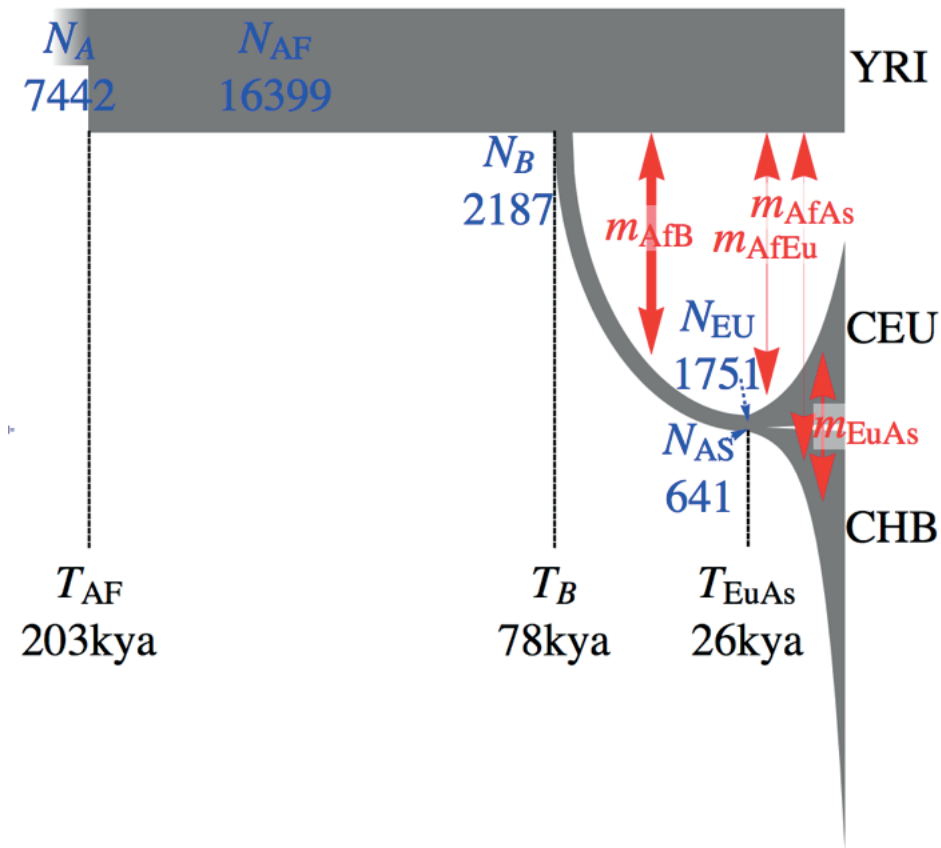


Supplementary information S2 (figure)



Demographic history based on the site frequency spectrum and sharing of rare alleles.

a) Updated three-population demographic model based on synonymous sites from 1000 Genomes Phase 1 data<sup>1</sup>, assuming a mutation rate of  $2.36 \times 10^{-8}$ /bp/g and a generation time of 25 years (for ease of comparison with Gravel *et al.*<sup>2</sup> and Tennessen *et al.*<sup>3</sup>). Estimated times and population sizes are inversely proportional to the assumed mutation rate.

1. Consortium, T. 1. G. P. *et al.* An integrated map of genetic variation from 1,092 human genomes. *Nature* **490**, 56–65 (2013).
2. Gravel, S. *et al.* Demographic history and rare allele sharing among human populations. *Proceedings of the National Academy of Sciences* **108**, 11983–11988 (2011).
3. Tennessen, J. A. *et al.* Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. *Science* **337**, 64–69 (2012).