

Supplementary Table 1. The number of sample and taxonomy of viruses detected by blastn

Accession No.	Species	Genus	Family	Genome	Case	Control
NC_014078.1	Torque teno virus 19	Alphatorquevirus	<i>Anelloviridae</i>	ssDNA(-)	1	-
NC_014081.1	Torque teno virus 3	Alphatorquevirus	<i>Anelloviridae</i>	ssDNA(-)	2	-
NC_014084.1	Torque teno virus 8	Alphatorquevirus	<i>Anelloviridae</i>	ssDNA(-)	1	-
NC_026809.1	Gemykibivirus humas3	Gemykibivirus	<i>Genomoviridae</i>	ssDNA	1	-
NC_048651.1	Aeribacillus virus AP45	Kamchatkavirus	<i>Siphoviridae</i>	dsDNA	1	-
NC_014076.1	Torque teno virus 10	Alphatorquevirus	<i>Anelloviridae</i>	ssDNA(-)	3	1
NC_022518.1	Human endogenous retrovirus K	-	<i>Retroviridae</i>	ssRNA-RT	100	100
NC_028045.1	Bat associated circovirus 4	Circovirus	<i>Circoviridae</i>	ssDNA(+/-)	59	45

The contig of each virus from individually sample had the genome completeness more than 5% of each viral genome.