Supplementary Information for Heredity Original Research Article:

Mitochondrial genomes from modern and ancient Turano-Mongolian cattle reveal an ancient diversity of taurine maternal lineages in East Asia

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Supplementary Figures and Table

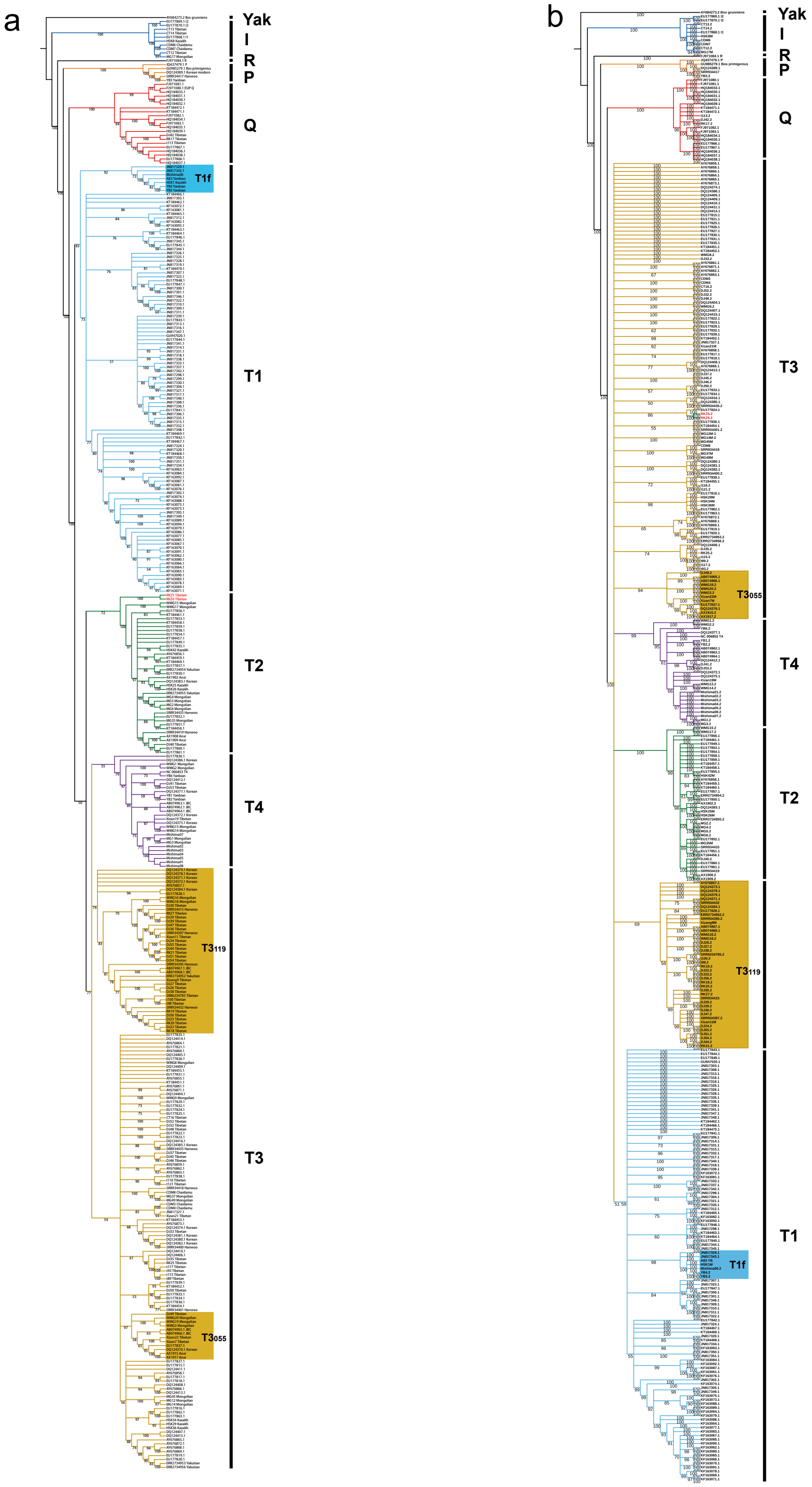

Fig. S1 Maximum Likelihood (ML) (a) and Bayesian Inference (BI) (b) phylogenetic trees for complete mitogenomes of 370 domestic cattle. Both trees were constructed with the yak sequence (AY684273) as outgroup. The values on the branch represent the bootstrap values (a) and posterior probability (b) respectively. The lineages color labeling of BI tree was consistent with ML approach. The labels of RKZ5 and RKZ6 are highlighted in red.

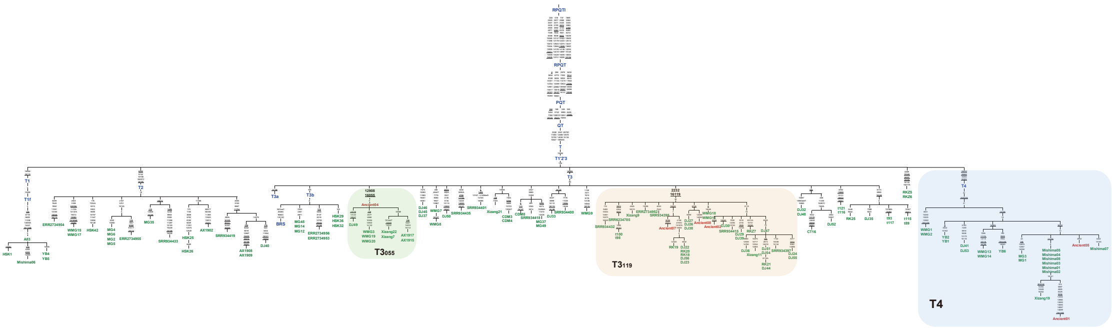

Fig. S2 Maximum parsimony (MP) tree of complete mitogenomes belonging to haplogroup T in Turano-Mongolian modern and ancient cattle. This tree was built and rooted as previously described by Achilli *et al.* (2008). The position of the Bovine Reference Sequence (BRS, V00654.1) is indicated for reading off-sequence motifs. Branches display mutations with numbers according to the BRS; they are transitions unless a base is explicitly indicated for transversions (to A, G, C, or T) or a suffix for indels (+, d) and heteroplasmy (h). Recurrent mutations within the phylogeny are underlined and back mutations are marked with the suffix @. Note that the reconstruction of recurrent mutations in the control region is in a number of cases ambiguous.

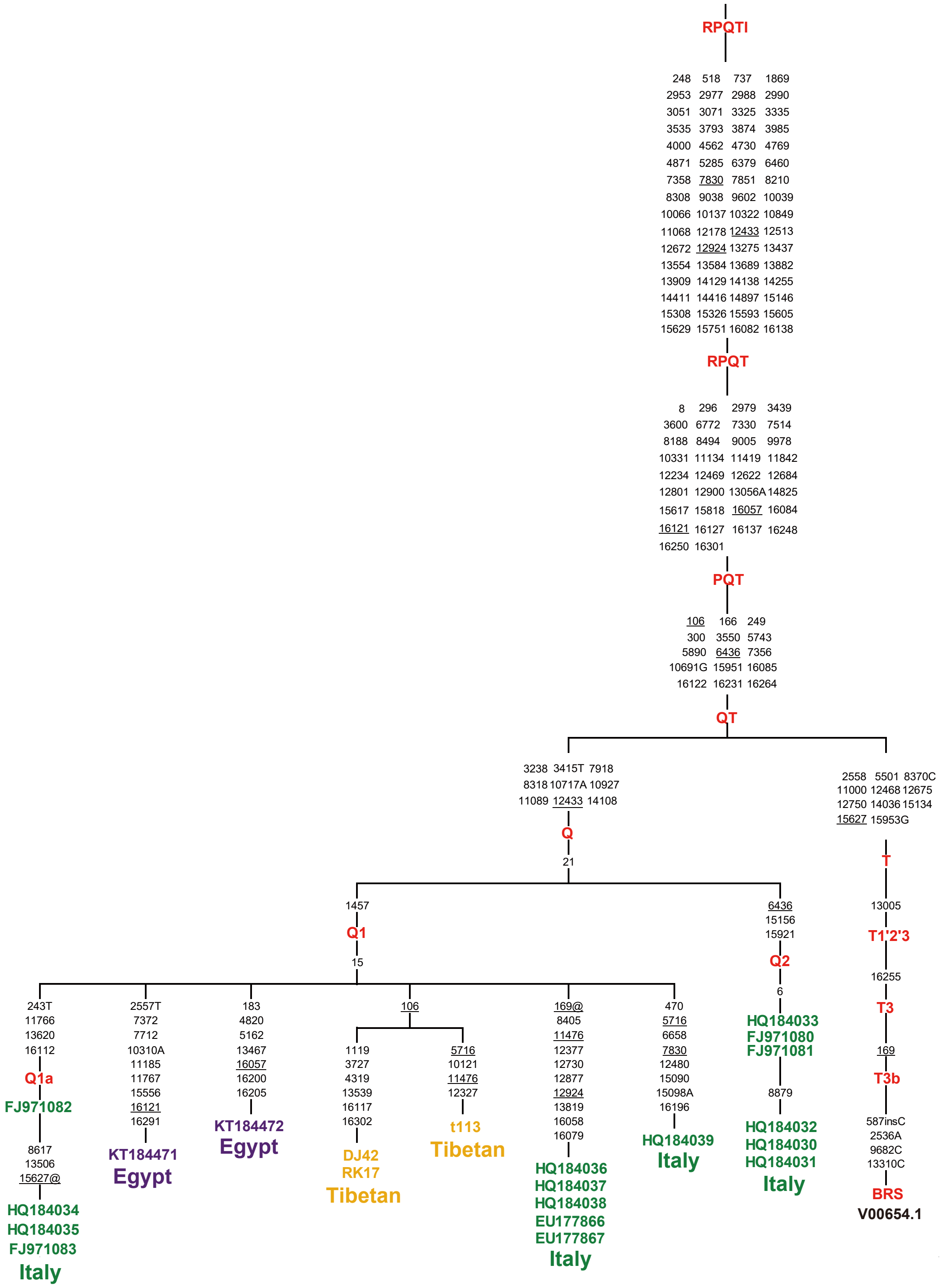

Fig. S3 Maximum parsimony (MP) tree of complete mitogenomes belonging to haplogroup Q. This tree was built and rooted as previously described by Achilli *et al*. (2008). The position of the Bovine Reference Sequence (BRS, V00654.1) is indicated for reading off-sequence motifs. Branches display mutations with numbers according to the BRS; they are transitions unless a base is explicitly indicated for transversions (to A, G, C, or T) or a suffix for indels (+, d) and heteroplasmy (h). Recurrent mutations within the phylogeny are underlined and back mutations are marked with the suffix @. Note that the reconstruction of recurrent mutations in the control region is in a number of cases ambiguous.

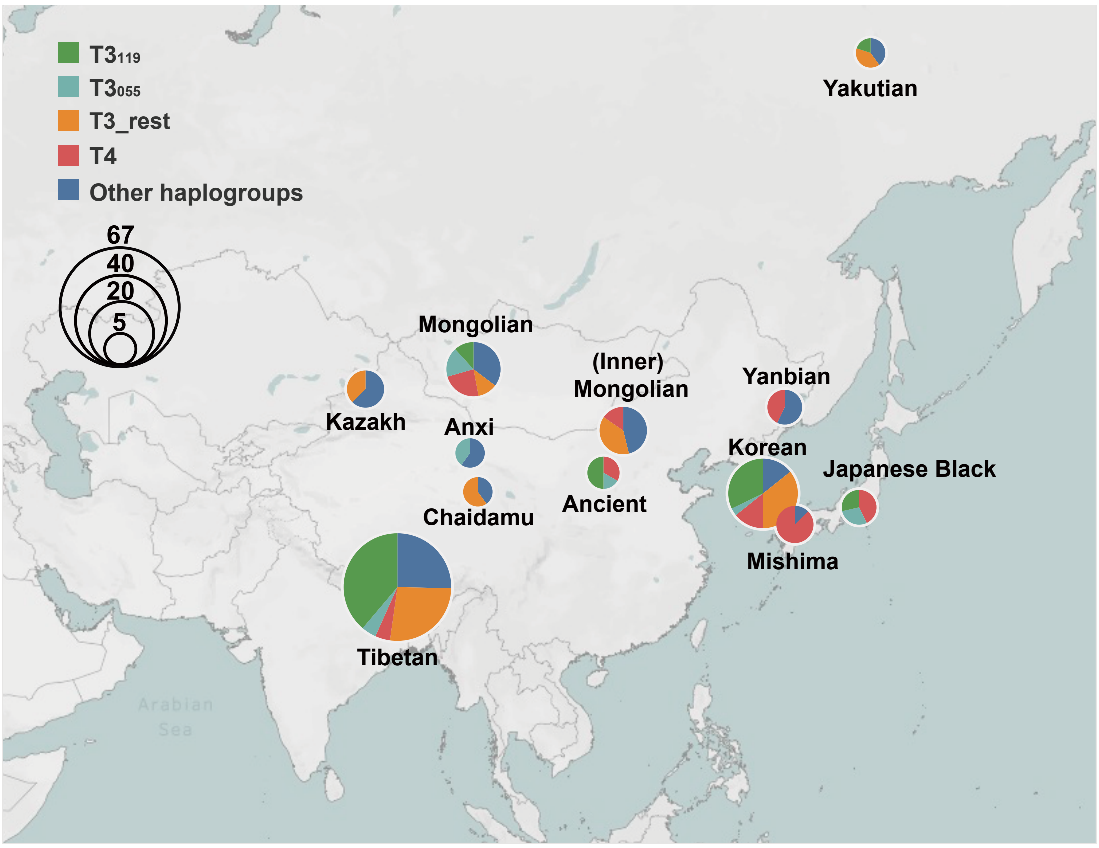

Fig. S4 The map of Asia shows the location of the specimens and associated the Turano-Mongolian-specific haplogroup/sub-haplogroups.

Dataset Table S1-S5

Table S1 Overview of sample information and sequencing statistics for Turano-Mongolian cattle.

Table S2 Whole mitochondrial genome sequences information used in this study.

Table S3 Polymorphic sites for the mitochondrial genome haplotypes in Turano-Mongolian cattle.

Table S4 Comparison of variation position information of T1f in Asia and Europe/Africa.

Table S5 Divergence time estimates of Turano-Mongolian cattle haplogroups based on coding region (from np 364 to np 15 791).