

Comparative genetic research on *Microtus mystacinus* (de Filippi, 1865) distributed in Asia and Europe inferred from mitochondrial (*CYTB* and *COXI*) and nuclear (*IRBP*) gene regions

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Supplementary material

Table S1.

M. mystacinus and outgroup sequences stored in GenBank used in this study.

Accession numbers	Localities	Gene region	References
MZ273990–MZ274002, MZ274004–MZ274006, MZ274008–MZ274013, MZ274024–MZ274036	Anatolia	<i>CYTB</i>	This study
MZ273989, MZ274003, MZ274007, MZ274014– MZ274023	Turkish Thrace	<i>CYTB</i>	This study
KX581053.1–KX581063.1	Iran	<i>CYTB</i>	Mahmoudi et al. (2017a)
AY513819.1	Finland	<i>CYTB</i>	Jaarola et al. (2004)
AY513820.1	Norway	<i>CYTB</i>	Jaarola et al. (2004)
DQ015676.1	Ukraine	<i>CYTB</i>	Triant and DeWoody (2006)
FJ641142.1–FJ641161.1	Greece	<i>CYTB</i>	Thanou et al. (2012)
U54472.1–U54472.1 U54493.1, U54495.1	Ukraine	<i>CYTB</i>	Barker et al. (1996)
KX380181.1–KX380185.1	Ukraine	<i>CYTB</i>	Stojak et al. (2016)
KX380186.1–KX380191.1	Armenia	<i>CYTB</i>	Stojak et al. (2016)
KX380179.1–KX380180.1	Romania	<i>CYTB</i>	Stojak et al. (2016)
KU957994.1–KU958001.1	Russia — Krasnodar region	<i>CYTB</i>	Balakirev et al. (2018)

MZ198210.1	Russia — Novosibirsk region	<i>CYTB</i>	Bogdanov et al. (2021)
LT970848.1–LT970849.1	Kazakhstan	<i>CYTB</i>	Holicová et al. (2018)
MW456004.1 (<i>M. arvalis</i>)	Turkey	<i>CYTB</i>	Çetintürk et al. (2021)
MW456015.1 (<i>M. arvalis</i>)	Hungary	<i>CYTB</i>	Çetintürk et al. (2021)
MZ234180–MZ234197, MZ234199–MZ234201, MZ234203–MZ234210, MZ234220–MZ234230	Anatolia	<i>COXI</i>	This study
MZ234179, MZ234198, MZ234202, MZ234211 - MZ234219	Turkish Thrace	<i>COXI</i>	This study
MW454918.1 (<i>M. arvalis</i>)	Turkey	<i>COXI</i>	Çetintürk et al. (2021)
MW454931.1 (<i>M. arvalis</i>)	Hungary	<i>COXI</i>	Çetintürk et al. (2021)
MZ419394–MZ419405, MZ419407–MZ419417, MZ419427–MZ419437, MZ419439–MZ419441	Anatolia	<i>IRBP</i>	This study
MZ419393, MZ419406, MZ419418–MZ419426, MZ419438	Turkish Thrace	<i>IRBP</i>	This study
MZ222064.1	Russia — Novosibirsk region	<i>IRBP</i>	Bogdanov et al. (2021)

KX455532.1	Russia — Kemerovo region	<i>IRBP</i>	Direct submission by Zoological Institute RAS
KX455523.1 (<i>M. longicaudus</i>)	Canada	<i>IRBP</i>	Direct submission by Abramson and Petrova
KJ556734.1 (<i>M. pennsylvanicus</i>)	Canada	<i>IRBP</i>	Kohli et al. (2014)

Table S2.

M. mystacinus sequences stored in Bold Systems used in this study.

Accession numbers	Localities	Gene region
BKMAM046-11	Bulgaria	<i>COXI</i>
BKMAM053-11	Bulgaria	<i>COXI</i>
SKMZM335.07	Russi_— Ryazanskaya	<i>COXI</i>
SKMZM621.08	Russia — Tyva Republic	<i>COXI</i>
NOMAM054.09	Norway	<i>COXI</i>
NOMAM055.09	Norway	<i>COXI</i>

Table S3.Genetic diversity values derived from *CYTB*, *COXI* and *IRBP* gene sequences.

<i>IRBP</i> (478 bp)	Populations	Number of samples	Number of haplotypes	Haplotype diversity (Hd)	Nucleotide diversity (Pi)
<i>CYTB</i> (500 bp)	Europe	19	7	0.608	0.003
	Thrace	33	14	0.939	0.007
	Anatolia	35	21	0.948	0.010
	Asia (Russia, Kazakhstan and Armenia)	17	5	0.728	0.010
	Iran	11	4	0.709	0.011
	<i>M. kermanensis</i>	2	2	1.000	0.002
	Total	117	52	0.962	0.017
<i>COXI</i> (578 bp)	Europe	5	1	0	0
	Thrace	14	3	0.385	0.0007
	Anatolia	40	17	0.896	0.006
	Total	59	21	0.914	0.009
<i>IRBP</i> (478 bp)	Anatolia	37	13	0.872	0.003
	Thrace	12	3	0.439	0.001
	Asia (Russia)	2	1	0.000	0.000
	Total	51	13	0.838	0.003

Table S4.

Mean genetic distance values (d) with standard errors and fixation index (F_{ST}) values between *M. mystacinus* populations based on p -distance (Hamming, 1950).

Gene	Populations	Genetic distance values	F_{ST}
<i>CYTB</i>	Anatolia–Thrace	0.016 ± 0.004	0.438
	Anatolia–Europe	0.020 ± 0.005	0.665
	Thrace–Europe	0.011 ± 0.003	0.561
	Anatolia–Asia	0.014 ± 0.004	0.277
	Europe–Asia	0.011 ± 0.003	0.413
	Thrace–Asia	0.011 ± 0.003	0.195
	Iran–Anatolia	0.032 ± 0.006	0.658
	Iran–Asia	0.035 ± 0.007	0.697
	Iran–Thrace	0.036 ± 0.007	0.741
	Iran– <i>M. kermanensis</i>	0.023 ± 0.006	0.709
	<i>M. kermanensis</i> –Anatolia	0.039 ± 0.008	0.837
	<i>M. kermanensis</i> –Thrace	0.043 ± 0.008	0.890
	<i>M. kermanensis</i> –Asia	0.042 ± 0.008	0.858
<i>COXI</i>	Anatolia–Thrace	0.014 ± 0.004	0.755
	Anatolia–Europe	0.012 ± 0.004	0.832
	Thrace–Europe	0.002 ± 0.002	0.747
<i>IRBP</i>	Anatolia–Thrace	0.003 ± 0.001	0.148
	Anatolia–Asia	0.002 ± 0.001	0.231
	Asia–Thrace	0.001 ± 0.001	0.654

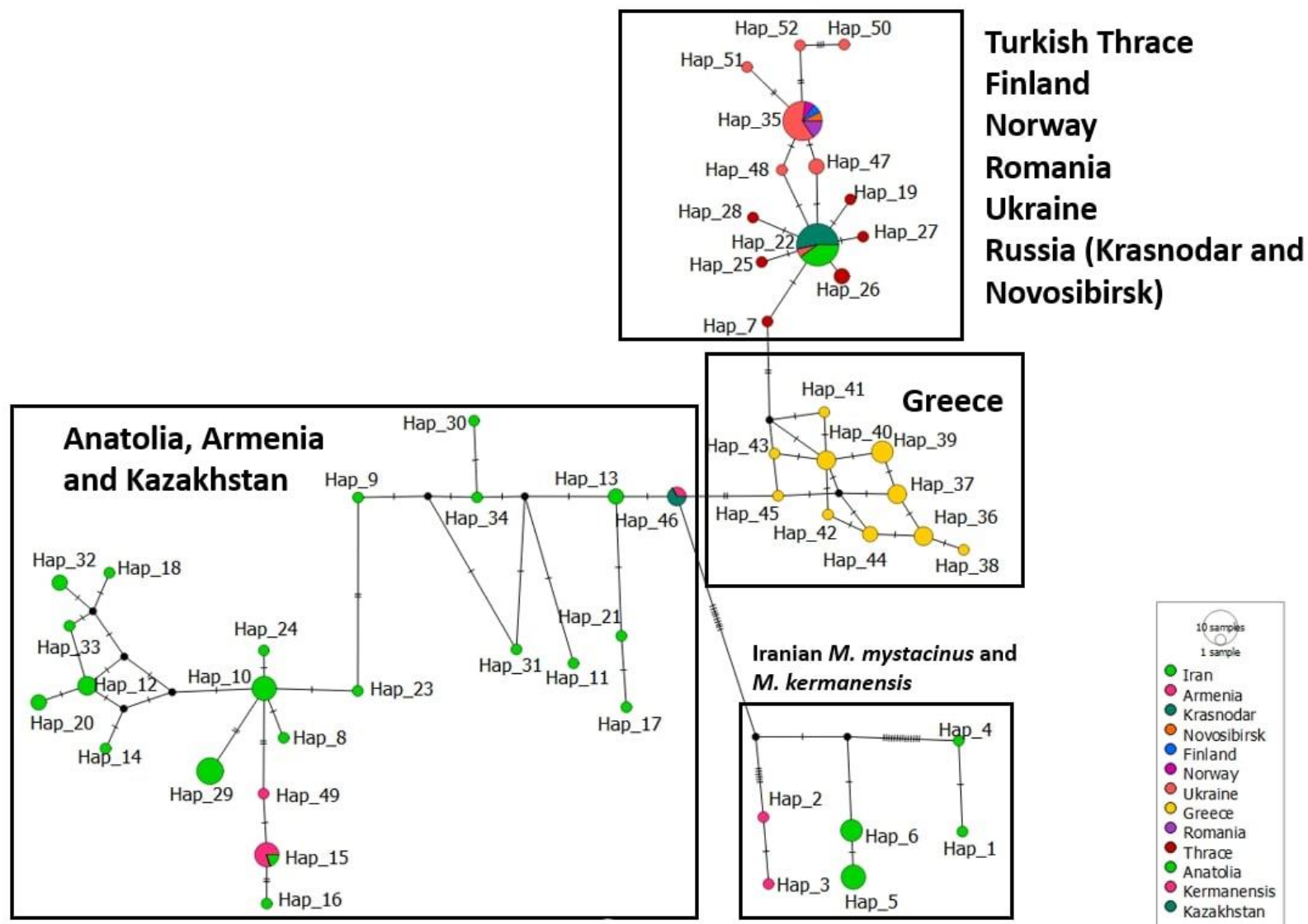


Figure S1. Median-joining network constructed using *CYTB* haplotypes. Mutations are shown with black dashes on branches.

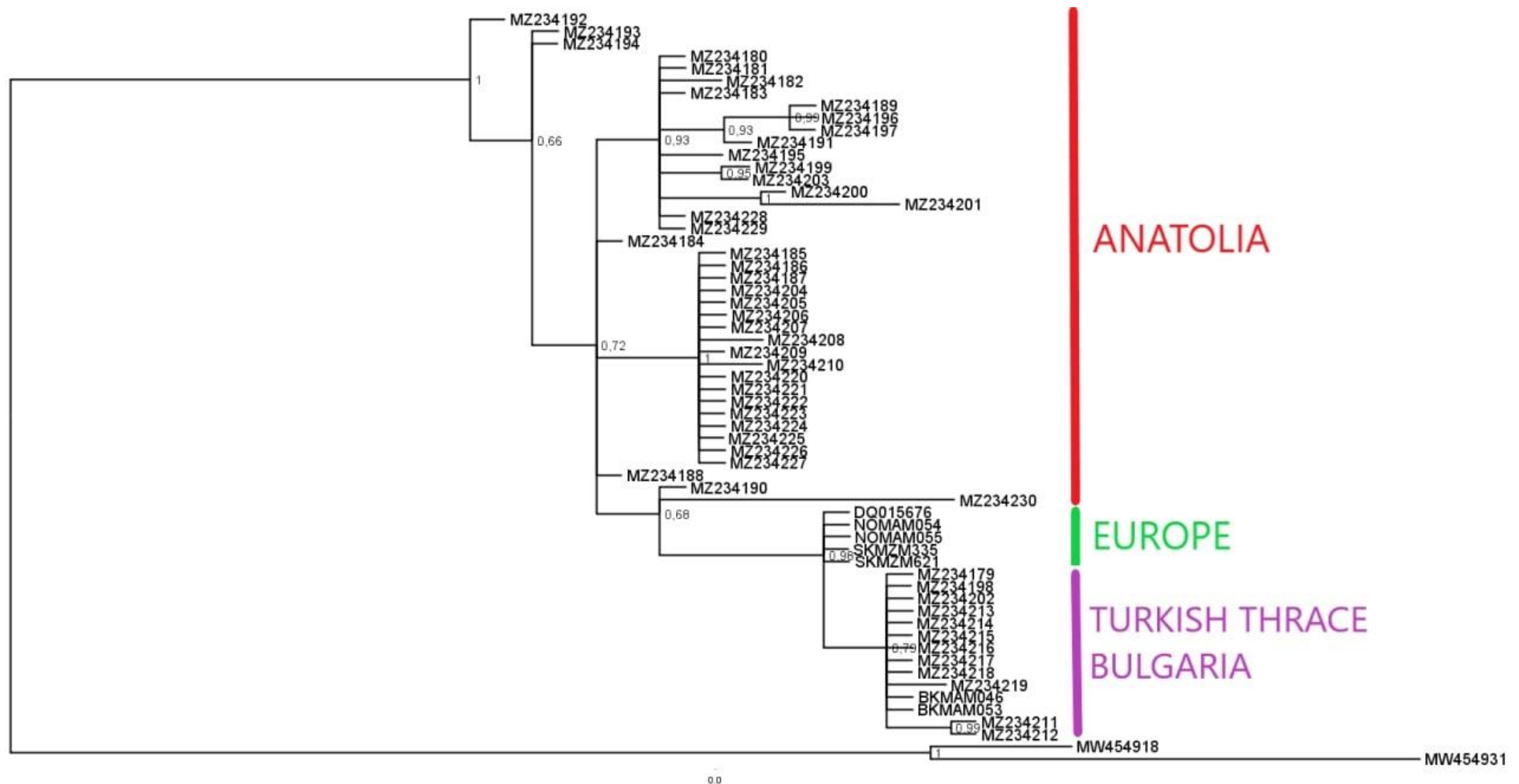


Figure S2. Bayesian Inference tree derived from *COXI* gene sequences. Numbers on branches show posterior probability (pp) values.

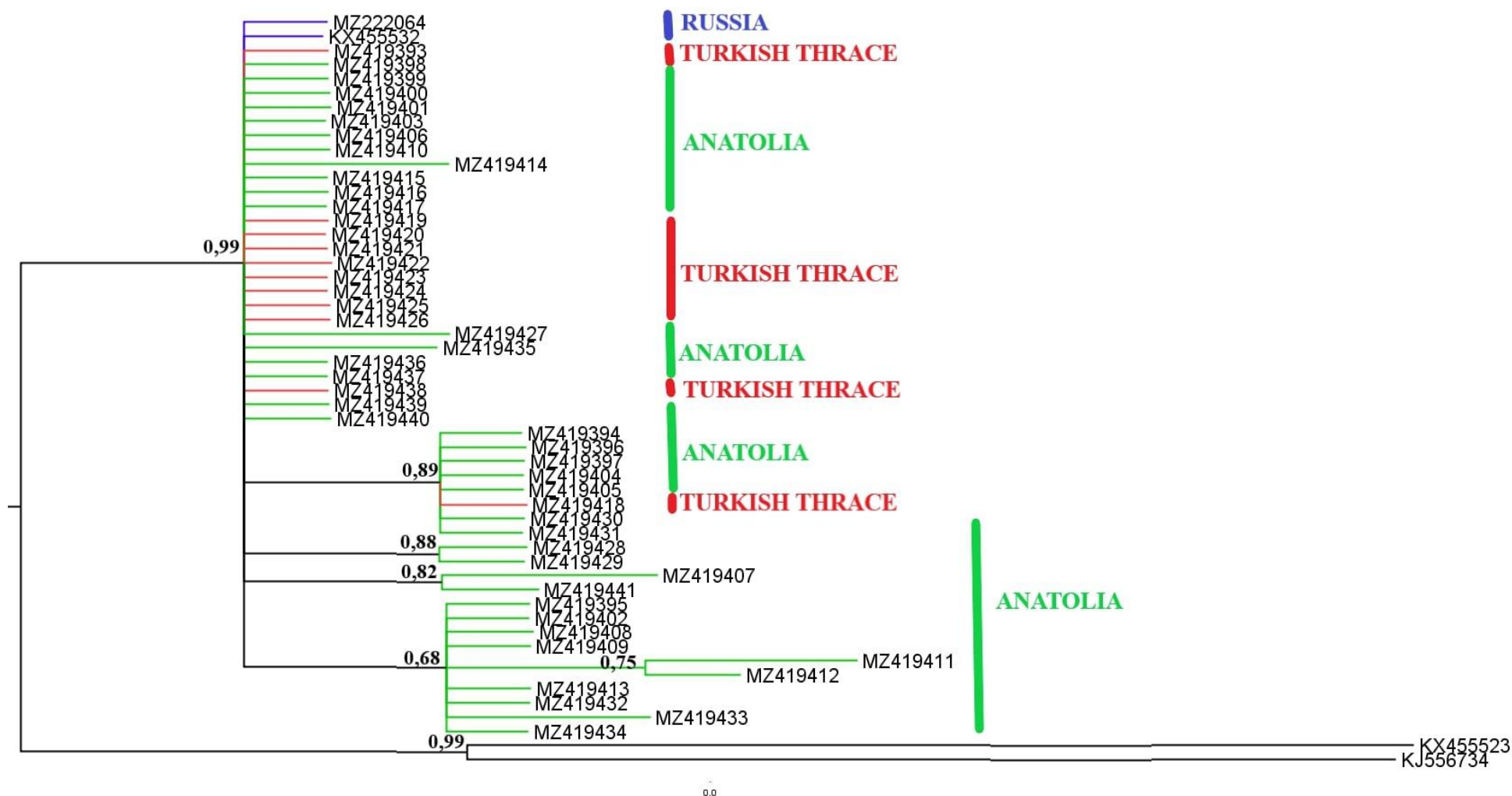


Figure S3. Bayesian Inference tree derived from *IRBP* gene sequences. Numbers on branches show posterior probability (pp) values.

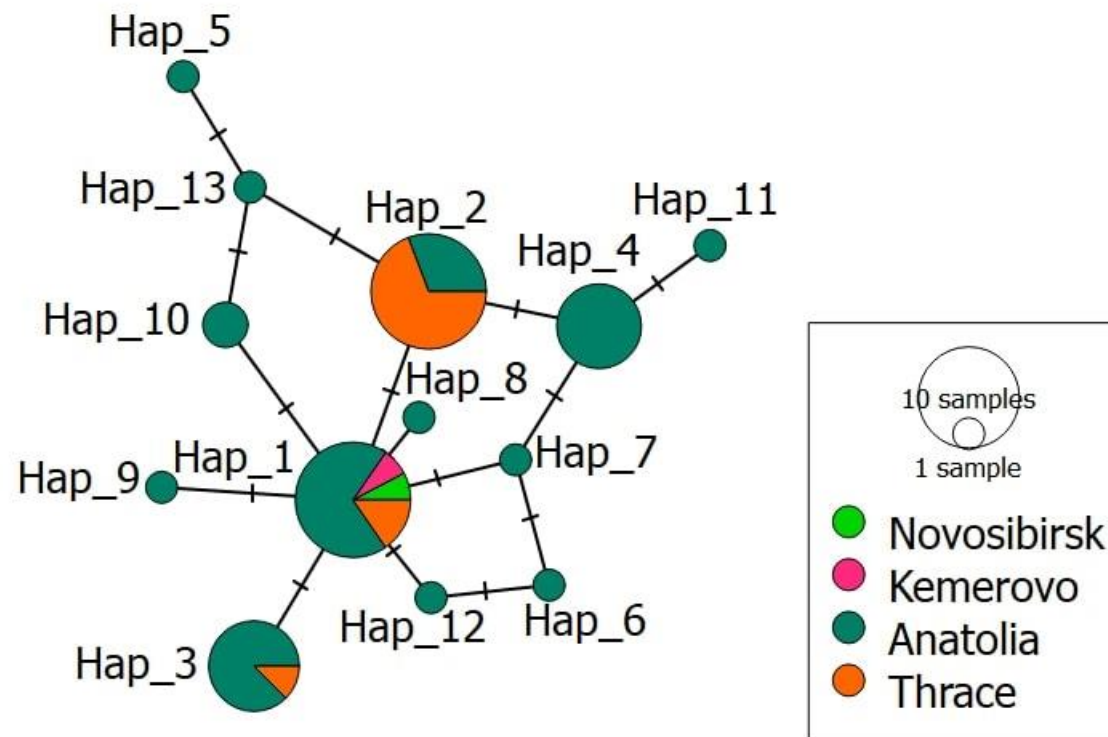


Figure S4. Median-joning network constructed using *IRBP* haplotypes. Mutations are shown with black dashes on branches.

Additional references

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