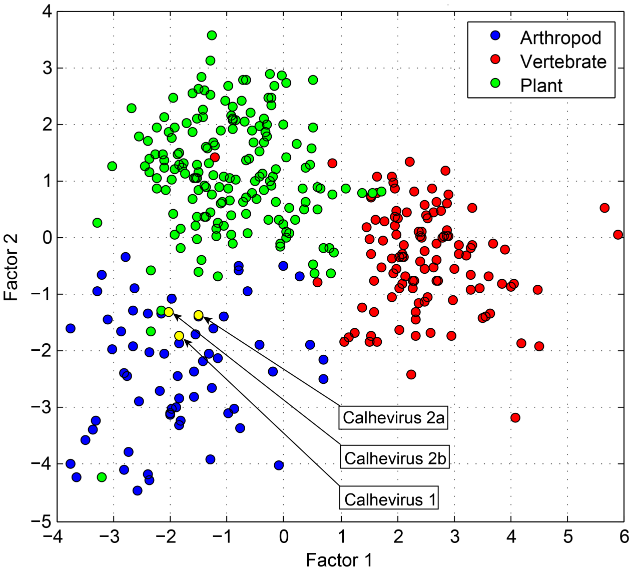
Title	Metagenomic analysis of the shrew enteric virome reveals novel viruses related to human stool-associated viruses
Author(s)	Sasaki, Michihito; Orba, Yasuko; Ueno, Keisuke; Ishii, Akihiro; Moonga, Ladslav; Hang'ombe, Bernard M.; Mweene, Aaron S.; Ito, Kimihito; Sawa, Hirofumi
Citation	Journal of General Virology, 96(2), 440-452 https://doi.org/10.1099/vir.0.071209-0
Issue Date	2015-02
Doc URL	http://hdl.handle.net/2115/60630
Type	article (author version)
Additional Information	There are other files related to this item in HUSCAP. Check the above URL.
File Information	Supplementary Figure.pdf



Supplementary Figure S1. Canonical discriminat analysis of Calhevirus 2a and Calhevirus 2b. The graph shows the separation of groups using the two most influential factors based on mononucleotide and dinucleotide frequencies. The genome sequences of 112 vertebrate-derived viruses, 64 arthropod-derived viruses, 171 plant-derived viruses were used as reference sequences for the analysis and shown as red circles, blue circles and green circles, respectively. Calhevirus 1, Calhevirus 2a and Calhevirus 2b are shown as yellow circles.