

**Supplementary material S6.** Identification of inter-species recombination event involving mongoose associated cyclovirus strain Mon-32, as determined by the Recombination Detection Program (RDP v.4.101). A sequence was identified as a recombinant if it was detected by more than two methods with a highest acceptable *p-value* of  $p < 0.01$  with Bonferroni's correction.

***Recombinant:*** Goat associated cyclovirus 1 (isolate PKgoat11), GenBank accession number HQ738636

***Major parent:*** Unknown

***Minor parent:*** Mongoose associated cyclovirus strain Mon-32

***Recombinant region:*** nt 1174-nt 45

Confirmation table generated by RDP v.4.101 program.

<b><i>Method</i></b>	<b><i>Average p-value</i></b>
RDP	$4.973 \times 10^{-15}$
GENECONV	$1.813 \times 10^{-12}$
BootScan	$8.837 \times 10^{-18}$
MaxChi	$7.541 \times 10^{-16}$
Chimaera	$2.776 \times 10^{-13}$
SiScan	$5.826 \times 10^{-26}$
3Seq	$2.226 \times 10^{-05}$