

Time to Most Recent Common Ancestor (Generations)

ID	Bav_1761a	Bav_1761b	Pol_1870	Bel_1650	Bel_1840	Bel_1880	Bav_1770	Fnc_1750	Hes_1750a	Fkf_1670	Hes_1750b	Hes_1540	Hes_1770	Hes_1750c	Hes_1750d	Cze_1820	Rom_1880	Cze_1840	Unknown	Ukraine	Hun_1820	Wert2	Wert1
Bav_1761a	-	11	11	8	8	11	17	17	18	14	14	11	11	14	14	21	14	14	11	11	17	20	14
Bav_1761b	11	-	17	14	14	11	24	24	21	20	20	17	17	20	20	25	20	20	17	17	11	27	20
Pol_1870	11	17	-	8	8	11	24	17	18	8	8	11	11	14	14	21	14	8	11	11	17	14	14
Bel_1650	8	14	8	-	4	8	20	14	14	11	11	8	8	11	11	18	11	11	8	8	14	17	11
Bel_1840	8	14	8	4	-	8	20	14	14	11	11	8	8	11	11	18	11	11	8	8	14	17	11
Bel_1880	11	11	11	8	8	-	24	17	18	14	14	11	11	14	14	21	14	14	11	11	11	20	14
Bav_1770	17	24	24	20	20	24	-	17	25	20	20	17	17	14	14	28	20	20	17	17	24	27	20
Fnc_1750	17	24	17	14	14	17	17	-	18	14	14	11	11	8	8	21	14	14	11	11	17	20	14
Hes_1750a	18	21	18	14	14	18	25	18	-	14	14	11	11	14	14	8	14	14	11	11	14	21	14
Fkf_1670	14	20	8	11	11	14	20	14	14	-	4	8	8	11	11	18	11	4	8	8	14	11	11
Hes_1750b	14	20	8	11	11	14	20	14	14	4	-	8	8	11	11	18	11	4	8	8	14	11	11
Hes_1540	11	17	11	8	8	11	17	11	11	8	8	-	4	8	8	14	8	8	4	4	11	14	8
Hes_1770	11	17	11	8	8	11	17	11	11	8	8	4	-	8	8	14	8	8	4	4	11	14	8
Hes_1750c	14	20	14	11	11	14	14	8	14	11	11	8	8	-	4	18	11	11	8	8	14	17	11
Hes_1750d	14	20	14	11	11	14	14	8	14	11	11	8	8	4	-	18	11	11	8	8	14	17	11
Cze_1820	21	25	21	18	18	21	28	21	8	18	18	14	14	18	18	-	18	18	14	14	18	25	18
Rom_1880	14	20	14	11	11	14	20	14	14	11	11	8	8	11	11	18	-	11	8	8	14	17	11
Cze_1840	14	20	8	11	11	14	20	14	14	4	4	8	8	11	11	18	11	-	8	8	14	11	11
Unknown	11	17	11	8	8	11	17	11	11	8	8	4	4	8	8	14	8	8	-	4	11	14	8
Ukraine	11	17	11	8	8	11	17	11	11	8	8	4	4	8	8	14	8	8	4	-	11	14	8
Hun_1820	17	11	17	14	14	11	24	17	14	14	14	11	11	14	14	18	14	14	11	11	-	20	14
Wert2	20	27	14	17	17	20	27	20	21	11	11	14	14	17	17	25	17	11	14	14	20	-	11
Wert1	14	20	14	11	11	14	20	14	14	11	11	8	8	11	11	18	11	11	8	8	14	11	-

- Infinite allele mutation model is used

- Average mutation rate varies: 0.0054 to 0.0054, from FTDNA derived rates

- Probability is 80% that the TMRCA is no longer than indicated