

Table S3. Diversity of viruses of public health relevance identified in this study

Bat species	Virus ID	Sampling sites	PCR	Lenght bp (Query cover %)	Percent Identity	GenBank Acession Number	Host/Year	RefSeq Percent Identity	RefSeq
Vertical transmission									
D. rotundus (n=1)	Rabies virus (pan-RhabV and LYSSAV)	CNS ¹	+	11922 (100)	98.2 (99.9)	KX148109.1 (RABV isolate 86117BRE)	Canine/1986	80.1	NC_001542.1 (RABV)
		GIT ²	-	11922 (100)	98.2 (99.9)	KX148109.1 (RABV isolate 86117BRE)	Canine/1986	80.1	NC_001542.1 (RABV)
		Kidney ³	+	9914 (100)	97.8 (99.9)	KX148109.1 (RABV isolate 86117BRE)	Canine/1986	80.4	NC_001542.1 (RABV)
		Fetus ⁴	+	1189 (100)	99.7	KX148109.1 (RABV isolate 86117BRE)	Canine/1986	80.9	NC_001542.1 (RABV)
M. molossus (n=4)		CNS ⁵	+	11907 (100)	97.9	KM594034.1 (RABV isolate IP 350/10)	Bat/2010	80.7	NC_001542.1 (RABV)
		GIT ⁶	-	611 (99)	99.33	KM594034.1 (RABV isolate IP 350/10)	Bat/2006	82.3	NC_001542.1 (RABV)
		CNS ⁸	+	11927 (100)	97.9	KM594034.1 (RABV isolate IP 350/10)	Bat/2010	80.6	NC_001542.1 (RABV)
		GIT ⁹	-	815 (87)	97.3	KX148109.1 (RABV isolate 86117BRE)	Canine/1986	79.3	NC_001542.1 (RABV)
		CNS ¹¹	+	11905 (100)	97.8	KM594034.1 (RABV isolate IP 350/10)	Bat/2010	80.6	NC_001542.1 (RABV)
		CNS ¹¹	+	11905 (100)	97.8	KM594034.1 (RABV isolate IP 350/10)	Bat/2010	80.6	NC_001542.1 (RABV)
		GIT ¹²	-	1270 (100)	93.3	KM594034.1 (RABV isolate IP 350/10)	Bat/2010	81.8	NC_001542.1 (RABV)
		GIT ¹²	-	748 (100)	98.3	AB618032.1 (RABV isolate MP19)	Bat/2006	82.6	NC_001542.1 (RABV)
		Anal swab ¹³	+	8555 (100)	98.5	KM594035.1 (RABV isolate IP 412)	Bat/2010	80.6	NC_001542.1 (RABV)
D. rotundus (n=1)	Adeno-associated virus	CNS ¹	-	420 (40)	78.4 (99.5)	NC_006152.1 (AAV5)	-	67.4	NC_006152.1 (AAV5)
		GIT ²	+	2730 (23)	80.09 (63.2)	OR998784.1 (Bat AAV1)	Bat	64.4	NC_006152.1 (AAV5)
		Kidney ³	+	809 (21)	79 (49.6)	NC_006152.1 (AAV5)	-	65.3	NC_006152.1 (AAV5)
		Fetus ⁴	-	936 (14)	79	NC_006152.1 (AAV5)	-	60.2	NC_006152.1 (AAV5)
M. molossus (n=2)	Hepatovirus H sp. 'sotense'	GIT ¹²	-	134 (100)	88.1 (100)	OR367421.1 (Hepatovirus sp. 'sotense' isolate CH-APSJS/2021)	Bat/2021	-	-
		Fetus ¹⁴	-	4179 (92)	82.12	OR367421.1 (Hepatovirus sp. 'sotense' isolate CH-APSJS/2021)	Bat/2021	-	-
D. rotundus (n=1)	Human betaherpesvirus 6	CNS ¹	-	354 (100)	86	KY290209.2 (HHV-6 isolate NY-353)	Homo sapiens	85.4	KY315532.2 (HHV-6 strain HP33A)
D. rotundus (n=1)	Mammalian Orthoreovirus 3	GIT ²	-	2267 (100)	97.7	KT224504.1 (MRV-3 isolate SD-14 segment L1)	Mink/2014	89.5	NC_077839.1 (MRV-3 Dearing strain T3D segment L1)
	Mammalian Orthoreovirus 2	GIT ²		2554 (100)	98.3	LC476907.1 (MRV-2 Osaka2005 lambda-1 protein)	Homo sapiens/2005	83.4	NC_077842.1 (MRV-3 Dearing strain T3D segment L3)
	Mammalian Orthoreovirus	GIT ²		1634 (100)	96.9	KC462154.1 (MRV isolate HB-A segment M3)	Mink/2013	83.8	NC_077845.1 (MRV-3 Dearing strain T3D segment M3)
	Mammalian Orthoreovirus 2	GIT ²		1673 (100)	98.3	LC476906.1 (MRV-2 Osaka2005 lambda-2 protein)	Homo sapiens/2005	77.6	NC_077840.1 (MRV-3 Dearing strain T3D segment L2)
	Mammalian Orthoreovirus	GIT ²		1594 (100)	99	PQ306480.1 (MRV HNU-XXS-2020 segment M1)	Domestic pig/2020	93.2	NC_077841.1 (MRV-3 Dearing strain T3D segment M1)
	Mammalian Orthoreovirus	GIT ²		1348 (90)	95.6	OR902355.1 (MRV mu-1 gene)	Sheep/2023	88.8	NC_077843.1 (MRV-3 Dearing strain T3D segment M2)
	Mammalian Orthoreovirus	GIT ²		1059 (99)	97.5	JF829217.1 (MRV isolate KPR150 sigma 1 gene)	Domestic pig/2005	85	NC_077844.1 (MRV-3 Dearing strain T3D segment S1)
	Mammalian Orthoreovirus	GIT ²		823 (100)	98	PQ306477.1 (MRV isolate HNU-XXS-2020 segment S2)	Domestic pig/2020	84	NC_077846.1 (MRV-3 Dearing strain T3D segment S2)
	Mammalian Orthoreovirus 2	GIT ²		657 (100)	99	LC121912.1 (MRV-2 segment S4)	Panthera leo/2011	87.5	NC_077838.1 (MRV-3 Dearing strain T3D segment S4)
	Mammalian Orthoreovirus	GIT ²		269 (100)	93.7	PQ306478.1 (MRV isolate HNU-XXS-2020 segment S3)	Domestic pig/2020	82.5	NC_077837.1 (MRV-3 Dearing strain T3D segment S3)
E. perotis / M. molossus (n=2)	Human papillomavirus	GIT ⁶	-	144 (100)	100	NC_001354.1 (HPV-41)	Homo sapiens	-	-

Virus ID: taxonomic classification assigned through BLAST search and phylogenetic analysis. **Length (query cover):** total length of viral contigs and percentage of query cover assigned by BLAST.

Percent identity: percentage of nucleotide identity assigned by BLAST; values in parentheses indicate overall identity between fetal and maternal tissues.

Sampling sites: RNA-seq pools (Pool1–Pool14), represented by superscript numbers indicating the origin of each sequence. The fetus positive for rabies virus is shown in bold.

RefSeq identical sites: number of identical nucleotide positions between the sequence and its reference genome.