

Supplementary Table 1. Primer and probe sequences used in this case-control study

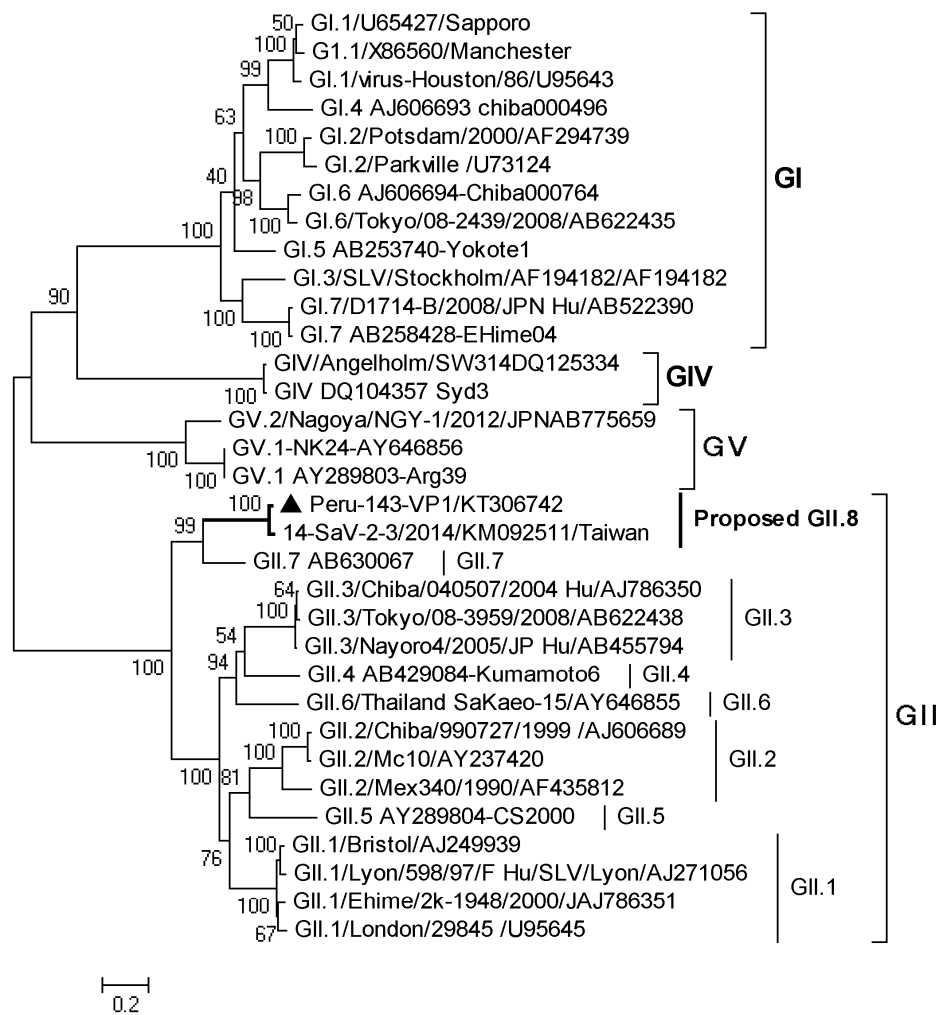
| Usage | Primer/Probe | Nucleotide Sequence (5'-3') | Position | Reference |
|----------------------|--------------|-----------------------------|------------------------|-----------|
| Real-time PCR | Sav 1F | TTGGCCCTCGCCACCTAC | 5077-5094 ^a | 1 |
| | Sav 5F | TTTGAACAAGCTGTGGCATGCTAC | 5112-5135 ^a | |
| | Sav124 F | GAYCASGCTCTCGCYACCTAC | 5074-5094 ^a | |
| | Sav1245 R | CCCTCCATYTCAAACACTA | 5159-5177 ^a | |
| | Sav124 probe | VIC-CCRCCTATRAACCA-MGB | 5101-5117 ^a | |
| | Sav5 probe | VIC-TGCCACCAATGTACCA-MGB | 5142-5157 ^b | |
| Genotyping | SV-F13 | GAYYWGGCYCTCGCYACCTAC | 5074-5094 ^a | 2 |
| | SV-F14 | GAACAAGCTGTGGCATGCTAC | 5074-5094 ^a | |
| | SaVF1245 | TAGTGTGGARATGGAGGG | 5159-5177 ^a | |
| | SaV5857R-1 | CWGGDGANAYHCCATTBTCCAT | 5857-5878 ^a | |
| | SaV5857R-2 | GGNGANMNNCCRTTNTSCAT | 5857-5876 ^a | |
| Amplification of VP1 | SV-F13 | GAYYWGGCYCTCGCYACCTAC | 5074-5094 ^a | Current |
| | SV-F14 | GAACAAGCTGTGGCATGCTAC | 5074-5094 ^a | study |
| | SaVGHIR | GCTCCWGTRAACCAAGACATTATTC | 6851-6875 ^c | |

- a. Position in complete sapovirus GI genogroup sequence (Manchester, X86560)
- b. Position in complete genome of sapovirus GV genogroup (NongKhai-24/Thailand, AY646856)
- c. Position in complete genome of GII genogroup (Bristol/98/UK, AJ249939)

1. **Oka T, Katayama K, Hansman GS, Kageyama T, Ogawa S, Wu FT, White PA,**

Takeda N. 2006. Detection of human sapovirus by real-time reverse transcription-polymerase chain reaction. *J Med Virol* 78:1347-1353.

2. **Okada M, Yamashita Y, Oseto M, Shinozaki K.** 2006. The detection of human sapoviruses with universal and genogroup-specific primers. *Arch Virol* 151:2503-2509.



Supplementary Figure 1. Phylogenetic analysis of full VP1 nucleotide sequences of sapovirus.

The phylogenetic tree was inferred using the maximum likelihood method (Kimura 2-parameter model) using MEGA5. The tree was drawn to scale, with branch lengths measured in the number of substitutions per site. The VP1 obtained in this study is marked with a filled triangle.