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Mapping the global diversity and surveillance landscape of medically important bat-borne viruses: a scoping review

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Annex 1A: distribution of bat-associated viral sequences by geographic region (2010–2024)		
Region	**Bat-borne viral sequences**	**Percentage of total assigned sequences**
Asia	6794	39.7%
Africa	5107	29.8%
North America	2000	11.7%
Europe	1613	9.4%
South America	1371	8.0%
Oceania	249	1.5%
Total Assigned	17,134	100.0%
Percentages are calculated from sequences with known geographic origin (N = 17,134); sequences with unknown origin (n = 92) are excluded; sequence deposition is an indirect proxy for surveillance effort, not true viral abundance		

Annex 1B: country-level surveillance intensity for bat-associated viruses (2010-2024)					
Sampling country	**Total detections**	**Virus families**	**Bat species**	**Bat families**	**High risk viruses**
Austria	1	1	1	1	0
Argentina	1	1	1	1	1
Australia	17	9	10	4	4
Bangladesh	1	1	1	1	0
Brazil	19	8	10	4	8
Cambodia	1	1	1	1	0
Canada	2	1	2	1	1
China	40	11	22	6	5
Costa Rica	1	1	1	1	1
Finland	4	2	3	1	4
France	3	2	2	1	1
France, Spain	1	1	1	1	0
French Guiana	3	3	3	2	1
Gabon	3	3	3	3	1
Germany	9	7	7	2	4
Ghana	6	4	3	2	1
Indonesia	1	1	1	1	0
Italy	5	4	4	1	0
Japan	2	1	2	2	0
Japan, China, Korea, Taiwan	1	1	1	1	0
Kenya	3	1	3	2	0
Korea, South	1	1	1	1	0
Latin America	1	1	1	1	1
Malaysia	1	1	1	1	0
Martinique	1	1	1	1	0
Mayotte	1	1	1	1	0
Mozambique, Madagascar, Mauritius, Mayotte, Reunion Island and Seychelles	1	1	1	1	0
Myanmar	1	1	1	1	0
New Zealand	2	2	1	1	0
Peru	1	1	1	1	0
Republic of Congo, Gabon, Central African Republic (CAR) and Senegal	1	1	1	1	1
Russia	1	1	1	1	0
Saudi Arabia	1	1	1	1	0
Serbia	1	1	1	1	0
Sierra Leone	1	1	1	1	0

Singapore	3	3	2	1	0
Spain	8	4	7	2	2
Spain, Portugal	1	1	1	1	0
Sri Lanka	1	1	1	1	0
Sweden	1	1	1	1	0
Switzerland	3	2	2	1	3
Taiwan, Province of China	1	1	1	1	0
Thailand	1	1	1	1	0
Trinidad and Tobago	1	1	1	1	0
Uganda	1	1	1	1	1
United States of America	5	3	3	2	1
Uruguay	1	1	1	1	0
Viet Nam	1	1	1	1	1
Vietnam	2	2	2	1	0
Vietnam and China	1	1	1	1	0
Zambia	2	1	2	2	0
Zimbabwe	3	2	2	2	0

Tier 4 = confirmed zoonotic; Tier 3 = high-potential zoonotic risk based on experimental evidence. 'Bat families' indicates the number of distinct bat families represented among the bat virus association records sampled in that country, not the total number of bat families known to occur there

Annex 1C: examples of zoonotic bat-borne viruses reported in Africa (2010-2024)

Viral Family	From bat	Bat diet type	Bat family	Sample type	Collection year	Sampling country	Sequence coding	Viruses
Coronaviridae	*Rousettus aegyptiacus*	Frugivore	*Pteropodidae*	Swabs	2016	Kenya	RdRp	229E-related bat coronavirus BatCoV5425/KEN/Trans Nzoia
Coronaviridae	*Hipposideros caffer*	Insectivore	*Rhinolophidae*	Swabs	2016	Kenya	RdRp	229E-related bat coronavirus BatCoV5743/KEN/Kwale
Coronaviridae	*Hipposideros caffer*	Insectivore	*Rhinolophidae*	Swabs	2016	Kenya	RdRp	229E-related bat coronavirus BatCoV5773/KEN/Kwale
Coronaviridae	*Hipposideros sp.*	Insectivore	*Rhinolophidae*	Feces	2016	Zimbabwe	RdRp	229E-related bat coronavirus BtCov-Zim001Mab
Coronaviridae	*Hipposideros sp.*	Insectivore	*Rhinolophidae*	Feces	2016	Zimbabwe	RdRp	229E-related bat coronavirus BtCov-Zim015Mab
Coronaviridae	*Hipposideros sp.*	Insectivore	*Rhinolophidae*	Feces	2016	Zimbabwe	RdRp	229E-related bat coronavirus BtCov-Zim019Mab
Coronaviridae	*Hipposideros sp.*	Insectivore	*Rhinolophidae*	Feces	2016	Zimbabwe	RdRp	229E-related bat coronavirus BtCov-Zim021Mab
Coronaviridae	*Hipposideros sp.*	Insectivore	*Rhinolophidae*	Feces	2016	Zimbabwe	RdRp	229E-related bat coronavirus BtCov-Zim034Mab
Coronaviridae	*Hipposideros sp.*	Insectivore	*Rhinolophidae*	Feces	2016	Zimbabwe	RdRp	229E-related bat coronavirus BtCov-Zim037Mab
Coronaviridae	*Hipposideros sp.*	Insectivore	*Rhinolophidae*	Feces	2016	Zimbabwe	RdRp	229E-related bat coronavirus BtCov-Zim040Mab
Coronaviridae	*Hipposideros abae*	Insectivore	*Rhinolophidae*	Feces	2010	Ghana	Full length	229E-related bat coronavirus BtCoV/AT1A-F1/Hip_aba/GHA/2010
Coronaviridae	*Hipposideros ruber*	Insectivore	*Rhinolophidae*	Feces	2010	Ghana	RdRp	229E-related bat coronavirus BtCoV/AT1A-F26/Hip_cf._rub/GHA/2010
Coronaviridae	*Hipposideros abae*	Insectivore	*Rhinolophidae*	Feces	2010	Ghana	RdRp, S	229E-related bat coronavirus BtCoV/AT1A-F41/Hip_aba/GHA/2010

RdRp = RNA-dependent RNA polymerase; S = Spike protein

Annex 1D: examples of zoonotic bat-borne viruses reported in Asia (2010-2024)

Viral Family	From bat	Bat diet type	Bat family	Sample type	Collection year	Sampling country	Sequence coding	Viruses
Adenoviridae	*Eonycteris spelaea*	Nectarivore	*Pteropodidae*	Mix	2013	Singapore	POL	Adenoviridae sp. DNUS-Bat-Polymerase-Esp
Picornaviridae	*Myotis fimbriatus*	Insectivore	*Vespertilionidae*	Swabs	2016	China	Polyprotein	Aichivirus F GD2016_288_738
Picornaviridae	*Rhinolophus sinicus*	Insectivore	*Rhinolophidae*	Swabs	2017	China	Polyprotein	Aichivirus F GD2017_085_7919
Picornaviridae	*Myotis ricketti*	Insectivore and piscivore	*Vespertilionidae*	Swabs	2017	China	Polyprotein	Aichivirus F GD2017_207_36806
Picornaviridae	*Myotis ricketti*	Insectivore and piscivore	*Vespertilionidae*	Swabs	2017	China	Polyprotein	Aichivirus F GD2017_210_473
Picornaviridae	*Myotis ricketti*	Insectivore and piscivore	*Vespertilionidae*	Swabs	2017	China	Polyprotein	Aichivirus F GD2017_210_5247
Picornaviridae	*Myotis chinensis*	Insectivore	*Vespertilionidae*	Swabs	2017	China	Polyprotein	Aichivirus F GD2017_279_5575
Picornaviridae	*Myotis ricketti*	Insectivore and piscivore	*Vespertilionidae*	Swabs	2019	China	Polyprotein	Aichivirus F GD2019_212_2679
Picornaviridae	*Myotis adversus*	Carnivore	*Vespertilionidae*	Swabs	2020	China	Polyprotein	Aichivirus F JX2020_264_61956
Picornaviridae	*Myotis chinensis*	Insectivore	*Vespertilionidae*	Swabs	2016	China	Polyprotein	Aichivirus F Pool-280_37268
Picornaviridae	*Myotis chinensis*	Insectivore	*Vespertilionidae*	Swabs	2018	China	Polyprotein	Aichivirus F SC2018_004_55519
Picornaviridae	*Myotis davidii*	Insectivore	*Vespertilionidae*	–	2016	China	Polyprotein	Aichivirus F WZ_My.davidii_picorna_1
Picornaviridae	*Myotis chinensis*	Insectivore	*Vespertilionidae*	Swabs	2020	China	Polyprotein	Aichivirus F YN2020_064_3297

Diet classifications follow IUCN bat diet categories (IUCN, International Union for Conservation of Nature). "Mix" indicates combined oral/rectal swabs or multiple sample types.
POL = Polymerase

Annex 1E: examples of zoonotic bat-borne viruses reported in Europe (2010-2024)

Viral family	From bat	Bat diet type	Bat family	Sample type	Collection year	Sampling country	Sequence coding	Viruses
Coronaviridae	*Pipistrellus kuhlii*	Insectivore	*Vespertilionidae*	Mix	2011	Italy	Full length	Alphacoronavirus Bat-CoV/P.kuhlii/Italy/206645-41/2011
Coronaviridae	*Pipistrellus kuhlii*	Insectivore	*Vespertilionidae*	Feces	2010	Italy	Full length	Alphacoronavirus Bat-CoV/P.kuhlii/Italy/206679-3/2010
Coronaviridae	*Pipistrellus kuhlii*	Insectivore	*Vespertilionidae*	Feces	2015	Italy	Full length	Alphacoronavirus Bat-CoV/P.kuhlii/Italy/3398-19/2015
Coronaviridae	*Hypsugo savii*	Insectivore	*Vespertilionidae*	Feces	2007	Spain	RdRp	Alphacoronavirus H.sav/L/Spain/2007
Coronaviridae	*Myotis blythii*	Insectivore	*Vespertilionidae*	Swabs	2004	Spain	RdRp	Alphacoronavirus M.bly/B/Spain/2004
Coronaviridae	*Myotis daubentonii*	Insectivore	*Vespertilionidae*	Feces	2007	Spain	RdRp	Alphacoronavirus M.dau/H/Spain/2007
Coronaviridae	*Myotis myotis*	Insectivore	*Vespertilionidae*	Feces	2007	Spain	RdRp	Alphacoronavirus M.myo/I/Spain/2007
Coronaviridae	*Miniopterus schreibersii*	Insectivore	*Vespertilionidae*	Swabs	2004	Spain	RdRp	Alphacoronavirus M.sch/A/Spain/2004
Coronaviridae	*Myotis blythii*	Insectivore	*Vespertilionidae*	Swabs	2012	Italy	RdRp	Alphacoronavirus Myotis/13rs384_31/Italy/2012
Coronaviridae	*Nyctalus lasiopterus*	Insectivore and bird-eating	*Vespertilionidae*	Feces	2007	Spain	RdRp	Alphacoronavirus N.las/C/Spain/2007
Coronaviridae	*Nyctalus lasiopterus*	Insectivore and bird-eating	*Vespertilionidae*	Feces	2007	Spain	RdRp	Alphacoronavirus N.las/D/Spain/2007
Coronaviridae	*Nyctalus lasiopterus*	Insectivore and bird-eating	*Vespertilionidae*	Feces	2007	Spain	RdRp	Alphacoronavirus N.las/E/Spain/2007

"Full length" indicates complete or near-complete genome sequence. "Mix" indicates combined oral/rectal swabs or multiple sample types. Abbreviations: RdRp = RNA-dependent RNA polymerase; HEL = helicase

Annex 1F: examples of zoonotic bat-borne viruses reported in South America (2010-2024)

Viral family	From bat	Bat diet type	Bat family	Sample type	Collection year	Sampling country	Sequence coding	Viruses
Coronaviridae	*Tadarida sp.*	Omnivore	*Molossidae*	Swabs	2011	Brazil	RdRp	Alphacoronavirus TadaridaM4/UNICAMP/Brazil/2014
Coronaviridae	*Carollia perspicillata*	Omnivore	*Phyllostomidae*	Mix	2009	Brazil	RdRp	Alphacoronavirus Trinidad/1FY2BA/2007 PREDICTAraguari-67
Coronaviridae	*Carollia perspicillata*	Omnivore	*Phyllostomidae*	Mix	2009	Brazil	RdRp	Alphacoronavirus Trinidad/1FY2BA/2007 PREDICTAraguari-69
Coronaviridae	*Carollia perspicillata*	Omnivore	*Phyllostomidae*	Swabs	2011	Bolivia	RdRp	Alphacoronavirus Trinidad/1FY2BA/2007 PREDICTEHA06811B00267
Coronaviridae	*Carollia perspicillata*	Omnivore	*Phyllostomidae*	Swabs	2011	Bolivia	RdRp	Alphacoronavirus Trinidad/1FY2BA/2007 PREDICTEHA06811B00294
Coronaviridae	*Carollia perspicillata*	Omnivore	*Phyllostomidae*	Swabs	2011	Bolivia	RdRp	Alphacoronavirus Trinidad/1FY2BA/2007 PREDICTEHA06811B00335
Coronaviridae	*Carollia perspicillata*	Omnivore	*Phyllostomidae*	Swabs	2011	Brazil	RdRp	Alphacoronavirus Trinidad/1FY2BA/2007 PREDICTWCS07611R00077
Coronaviridae	*Artibeus planirostris*	Frugivore	*Phyllostomidae*	Tissue	2018	Brazil	RdRp	Alphacoronavirus sp. BatCoV-801
Coronaviridae	*Artibeus planirostris*	Frugivore	*Phyllostomidae*	Tissue	2018	Brazil	RdRp	Alphacoronavirus sp. BatCoV-804
Hantaviridae	*Carollia perspicillata*	Omnivore	*Phyllostomidae*	Blood	2013	Brazil	N	Andes orthohantavirus gsj169blood
Hantaviridae	*Carollia perspicillata*	Omnivore	*Phyllostomidae*	Blood	2013	Brazil	N	Andes orthohantavirus gsj169s
Hantaviridae	*Desmodus rotundus*	Sanguivore	*Phyllostomidae*	Urine	2013	Brazil	N	Andes orthoserelogica gsj174urine
Anelloviridae	*Diaemus youngi*	Sanguivore	*Phyllostomidae*	Mix	2019	Brazil	Full length	Anelloviridae sp. ViroVet11

"PREDICT" entries refer to sequences generated under the USAID PREDICT project (USAID, United States Agency for International Development). Virus names follow ICTV nomenclature where available (ICTV, International Committee on Taxonomy of Viruses). "Full length" indicates complete or near-complete genome sequence. Abbreviations: RdRp = RNA dependent RNA polymerase; N = nucleocapsid gene

Annex 1G: examples of zoonotic bat-borne viruses reported in North America (2010-2024)

Viral Family	From bat	Bat diet type	Bat family	Sample type	Collection year	Sampling country	Sequence coding	Viruses
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	RdRp	Alphacoronavirus Eptesicus fuscus ARCoV.1
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2010	USA	HEL	Alphacoronavirus Eptesicus fuscus NeCoV
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	–	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-239577/IT/USA/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	S	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-265225/IT/USA/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	S	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-287740/IT/USA/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	–	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-293985/IT/USA/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	ORF1a	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-5088/IT/USA/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	–	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-66604/IT/USA/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	ORF1ab	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-C1148/IT/USA/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	ORF1ab	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-C146/IT/USA/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	HEL	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-C149/IT/USA/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	–	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-C264/IT/USA/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	USA	M	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-C265/IT/USA/20

Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	United States of America	RdRp	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-C328/IT/USA/2009 ARCoV/P1C328/IT/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	United States of America	RdRp	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-C348/IT/USA/2009 ARCoV/P1C348/IT/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	United States of America	RdRp	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-C362/IT/USA/2009 ARCoV/P1C362/IT/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	United States of America	ORF1ab	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-C368/IT/USA/2009 ARCoV/P1C368/IT/2009
Coronaviridae	*Eptesicus fuscus*	Insectivore	*Vespertilionidae*	Feces	2009	United States of America	ORF1ab	Alphacoronavirus Eptesicus fuscus/Appalachian Ridge/P1-C412/IT/USA/2009 ARCoV/P1C412/IT/2009

A dash (–) indicates that sequence coding information was not reported in the source. Sequences from the USA were submitted under the "Appalachian Ridge" surveillance program. Abbreviations: RdRp = RNA-dependent RNA polymerase; HEL = helicase; S = spike; M = membrane; ORF1a/ORF1ab = replicase polyprotein.

Annex 1H: examples of zoonotic bat-borne viruses reported in Oceania (2010-2024)

Viral family	From bat	Bat diet Type	Bat Family	Sample Type	Collection Year	Sampling Country	Sequence Coding	Viruses
Paramyxoviridae	*Pteropus sp.*	Frugivore	*Pteropodidae*	Urine	2011	Australia	Full length	Alston virus Alstonville
Paramyxoviridae	*Pteropus poliocephalus*	Frugivore	*Pteropodidae*	Tissue	2013	Australia	Full length	Auskunsag virus GHFF09/Li/1
Rhabdoviridae	*Pteropus alecto*	Frugivore	*Pteropodidae*	Tissue	1998	Australia	G	Australian bat lyssavirus 0331-14
Rhabdoviridae	*Pteropus alecto*	Frugivore	*Pteropodidae*	Tissue	1997	Australia	G	Australian bat lyssavirus 092-5
Rhabdoviridae	*Pteropus scapulatus*	Frugivore	*Pteropodidae*	Tissue	1997	Australia	G	Australian bat lyssavirus 174-19
Rhabdoviridae	*Acclaim's flaviventris*	Insectivore	*Emballonuridae*	Tissue	2009	Australia	N	Australian bat lyssavirus 2009/233
Rhabdoviridae	*Pteropus poliocephalus*	Frugivore	*Pteropodidae*	Tissue	1997	Australia	G	Australian bat lyssavirus 292-7
Rhabdoviridae	*Pteropus alecto*	Frugivore	*Pteropodidae*	Tissue	2000	Australia	G	Australian bat lyssavirus 366-36
Rhabdoviridae	*Saccolaimus flaviventris*	Insectivore	*Emballonuridae*	Tissue	1997	Australia	G	Australian bat lyssavirus 375-11
Rhabdoviridae	*Pteropus alecto*	Frugivore	*Pteropodidae*	Tissue	1998	Australia	G	Australian bat lyssavirus 455-1
Rhabdoviridae	*Pteropus poliocephalus*	Frugivore	*Pteropodidae*	Tissue	1998	Australia	G	Australian bat lyssavirus 5331-13
Rhabdoviridae	*Saccolaimus flaviventris*	Insectivore	*Emballonuridae*	Tissue	1998	Australia	G	Australian bat lyssavirus 576-15
Rhabdoviridae	*Pteropus alecto*	Frugivore	*Pteropodidae*	Tissue	2000	Australia	G	Australian bat lyssavirus 632-37
Rhabdoviridae	*Pteropus alecto*	Frugivore	*Pteropodidae*	Tissue	1998	Australia	G	Australian bat lyssavirus 634-26
Rhabdoviridae	*Pteropus alecto*	Frugivore	*Pteropodidae*	Tissue	1997	Australia	G	Australian bat lyssavirus 661-22

Australian bat lyssavirus entries include strain identifiers from national surveillance records. "Full length" indicates complete or near-complete genome sequence. Tissue samples include brain, salivary gland, and kidney homogenates. Abbreviations: G = glycoprotein gene; N = nucleoprotein gene

Annex 1I: abundance of bat-associated virus records per bat family (2010–2024)	
Bat family	**Virus number**
Megachiroptera	3554
Microchiroptera	12661
Emballonuridae	175
Megadermatidae	16
Molossidae	1169
Mormoopidae	106
Mystacinidae	12
Natalidae	2
Nycteridae	51
Phyllostomidae	768
Rhinolophidae	3884
Rhinopomatidae	27
Vespertilionidae	6028
unclassified *Chiroptera*	1011
Records were extracted from the ZOVER database (formerly DBatVir) in November 2024. "Virus number" reflects total unique sequence records, not unique virus species. "Unclassified Chiroptera" includes records for which bat family was not specified in the source. Megachiroptera and Microchiroptera are suborders; individual families are listed below them	

Annex 1J: bat-borne zoonotic viruses with documented or suspected spillover potential identified from literature analysis (2010-2024)

Virus	**Genus, species**	**Host reservoir**	**Intermediate hosts**
Kolente virus	*Ledantevirus kolentevirus*	*Hipposideros spp.*	Unknown
Nepuyo virus	*Orthobunyavirus neurons*	Bats	Mosquitoes
Catu virus	*Orthobunyavirus catuense*	Bats	Mosquitoes
Hantavirus	*Orthohantavirus sp.*	Rodents	None (direct)
Toscana virus	*Phlebovirus toscanense*	Sandflies	Bats
Rift Valley fever virus	*Phlebovirus riftvalleyense*	Mosquitoes/Livestock	None (direct)
Kaeng Khoi virus	*Orthobunyavirus kaengkhoiense*	Bats	Bats, bedbugs
Japanaut virus	*Orthobunyavirus japanautense*	Bats	Unknown
Ife virus	*Orthobunyavirus ifense*	Bats	Unknown
Fomede virus	*Orthobunyavirus fomedense*	Bats	Unknown
Bangui virus	*Orthobunyavirus bangense*	Bats	Unknown
SARS virus	*Betacoronavirus Sarbecovirus*	*Rhinolophus spp.*	Palm civets
SARS-like coronavirus	*Betacoronavirus Sarbecovirus*	*Rhinolophus spp.*	Unknown
MERS virus	*Betacoronavirus Merbecovirus*	Bats	Camels
MERS-like coronavirus	*Betacoronavirus Merbecovirus*	Bats	Unknown
Other coronavirus in bats	*Alpha and Betacoronavirus*	Bats	Various
Reston Ebola virus	*Ebolavirus restonense*	Bats	Non-human primates
Zaire Ebola virus	*Ebolavirus zairense*	Bats	Non-human primates
Bombali virus	*Ebolavirus bombaliense*	Molossidae bats	Unknown
Marburg virus	*Marburgvirus marburgense*	*Rousettus aegyptiacus*	Non-human primates
Lloviu virus	*Cuevavirus lloviuense*	*Miniopterus schreibersii*	Unknown
Ileus virus	*Flavivirus ileuse*	Birds	Mosquitoes
Zika Virus	*Flavivirus zikense*	Primates	Mosquitoes
Western equine encephalitis virus (WEEV)	*Alphavirus weevense*	Birds	Mosquitoes

: Intermediate hosts are listed based on epidemiological studies from the cited literature. Virus names follow ICTV nomenclature (International Committee on Taxonomy of Viruses). This table is derived from the curated subset of 244 bat–virus association records validated against the full corpus of 17,134 sequences.

Annex 1K: regional surveillance efforts by sample type for bat-associated viruses (2010-2024)

Sample category	Total detections	Virus families detected	Bat species sampled	High-risk detections
Blood	4	4	4	1
Feces	45	14	32	5
Other	4	2	4	3
Swabs	54	16	39	5
Tissue	61	18	38	27
Urine	7	1	4	1

Total detections are unique virus–bat association records; high-risk detections are viruses classified as Tier 4 or Tier 3. Tier 4 = confirmed zoonotic; Tier 3 = high-potential zoonotic risk.

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Annex 1L: Zoonotic risk classification of bat-associated viruses stratified by bat diet type (2010-2024)

Bat diet type	Total detections	Tier4 count	Tier3 count	Tier2 count	Tier4 %	Tier3 %	Tier2 %
Frugivore	34	7	18	**9**	20.6	52.9	23.5
Insectivore	108	27	51	30	25.0	47.2	27.8
Insectivore and piscivore	4	0	0	4	0	0	100
Nectarivore	3	0	1	2	0	33.3	66.7
Omnivore	5	0	4	1	0	80.0	20.0
Piscivorous	1	0	1	0	0	100	0
Sanguivore	8	4	2	2	50.0	25.0	25.0
Unknown	11	3	6	2	27.3	54.5	18.2
Various	1	1	0	0	100	0	0

: "Various" indicates mixed or unclassifiable diet in the source literature. Diet classifications follow bat ecological guilds. Tier 4 = confirmed zoonotic; Tier 3 = high potential; Tier 2 = moderate potential; Tier 1 = low potential