

Phylogeographic and genome-wide investigations of Vietnam ethnic groups reveal signatures of complex historical demographic movements

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Supplementary Data

Figure S1. Phylogenetic networks of HVS-I mtDNA Vietnamese sequences.

Figure S2. Maximum parsimony trees based on CR sequences representing haplogroup M7b1a1f (A) and F1f (B). See Figure 3 for more information.

Figure S3. EBSPs (with 95% CI) of haplogroup F1f and M7b1a1f obtained from complete mitogenomes.

Figure S4. EBSP of main Vietnamese ethnics.

Figure S5. MDS plot of IBS values considering different SEA populations (Table S2) and one European (CEU) and one African population (YRI).

Figure S1.

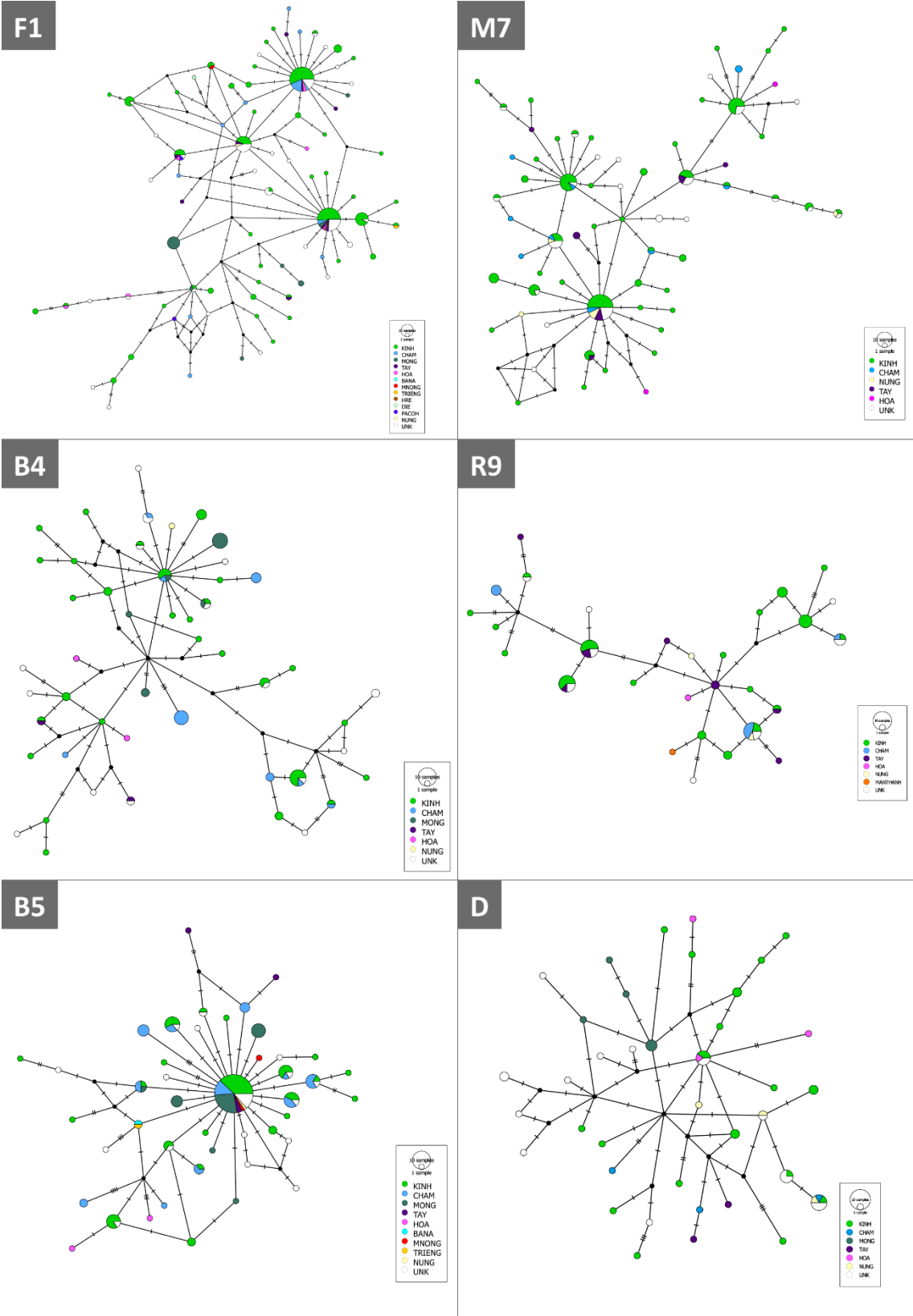


Figure S1.

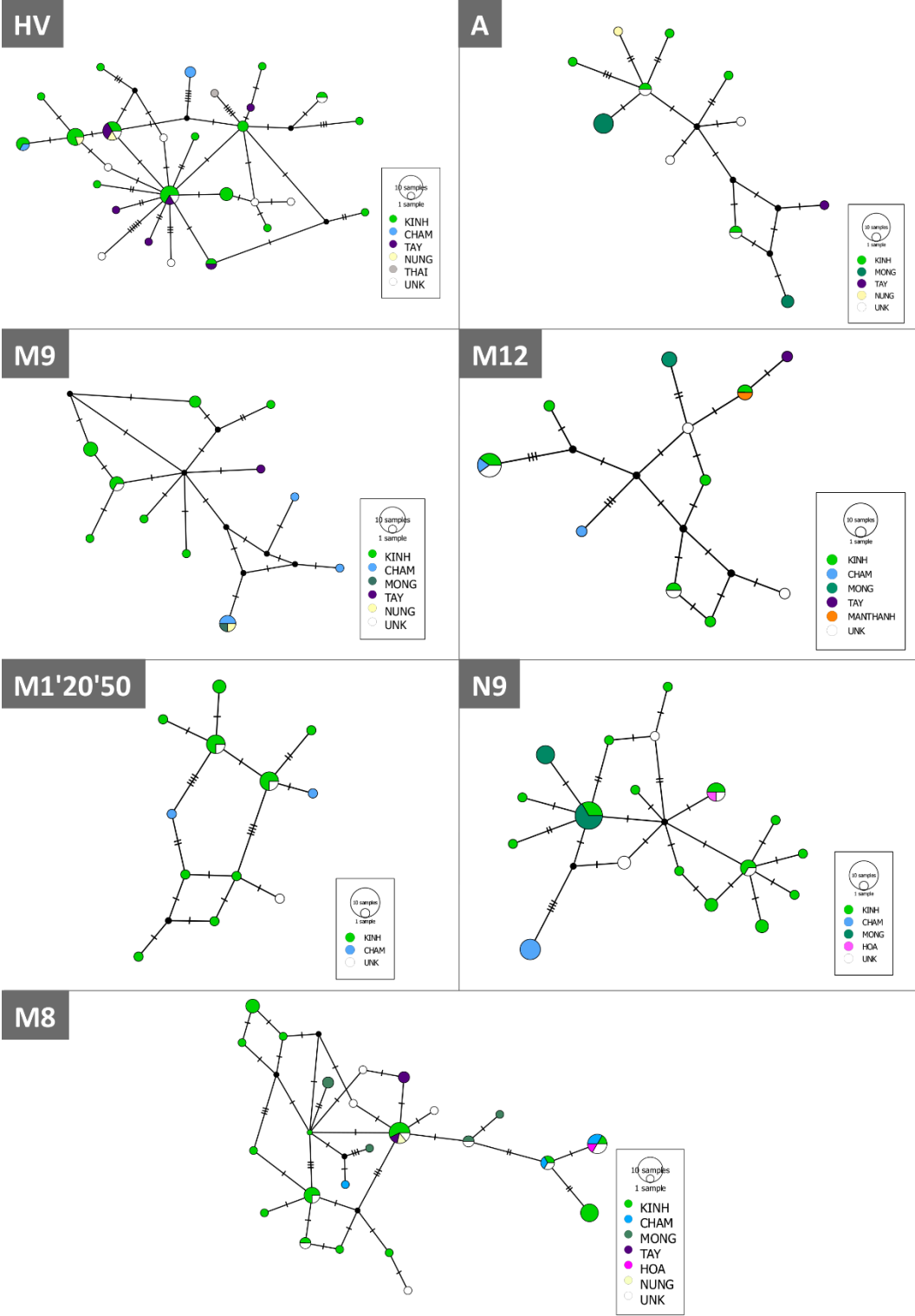
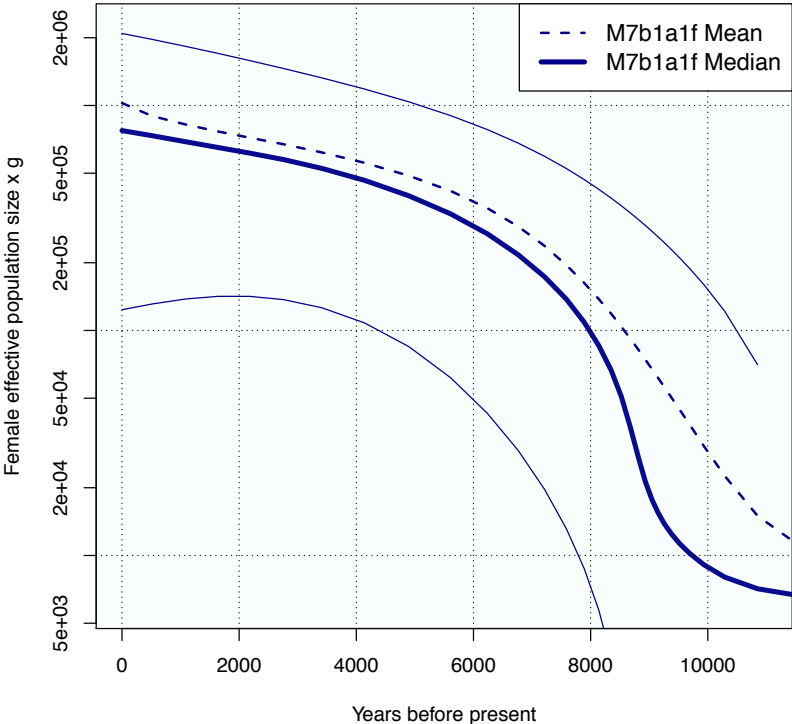


Figure S3.

A



B

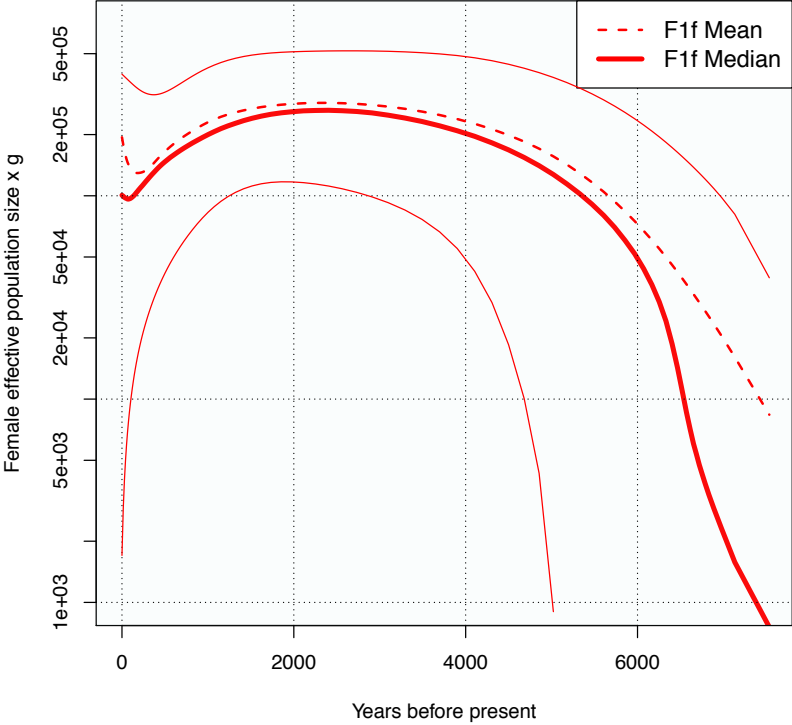


Figure S4.

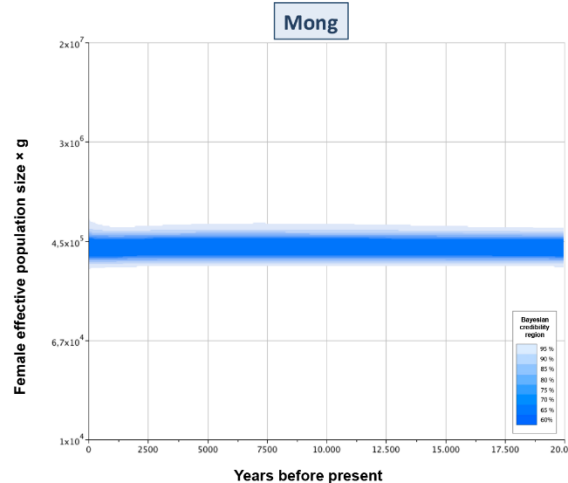
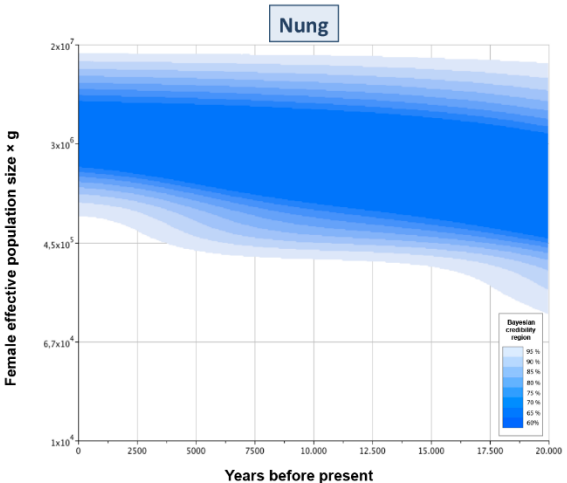
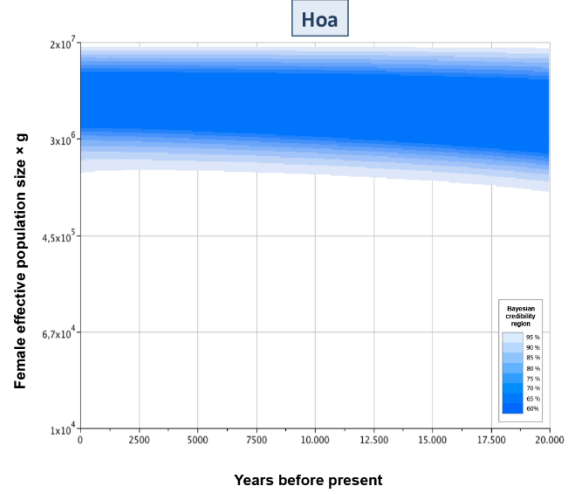
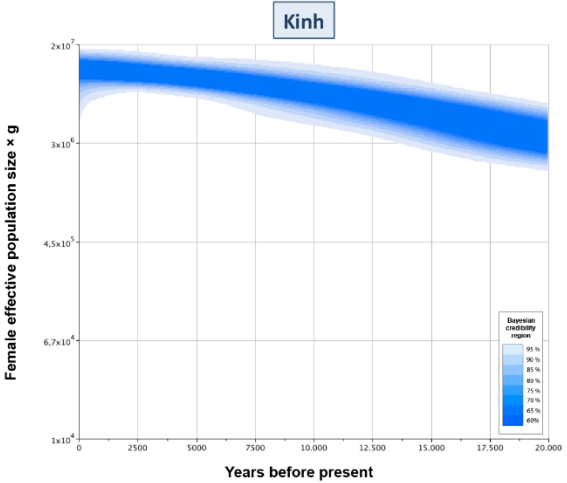
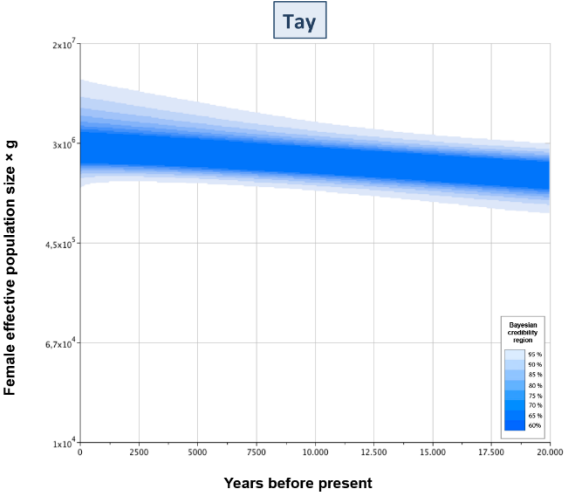
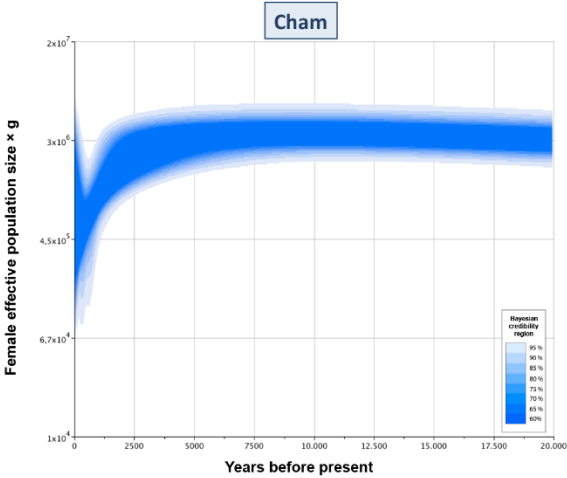
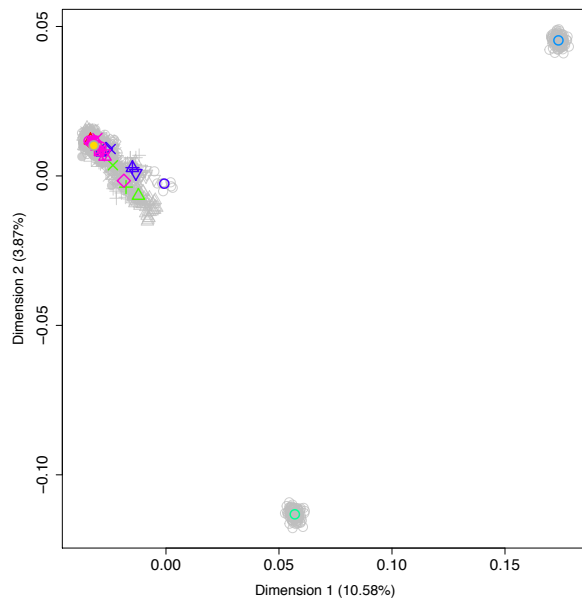
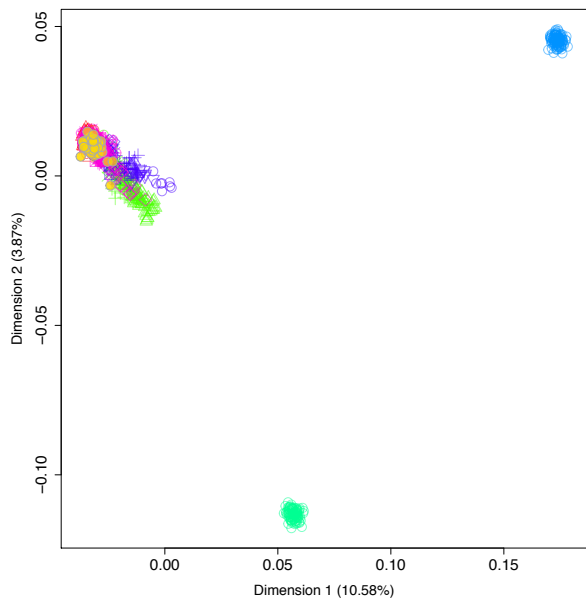


Figure S5.



- Europe**
- CEU
- Africa**
- YRI
- China**
- CHS
- △ CDX
- Malaysia**
- Bidayuh
- △ Negrito
- + Malay
- × Proto-Malay
- Philippines**
- Ayta
- △ Agta
- + Ati
- × Iraya
- ◇ Minanubu
- ▽ Mamanwa
- Filipino
- Thailand**
- Hmong (Miao)
- △ Karen
- + Lawa
- × Mlabri
- ◇ Mon
- ▽ Paluang
- Plang
- * Tai Khuen
- ◇ Tai Lue
- ⊗ H'tin
- ▲ Tai Yuan
- Tai Yong
- ⊗ Yao
- Vietnam**
- KHV