

Supplementary Table S1. Accession-level annotations and clade classification of non-self BLAST hits with $\geq 99.5\%$ *cox1* percent identity to AB780998.1

Sequence identity ^a	Accession no.	Percent identity	GeoLocName	Clade	Reference
Lower	OR263180	99.5025	China: Xinjiang, Yili	Asian	SR1
	MN387224	99.5025	USA: Vermont	European	SR2
	OK330093	99.5025	Unknown	European	SR3
	OR060940	99.5025	Poland: Podkarpacke Province	European	SR4
	OK330092	99.5025	Unknown	European	SR3
	OR060939	99.5025	Latvia: Pinupi	European	SR4
	AB461412	99.5025	Austria	European	SR5
	PV055283	99.5025	Poland: Warminsko-Mazurskie Voivodship	European	SR6
	OQ874679	99.5025	Poland	European	SR7
	PV055353	99.5025	Poland: Warminsko-Mazurskie Voivodship	European	SR6
	OQ874675	99.5647	Poland	European	SR7
	MW255910	99.5647	Poland	European	SR8
	MW255909	99.5647	Poland	European	SR8
	OR060936	99.5647	Czech Republic: Brezinka pod Bezdezem	European	SR4
	OR060941	99.5647	Switzerland	European	SR4
	AB461413	99.5647	France	European	SR5
	AB777919	99.5647	Russia	European	SR9
	KY205684	99.5647	Poland	European	SR10
	KY205677	99.5647	Poland	European	SR10
	OR060934	99.5647	Croatia: Krizevci	European	SR4
	OR263183	99.5647	China: Xinjiang, Yili	Asian	SR1
	MK843309	99.5647	Canada	European	SR11
	MW255894	99.5647	Poland	European	SR8
	MK843308	99.5647	Canada	European	SR11
	KY205689	99.5647	Poland	European	SR10
	OQ607803	99.5647	Poland: Pomerania	European	SR6
	MW255901	99.5647	Poland	European	SR8
	KY205682	99.5647	Poland	European	SR10
	OR060928	99.5647	Austria	European	SR4
	KY205690	99.5647	Poland	European	SR10
	MW255900	99.5647	Poland	European	SR8
	MW255908	99.5647	Poland	European	SR8
	KY205683	99.5647	Poland	European	SR10
	MW255911	99.5647	Poland	European	SR8
	MW255899	99.5647	Poland	European	SR8
	LC380931	99.6269	USA: Missouri	European	SR12
	KY205691	99.6269	Poland	European	SR10

	KY205678	99.6269	Poland	European	SR10
	AB461414	99.6269	Slovakia	European	SR5
	MT461410	99.6269	Switzerland	European	SR13
	KY205687	99.6269	Poland	European	SR10
	MW255892	99.6269	Poland	European	SR8
	MT461411	99.6269	Switzerland	European	SR13
	KY205686	99.6269	Poland	European	SR10
	KY205688	99.6269	Poland	European	SR10
	MW255891	99.6269	Poland	European	SR8
	MW255893	99.6269	Poland	European	SR8
	KY205679	99.6269	Poland	European	SR10
	KY205680	99.6269	Poland	European	SR10
	KY205681	99.6269	Poland	European	SR10
Higher	AB688133	99.6891	Russia:Altai	Asian	SR9
	OR263177	99.7512	China: Xinjiang, Yili	Asian	SR1
	MH259772	99.7512	Unknown	Asian	SR14
	MN829538	99.7512	Kyrgyzstan	Asian	SR15
	MN829529	99.7512	Kyrgyzstan	Asian	SR15
	MH259771	99.7512	Unknown	Asian	SR14
	MH259764	99.8133	Unknown	Asian	SR14
	MN829537	99.8134	Kyrgyzstan	Asian	SR15
	MN829539	99.8134	Kyrgyzstan	Asian	SR15
	AB688127	99.8134	Russia:Altai	Asian	SR9
	MH259765	99.8134	Unknown	Asian	SR14
	AB777915	99.8134	Russia	Asian	SR9
	OR263182	99.8134	China: Xinjiang, Yili	Asian	SR1
	AB688128	99.8134	Russia:Altai	Asian	SR9
	MN829536	99.8134	Kyrgyzstan	Asian	SR15
	AB461415	99.8134	Kazakhstan	Asian	SR5
	MN251847	99.8134	China: Sichuan	Asian	SR16
	AB688126	99.8134	Russia:Altai	Asian	SR9
	AB688132	99.8134	Russia:Altai	Asian	SR9
	AB688134	99.8134	Russia:Altai	Asian	SR9
	AB688131	99.8134	Russia:Altai	Asian	SR9
	MN829531	99.8134	Kyrgyzstan	Asian	SR15
	AB688130	99.8134	Russia:Altai	Asian	SR9
	MH259770	99.8134	Unknown	Asian	SR14
	OR263181	99.8134	China: Xinjiang, Yili	Asian	SR1
	MN829532	99.8134	Kyrgyzstan	Asian	SR15
	AB688129	99.8134	Russia:Altai	Asian	SR9

OR263178	99.8756	China: Xinjiang, Yili	Asian	SR1
MN251849	99.8756	China: Sichuan	Asian	SR16
AB477011	99.8756	China: Sichuan	Asian	SR5
MH259766	99.8756	Unknown	Asian	SR14
OR263184	99.8756	China: Xinjiang, Yili	Asian	SR1
MH259767	99.8756	Unknown	Asian	SR14
AB477010	99.8756	China: Sichuan	Asian	SR5
PV055397	99.8756	Poland: Warminsko-Mazurskie Voivodship	Asian	SR6
MH259773	99.8756	Unknown	Asian	SR14
MH259769	99.8756	Unknown	Asian	SR14
MH259774	99.8756	Unknown	Asian	SR14
MN251846	99.8756	China: Sichuan	Asian	SR16
AB385610	99.8756	Japan: Fukui	Asian	SR9
MT461409	99.8756	Canada	Asian	SR13
AB477012	99.8756	China: Sichuan	Asian	SR5
KY205685	99.9378	Poland	Asian	SR10
MW255914	99.9378	Poland	Asian	SR8
MW255912	99.9378	Poland	Asian	SR8
AB461417	99.9378	China: Sichuan	Asian	SR5
MW255907	99.9378	Poland	Asian	SR8
MW255895	99.9378	Poland	Asian	SR8
MW255898	99.9378	Poland	Asian	SR8
MW255896	99.9378	Poland	Asian	SR8
MW255903	99.9378	Poland	Asian	SR8
MH259768	99.9378	Unknown	Asian	SR14
MW255904	99.9378	Poland	Asian	SR8
MW255906	99.9378	Poland	Asian	SR8
MW255913	99.9378	Poland	Asian	SR8
MW255897	99.9378	Poland	Asian	SR8
MW255915	99.9378	Poland	Asian	SR8
MW255902	99.9378	Poland	Asian	SR8
MW255916	99.9378	Poland	Asian	SR8
MW255905	99.9378	Poland	Asian	SR8

^a*coxI* percent identity values are relative to AB780998.1. The lower and higher sequence identity bands correspond to 99.5025%–99.6269% and 99.6891%–99.9378%, respectively. Source reference numbers correspond to the Supplementary References listed below.

Supplementary References

- SR1. Guo B, Cairen, Wu J, et al. The A2 haplotype of *Echinococcus multilocularis* is the predominant variant infecting humans and dogs in Yili Prefecture, Xinjiang. *Infect Genet Evol* 2024;119:105581. <https://doi.org/10.1016/j.meegid.2024.105581>
- SR2. Polish LB, Pritt B, Barth TFE, et al. First European haplotype of *Echinococcus multilocularis* identified in the United States: an emerging disease? *Clin Infect Dis* 2021;72:1117-23. <https://doi.org/10.1093/cid/ciaa245>
- SR3. Polish LB, O'Connell EM, Barth TFE, et al. European haplotype of *Echinococcus multilocularis* in the United States. *N Engl J Med* 2022;387:1902-4. <https://doi.org/10.1056/NEJMc2210000>
- SR4. Santoro A, Santolamazza F, Cacciò SM, et al. Mitochondrial genetic diversity and phylogenetic relationships of *Echinococcus multilocularis* in Europe. *Int J Parasitol* 2024;54:233-45. <https://doi.org/10.1016/j.ijpara.2024.01.003>
- SR5. Nakao M, Xiao N, Okamoto M, et al. Geographic pattern of genetic variation in the fox tapeworm *Echinococcus multilocularis*. *Parasitol Int* 2009;58:384-9. <https://doi.org/10.1016/j.parint.2009.07.010>
- SR6. Gładysz P, Bielińska-Wąż D, Wąż P, et al. Euro-Asian hybrids of *Echinococcus multilocularis* from red foxes in northern and northeastern Poland result from secondary contact between long-isolated populations. *Sci Rep* 2026. <https://doi.org/10.1038/s41598-026-40313-z>. Epub ahead of print.
- SR7. Karamon J, Samorek-Pieróg M, Bilska-Zajac E, et al. *Echinococcus multilocularis* genetic diversity based on isolates from pigs confirmed the characteristic haplotype distribution and the presence of the Asian-like haplotype in Central Europe. *J Vet Res* 2023;67:567-74. <https://doi.org/10.2478/jvetres-2023-0056>
- SR8. Umhang G, Knapp J, Wassermann M, et al. Asian admixture in European *Echinococcus multilocularis* populations: new data from Poland comparing EmsB microsatellite analyses and mitochondrial sequencing. *Front Vet Sci* 2021;7:620722. <https://doi.org/10.3389/fvets.2020.620722>
- SR9. Konyaev SV, Yanagida T, Nakao M, et al. Genetic diversity of *Echinococcus* spp. in Russia. *Parasitology* 2013;140:1637-47. <https://doi.org/10.1017/S0031182013001340>
- SR10. Karamon J, Stojcki K, Samorek-Pieróg M, et al. Genetic diversity of *Echinococcus multilocularis* in red foxes in Poland: the first report of a haplotype of probable Asian origin. *Folia Parasitol* 2017;64:2017.007. <https://doi.org/10.14411/fp.2017.007>
- SR11. Massolo A, Klein C, Kowalewska-Grochowska K, et al. European *Echinococcus multilocularis* identified in patients in Canada. *N Engl J Med* 2019;381:384-5. <https://doi.org/10.1056/NEJMc1814975>
- SR12. Kuroki K, Morishima Y, Neil J, et al. Intestinal echinococcosis in a dog from Missouri. *J Am Vet Med Assoc* 2020;256:1041-6. <https://doi.org/10.2460/javma.256.9.1041>

- SR13. Laurimäe T, Kronenberg PA, Alvarez Rojas CA, et al. Long-term (35 years) cryopreservation of *Echinococcus multilocularis* metacestodes. *Parasitology* 2020;147:1048-54. <https://doi.org/10.1017/S003118202000075X>
- SR14. Li JQ, Li L, Fan YL, et al. Genetic diversity in *Echinococcus multilocularis* from the plateau vole and plateau pika in Jiuzhi County, Qinghai Province, China. *Front Microbiol* 2018;9:2632. <https://doi.org/10.3389/fmicb.2018.02632>
- SR15. Alvarez Rojas CA, Kronenberg PA, Aitbaev S, et al. Genetic diversity of *Echinococcus multilocularis* and *Echinococcus granulosus* sensu lato in Kyrgyzstan: the A2 haplotype of *E. multilocularis* is the predominant variant infecting humans. *PLoS Negl Trop Dis* 2020;14:e0008242. <https://doi.org/10.1371/journal.pntd.0008242>
- SR16. Shang JY, Zhang GJ, Yu WJ, et al. Genetic polymorphism of *Echinococcus multilocularis* in northwestern China inferred from *cox1* gene sequences. *J Pathog Biol* 2021;16:137-42. <https://doi.org/10.13350/j.cjpb.210203>