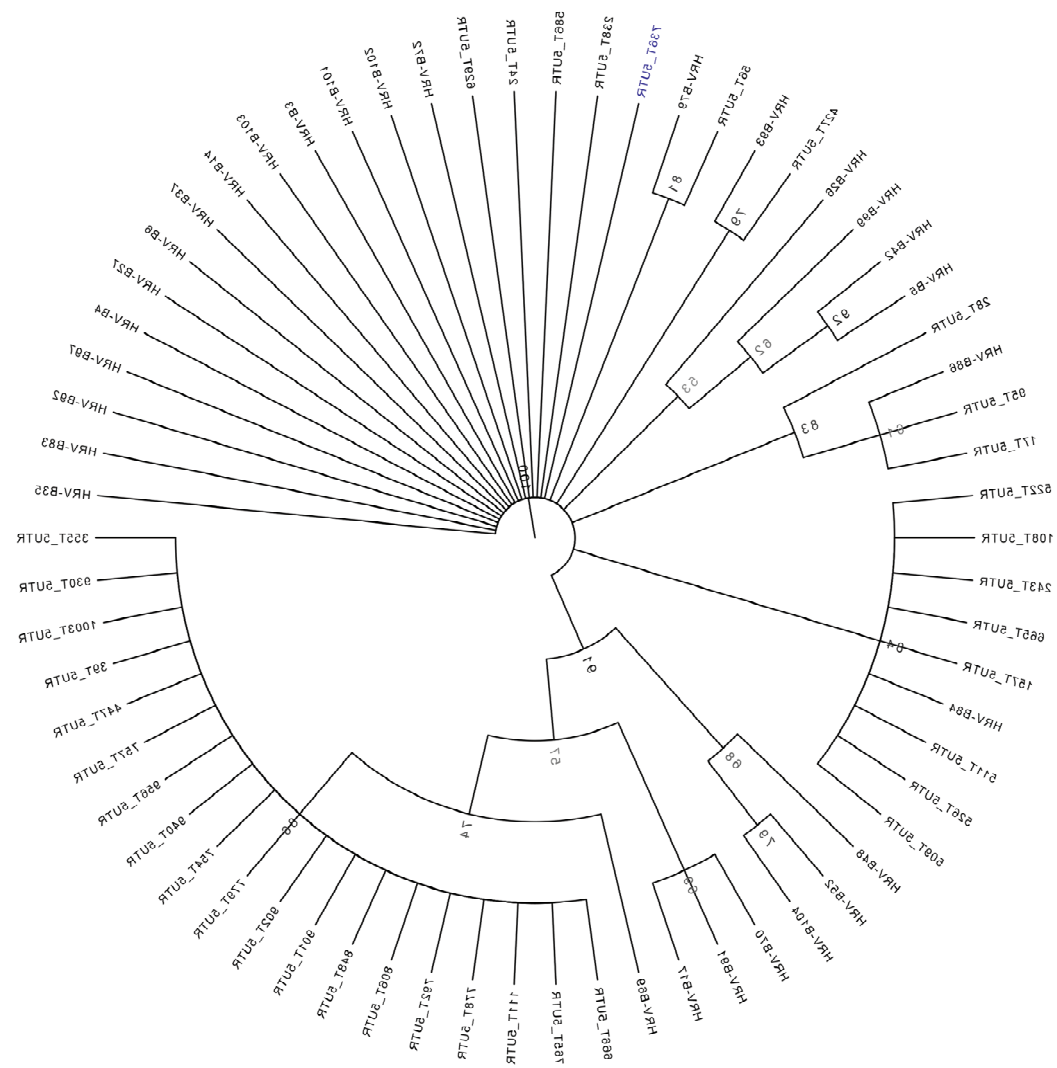
Table S8. HEV-C genotyping according to sequenced genome regions.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2	Other
590	38.05	CV-A13	NT	NT	VP1: CV-A13 ^a
648	38.57	CV-A13	CV-A13	NT	VP1: CV-A13
207	39.03	CV-A24	NT ^b	CV-A24	
546	25.33	HEV-C99 ^c		HEV-C99	
593	33.36	PV Sabin1	PV1A Access nr: KR997879	PV1A Access nr: KR997879	PV1A ^{d,e} VP3/VP1: Access nr: KR9978952C: Access nr: KR9978963A/3C: Access nr: KR997897
948	39.32	NT	NT	NT	
CT value, mean ± SD		35.6 ± 5.5			

NT: Not typable;^a NCBI GenBank entry: JF260920.1; ^b The first 787 nucleotides had 97% similarity with CV-A24 (GenBank entry: EU221292.1); ^c Co-infection with HRV-A67; ^d NCBI GenBank entry: AB467606.1; ^e NCBI GenBank entry: KJ170532.1.

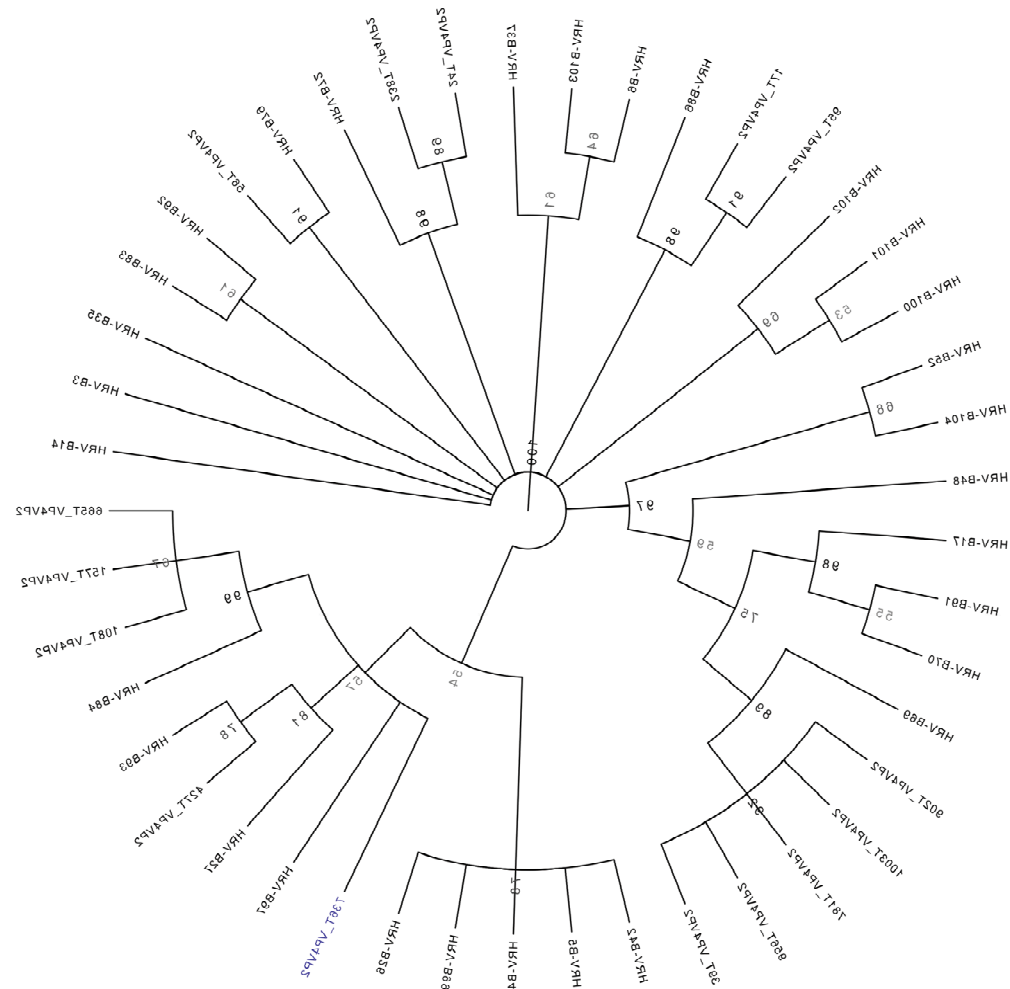
Table S9. HEV-D genotyping according to sequenced genome regions.

Patient ID	CT Value	Genotype	5'UTR	VP4/VP2
202	32.86	HEV-D68	HEV-D68	HEV-D68
487	32.11	HEV-D68	HEV-D68	HEV-D68
525	35.96	HEV-D68	HEV-D68	HEV-D68
CT value, mean ± SD		33.6 ± 2.0		



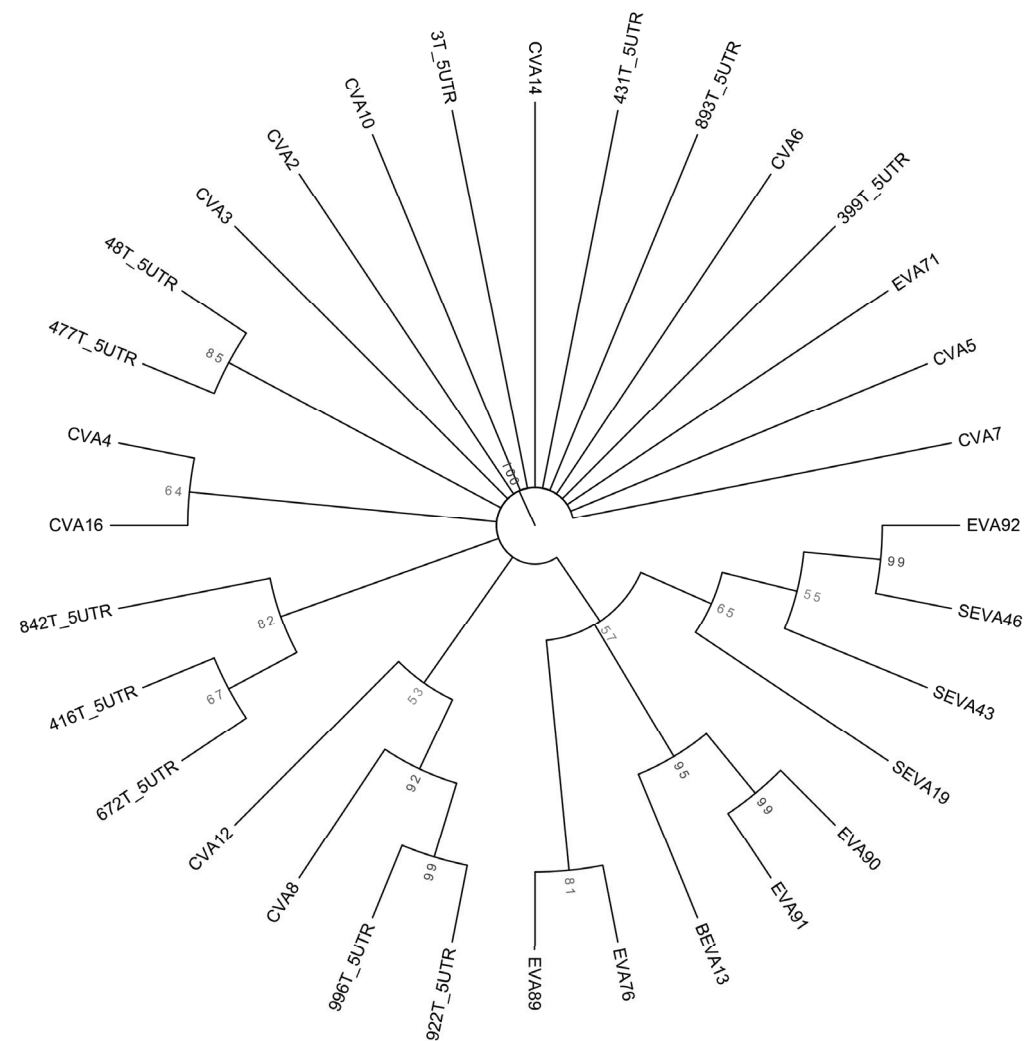
(A)

Figure S2. Cont.



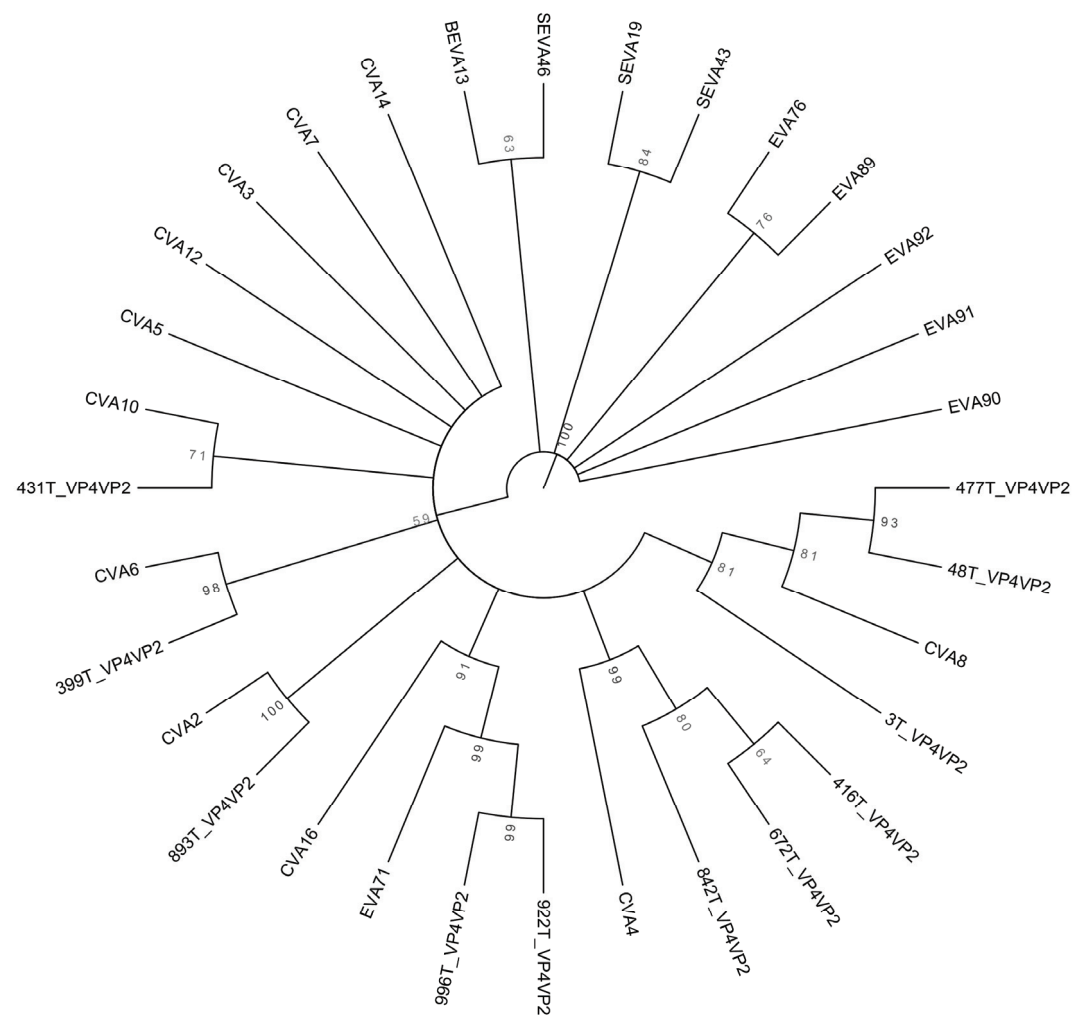
(B)

Figure S2. (A) HRV-B 5'UTR tree (nt 177 to 449 relative to HRV-A2_X02316); (B) HRV-B VP4/VP2 tree (nt 611 to 1018 relative to HRV-A2_X02316).



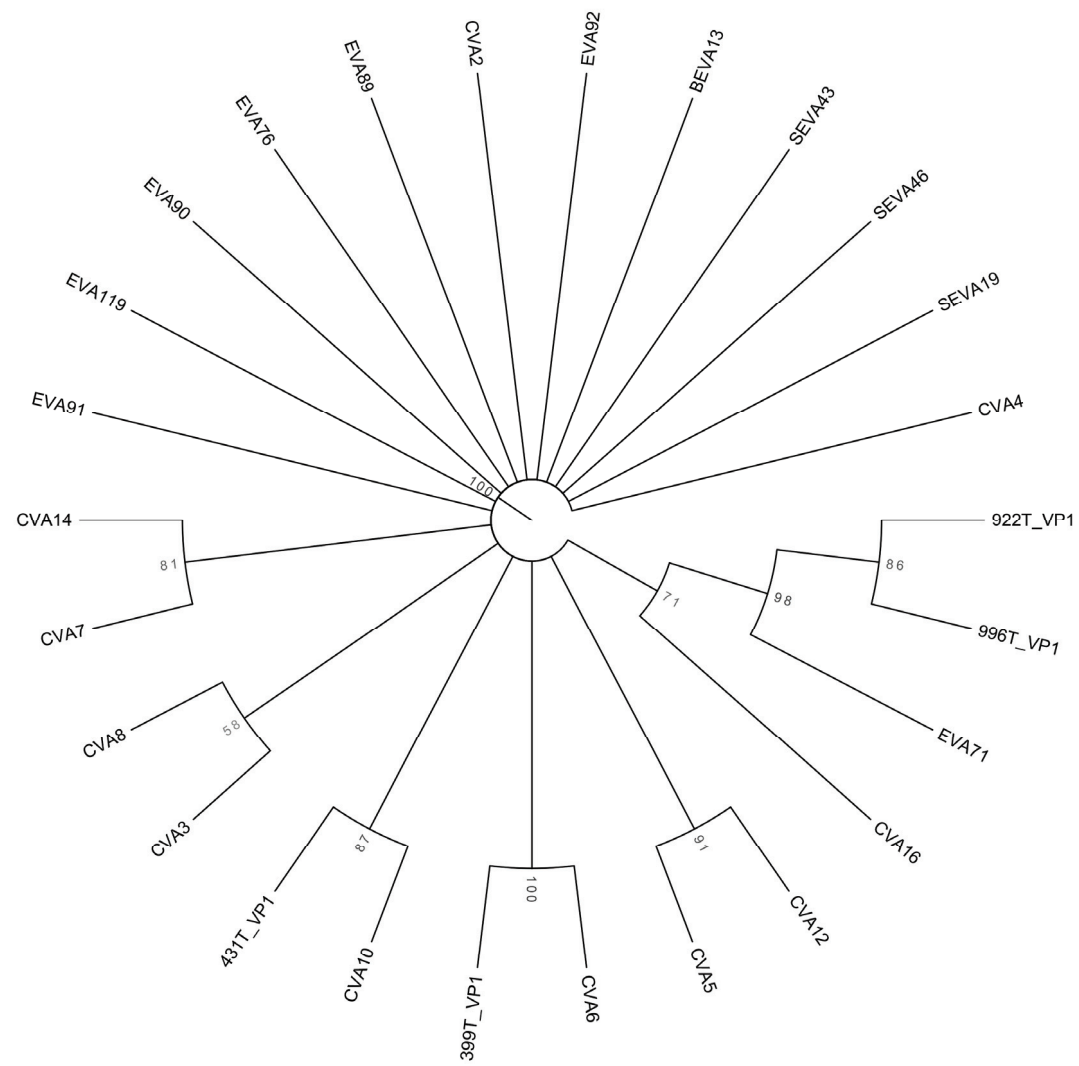
(A)

Figure S4. *Cont.*



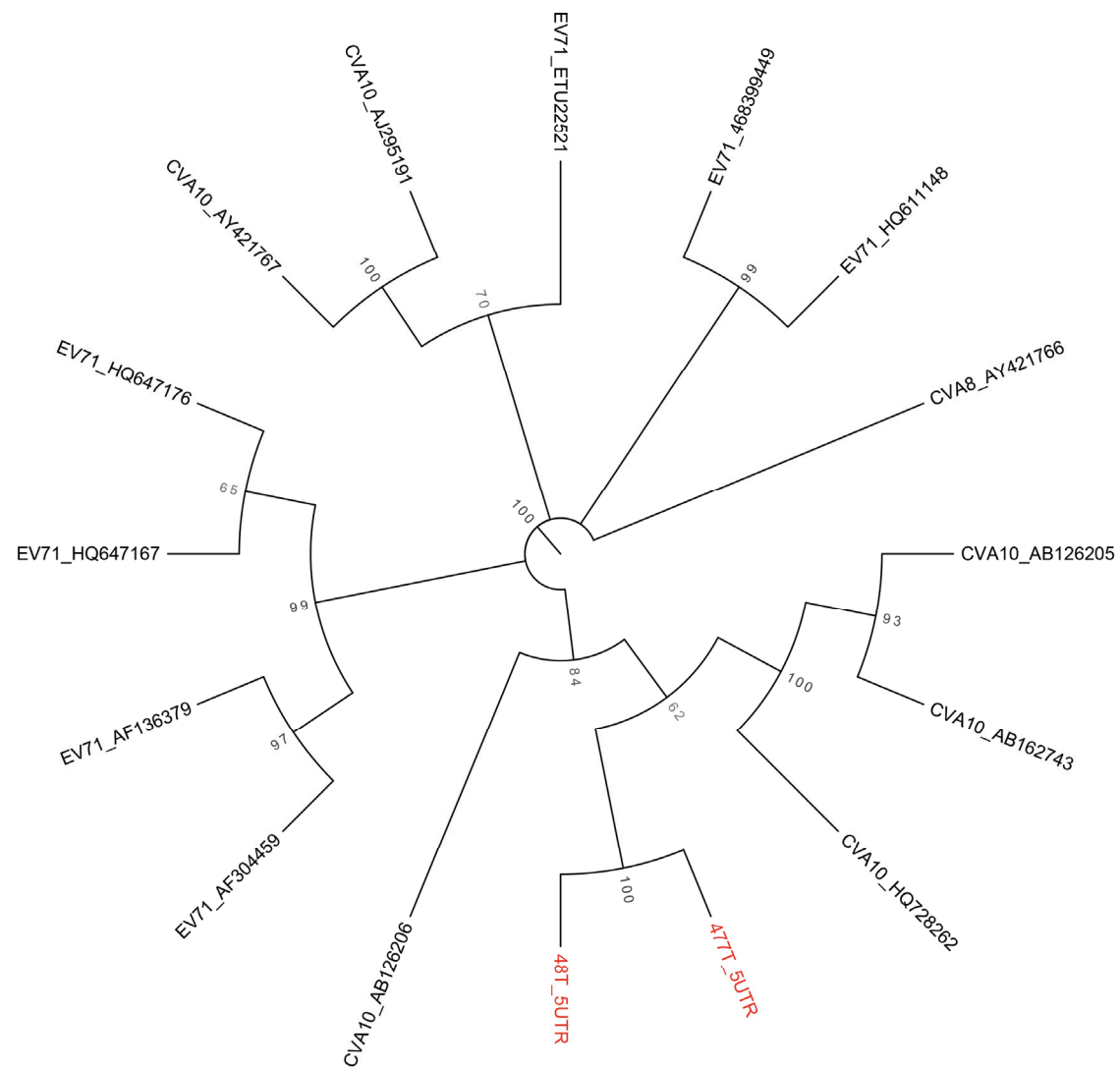
(B)

Figure S4. *Cont.*



(C)

Figure S4. *Cont.*



(D)

Figure S4. Cont.

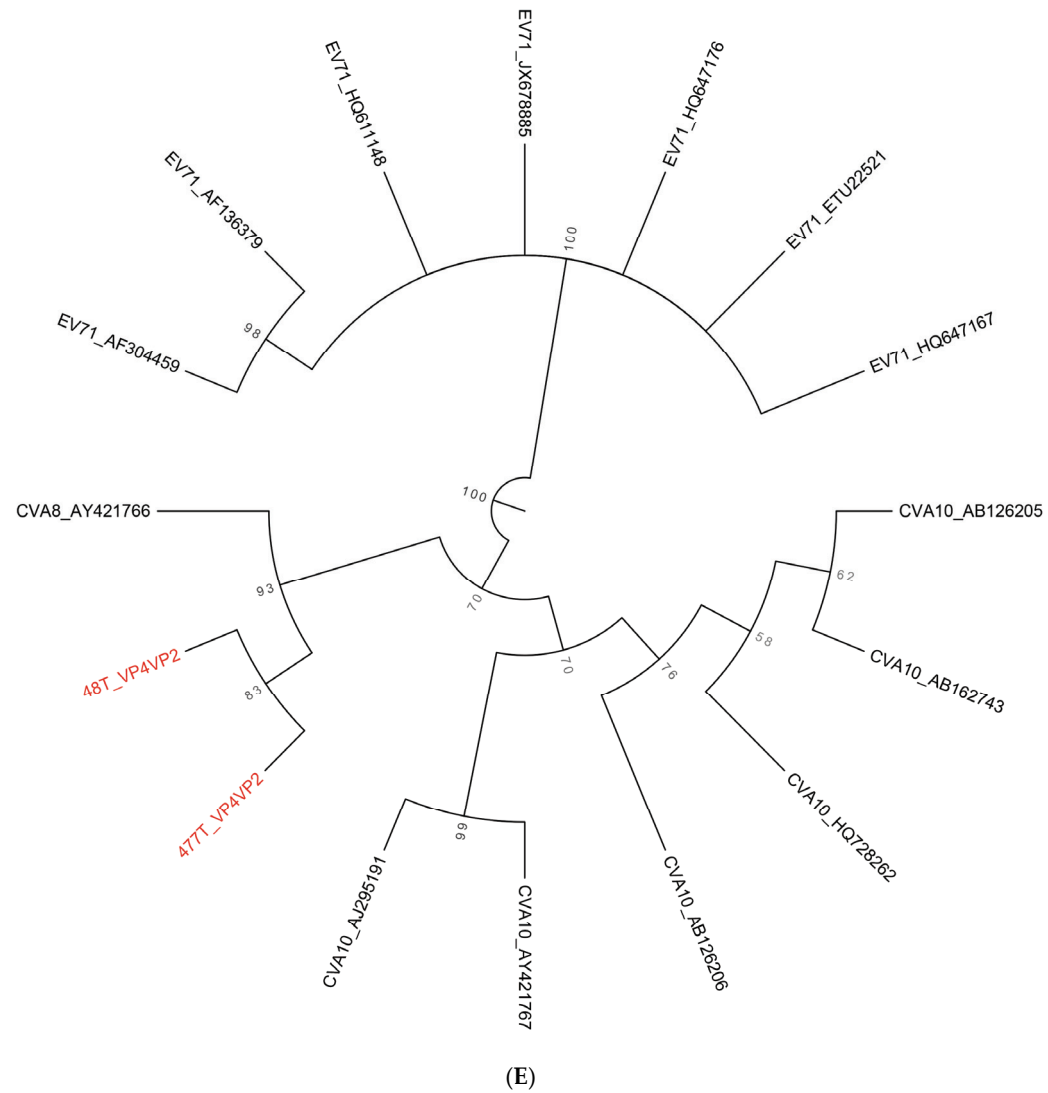


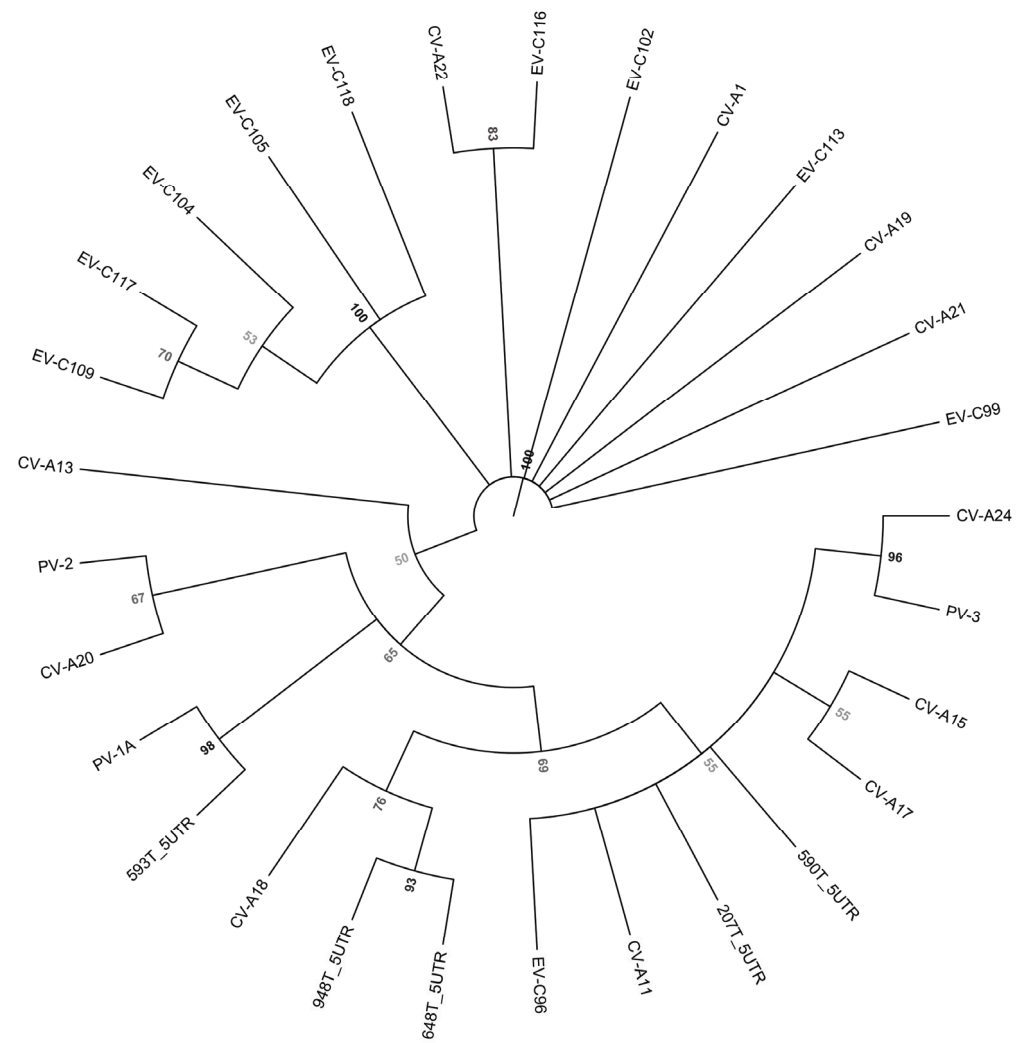
Figure S4. (A) HEV-A 5'UTR tree (nt 177 to 370 relative to HRV-A2_X02316); (B) HEV-A VP4/VP2 tree (nt 611 to 1030 relative to HRV-A2_X02316); (C) HEV-A VP1 tree (nt 2429 to 2709 relative to HRV-A2_X02316); (D) HEV-A 5'UTR recombinant tree (nt 169 to 611 relative to HRV-A2_X02316); (E) HEV-A VP4/VP2 recombinant tree (nt 611 to 1038 relative to HRV-A2_X02316).



S33

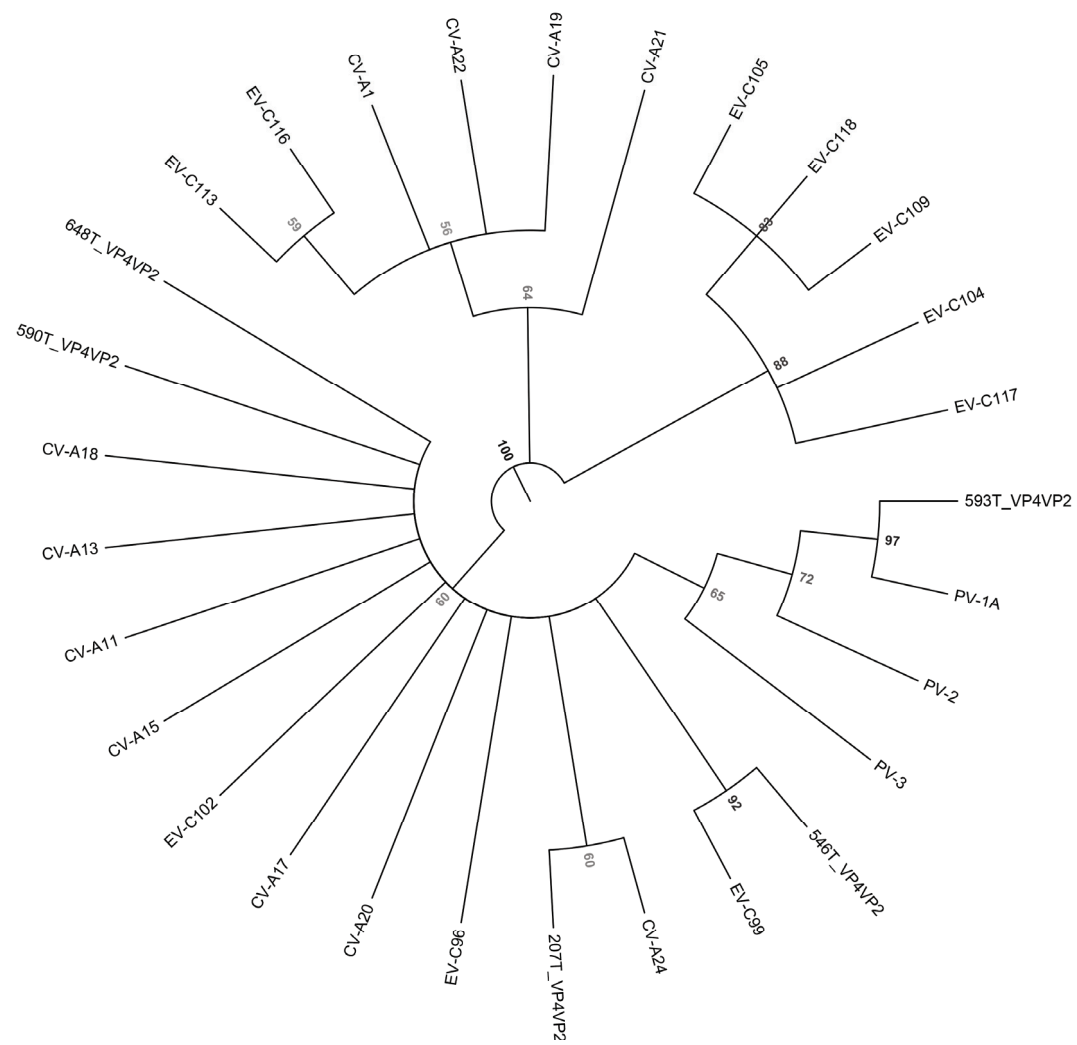


S34



(A)

Figure S6. *Cont.*



(B)

Figure S6. Cont.

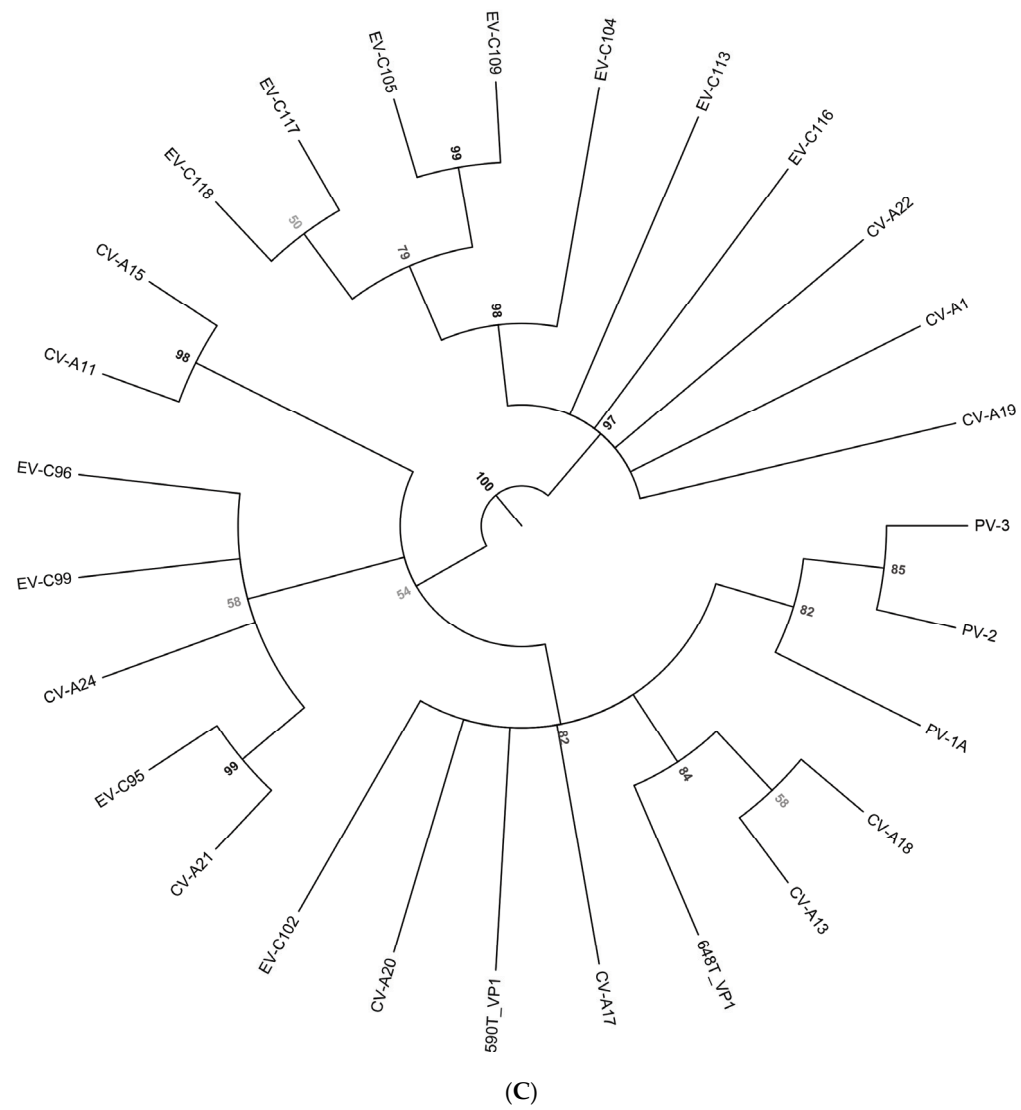


Figure S6. (A) HEV-C 5'UTR tree (nt 281 to 557 relative to HRV-A2_X02316); (B) HEV-C VP4/VP2 tree (nt 611 to 934 relative to HRV-A2_X02316); (C) HEV-C VP1 tree (nt 2450 to 2743 relative to HRV-A2_X02316).

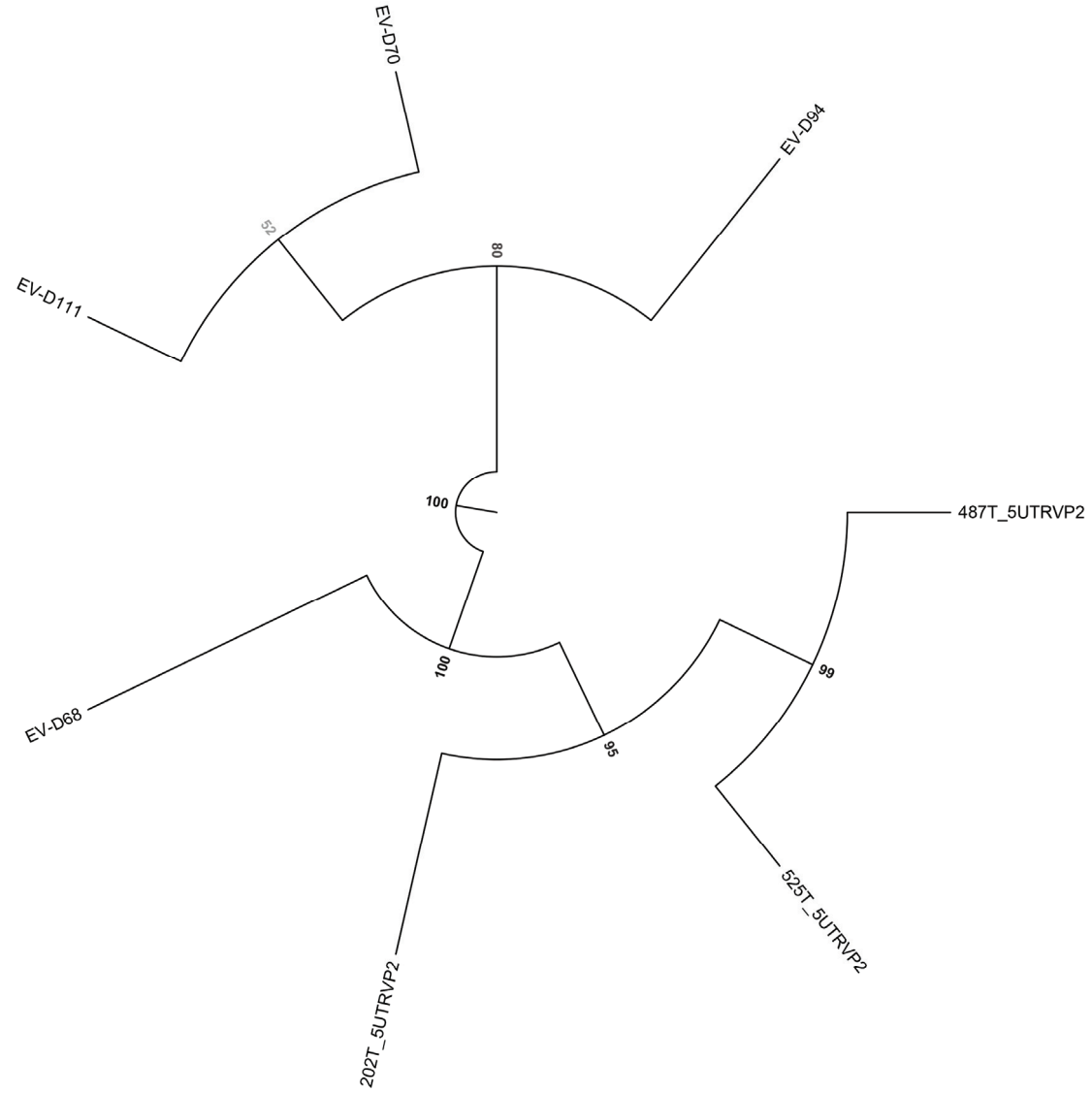


Figure S7. HEV-D 5'UTR/VP2 tree (nt 661 to 993 relative to HRV-A2_X02316).

Reference

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