Whole mitochondrial DNA sequencing in Alpine populations and the genetic history of the Neolithic Tyrolean Iceman

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Figure S1. Approximate places of origin of the K alpine samples (yellow stars) analyzed in this study and place of discovery of the Tyrolean Iceman (red star). Map was created by Kathrin Renner (Eurac-Research) using ESRI 2011 ArcGIS Desktop: Release 10.

Figure S2. Median Joining network of 42 K sequences from alpine populations analyzed in this study more 6 K sequences from south Tyrolean area[1] (see also Table S2). Weight at the different positions were assigned according to[2].

Figure S3. Bayesian skyline plot showing changes thought the time (kya, abscissa) of the effective population size (Ne, ordinate) of haplogroup K1 in the Alps.

Table S1. Total K Alpine samples analyzed in this study. This table is provided in a separate file.

Table S2. Total K1 mitogenomes used in this study. This table is provided in a separate file.

Table S3. TMCRA estimates of K1 haplogroup and ist sub-clades. This table is provided in a separate file.

References

1. Pichler, I. *et al.* Drawing the history of the Hutterite population on a genetic landscape: inference from Y-chromosome and mtDNA genotypes. *Eur. J. Hum.Genet*. **18,** 463–470 (2010).
2. Brandstätter, A. *et al.* Timing and deciphering mitochondrial DNA macro-haplogroup R0 variability in Central Europe and Middle East. *BMC Evol. Biol*. **8,** 191 (2008).
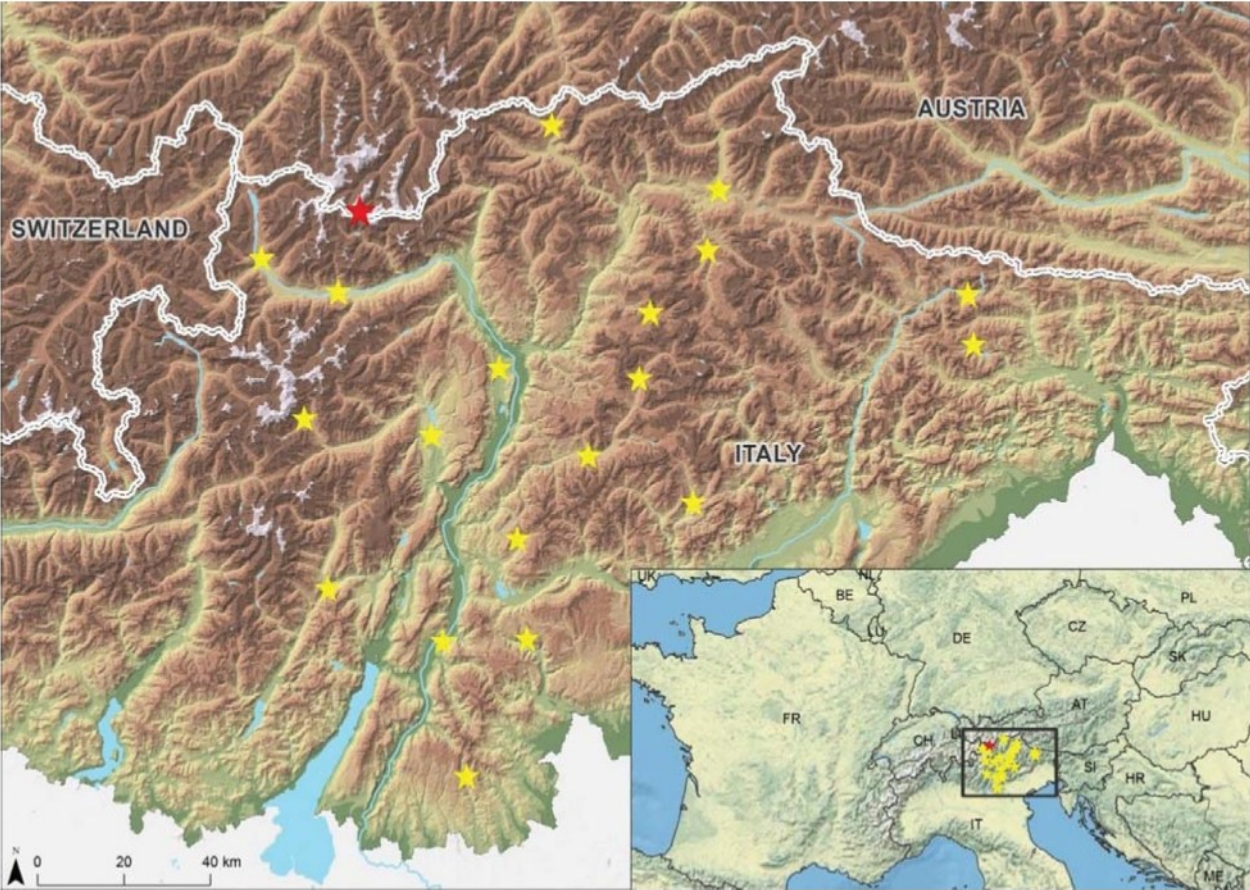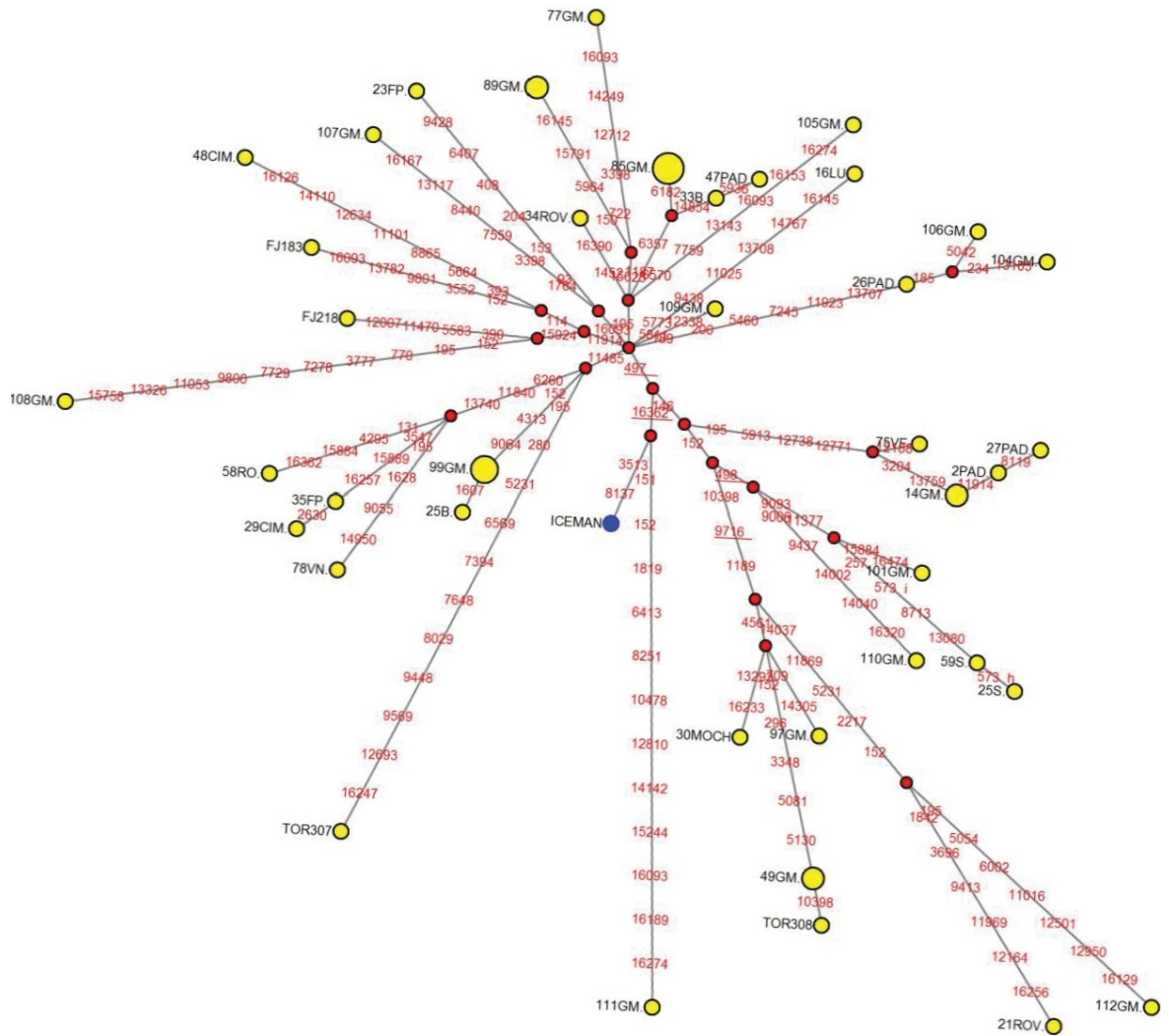
Figure S1

Figure S2

Figure S3