C:\Users\Nica01\Downloads\Phylogenetic tree consecutive infections.tif**Supplement 1.** The nucleotide (nt) sequences homology from children experiencing consecutive sapovirus infections with the same genotype within 42 days and phylogenetic tree based in pairwise alignment of the nt sequences of the N-terminal and Shell region of the capsid gene. Nucleotide sequence homology was determined by using BioEdit, 7.2. Sequence alignment was performed by using the clustalW algorithm, version 1.83. Phylogenetic analysis and pairwise nucleotide identities were performed by the Mega 11.0.13 software package.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Subject ID followed by tested sample** | **Genotype** | **Days between infections** | **Compared segments (bp)** | | **Nucleotide homology (%)** | |
| 3-D1 | GI.1 | 42 | 354 | | 100.0 | |
| 3-D2 | GI.1 |
| 5-D1 | GII.3 | 21 | 399 | | 99.2 | |
| 5-D2 | GII.3 |
| 11-D1 | GI.1 | 29  36 | 361 | | 100.0 | |
| 11-F11 | GI.1 |
| 11-F12 | GI.1 |
| 16-D3 | GI.1 | 7 | 396 | | 100.0 | |
| 16-F10 | GI.1 |
| 18-F20 | GV.1 | 27 | 254 | | 100.0 | |
| 18-F21 | GV.1 |
| 29-D5 | GII.1 | 5 | 351 | | 96.6 | |
| 29-F19 | GII.1 |
| 36-D1 | GI.1 | 16 | 363 | | 100.0 | |
| 36-F7 | GI.1 |
| 37-F19 | GI.1 | 2 | 357 | | 100.0 | |
| 37-D4 | GI.1 |
| 38-D1 | GI.1 | 16 | 355 | | 100.0 | |
| 38-F16 | GI.1 |
| "D" stand for Acute Gastroenteritis Episode, | | | | | |
| and for monthly routine stool | | | |  | |