

**Figure SF 1. Simulated examples employed for the qualitative evaluation.** A) simulated scenario employed to perform a parameter estimation analysis. It contains nine parameters: effective population sizes of the present populations (*Ne*1, *Ne*2 and *Ne*3), as well as the ancestral populations (*Ne*4, *Ne*5 and *Ne*6), the time to the demographic expansion of population 2 (*t1*) and the time to two split events (*t*2 and *t*3). Real values were *Ne*1 = 10 000, *Ne*2 = 15 000, *Ne*3 = 5 000, *Ne*4 = 2 814, *Ne*5 = 17 814, *Ne*6 = 6 284,*t1* = 5 000, *t*2 = 10 000, and *t*3 = 40 000. B-E) four competing models that were used for model choice analysis (where third model -bottleneck- was the right one). In the scenario for parameters estimation (A), the generation time was one per year, the mutation rate was set to 0.15 per site per million years (/site/106y), the transition/transversion bias was 0.875 and the gamma shape parameter was 0.15. The sample consisted of 51 heterochronous DNA sequences with ages ranging from 0 - 38 910 years before present, and DNA sequences were 1 000 bp long. In the scenarios for model choice (B - E) the generation time was 15 years, the mutation rate was set to 0.247 /site/106y , the transition/transversion bias was 0.9798 and the gamma shape parameter was 0.05. The sample consisted of 59 heterochronous DNA sequences with ages ranging from 3 685 to 61 600 years before present. Analyzed sequences were 741 bp long. Both analyses were inspired by real data from case studies of ancient DNA.