Erratum to: A field guide to eukaryotic circular single-stranded DNA viruses: insights gained from metagenomics

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In the original publication of the article, Fig. 5 depicted the wrong color scheme for genome SsHADV-1 since the 'Cap' open reading was miscolored.

The online version of the original article can be found under
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Fig. 5 Schematic genome organization of selected ssDNA viruses discovered through metagenomics with previously described genome architectures. Genome types were classified based on the features listed in Table 2. Each circle shows the genome size and top BLAST similarities (colors) for each open reading frame (ORF), including matches to virus-like replication-associated proteins (Rep) found in protists. ORFs that are known or have significant matches are labeled as Rep or capsid (Cap) based on putative function. Genomes

containing a canonical nonanucleotide motif ('NANTATTAC') at the apex of a potential stem-loop structure are indicated with a star. 'RRR' indicates the presence of an N-terminal region rich in basic amino acids, which is a characteristic of the circovirus Cap. The presence of a unique SF3helicase Walker-A motif (i.e., [D(E)xxGgxGK(T/S)]) in putative Rep ORFs is indicated with 'W-A'. Note that ORFs within a single genome may have similarities to different ssDNA viruses