

Table S1. Viruses and GenBank accession numbers of nucleotide (nt) and amino acid (aa) sequences of YEZV and nucleic acid sequences of SULV isolates used in phylogenetic and other comparative analyses.

Virus (strain or isolate)	Segment	GenBank accession number nt/aa
Yezo virus (24 2 K43 6)	L	PV683040.1 / XUJ59931.1
Yezo virus (24 2 K43 4)	M	PV683027.1 / XUJ59927.1
Yezo virus (24 2 K43 5)	S	PV683026.1 / XUJ59925.1
Yezo virus (24 2 K71 2)	L	PV683021.1 / XUJ59930.1
Yezo virus (24 2 K71 3)	M	PV683037.1 / XUJ59928.1
Yezo virus (24 2 K71 4)	S	PV683020.1 / XUJ59924.1
Yezo virus (24 L 3 R 2)	L	PV683017.1 / XUJ59929.1
Yezo virus (24 L 3 R 3)	M	PV683016.1 / XUJ59926.1
Yezo virus (24 L3 R 4)	S	PV683015.1 / XUJ59923.1
Yezo virus (Khabarovsk 2024-1)	L	PV061572.1 / XPK55866.1
Yezo virus (Khabarovsk 2024-1)	M	PV061577.1 / XPK55871.1
Yezo virus (Khabarovsk 2024-1)	S	PV061582.1 / XPK55876.1
Yezo virus (Chita 2024-1)	L	PV061571.1 / XPK55865.1
Yezo virus (Chita 2024-1)	M	PV061576.1 / XPK55870.1
Yezo virus (Chita 2024-1)	S	PV061581.1 / XPK55875.1
Yezo virus (Primorye 2024-3)	L	PV061570.1 / XPK55864.1
Yezo virus (Primorye 2024-3)	M	PV061575.1 / XPK55869.1
Yezo virus (Primorye 2024-3)	S	PV061580.1 / XPK55874.1
Yezo virus (Primorye 2024-2)	L	PV061569.1 / XPK55863.1
Yezo virus (Primorye 2024-2)	M	PV061574.1 / XPK55868.1
Yezo virus (Primorye 2024-2)	S	PV061579.1 / XPK55873.1
Yezo virus (Primorye 2024-1)	L	PV061568.1 / XPK55862.1
Yezo virus (Primorye 2024-1)	M	PV061573.1 / XPK55867.1
Yezo virus (Primorye 2024-1)	S	PV061578.1 / XPK55872.1
Yezo virus (NE-WQ)	L	PQ475625.1 / XJP49228.1
Yezo virus (NE-WQ)	M	PQ485629.1 / XJP49232.1
Yezo virus (NE-WQ)	S	PQ475633.1 / XJP49236.1
Yezo virus (NE-DN2)	L	PQ475624.1 / XJP49227.1
Yezo virus (NE-DN2)	M	PQ475628.1 / XJP49231.1
Yezo virus (NE-DN2)	S	PQ475632.1 / XJP49235.1
Yezo virus (NE-ALH2)	L	PQ475623.1 / XJP49226.1
Yezo virus (NE-ALH2)	M	PQ475627.1 / XJP49230.1
Yezo virus (NE-ALH2)	S	PQ475631.1 / XJP49234.1
Yezo virus (NE-YTLH1)	L	PQ475622.1 / XJP49225.1
Yezo virus (NE-YTLH1)	M	PQ475626.1 / XJP49229.1
Yezo virus (NE-YTLH1)	S	PQ475630.1 / XJP49233.1
Yezo virus (TIGMIC 5)	L	PQ231079.1 / XJO53607.1
Yezo virus (TIGMIC 5)	M	PQ231077.1 / XJO53605.1
Yezo virus (TIGMIC 5)	S	PQ231072.1 / XJO53600.1
Yezo virus (TIGMIC 4)	L	PQ231078.1 / XJO53606.1
Yezo virus (TIGMIC 4)	M	PQ231076.1 / XJO53604.1
Yezo virus (TIGMIC 4)	S	PQ231071.1 / XJO53599.1
Yezo virus (MDJ2209)	L	PQ220372.1 / XJQ61057.1
Yezo virus (MDJ2209)	M	PQ220367.1 / XJQ61052.1
Yezo virus (MDJ2209)	S	PQ220362.1 / XJQ61047.1
Yezo virus (MDJ486)	L	PQ220371.1 / XJQ61056.1
Yezo virus (MDJ486)	M	PQ220366.1 / XJQ61051.1
Yezo virus (MDJ486)	S	PQ220361.1 / XJQ61047.1

Yezo virus (MDJ025)	L	PQ220370.1 / XJQ61055.1
Yezo virus (MDJ025)	M	PQ220365.1 / XJQ61050.1
Yezo virus (MDJ025)	S	PQ220360.1 / XJQ61045.1
Yezo virus (MDJ014)	L	PQ220369.1 / XJQ61054.1
Yezo virus (MDJ014)	M	PQ220364.1 / XJQ61049.1
Yezo virus (MDJ014)	S	PQ220359.1 / XJQ61044.1
Yezo virus (MDJ003)	L	PQ220368.1 / XJQ61053.1
Yezo virus (MDJ003)	M	PQ220363.1 / XJQ61048.1
Yezo virus (MDJ003)	S	PQ220358.1 / XJQ61043.1
Yezo virus (YEZV YBQG1739)	L	OR148889.1 / WWT48703.1
Yezo virus (YEZV YBQG1739)	M	OR148887.1 / WWT48697.1
Yezo virus (YEZV YBQG1739)	S	OR148888.1 / WWT48700.1
Yezo virus (YEZV YBQG1712)	L	OR148886.1 / WWT48702.1
Yezo virus (YEZV YBQG1712)	M	OR148884.1 / WWT48696.1
Yezo virus (YEZV YBQG1712)	S	OR148885.1 / WWT48699.1
Yezo virus (YEZV THQG1707B)	L	OR148883.1 / WWT48701.1
Yezo virus (YEZV THQG1707B)	M	OR148881.1 / WWT48695.1
Yezo virus (YEZV THQG1707B)	S	OR148882.1 / WWT48698.1
Yezo virus (H-IM01)	L	ON563283.1 / UYR58267.1
Yezo virus (H-IM01)	M	ON563284.1 / UYR58268.1
Yezo virus (H-IM01)	S	ON563285.1 / UYR58269.1
Yezo virus (T-JL01)	L	ON563280.1 / UYR58264.1
Yezo virus (T-JL01)	M	ON563281.1 / UYR58265.1
Yezo virus (T-JL01)	S	ON563282.1 / UYR58266.1
Yezo virus (T-IM01)	L	ON563277.1 / UYR58261.1
Yezo virus (T-IM01)	M	ON563278.1 / UYR58262.1
Yezo virus (T-IM01)	S	ON563279.1 / UYR58263.1
Yezo virus (T-HLJ03)	L	ON563274.1 / UYR58258.1
Yezo virus (T-HLJ03)	M	ON563275.1 / UYR58259.1
Yezo virus (T-HLJ03)	S	ON563276.1 / UYR58260.1
Yezo virus (T-HLJ02)	L	ON563271.1 / UYR58255.1
Yezo virus (T-HLJ02)	M	ON563272.1 / UYR58256.1
Yezo virus (T-HLJ02)	S	ON563273.1 / UYR58257.1
Yezo virus (T-HLJ01)	L	ON563268.1 / UYR58252.1
Yezo virus (T-HLJ01)	M	ON563269.1 / UYR58253.1
Yezo virus (T-HLJ01)	S	ON563270.1 / UYR58254.1
Yezo virus (HH003-2020)	L	NC 079099.1 / YP 010840880.1
Yezo virus (HH003-2020)	M	NC 079098.1 / YP 010840879.1
Yezo virus (HH003-2020)	S	NC 079100.1 / YP 010840881.1
Yezo virus (BT-2155)	L	LC790680.1 / BEV30402.1
Yezo virus (BT-2155)	M	LC790681.1 / BEV30403.1
Yezo virus (BT-2155)	S	LC790682.1 / BEV30404.1
Yezo virus (BT-2135)	L	LC790677.1 / BEV30399.1
Yezo virus (BT-2135)	M	LC790678.1 / BEV30400.1
Yezo virus (BT-2135)	S	LC790679.1 / BEV30401.1
Yezo virus (BT-1968)	L	LC790674.1 / BEV30396.1
Yezo virus (BT-1968)	M	LC790675.1 / BEV30397.1
Yezo virus (BT-1968)	S	LC790676.1 / BEV30398.1
Yezo virus (BT-1864)	L	LC735734.1 / BDT53108.1
Yezo virus (BT-1864)	M	LC735735.1 / BDT53109.1
Yezo virus (BT-1864)	S	LC735736.1 / BDT63110.1
Yezo virus (BT-1844)	L	LC735731.1 / BDT53105.1

Yezo virus (BT-1844)	M	LC735732.1 / BDT53106.1
Yezo virus (BT-1844)	S	LC735733.1 / BDT53107.1
Yezo virus (BT-1826)	L	LC735728.1 / BDT53102.1
Yezo virus (BT-1826)	M	LC735729.1 / BDT53103.1
Yezo virus (BT-1826)	S	LC735730.1 / BDT53104.1
Yezo virus (BT-1821)	L	LC735725.1 / BDT53099.1
Yezo virus (BT-1821)	M	LC735726.1 / BDT53100.1
Yezo virus (BT-1821)	S	LC735727.1 / BDT53101.1
Sulina virus (b31)	L	PP260006.1
Sulina virus (b31)	M	PP260007.1
Sulina virus (b31)	S	PP260008.1
Sulina virus (Alsace)	L	OR613124.1
Sulina virus (Alsace)	M	OR613123.1
Sulina virus (Alsace)	S	OR613122.1
Sulina virus (IxriSL 16-01)	L	NC 078999.1
Sulina virus (IxriSL 16-01)	M	NC 078997.1
Sulina virus (IxriSL 16-01)	S	NC 078998.1

Table S2. Viruses and GenBank accession numbers of amino acid sequences of RdRp of species of the *Orthonairovirus* used in phylogenetic analyses.

Virus (strain or isolate)	Position of the virus within the genus <i>Otrhonairovirus</i>	GenBank accession number
Abu Hammad virus	member species	AMT75371.1
Abu Mina virus	member species	AMT75374.1
Aigai virus	member species	ABB30012.1
Antu virus	related, unclassified virus	WGL08458.1
Artashat virus	member species	AKC89358.1
Avalon virus	member species	AMT75377.1
Bandia virus (IPD/A611)	member species	NC 078253.1
Bandia virus (RV611)	member species	AMT75383.1
Burana virus	member species	AKC89349.1
Caspiy virus	member species	AKC89346.1
cencurut virus	related, unclassified virus	WAX23731.1
Chim virus	member species	AKC89343.1
Clo Mor virus	member species	KU343163.1
Clo Mor virus (ScotAr7)	member species	KU343139.1
Crimean-Congo hemorrhagic fever virus	member species	AAR25663.1
Dera Ghazi Khan virus	member species	KU343151.1
Dugbe virus	member species	AAB18834.1
Erve virus	member species	AFH89032.1
Estero Real virus	member species	AXP33563.1
Farralon virus	member species	KU343154.1
Finch creek virus	related, unclassified virus	ULT85602.1
Geran virus	member species	AKC89340.1
Gossas virus	member species	ALD83626.1
Great Saltee virus	member species	AMT75404.1
Gubbo nairovirus	related, unclassified virus	UZO29916.1
Hazara virus	member species	AJW66841.1
Huangpi tick virus 1	member species	AJG39237.1
Hughes virus	member species	AMT75407.1

Issyk-Kul virus	member species	AII79373.1
Kasokero virus	member species	ALD84349.1
Keterah virus	member species	ALD84352.1
Kupe virus	member species	ABY82502.1
Lamusara virus	related, unclassified virus	BDE11047.1
Leopards Hill virus	member species	BAP90965.1
Meihua Mountain virus	related, unclassified virus	UQM93876.1
Meram virus	member species	QNH88011.1
Nairobi sheep disease virus	member species	AIZ00432.1
Orthonairovirus sp. isolate YS	related, unclassified virus	UCR91749.1
Pacific coast tick nairovirus	member species	ARF07704.1
Pangolin orthonairovirus	related, unclassified virus	URZ29345.1
Paramushir virus	related, unclassified virus	AZB49553.1
Punta Salinas virus	member species	AMT75410.1
Qalyub virus	member species	KU343160.1
Raza virus	member species	AMT75416.1
Sakhalin virus	member species	AMT75419.1
Sapphire II virus	member species	QLA46845.1
Sapphire II virus (RML 52323-14)	member species	AMT75422.1
Soldado virus	member species	AMT75425.1
Songling virus	member species	QPO14991.1
Sulina virus	member species	QRR19149.1
Tacheng tick virus 1	member species	AJG39253.1
Taggart virus	member species	AMR73395.1
Tamdy virus (TT1)	member species	QNH88007.1
Tamdy virus (XJ01)	member species	QFU19352.1
Thiafora virus	member species	ALD84355.1
Tillamook virus	member species	AMT75431.1
Tofla virus	member species	BAU21075.1
Tunis virus	member species	AMT75434.1
Uzun-Agach virus	member species	AKC89313.1
Vinegar Hill virus	member species	AUD40046.1
Wenzhou tick virus	member species	AJG39255.1
Wufeng Crocidura attenuata orthonairovirus 1	related, unclassified virus	UOL48895.1
Yogue virus	member species	ALD84358.1
Zirqa virus (A2070-1)	member species	KU343169.1
Zirqa virus (Por 7866)	member species	AMT75437.1

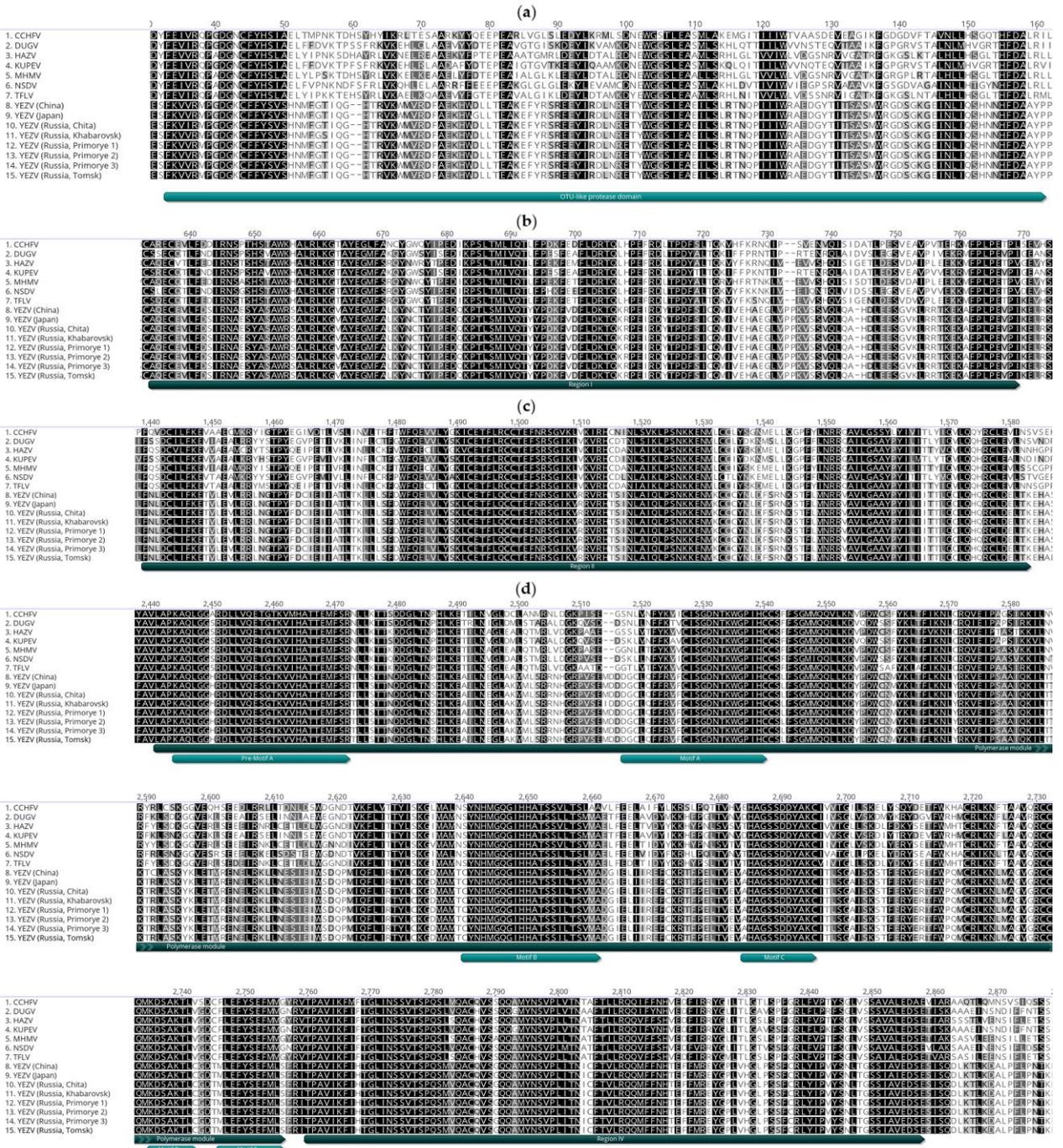


Figure S3. Amino acid sequence alignment of the conserved regions of NSD viruses and YEZV isolates. (a) OUT-like protease domain; (b) Region I; (c) Region II; (d) Polymerase module (pre-Motif A and Motif A-E) and region IV are highlighted and highly conserved in bunyaviruses. The selected orthonairoviruses: CCHFV – Crimean-Congo hemorrhagic fever virus (*O. haemorrhagiae*), DUGV – Dugbe virus (*O. dugbeense*), HAZV – Hazara virus (*O. hazaraense*), KUPEV – Kupe virus (*O. amblyomae*), MHMV – Meihua Mountain virus, NSDV – Nairobi sheep disease virus (*O. nairobiense*), TFLV – Tofla virus (*O. japonicum*).

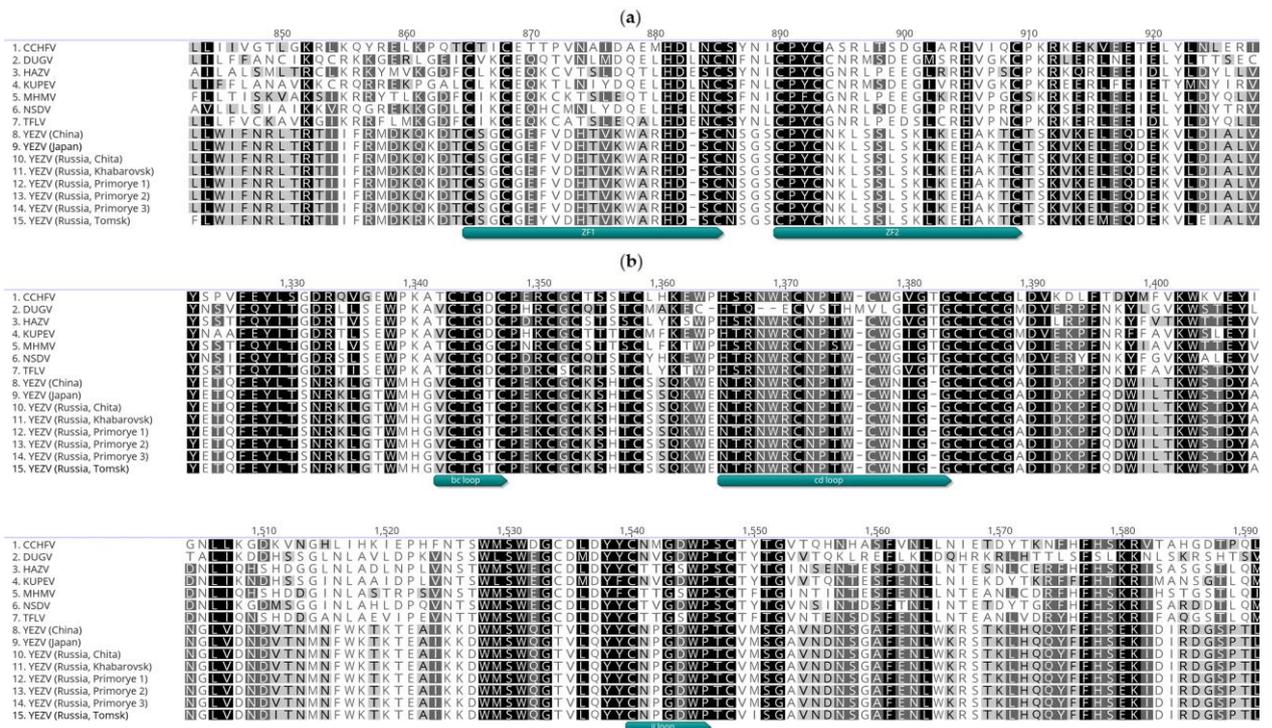


Figure S4. Amino acid sequence alignment of the Gns and Gcs of NSD genogroup viruses and YEZV isolates. **(a)** Glycoprotein Gn, two C-terminus localized zinc-finger motifs are highlighted; **(b)** Glycoprotein Gc, fusion loops are highlighted. The selected orthonairoviruses: CCHFV – Crimean-Congo hemorrhagic fever virus (*O. haemorrhagiae*), DUGV – Dugbe virus (*O. dugbeense*), HAZV – Hazara virus (*O. hazaraense*), KUPEV – Kupe virus (*O. amblyomae*), MHMV – Meihua Mountain virus, NSDV – Nairobi sheep disease virus (*O. nairobiense*), TFLV – Tofla virus (*O. japonicum*).



Figure S5. Amino acid sequence alignment of the nucleoproteins of NSD genogroup viruses and YEZV isolates. The flexible stalk domain is highlighted. The selected orthonairoviruses: CCHFV – Crimean-Congo hemorrhagic fever virus (*O. haemorrhagiae*), DUGV – Dugbe virus (*O. dugbeense*), HAZV – Hazara virus (*O. hazaraense*), KUPEV – Kupe virus (*O. amblyomae*), MHMV – Meihua Mountain virus, NSDV – Nairobi sheep disease virus (*O. nairobiense*), TFLV – Tofla virus (*O. japonicum*).

