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Supplemental Data

Mitochondrial DNA Signals

of Late Glacial Recolonization of Europe

from Near Eastern Refugia

Maria Pala, Anna Olivieri, Alessandro Achilli, Matteo Accetturo, Ene Metspalu, Maere Reidla, Erika Tamm, Monika Karmin, Tuuli Reisberg, Baharak Hooshiar Kashani, Ugo A. Perego, Valeria Carossa, Francesca Gandini, Joana B. Pereira, Pedro Soares, Norman Angerhofer, Sergei Rychkov, Nadia Al-Zahery, Valerio Carelli, Mohammad Hossein Sanati, Massoud Houshmand, Jiří Hatina, Vincent Macaulay, Luísa Pereira, Scott R. Woodward, William Davies, Clive Gamble, Douglas Baird, Ornella Semino, Richard Villems, Antonio Torroni, and Martin B. Richards

Figure S1. Maximum-Parsimony Phylogenetic Tree of 451 Complete mtDNA Sequences Belonging to Haplogroup J

Figure S2. Maximum-Parsimony Phylogenetic Tree of 451 Complete mtDNA Sequences Belonging to Haplogroup T

Figure S3. Frequency Distribution Maps and Corresponding HVS-I Networks Obtained for Haplogroups J (and Subclades) and T (and Subclades)

Table S1. Origin and Subhaplogroup Affiliation of the Hg J mtDNA Complete Sequences Considered in this Study (.xls)

Table S2. Origin and Subhaplogroup Affiliation of the Hg T mtDNA Complete Sequences Considered in this Study (.xls)

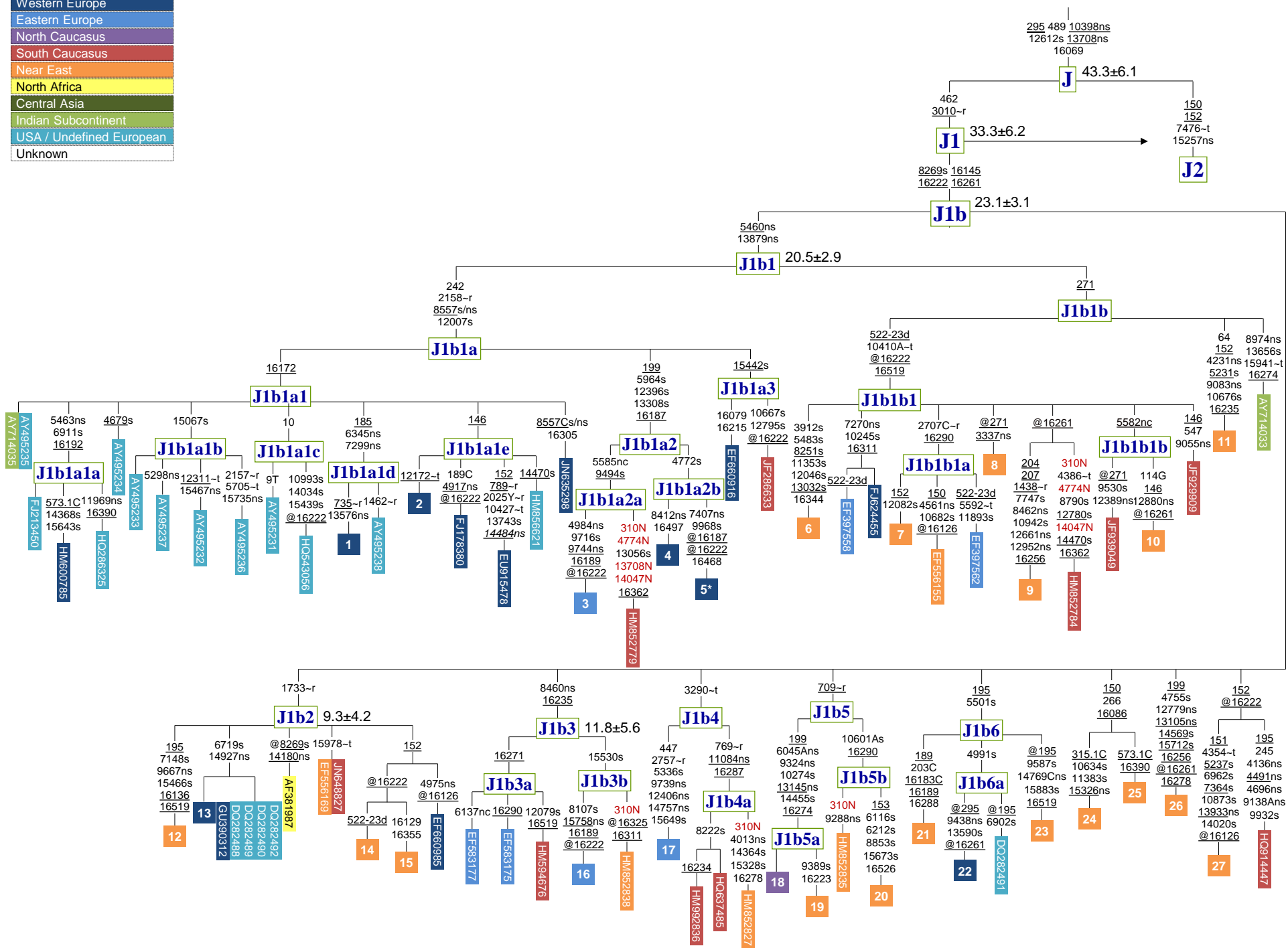
Table S3. Dataset of 37,239 Samples, from 106 Populations, Used to Generate Frequency Maps for T and Subclades and J, J1, and J2 (.xls)

Table S4. Dataset of 29,710 Samples, from 83 Populations, Used to Generate Frequency Maps for J1b'c'd and J2a'b Clades (.xls)

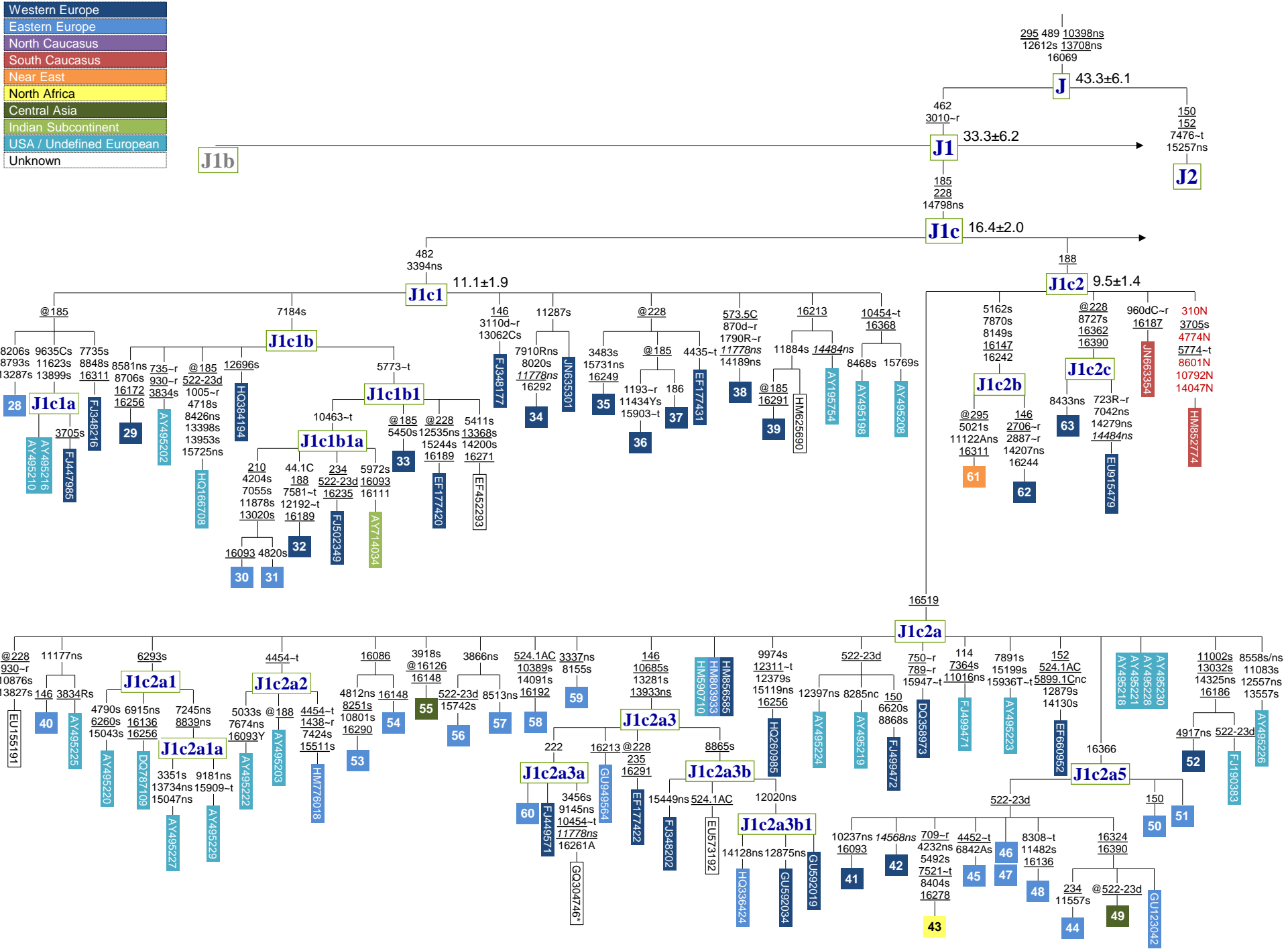
Table S5. Diversity Values of JT Lineages Observed in Near East, Eastern, and Western Europe

Supplemental References

Western Europe
Eastern Europe
North Caucasus
South Caucasus
Near East
North Africa
Central Asia
Indian Subcontinent
USA / Undefined European
Unknown

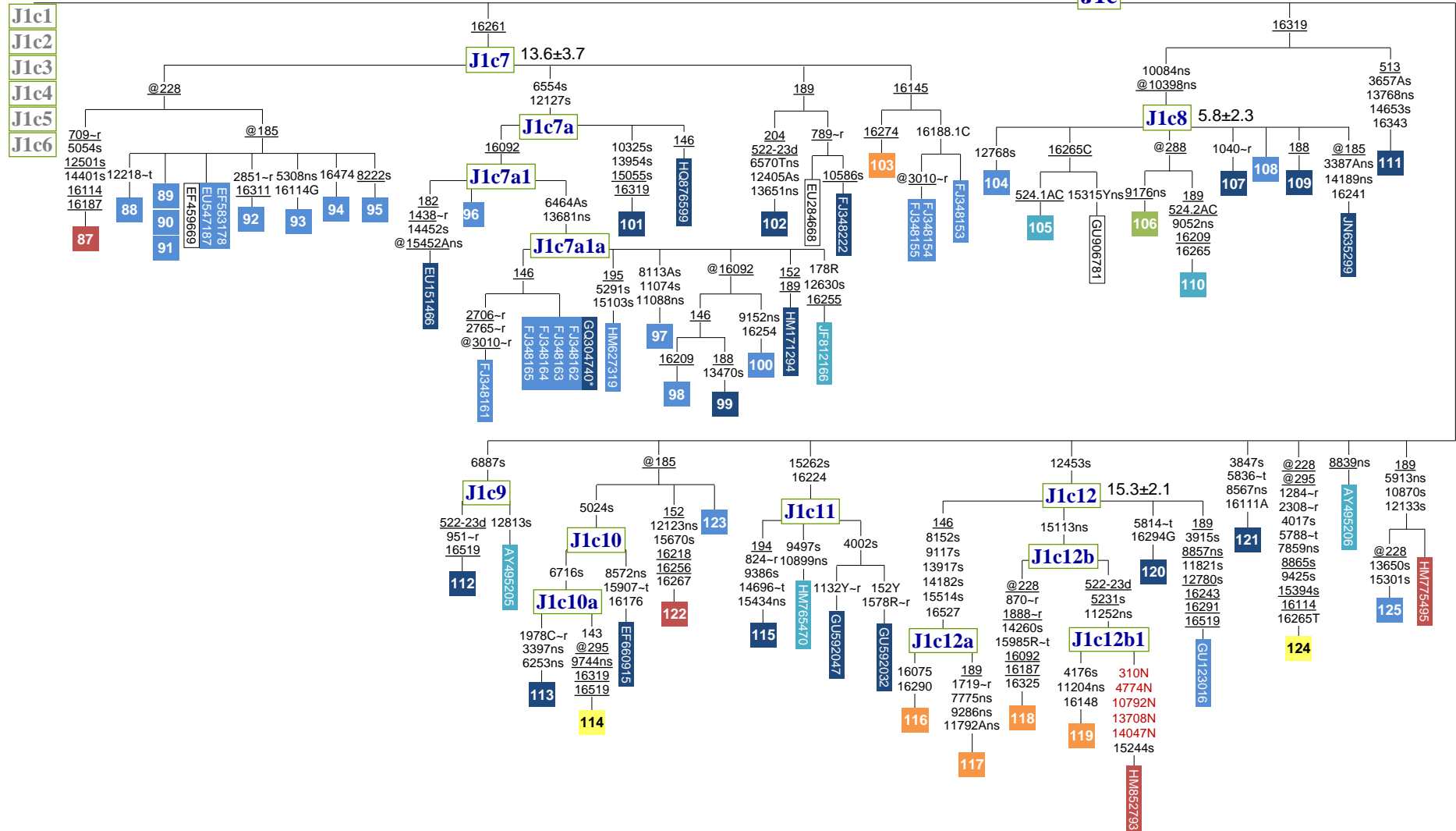
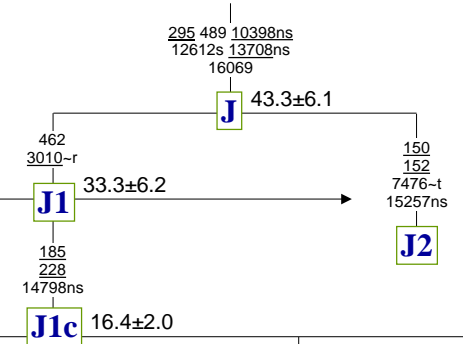


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North Caucasus
South Caucasus
Near East
North Africa
Central Asia
Indian Subcontinent
USA / Undefined European
Unknown

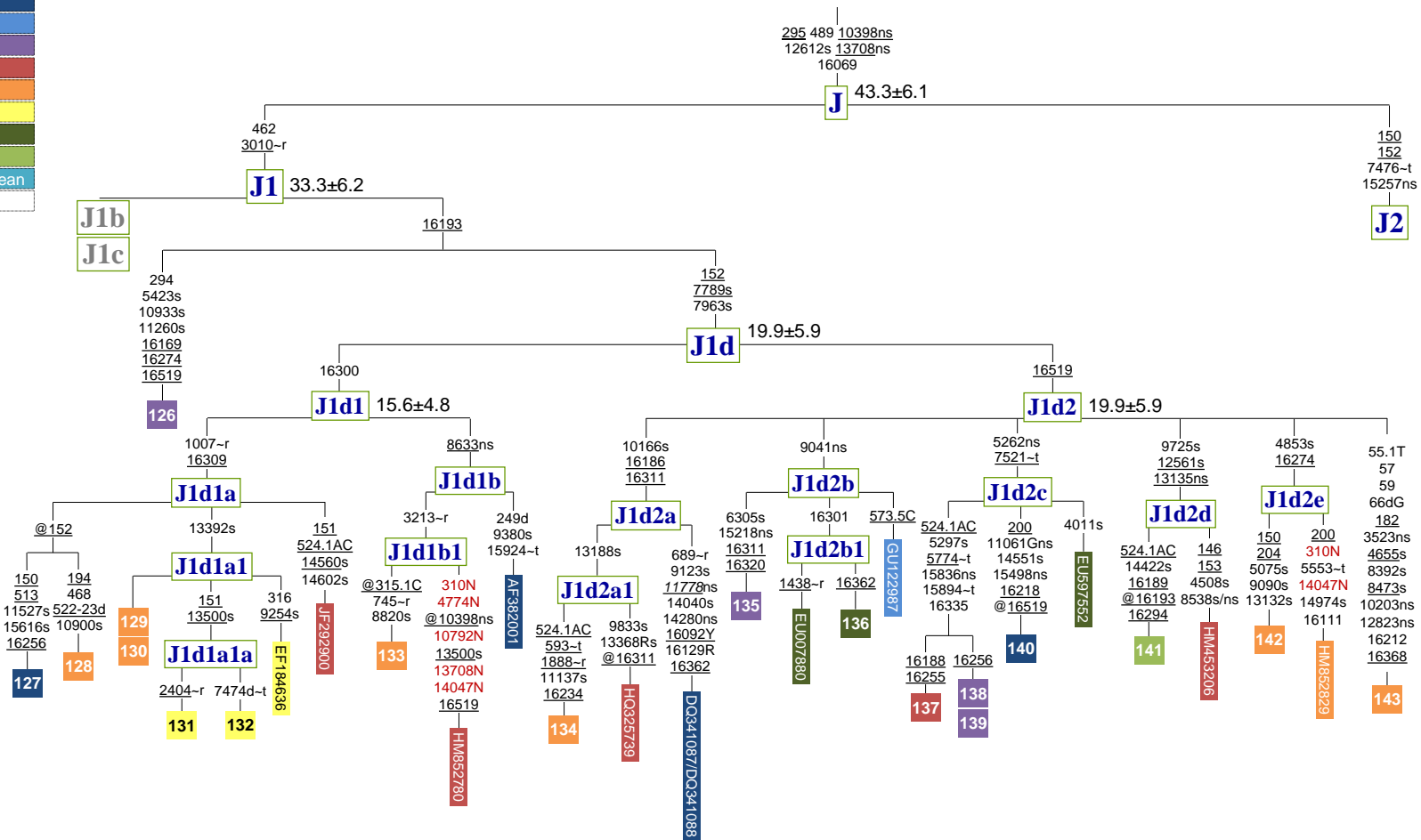


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North Caucasus
South Caucasus
Near East
North Africa
Central Asia
Indian Subcontinent
USA / Undefined European
Unknown

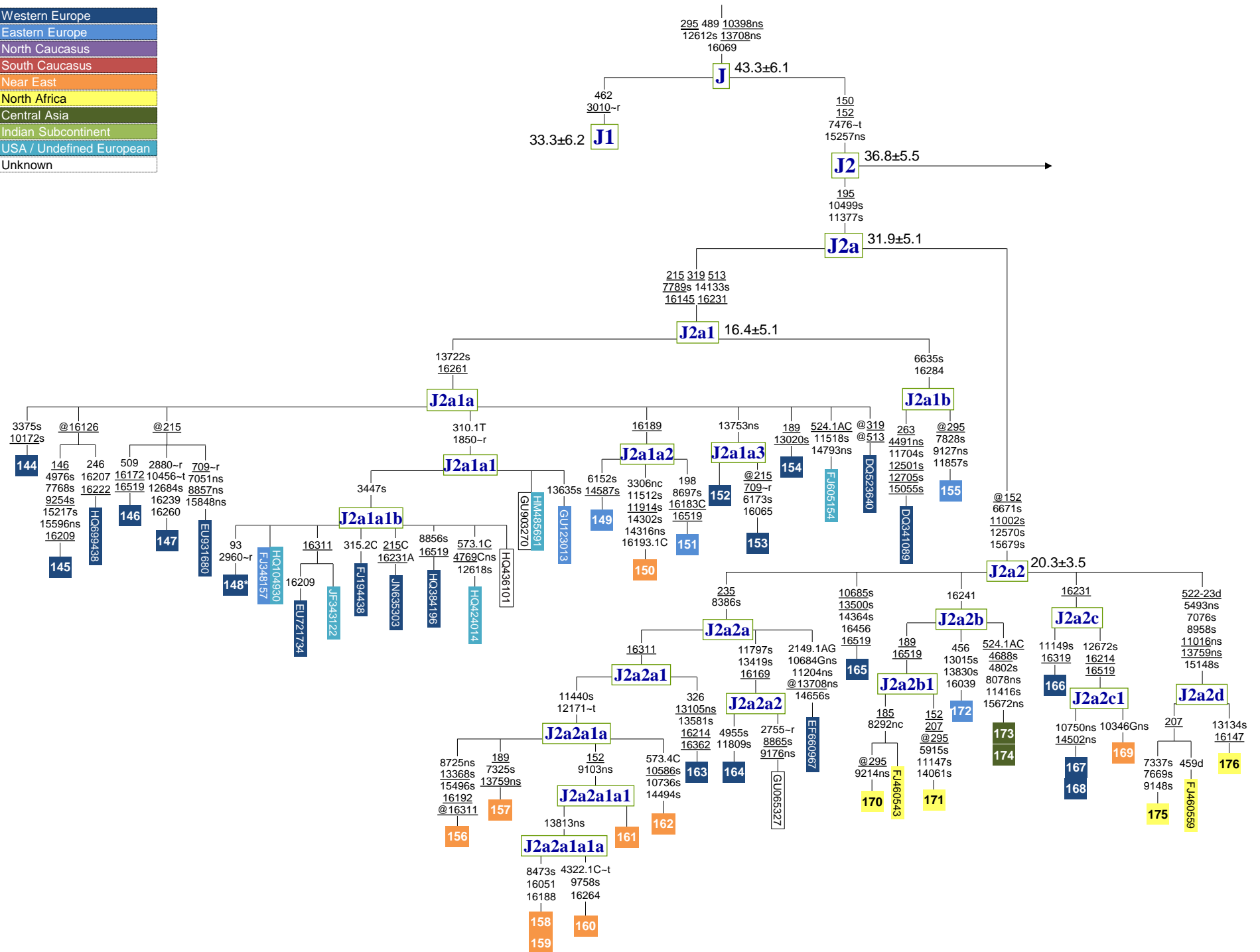
J1b



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South Caucasus
Near East
North Africa
Central Asia
Indian Subcontinent
USA / Undefined European
Unknown



Western Europe
Eastern Europe
North Caucasus
South Caucasus
Near East
North Africa
Central Asia
Indian Subcontinent
USA / Undefined European
Unknown



Western Europe
Eastern Europe
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South Caucasus
Near East
North Africa
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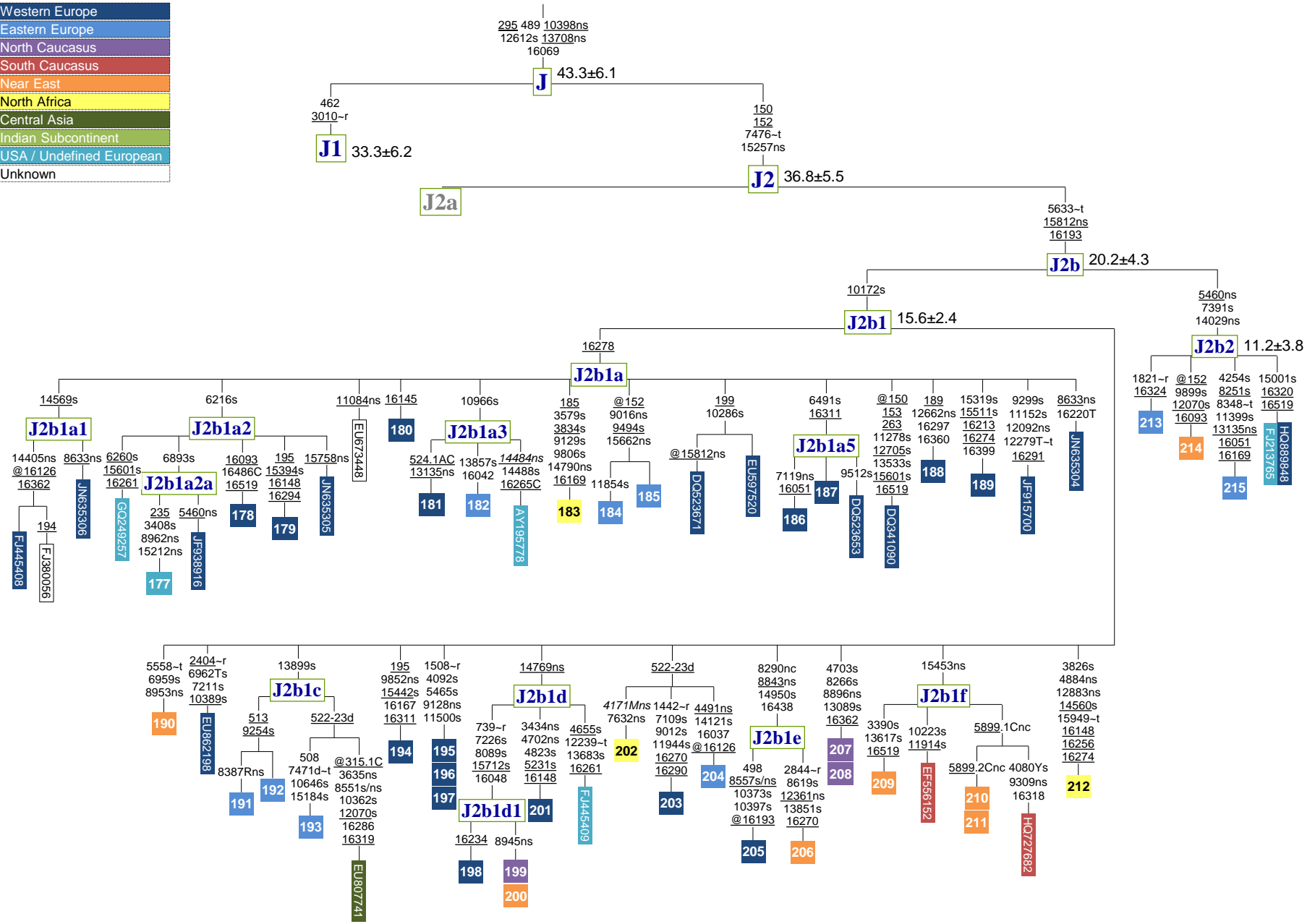
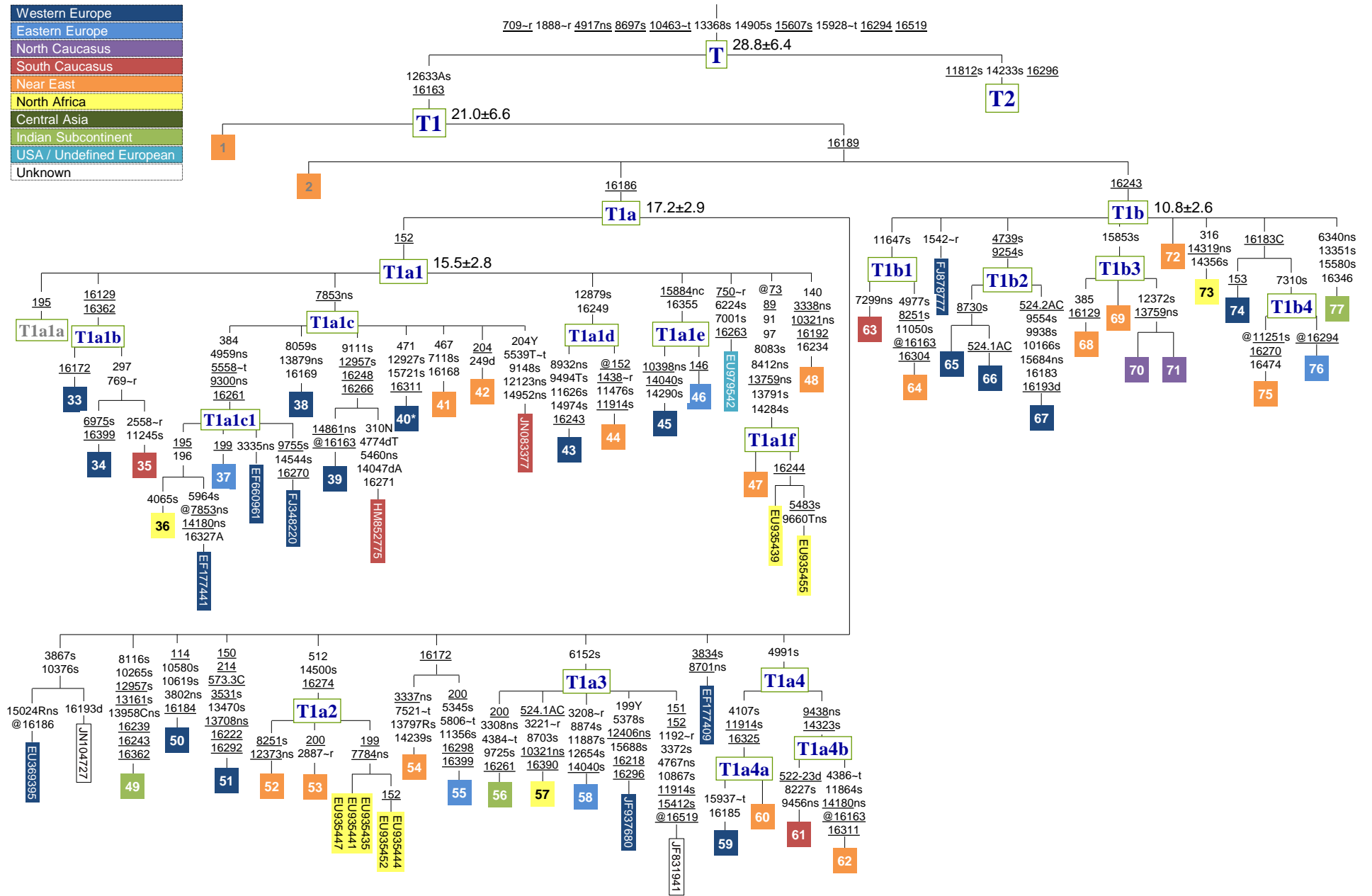


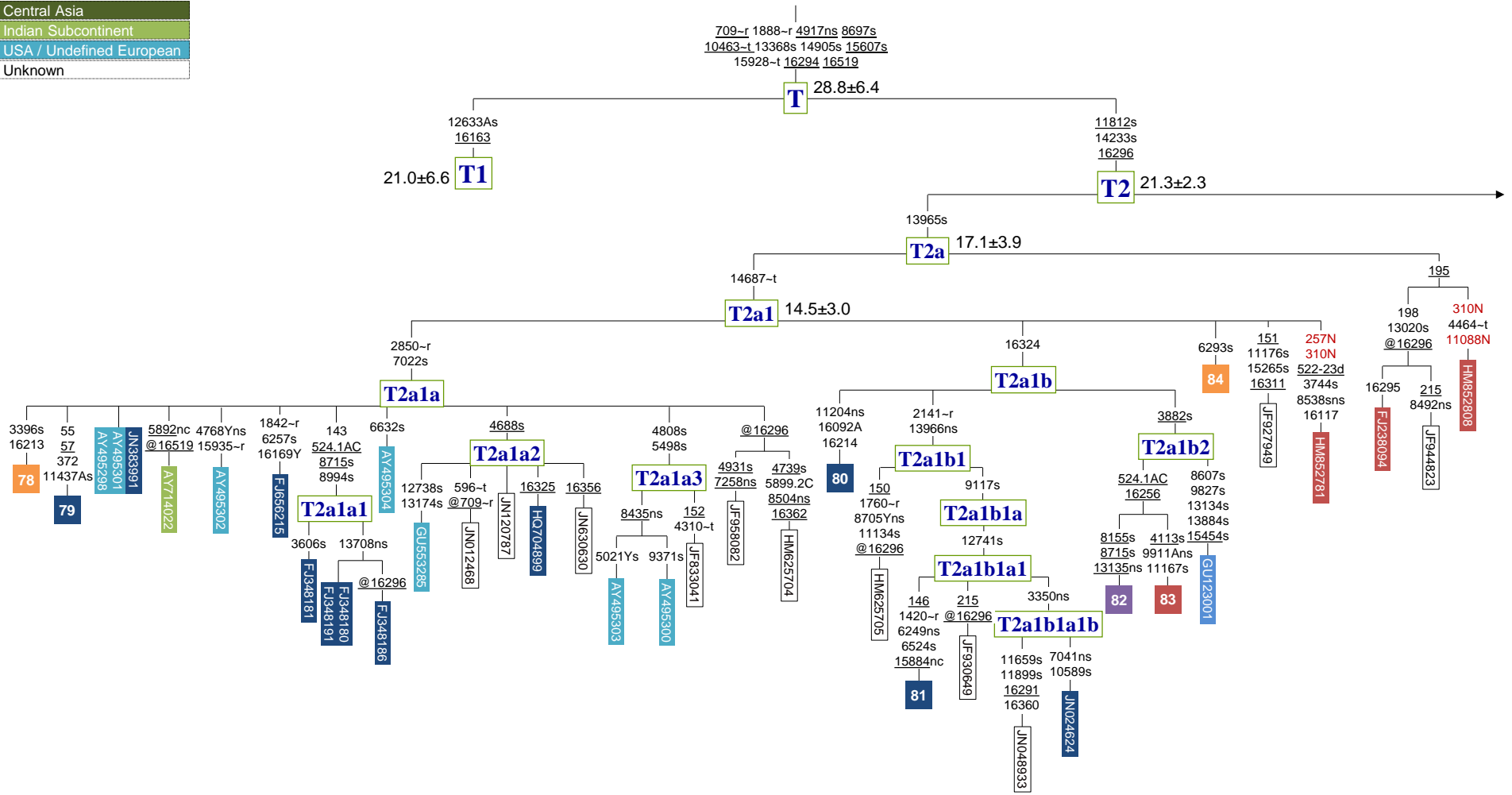
Figure S1. Maximum-Parsimony Phylogenetic Tree of 451 Complete mtDNA Sequences Belonging to Haplogroup J

Mutations are shown on the branches; they are transitions unless the base change is explicitly indicated. The prefix “@” designates reversions, whereas suffixes indicate: transversions (to A, G, C, or T), deletions “d”, gene locus (~t, tRNA; ~r, rRNA; ~nc, noncoding region outside of the control region), synonymous or non-synonymous changes (s or ns), and heteroplasmies (R, Y, M). Insertions are also suffixed with a dot followed by a number indicating how many bases were inserted and the inserted nucleotide/s (.1C). Recurrent mutations are underlined. The variation in number of Cs at np 309 was not included in the phylogeny. Italics highlight pathological mutations while brown labels indicate potential phantom mutations or documentation errors that have not been considered for the age calculations. DNA of samples marked with an asterisk (*) derived from cybrid cell lines. Each rectangle represents a sample, they are numbered according to the order they appear on the tree, while previously published sequences are identified by their GenBank accession number. All the samples are coloured according to their geographic origin, as shown in the legend.

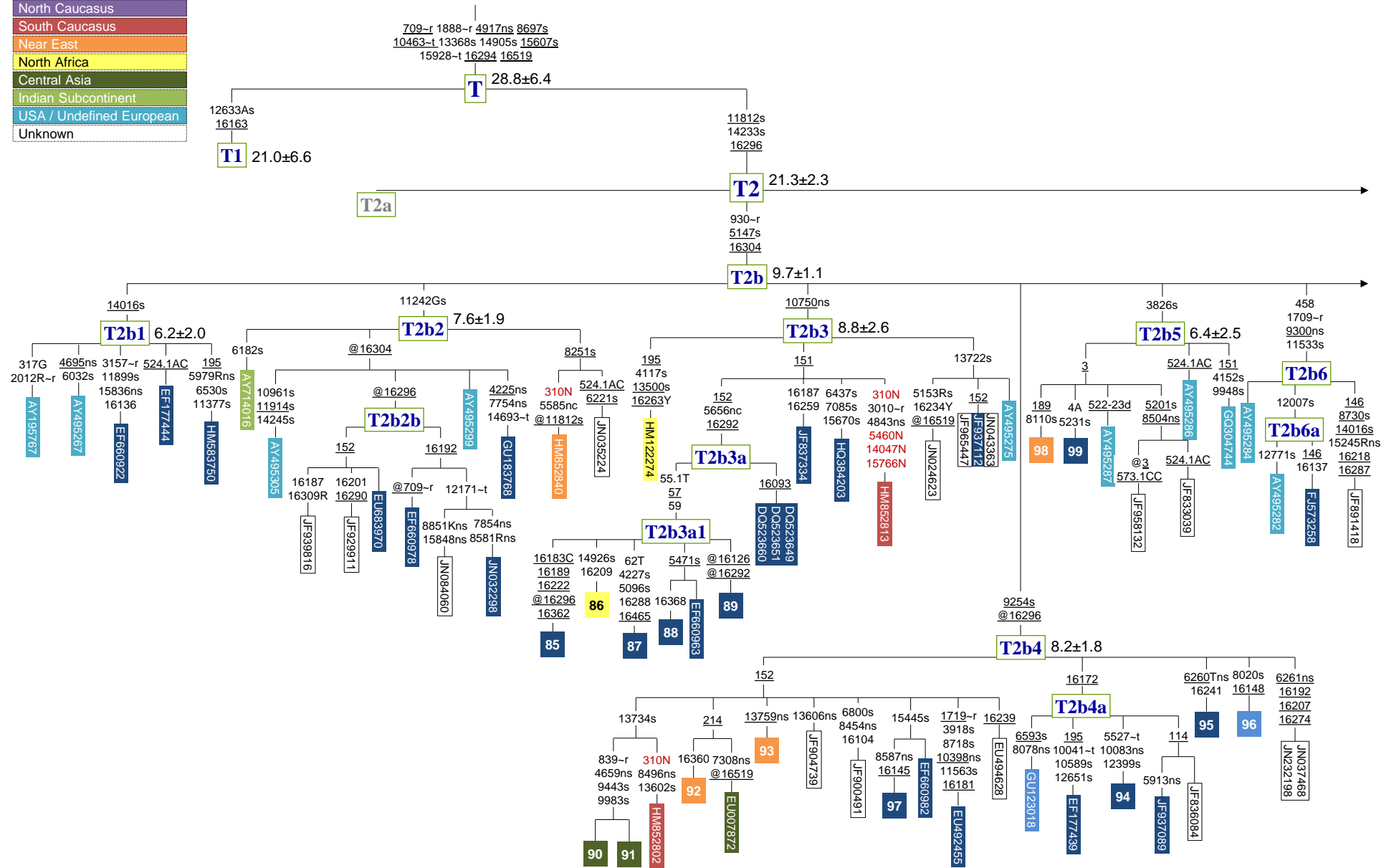
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South Caucasus
Near East
North Africa
Central Asia
Indian Subcontinent
USA / Undefined European
Unknown



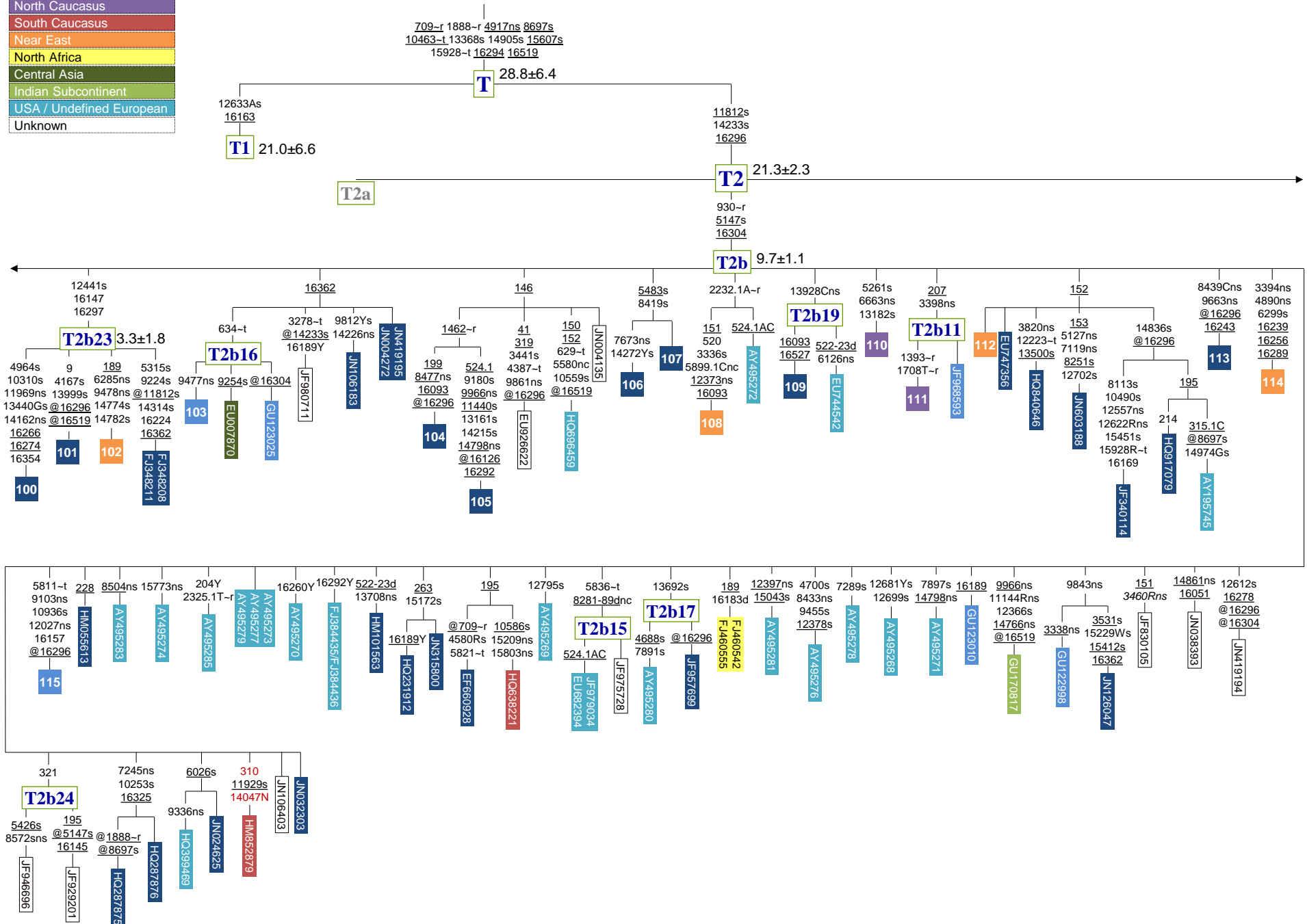
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North Caucasus
South Caucasus
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Central Asia
Indian Subcontinent
USA / Undefined European
Unknown



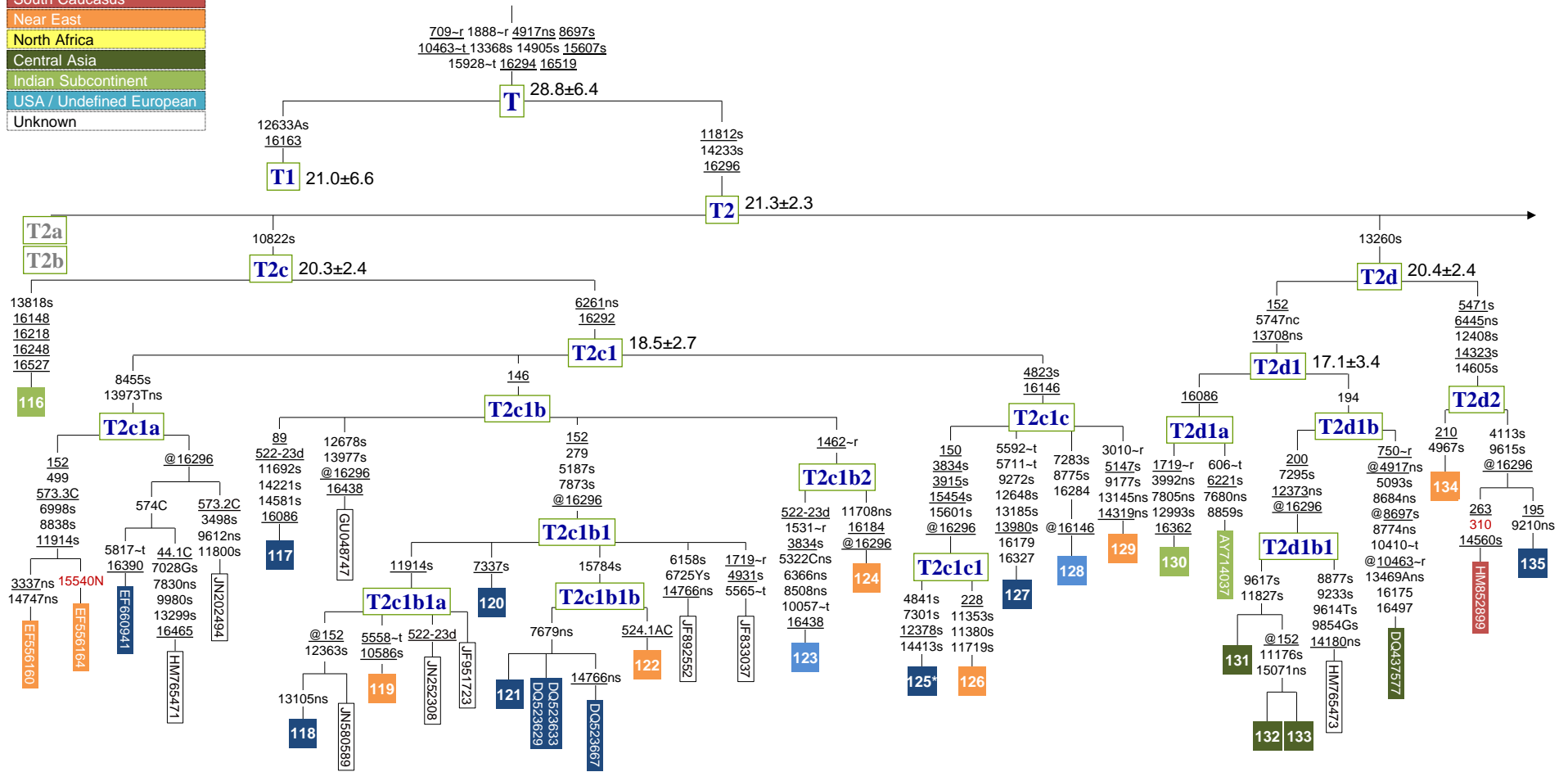
Western Europe
Eastern Europe
North Caucasus
South Caucasus
Near East
North Africa
Central Asia
Indian Subcontinent
USA / Undefined European
Unknown



Western Europe
Eastern Europe
North Caucasus
South Caucasus
Near East
North Africa
Central Asia
Indian Subcontinent
USA / Undefined European
Unknown



Western Europe
Eastern Europe
North Caucasus
South Caucasus
Near East
North Africa
Central Asia
Indian Subcontinent
USA / Undefined European
Unknown



- Western Europe
- Eastern Europe
- North Caucasus
- South Caucasus
- Near East
- North Africa
- Central Asia
- Indian Subcontinent
- USA / Undefined European
- Unknown

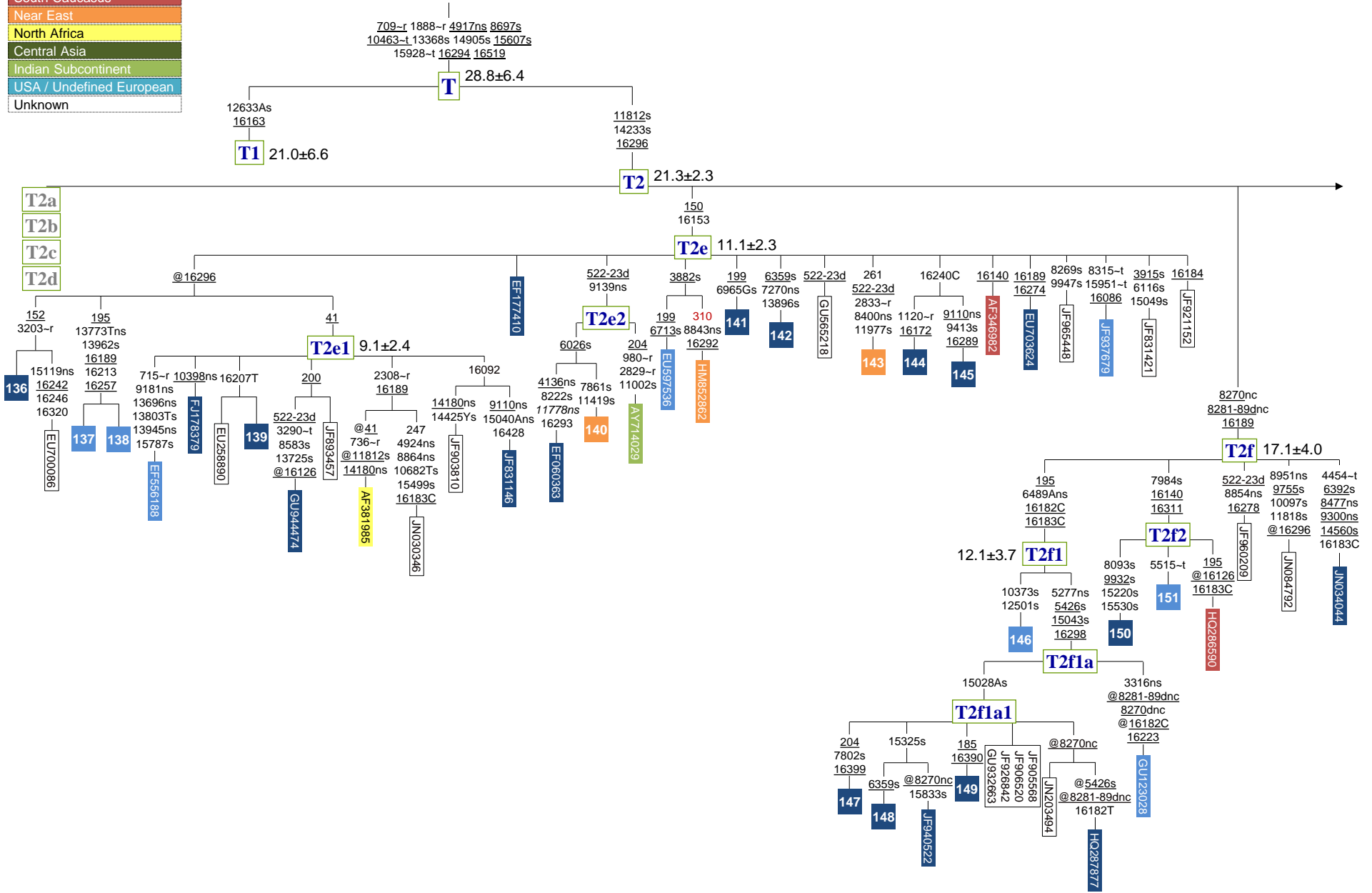
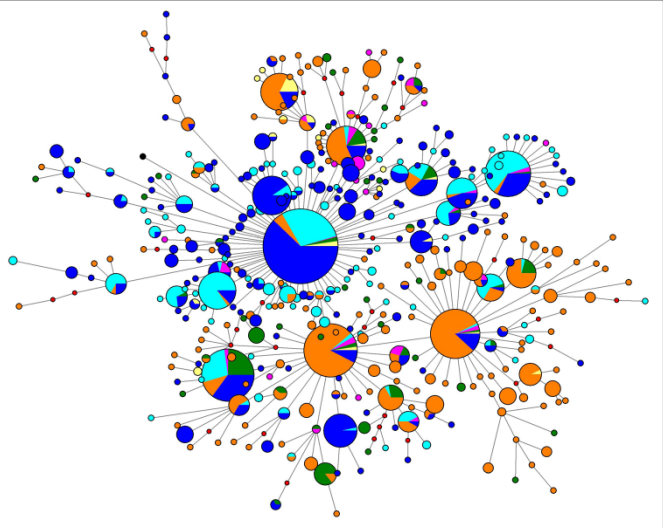
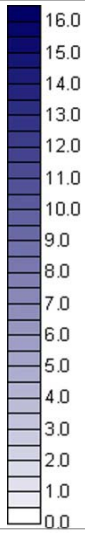
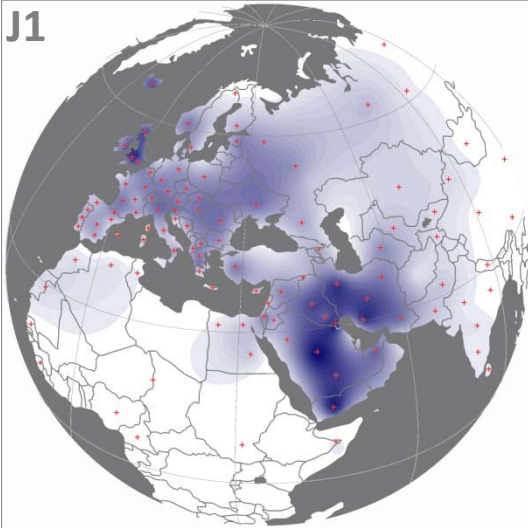


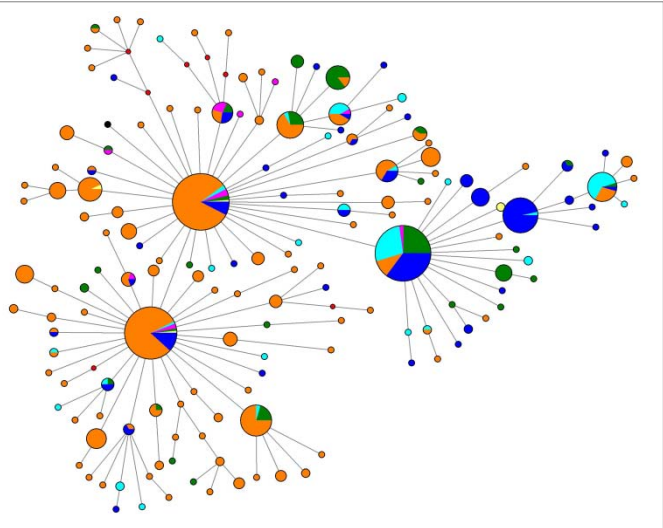
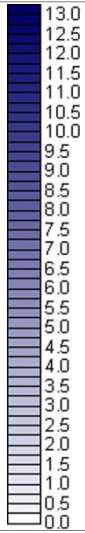
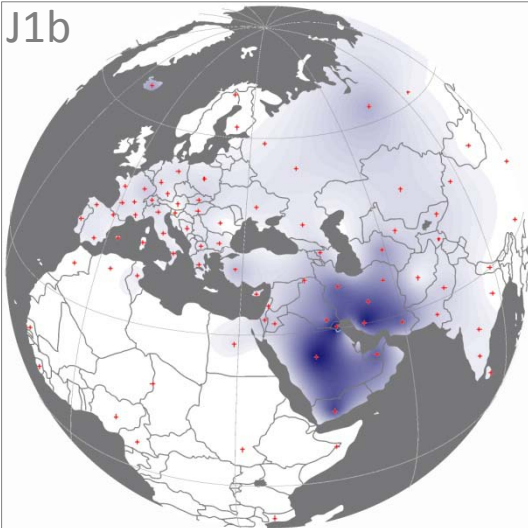
Figure S2. Maximum-Parsimony Phylogenetic Tree of 451 Complete mtDNA Sequences Belonging to Haplogroup T

Mutations are shown on the branches; they are transitions unless the base change is explicitly indicated. The prefix “@” designates reversions, whereas suffixes indicate: transversions (to A, G, C, or T), deletions “d”, gene locus (~t, tRNA; ~r, rRNA; ~nc, noncoding region outside of the control region), synonymous or non-synonymous changes (s or ns), and heteroplasmies (R, Y, W, K). Insertions are also suffixed with a dot followed by a number indicating how many bases were inserted and the inserted nucleotide/s (.1C). Recurrent mutations are underlined. Italics highlight pathological mutations while brown labels indicate potential phantom mutations or documentation errors that have not been considered for the age calculations. DNA of samples marked with an asterisk (*) derived from cybrid cell lines. The variation in number of Cs at np 309 was not included in the phylogeny. Each rectangle represents a sample, they are numbered according to the order they appear on the tree, while previously published sequences are identified by their GenBank accession number. All the samples are coloured according to their geographic origin, as shown in the legend.

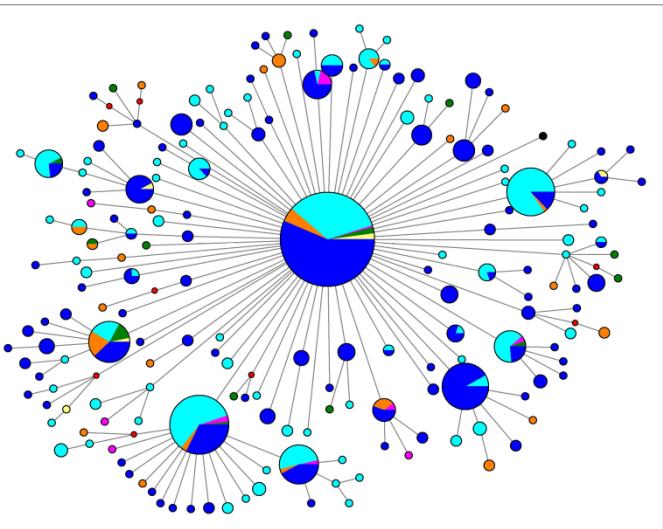
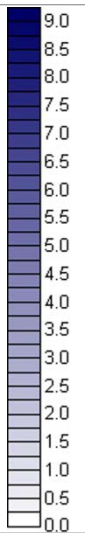
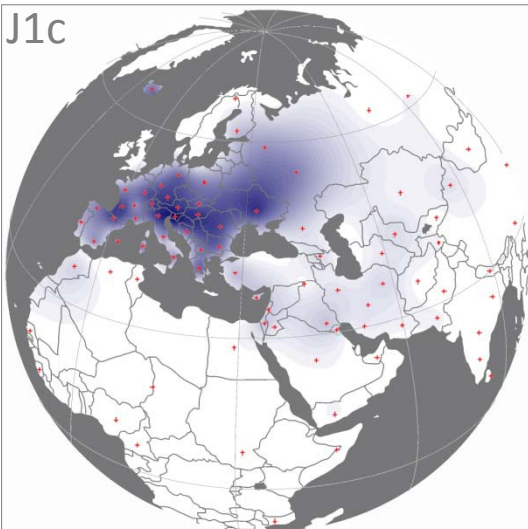
J1



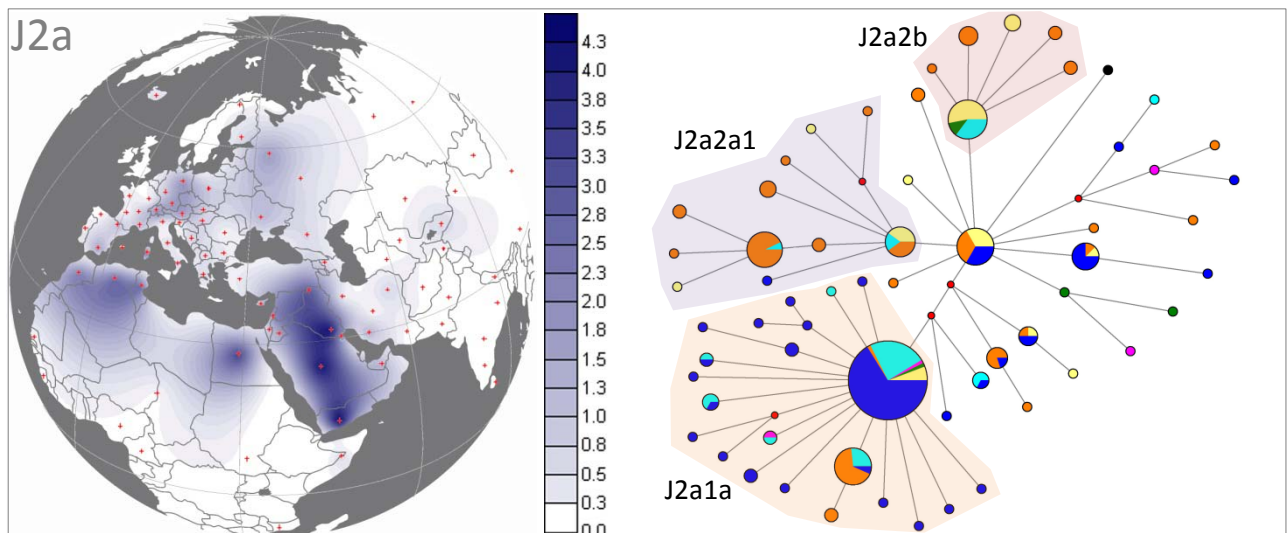
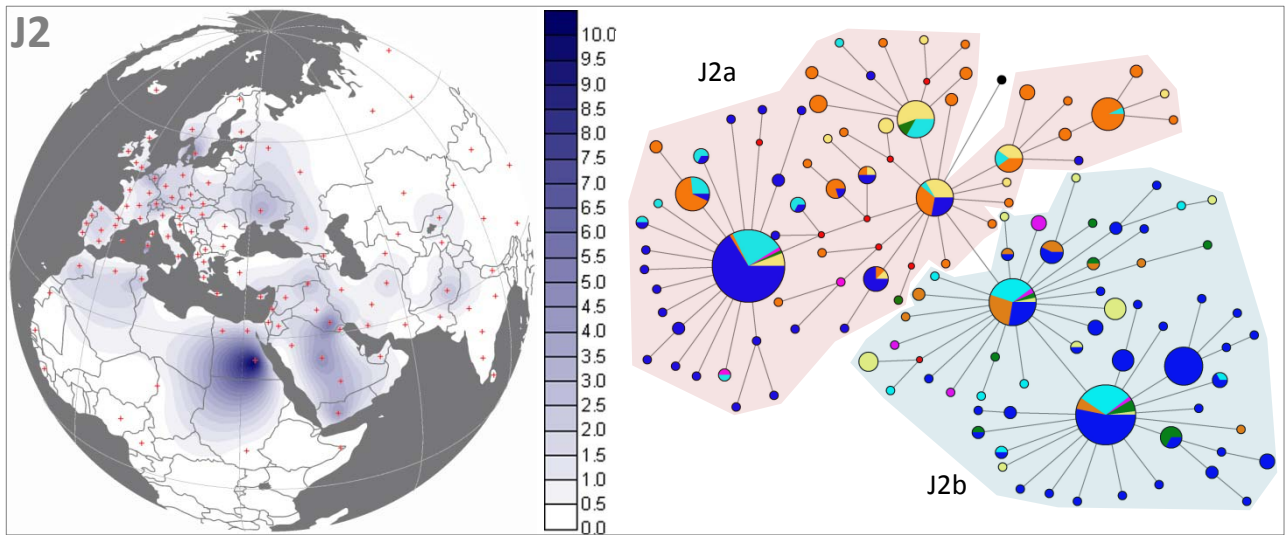
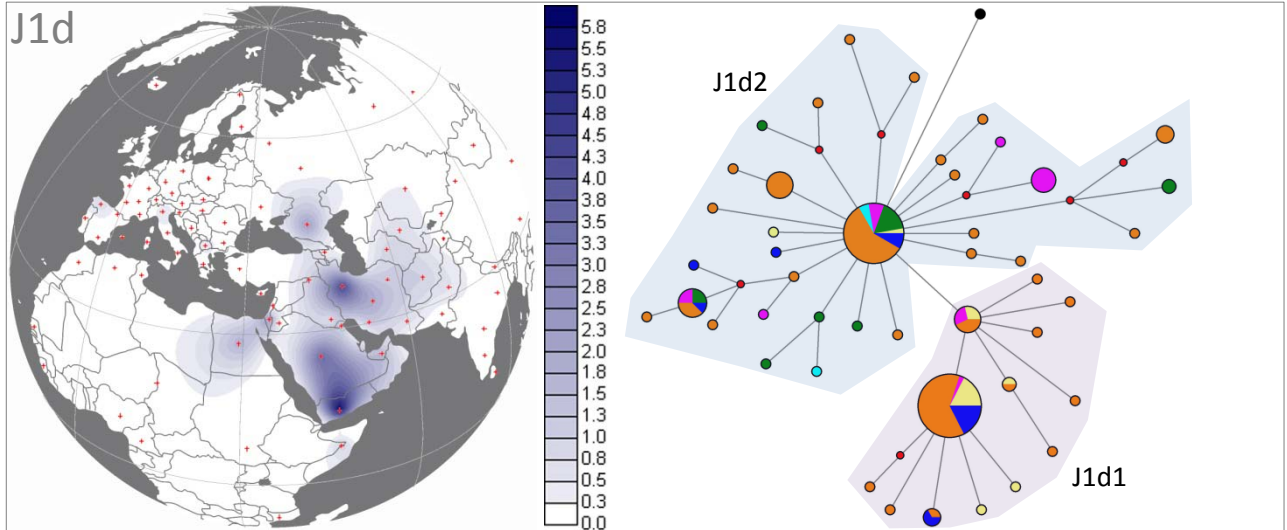
J1b



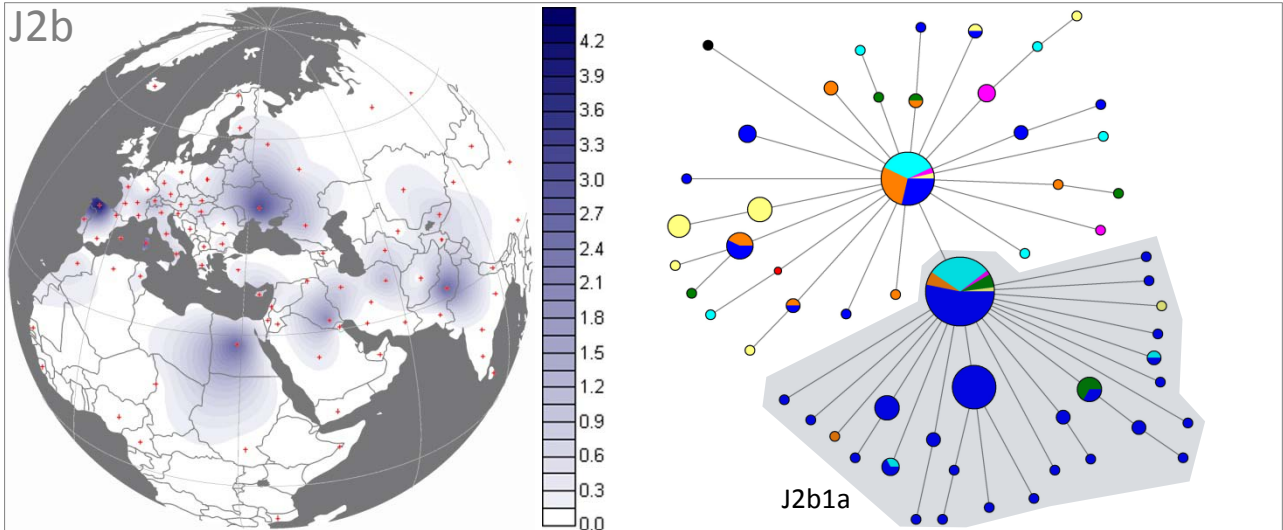
J1c



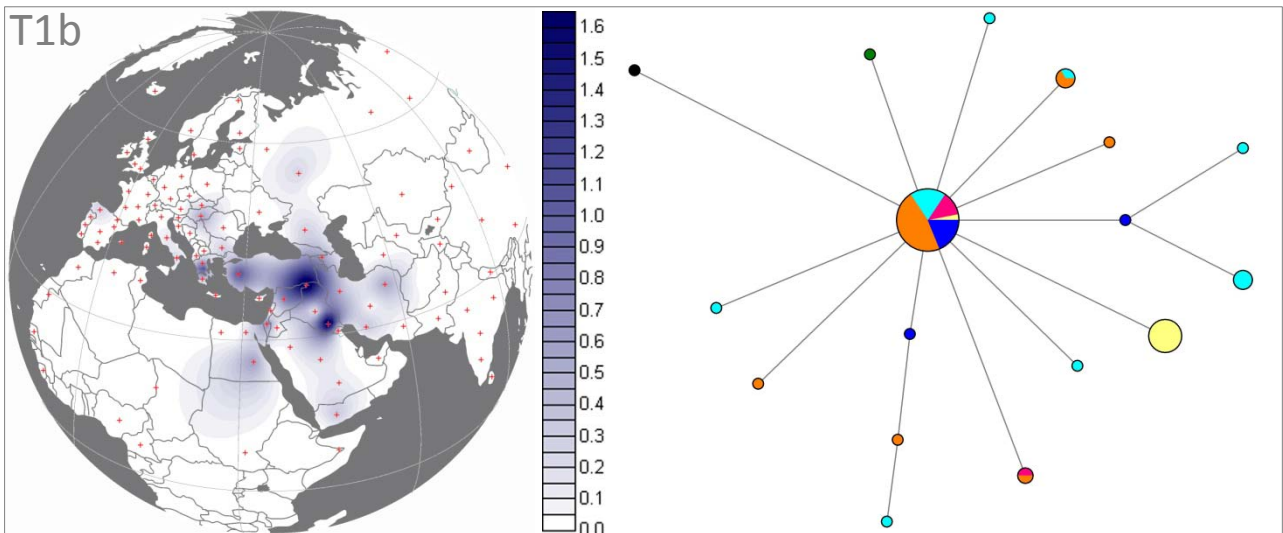
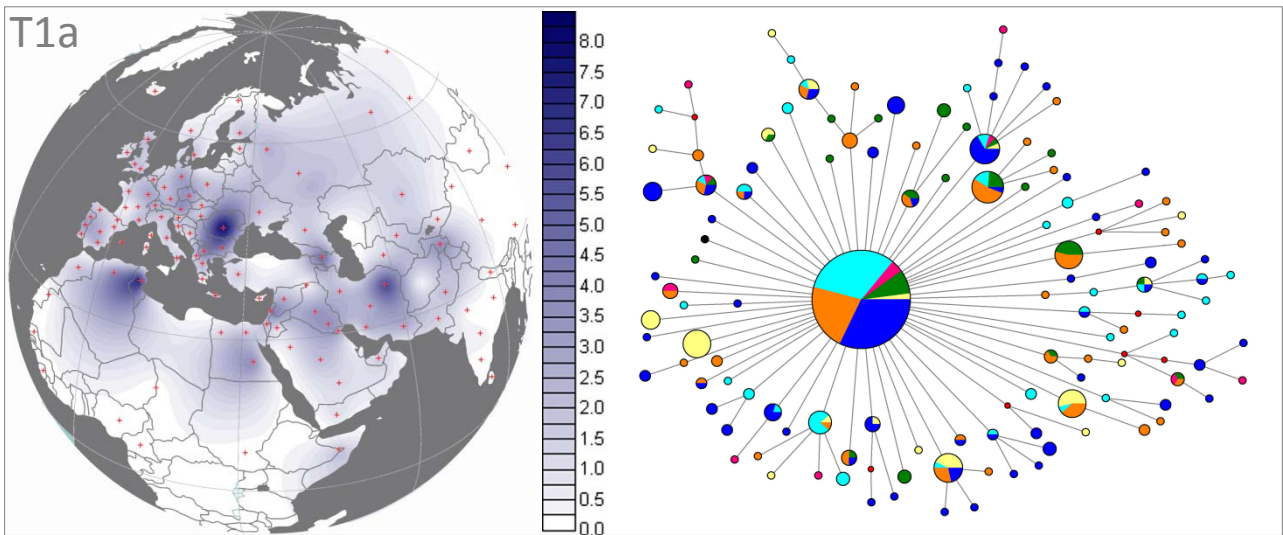
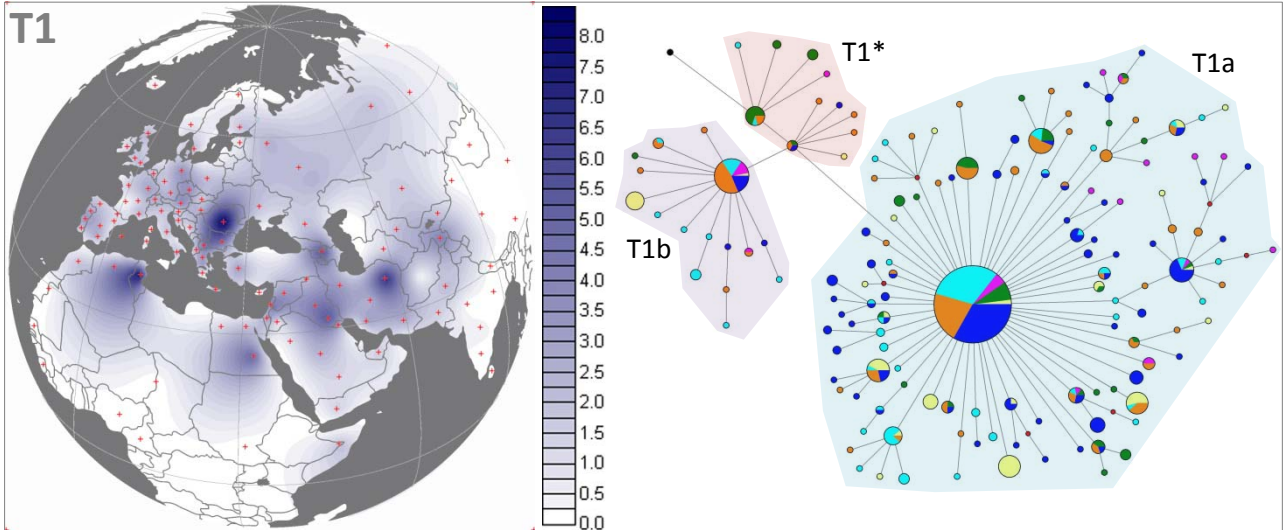
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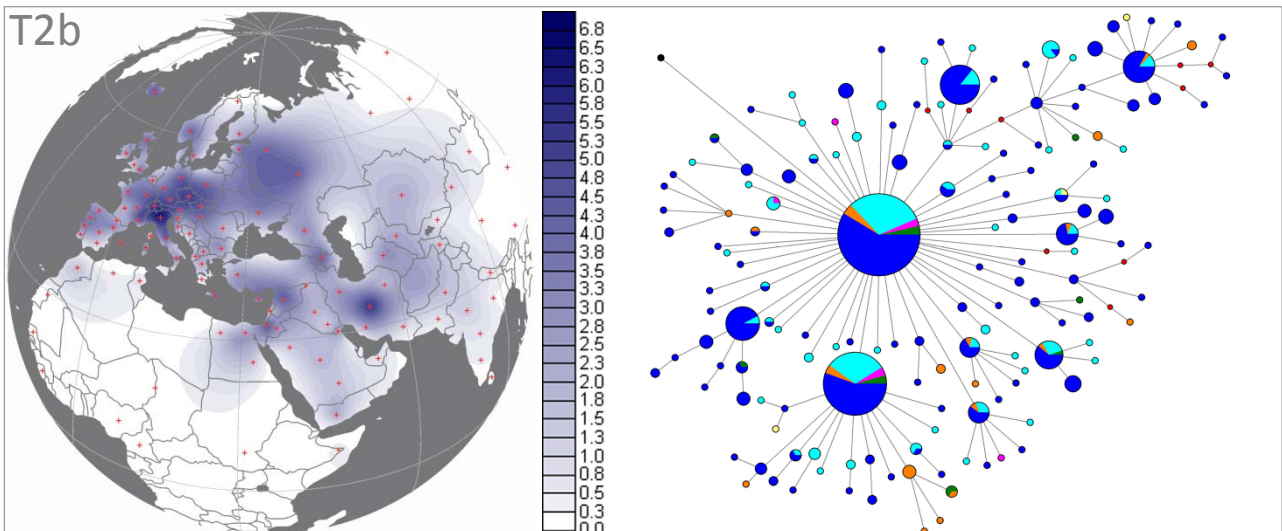
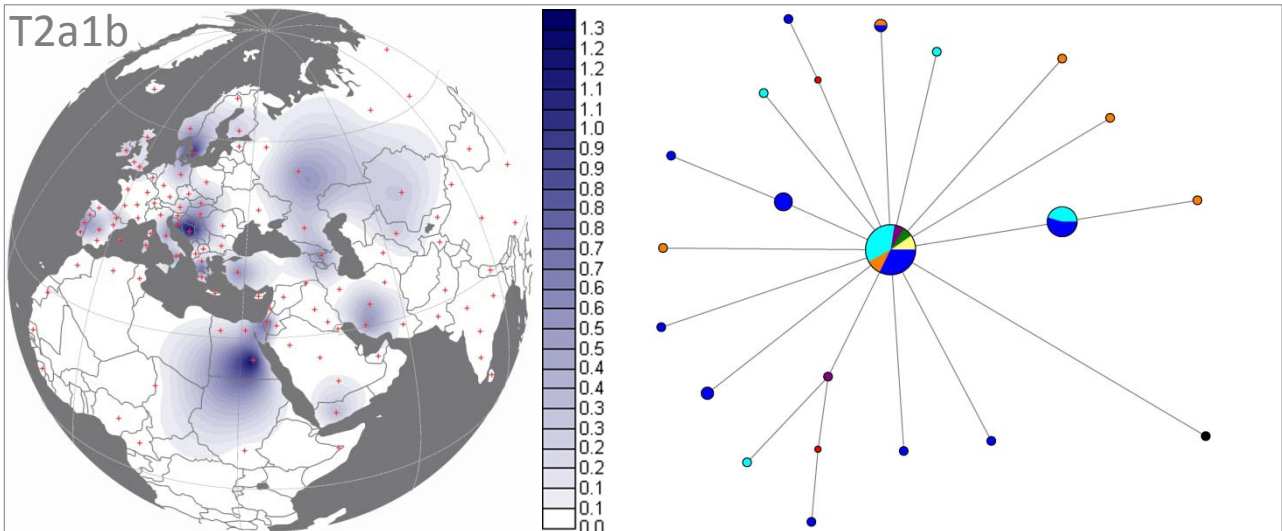
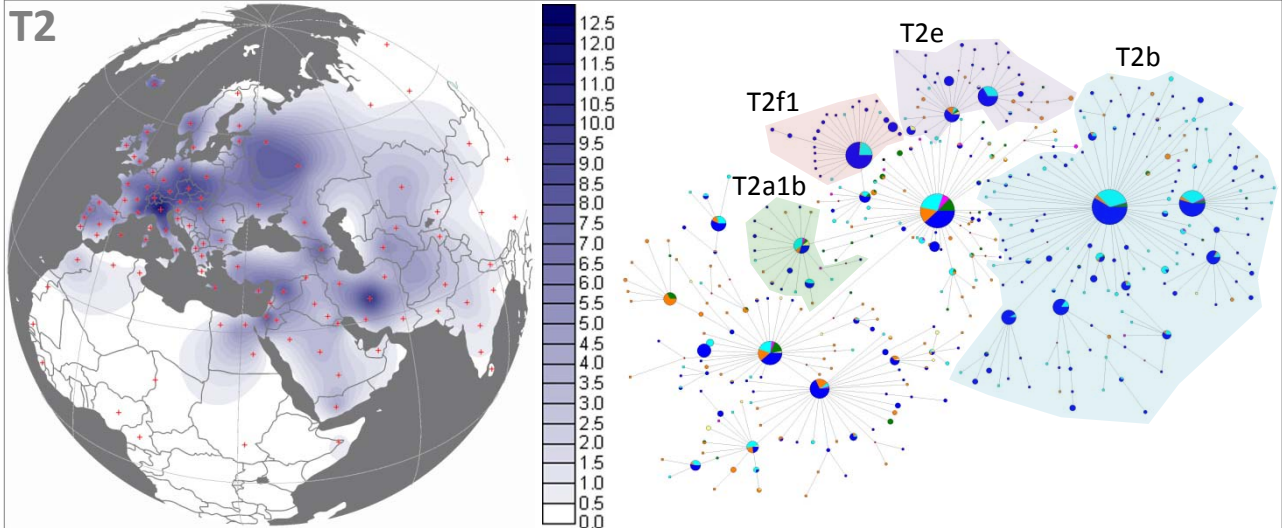
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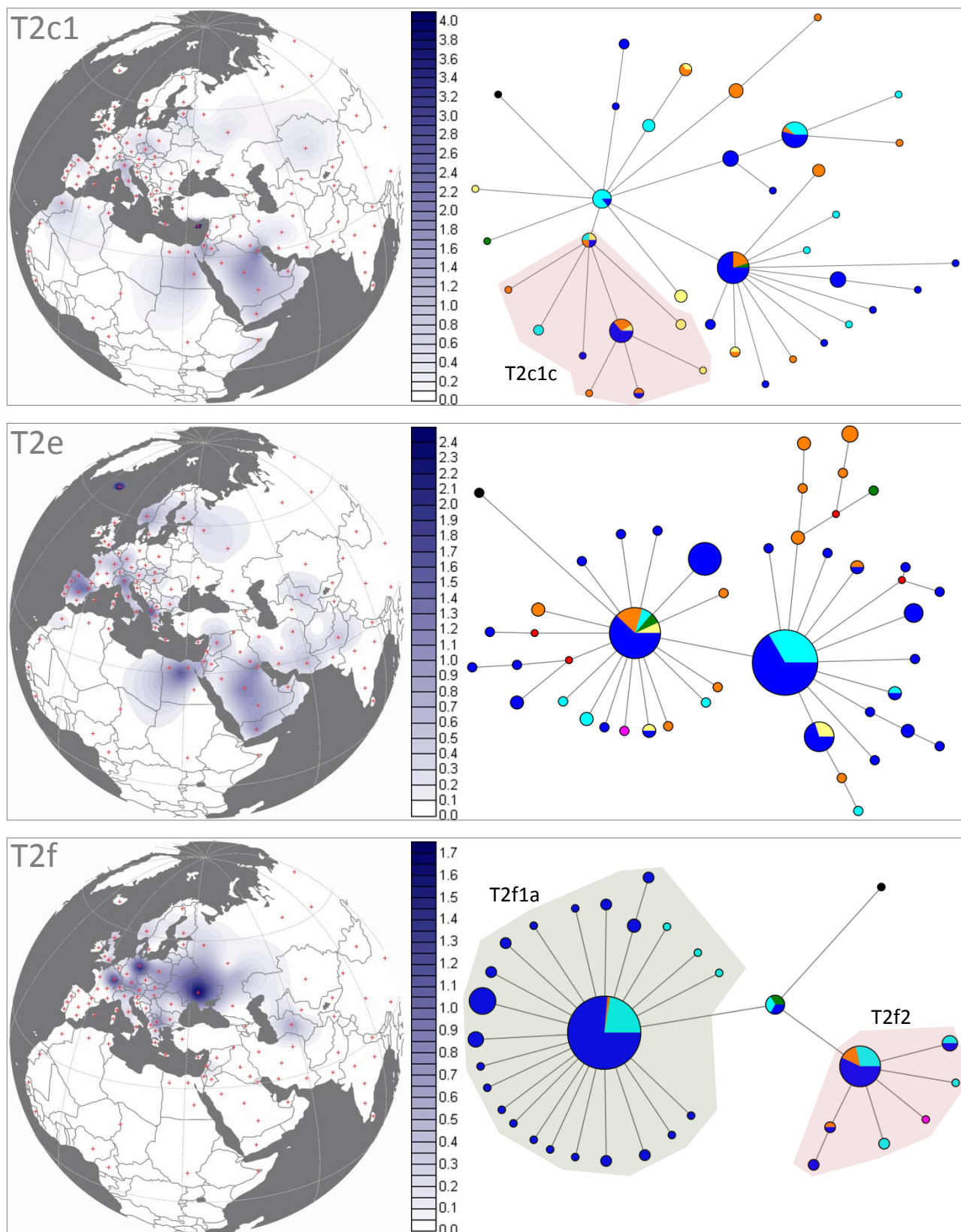


Figure S3. Frequency Distribution Maps and Corresponding HVS-I Networks Obtained for Haplogroups J (and Subclades) and T (and Subclades)

Table S5. Diversity Values of JT Lineages Observed in Near East, Eastern, and Western Europe

Clade	Geographic Area	No. of MtDNAs	No. of Haplotypes ^a	ρ^b	π^c	h^d
J	Near East	615	193	4.119 ± 1.199	0.970 ± 0.003	1.135 ± 0.024
	Eastern Europe	501	120	1.633 ± 0.424	0.906 ± 0.010	0.756 ± 0.027
	Western Europe	973	222	1.673 ± 0.314	0.889 ± 0.009	0.807 ± 0.022
	Total	2089				
J1	Near East	523	163	3.756 ± 1.274	0.963 ± 0.004	1.064 ± 0.028
	Eastern Europe	423	102	1.530 ± 0.363	0.885 ± 0.013	0.701 ± 0.030
	Western Europe	753	162	1.545 ± 0.339	0.849 ± 0.013	0.700 ± 0.025
	Total	1699				
J1b	Near East	363	100	1.540 ± 0.472	0.937 ± 0.008	0.727 ± 0.029
	Eastern Europe	67	26	1.702 ± 0.691	0.863 ± 0.032	0.656 ± 0.064
	Western Europe	126	37	1.651 ± 0.744	0.887 ± 0.018	0.588 ± 0.034
	Total	556				
J1c	Near East	54	25	1.241 ± 0.263	0.898 ± 0.033	0.680 ± 0.075
	Eastern Europe	324	73	0.988 ± 0.259	0.856 ± 0.016	0.507 ± 0.026
	Western Europe	461	98	0.833 ± 0.156	0.829 ± 0.017	0.460 ± 0.021
	Total	839				
J1d	Near East	86	30	1.616 ± 0.576	0.852 ± 0.027	0.683 ± 0.063
	Eastern Europe	3	2	0.667 ± 0.471	0.667 ± 0.314	0.381 ± 0.180
	Western Europe	15	6	1.800 ± 0.887	0.762 ± 0.096	0.550 ± 0.116
	Total	104				
J2	Near East	91	36	2.297 ± 0.554	0.951 ± 0.010	1.091 ± 0.051
	Eastern Europe	69	21	2.348 ± 0.845	0.881 ± 0.022	0.935 ± 0.045
	Western Europe	186	63	2.747 ± 0.942	0.910 ± 0.014	1.029 ± 0.028
	Total	346				
J2a	Near East	67	25	2.552 ± 0.722	0.928 ± 0.017	1.139 ± 0.056
	Eastern Europe	37	11	2.811 ± 1.260	0.784 ± 0.059	0.707 ± 0.096
	Western Europe	85	29	2.906 ± 1.378	0.715 ± 0.055	0.564 ± 0.065
	Total	189				
J2b	Near East	21	9	0.667 ± 0.278	0.833 ± 0.066	0.354 ± 0.056
	Eastern Europe	31	9	0.871 ± 0.527	0.708 ± 0.061	0.350 ± 0.072
	Western Europe	100	35	1.610 ± 0.814	0.893 ± 0.020	0.535 ± 0.038
	Total	152				
T	Near East	385	166	3.725 ± 0.944	1.208 ± 0.025	0.963 ± 0.006
	Eastern Europe	550	156	2.967 ± 0.939	1.043 ± 0.021	0.940 ± 0.006
	Western Europe	1127	274	2.800 ± 0.616	1.071 ± 0.016	0.965 ± 0.002
	Total	2062				
T1	Near East	158	46	2.608 ± 1.303	0.506 ± 0.036	0.822 ± 0.029
	Eastern Europe	158	43	2.525 ± 1.338	0.409 ± 0.045	0.651 ± 0.045
	Western Europe	193	57	1.782 ± 0.954	0.470 ± 0.040	0.758 ± 0.034
	Total	509				
T1a	Near East	131	35	0.733 ± 0.172	0.377 ± 0.036	0.753 ± 0.040
	Eastern Europe	140	32	0.586 ± 0.148	0.260 ± 0.034	0.557 ± 0.052
	Western Europe	183	52	0.874 ± 0.156	0.433 ± 0.040	0.732 ± 0.037
	Total	454				
T1b	Near East	21	6	0.333 ± 0.143	0.188 ± 0.063	0.495 ± 0.130
	Eastern Europe	16	9	1.313 ± 0.455	0.586 ± 0.116	0.850 ± 0.077
	Western Europe	8	3	0.250 ± 0.177	0.143 ± 0.068	0.464 ± 0.200
	Total	45				
T2	Near East	227	120	2.586 ± 0.551	1.009 ± 0.036	0.979 ± 0.004
	Eastern Europe	392	113	2.227 ± 0.616	0.775 ± 0.025	0.939 ± 0.007
	Western Europe	934	217	2.664 ± 0.640	0.902 ± 0.016	0.960 ± 0.003
	Total	1553				
T2a1b	Near East	8	6	0.750 ± 0.306	0.429 ± 0.106	0.893 ± 0.111
	Eastern Europe	19	5	0.474 ± 0.283	0.237 ± 0.061	0.620 ± 0.099
	Western Europe	28	11	0.893 ± 0.337	0.462 ± 0.072	0.847 ± 0.047
	Total	55				
T2b	Near East	36	19	1.333 ± 0.375	0.651 ± 0.073	0.919 ± 0.032
	Eastern Europe	187	53	0.904 ± 0.246	0.466 ± 0.034	0.807 ± 0.027
	Western Europe	421	97	1.097 ± 0.274	0.541 ± 0.022	0.870 ± 0.014
	Total	644				
T2c1	Near East	25	14	1.800 ± 0.584	0.747 ± 0.084	0.937 ± 0.026
	Eastern Europe	21	9	1.286 ± 0.493	0.626 ± 0.079	0.862 ± 0.048
	Western Europe	54	18	1.630 ± 0.635	0.614 ± 0.051	0.882 ± 0.028
	Total	100				
T2e	Near East	20	11	2.050 ± 0.779	0.868 ± 0.096	0.916 ± 0.041
	Eastern Europe	23	6	1.000 ± 0.749	0.262 ± 0.075	0.518 ± 0.122

	Western Europe	94	24	1.181 ± 0.601	0.457 ± 0.039	0.830 ± 0.027
	Total	137				
T2f	Near East	6	3	2.000 ± 1.202	0.354 ± 0.171	0.600 ± 0.215
	Eastern Europe	38	9	1.526 ± 0.781	0.498 ± 0.057	0.686 ± 0.070
	Western Europe	130	25	1.554 ± 0.870	0.424 ± 0.041	0.712 ± 0.041
	Total	274				

^a HVS-I haplotypes (from np 16051 to np 16400)
^b average divergence from the root
^c mean pairwise divergence (%)
^d gene diversity
Peak values are in bold.

Supplemental References

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