Table S1. Primers used in the study for typing and sequencing of HuNoV. Nucleotide position corresponds to MD-145 strain (GenBank accession number AY032605).

Primer name	Sense/ Antisense	Sequence	Target nucleotide position	Reference
		Molecular typing		
Mon431	S	TGG ACI AGR GGI CCY AAY CA	4820-4839	[9,10]
GIISKR	A	CCR CCN GCA TRH CCR TTR TAC AT	5367-5389	[9,11]
		Sequencing of the VP1 P2 domain for phylogenetic analysis		
NV 347a	S	GAI GAT GTC TTC ACA GTY TCT T	5661-5682	[12]
NV 347b	S	GAT GAT GTK TTC ACW GTI TCT T	5661-5682	[12]
NV347c	S	GAT GAY GTI TTC ACI GTI TCM T	5661-5682	[12]
NV348a	A	GGT TRA CCC ARG AAT CAA A	6630-6648	[12]
NV348b	A	GRT TMA CCC AAG AIT CAA A	6630-6648	[12]
NV348c	A	GRT TRA CCC AIA CTT CAA A	6630-6648	[12]

Figure S1. Amino acid alignment of GII.4 HuNoV sequences included in the sequence analysis. The alignment corresponds to a highly variable region at sequence positions 5807–6365 (strain AB972487).

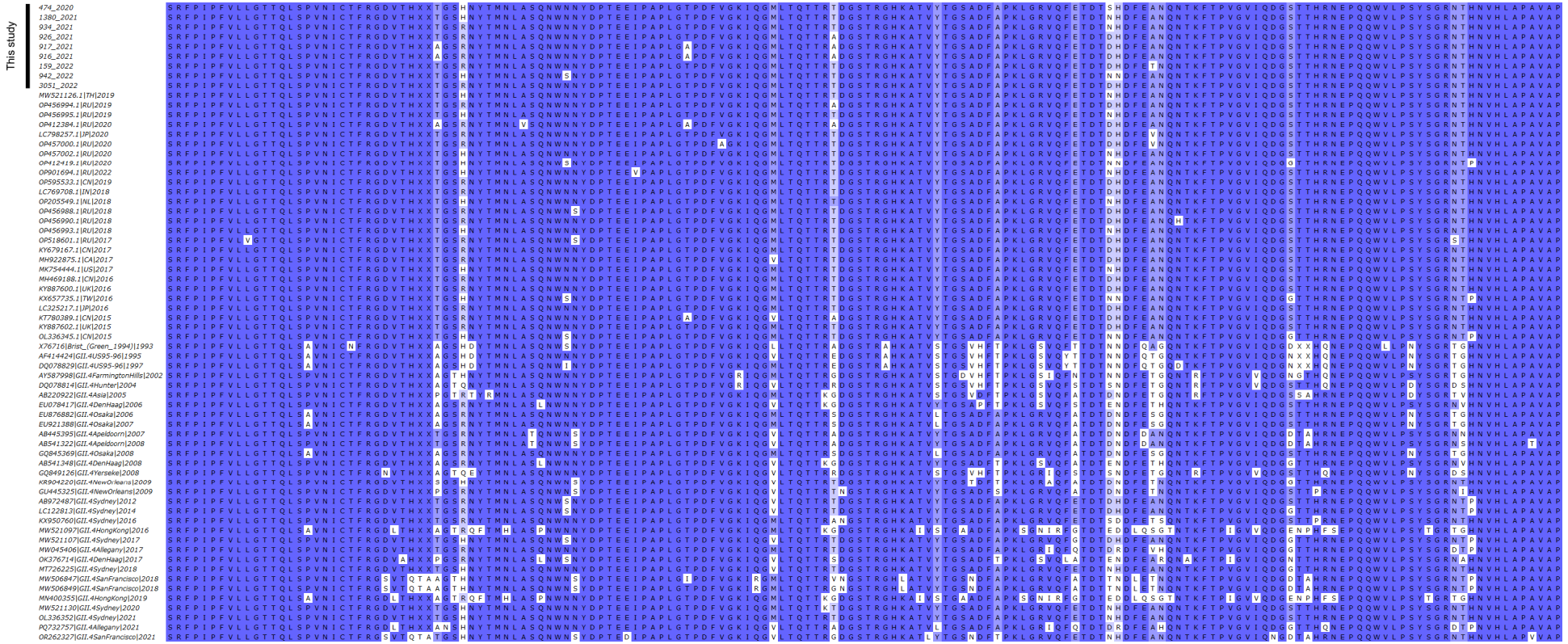


Figure S2. Amino acid alignment of GII.17 HuNoV sequences included in the sequence analysis. The alignment corresponds to a highly variable region at sequence positions 5926–6341 (strain PQ308687).

