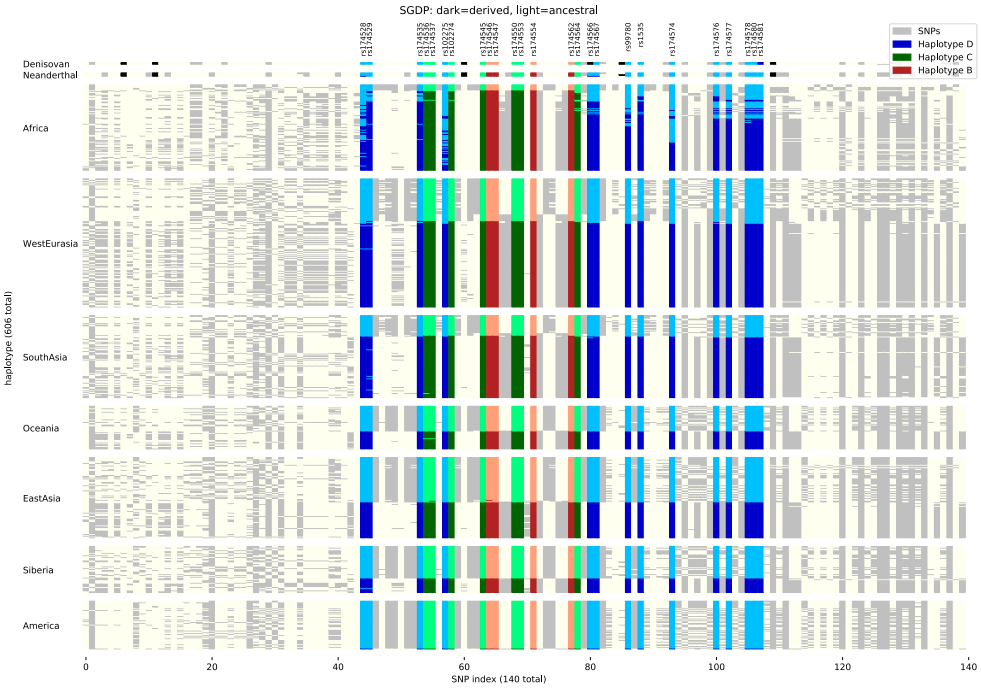
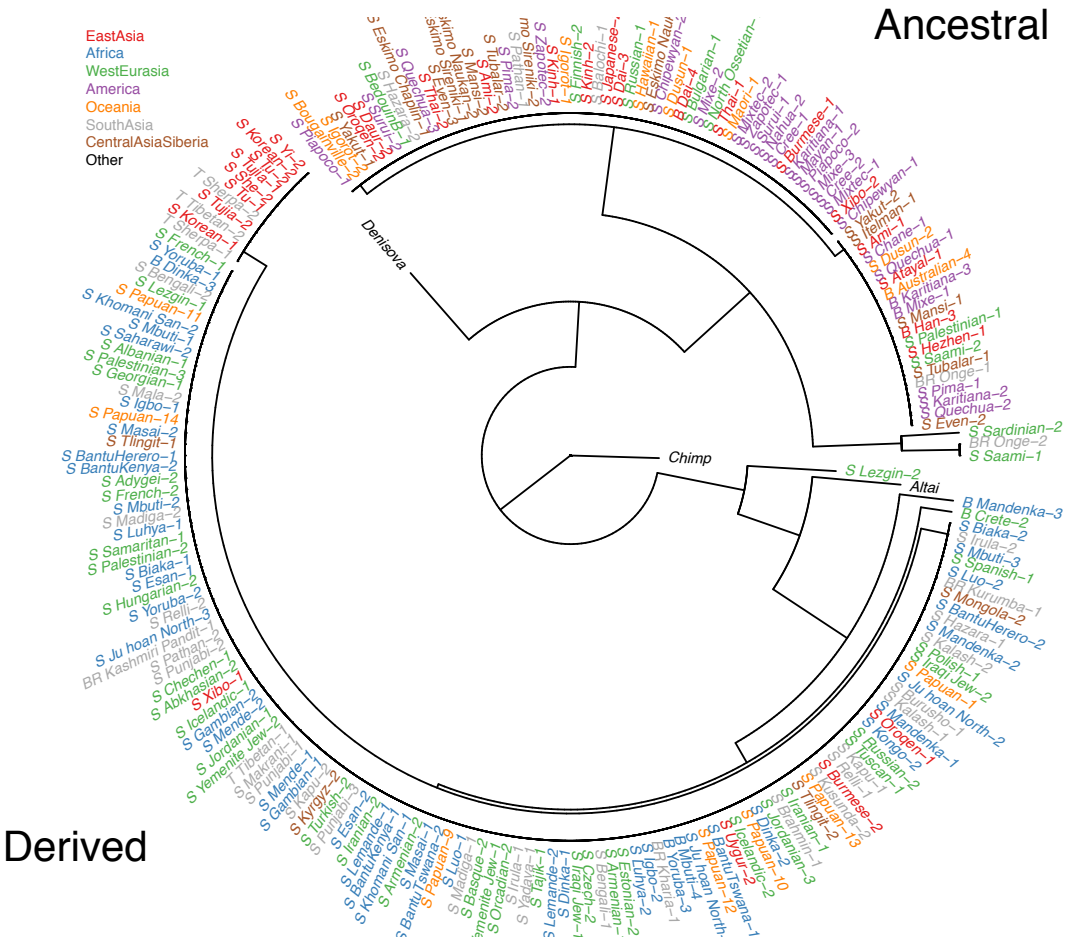
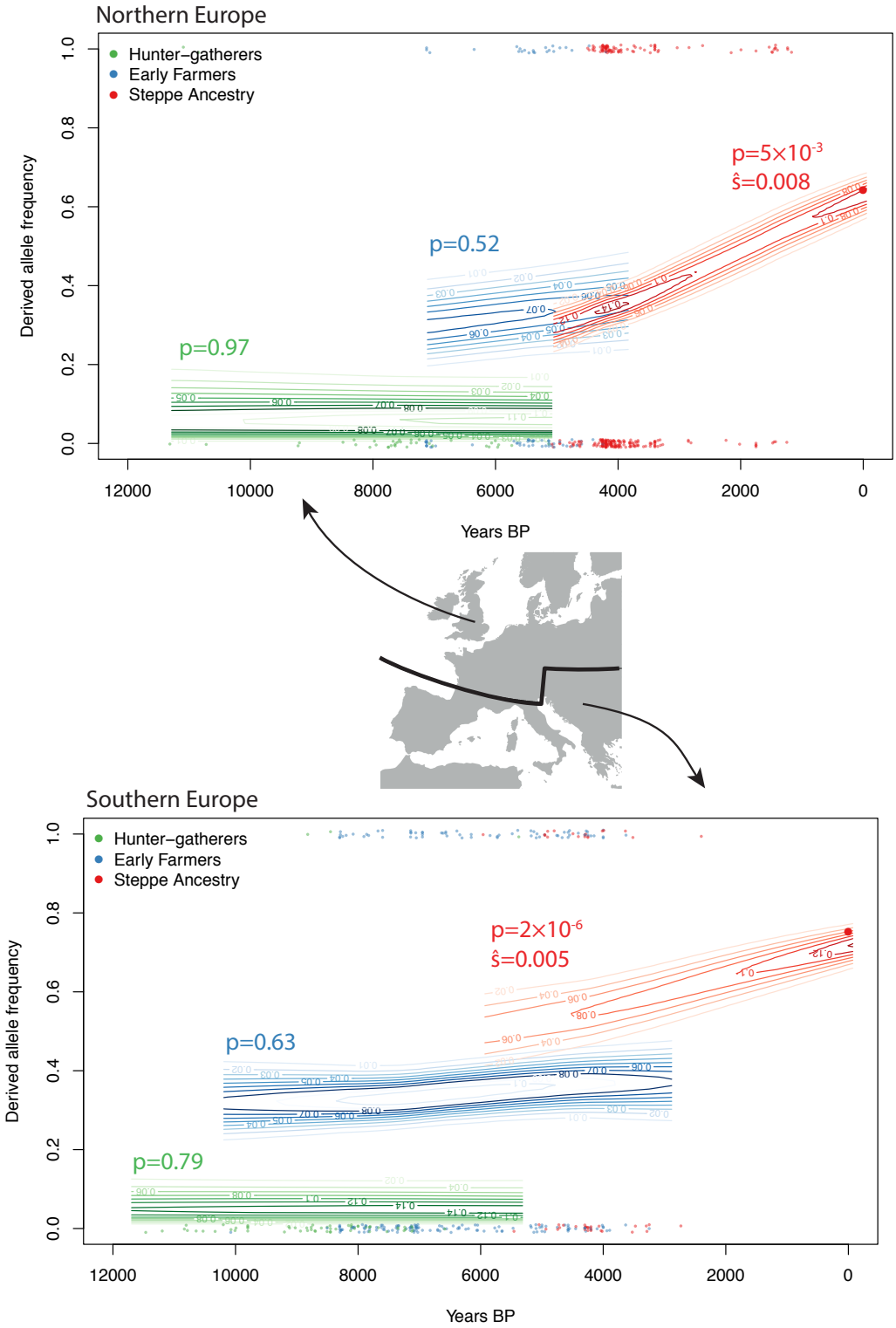


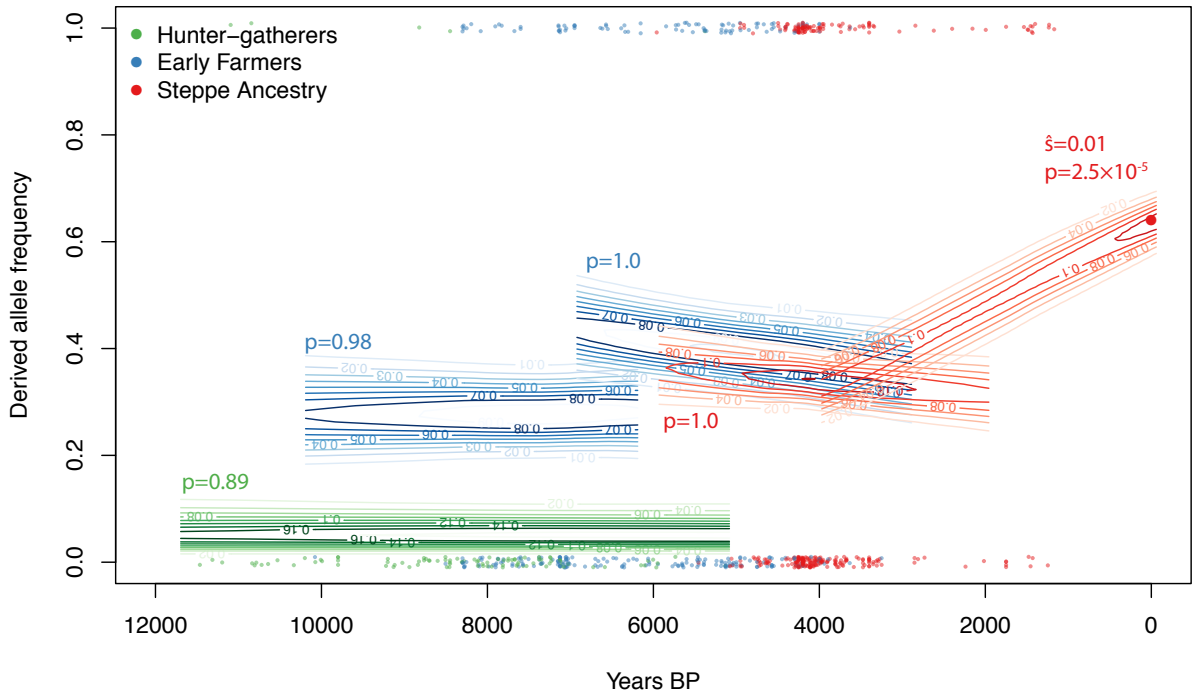
Supplementary Figure 1: As Figure 1A, including all 300 SGDP individuals.



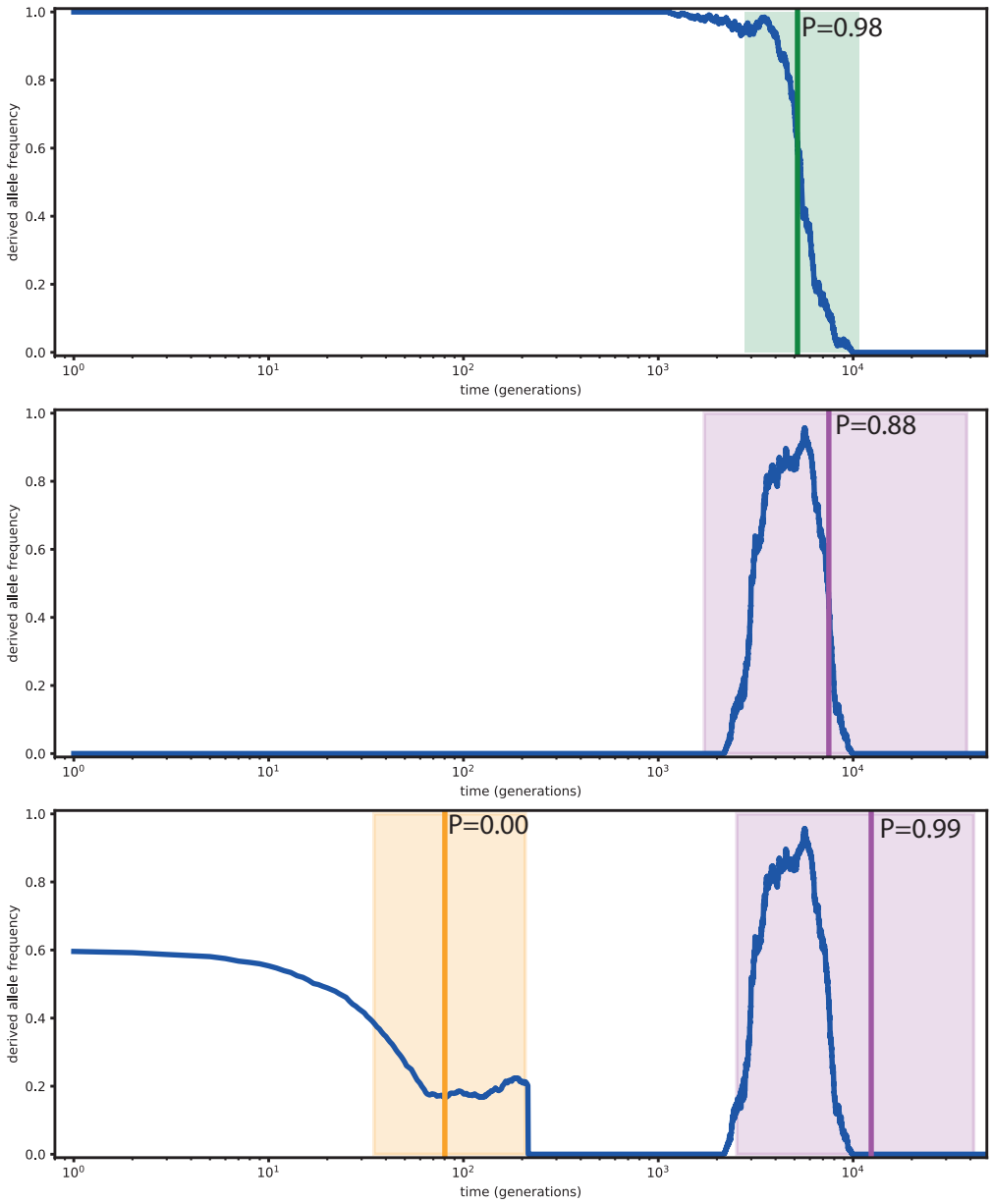
Supplementary Figure 2: UPGMA tree of haplotype B region including all 211 SGDP individuals homozygous at rs174546.



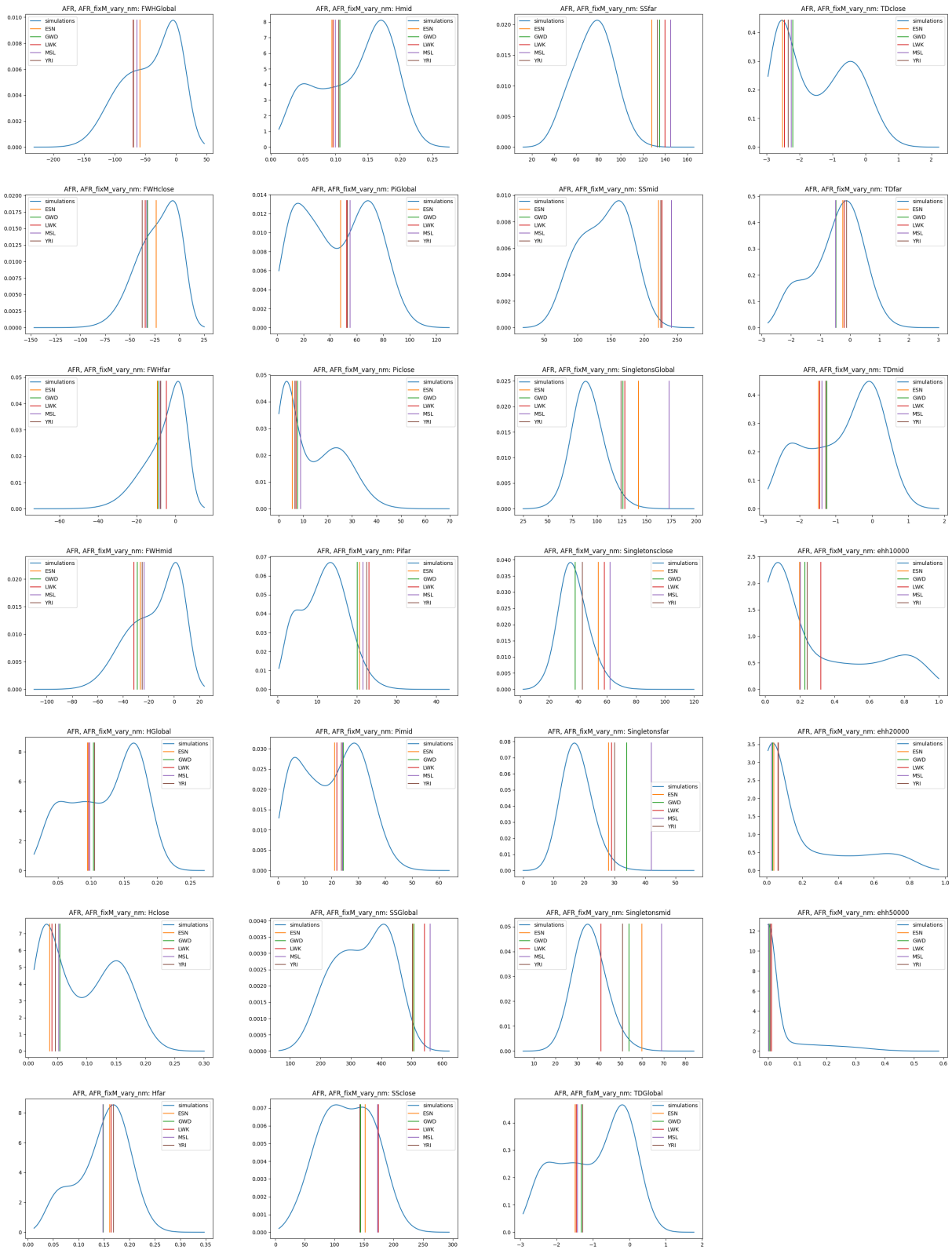
Supplementary Figure 3: Ancient DNA based allele frequency trajectories for rs174546, as in Figure 2C, computed separately for Northern and Southern Europe – border chosen to approximately represent the extent of the Neolithic in 7000 BP.



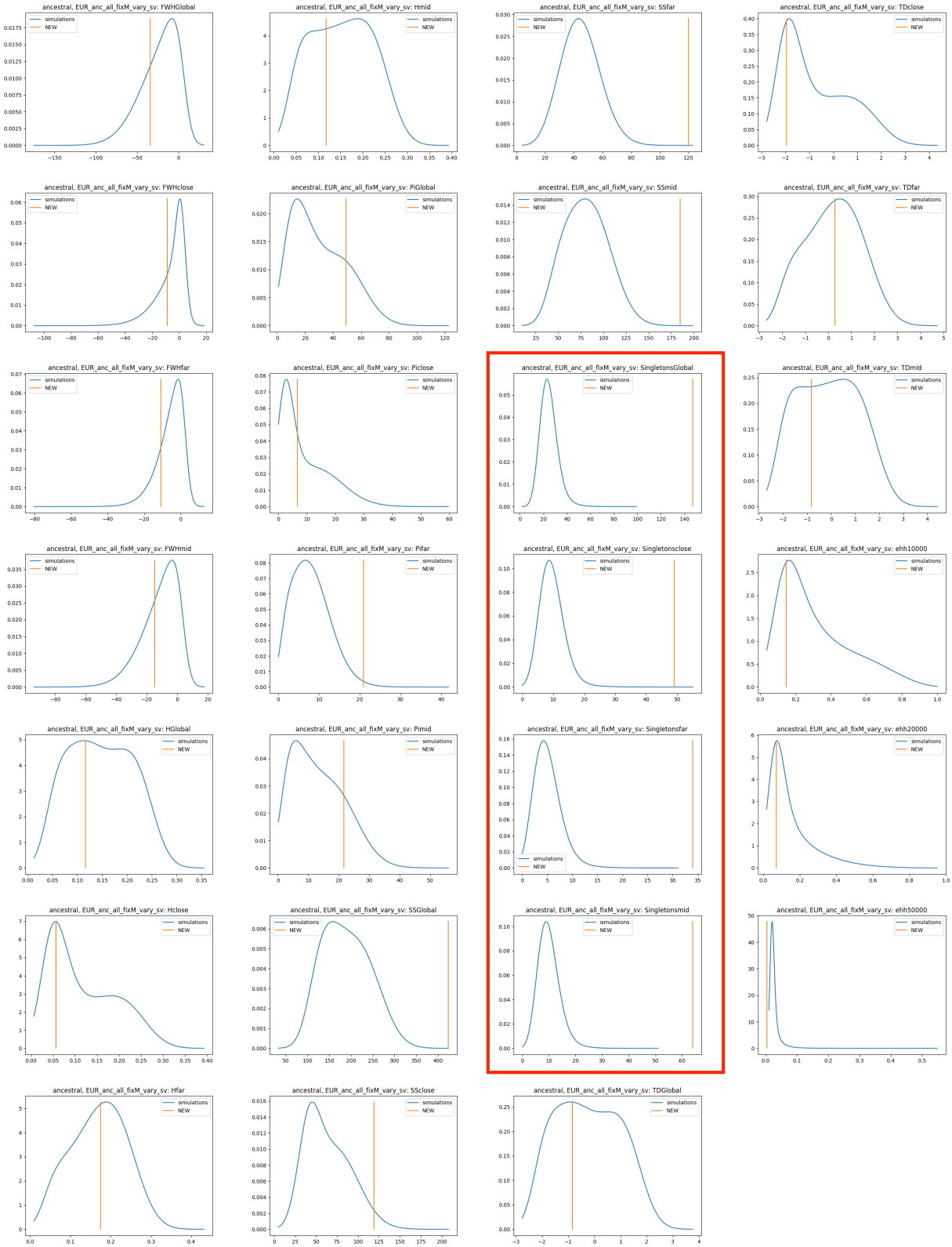
Supplementary Figure 4: Ancient DNA based allele frequency trajectories for rs174546, as in Figure 2C, but with Early Farmer and Steppe ancestry populations split into (overlapping) 4,000 year blocks.



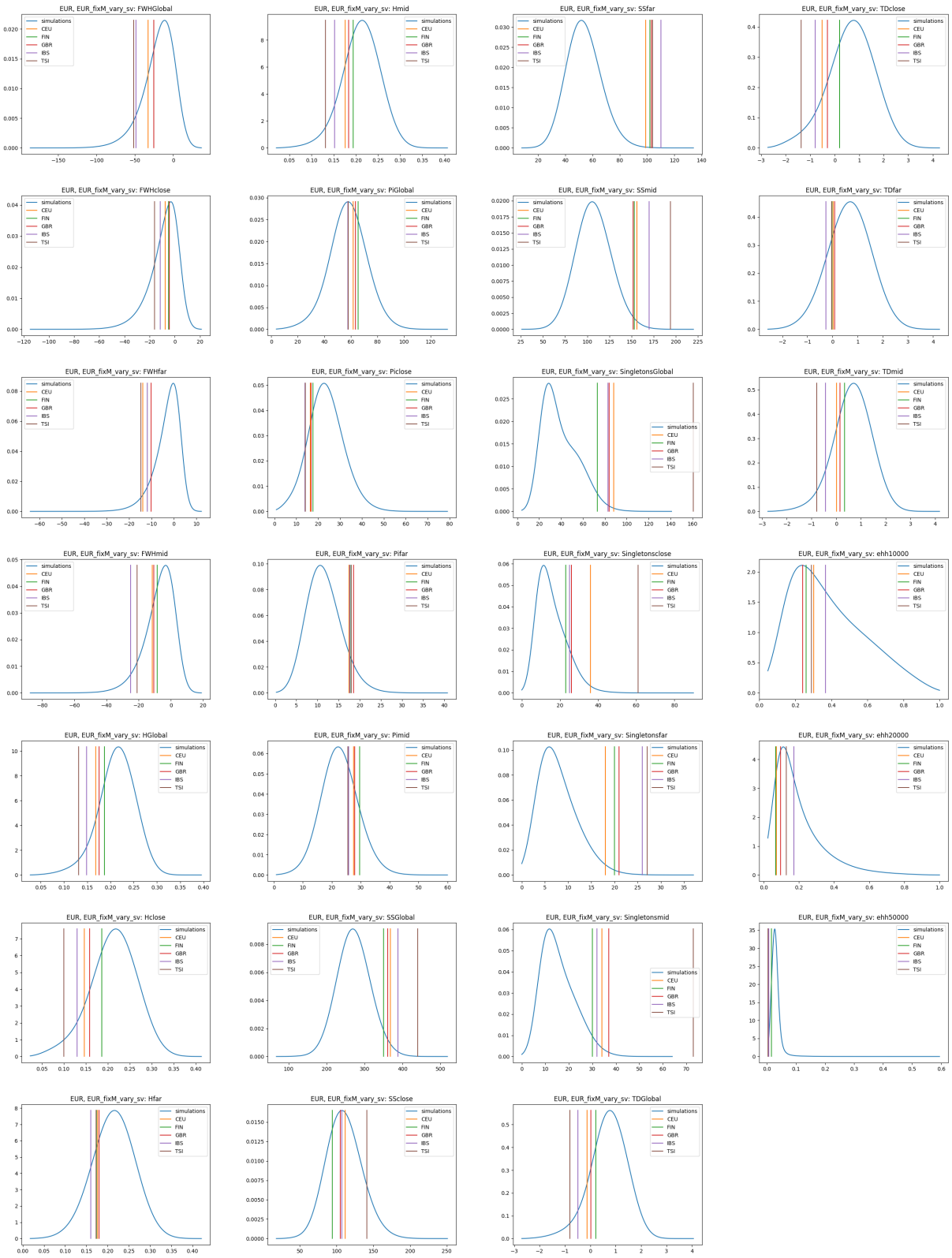
Supplementary Figure 5: ABC results on complex histories. Each plot shows the allele frequency trajectory, and ABC credible intervals for selection under complex histories. Top: ancient selection on the derived allele (green). Middle: ancient selection on the ancestral allele (purple) following ancient selection for the derived allele. Bottom: recent selection for the derived allele (orange) and ancient selection for the ancestral allele (purple), following ancient selection for the derived allele. Probability of selection on new mutation indicated by P. Ancient selection does not affect inference of recent selection, but selection on the ancestral allele is uncertain and may be misclassified as selection on a new mutation.



Supplementary Figure 6: Simulated summary statistic distributions (blue density) and observed values (vertical lines) for ancient selection on the derived allele in Africa, for a new mutation. See Peter, et al. (2012) for descriptions of the statistics.



Supplementary Figure 7: Simulated summary statistic distributions (blue density) and observed values (vertical lines) for selection on standing variation on the ancestral allele in Europeans. See Peter, et al. (2012) for descriptions of the statistics. The Fay and Wu's H statistics (red box) are excluded from ABC.



Supplementary Figure 8: Simulated summary statistic distributions (blue density) and observed values (vertical lines) for recent selection on standing variation on the derived allele in Europeans. See Peter, et al. (2012) for descriptions of the statistics.