

Supporting Information

Zhao et al. 10.1073/pnas.0907844106

SI Text

1. Andrews RM, et al. (1999) Reanalysis and revision of the Cambridge reference sequence for human mitochondrial DNA. *Nat Genet* 23:147.
2. Kong Q-P, et al. (2003) Phylogeny of East Asian mitochondrial DNA lineages inferred from complete sequences. *Am J Hum Genet* 73:671–676.
3. Palanichamy MG, et al. (2004) Phylogeny of mitochondrial DNA macrohaplogroup N in India, based on complete sequencing: Implications for the peopling of South Asia. *Am J Hum Genet* 75:966–978.
4. Kong Q-P, et al. (2006) Updating the East Asian mtDNA phylogeny: A prerequisite for the identification of pathogenic mutations. *Hum Mol Genet* 15:2076–2086.
5. Sun C, et al. (2006) The dazzling array of basal branches in the mtDNA macrohaplogroup M from India as inferred from complete genomes. *Mol Biol Evol* 23:683–690.
6. Olivieri A, et al. (2006) The mtDNA legacy of the Levantine early Upper Palaeolithic in Africa. *Science* 314:1767–1770.
7. Bandelt H-J, Macaulay V, Richards M (2000) Median networks: Speedy construction and greedy reduction, one simulation, and two case studies from human mtDNA. *Mol Phylogenet Evol* 16:8–28.
8. Soares P, et al. (2009) Correcting for purifying selection: An improved human mitochondrial molecular clock. *Am J Hum Genet* 84:740–759.

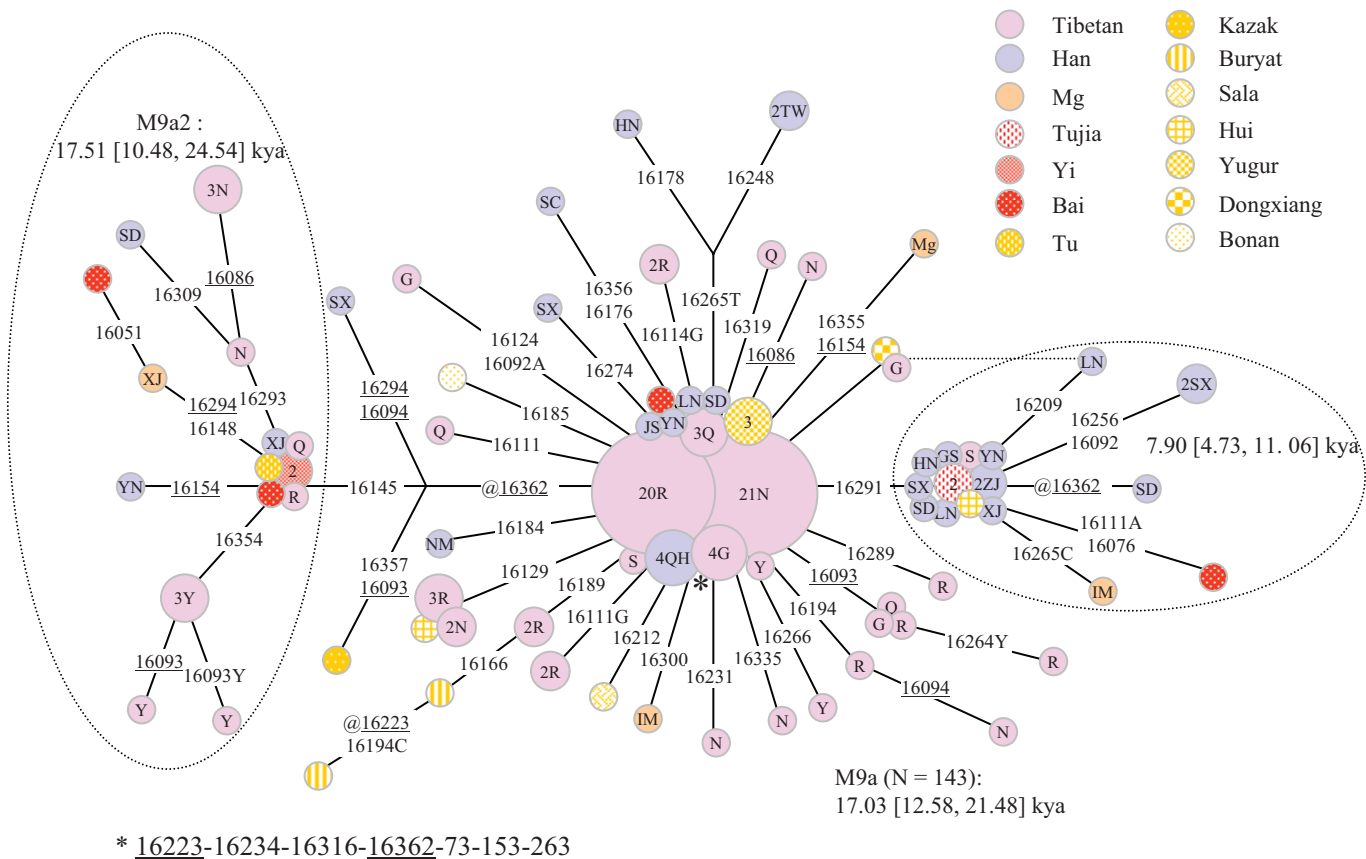
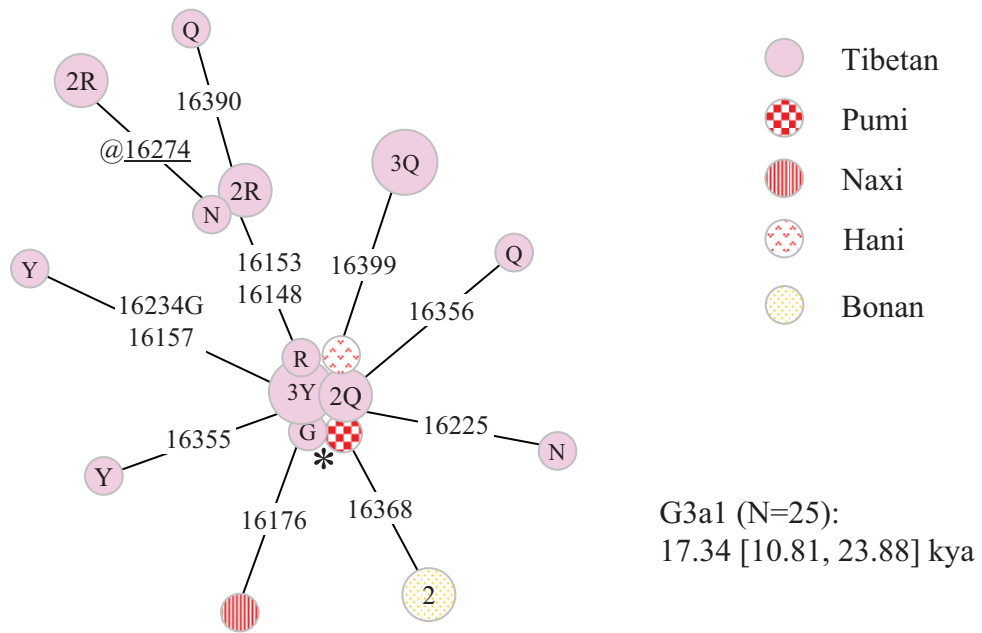
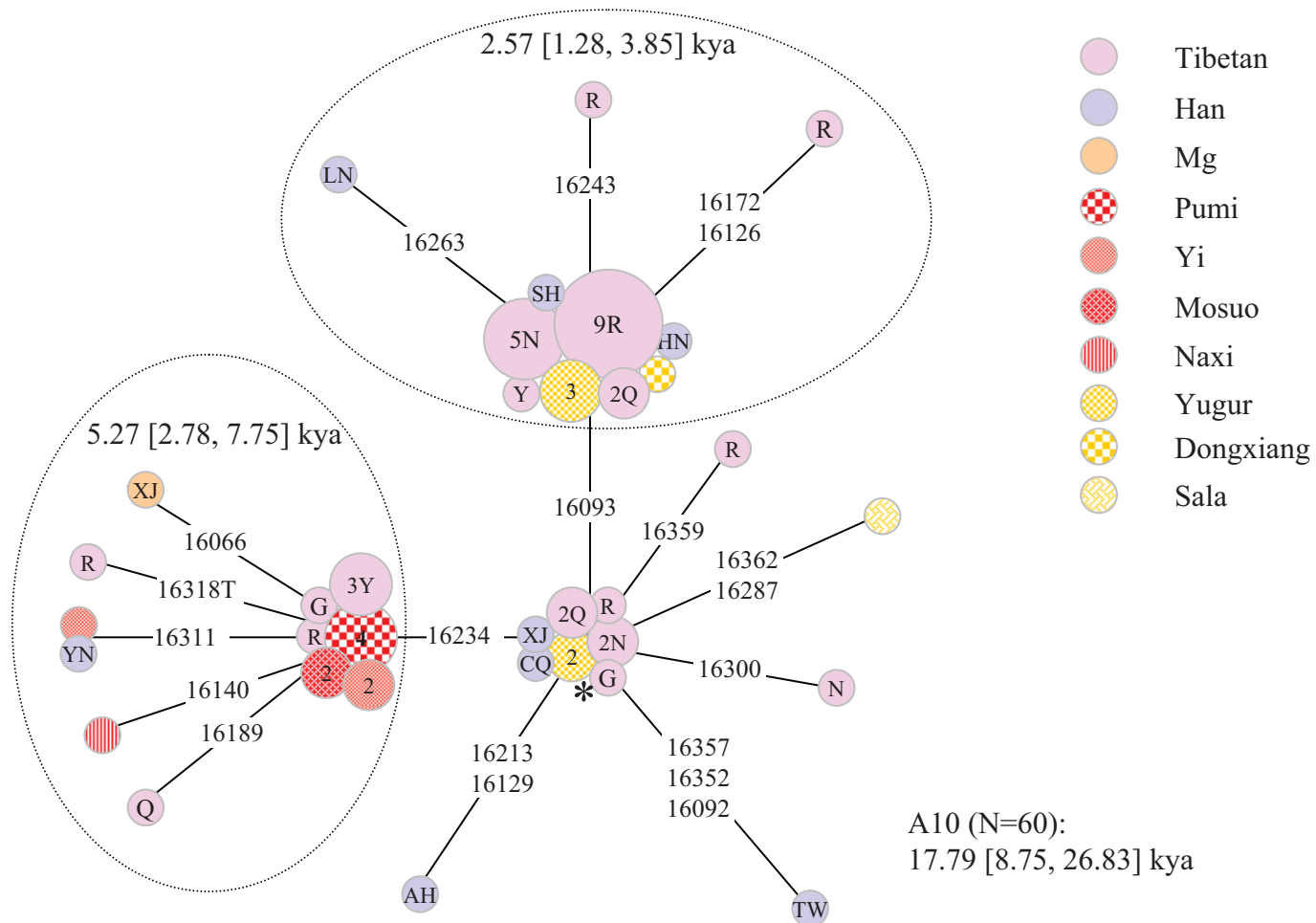


Fig. S2. Median network of haplogroup M9a. This network was constructed manually according to Bandelt et al. (7). The data used here were collected from the literature (Table S2) and the present study (Tables S3 and S5). The sequence information used for network construction was confined to segment 16047–16497. Suffixes “A,” “C,” “G,” and “T” refer to transversions; “Y” specifies heteroplasmic status *CT* at the site; recurrent mutations are underlined; and “@” denotes a reverse mutation. Time estimation was carried out based on segment 16051–16400 as described previously (8). Codes “N,” “R,” “Q,” “Y,” “S,” and “G” refer to sampling locations (Nakchu, Shigatse, Qinghai, Yunnan, Sichuan, and Gansu, respectively) of different regional Tibetan populations. The asterisk denotes the ancestral node of the haplogroup defined by motif 16223-16234-16316-16362-73-153-263.



* 16215-16223-16274-16T-73-143-150-263

Fig. S5. Median network of haplogroup G3a1. The asterisk denotes the ancestral node of the haplogroup defined by motif 16215-16223-16274-16T-73-143-150-263. For more information, see Fig. S2.



* 16223-16290-16293C-16319-73-152-235-263

Fig. S6. Median network of haplogroup A10. The asterisk denotes the ancestral node of the haplogroup defined by motif 16223-16290-16293C-16319-73-152-235-263. For more information, see Fig. S2.

Other Supporting Information Files

- [Table S1](#)
- [Table S2](#)
- [Table S3](#)
- [Table S4](#)
- [Table S5](#)