Supplementary Material

Supplementary Table 1. Summary of next generation sequencing results and contigs obtained

Sample ID	QC[1] (original samples and libraries)	No. of raw reads obtained	No. of contigs obtained	Contig length(s) (nt)	No. of reads mapping to contig(s)	Final sequence length
Alleys-Red (GRF0085)	PASS	2,585,444	3	3,270 4,020 4,050	1,121	7,274
Beni-Aka (GRF0096)	PASS	2,279,642	1	10,857	3,439	7,712

[1]The quality and concentration of the original samples were determined with Picogreen™ (ThermoFisher Scientific, Australia) using a Victor[3] fluorometer (PerkinElmer, Australia) and by gel electrophoresis. The NGS libraries were prepared using the Nextera XT DNA Library Preparation Kit (Illumina, Australia) and the quality and concentration of the libraries were determined using a Agilent Bioanalyzer 2100. Both the original samples and libraries passed the QC, and libraries were sequenced using the Illumina MiSeq platform.

Supplementary Table 2. Genome organisation of sweet potato collusive virus isolates and other *Cavemovirus* members

Virus sp. (isolate)	**Complete genome length (bp)**	**Size of predicted ORFs in bp[a] (conserved protein domains)**				
		ORF 1 (CP/MP)	ORF 2 (Unknown)	ORF 3 (AP/RT/RH)	ORF 4 (IBP)	ORFa (Unknown)
CsVMV	8159	4119	216	1959	1179	165
EpV-4	7296	3600	n/a	1959	1077	153
ChiMV	7775	3837	n/a	1953	1155	195
SPCV (Mad1)	7723	3795	n/a	1926	1197	150
SPCV (Aus1)	7712	3786	n/a	1926	1197	111
SPCV (Aus2)	7274	3345	n/a	1926	1197	111

[a]Numbering of ORFs follows the Cassava vein mosaic virus (CsVMV) genome organisation. EpV – Epiphyllum virus, ChiMV– Chicory mosaic cavemovirus, SPCV– sweet potato collusive virus, CP – coat protein, MP – movement protein, AP – aspartic protease, RT – reverse transcriptase, RH – ribonuclease H, IBP – inc