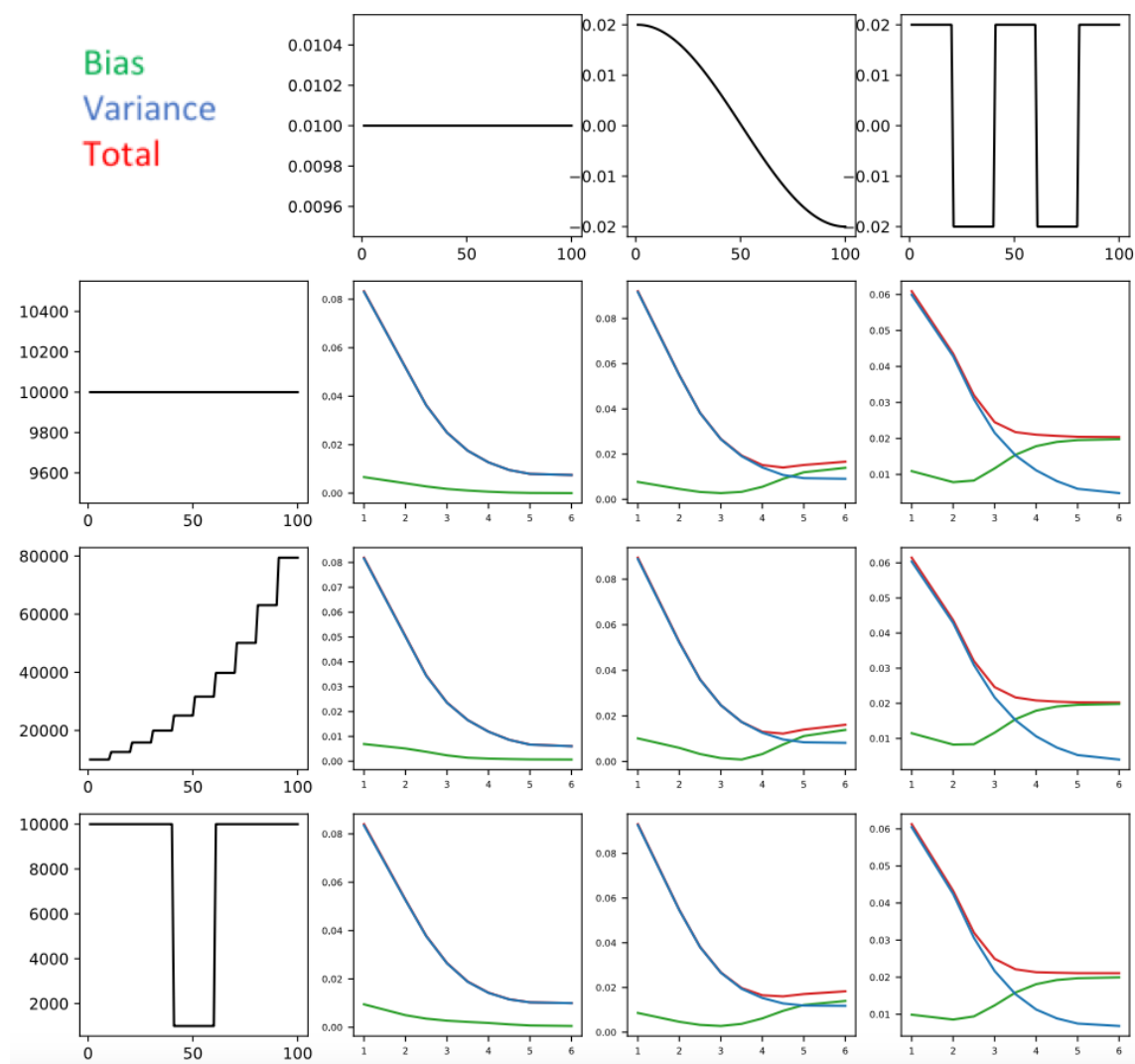
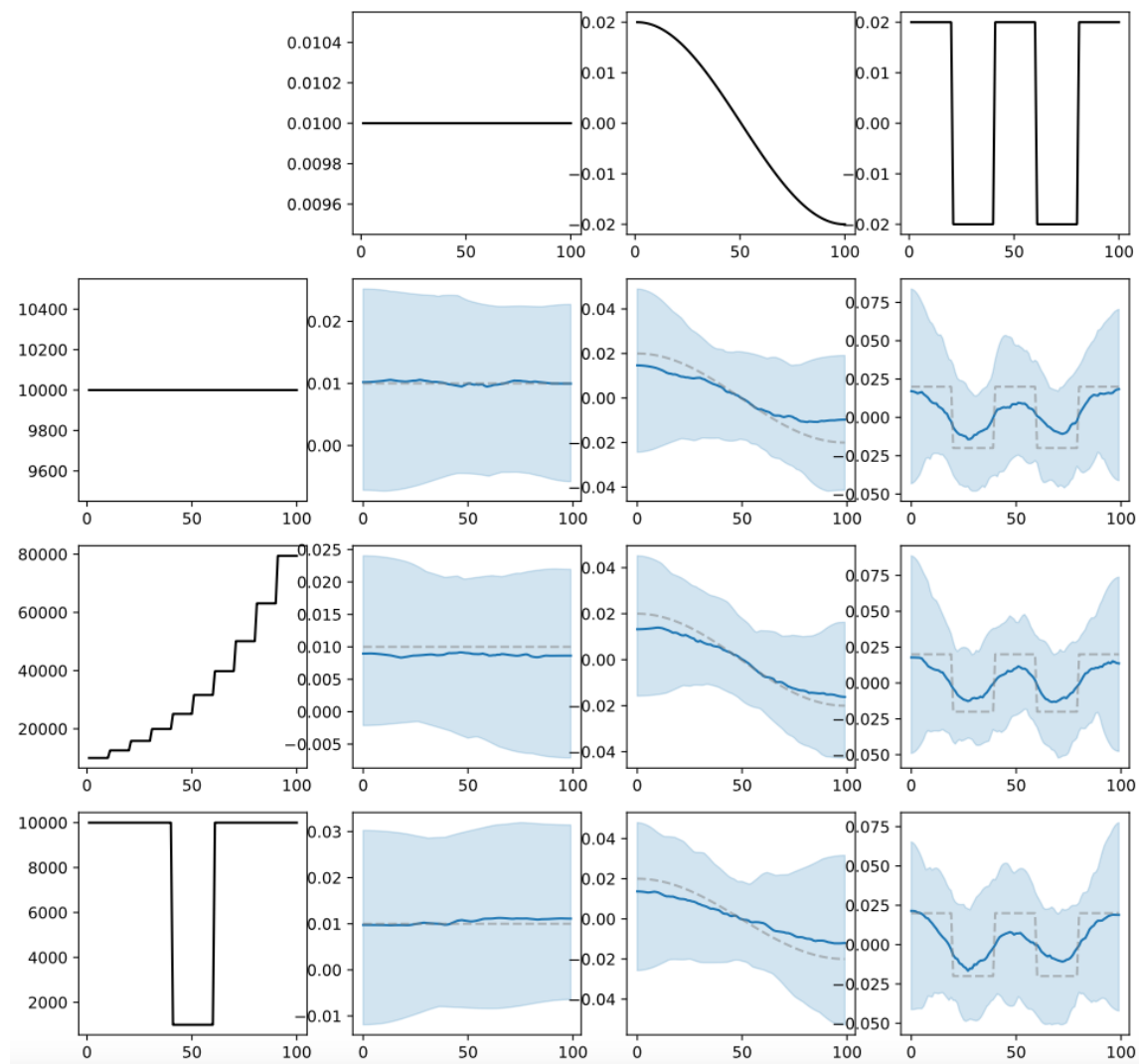
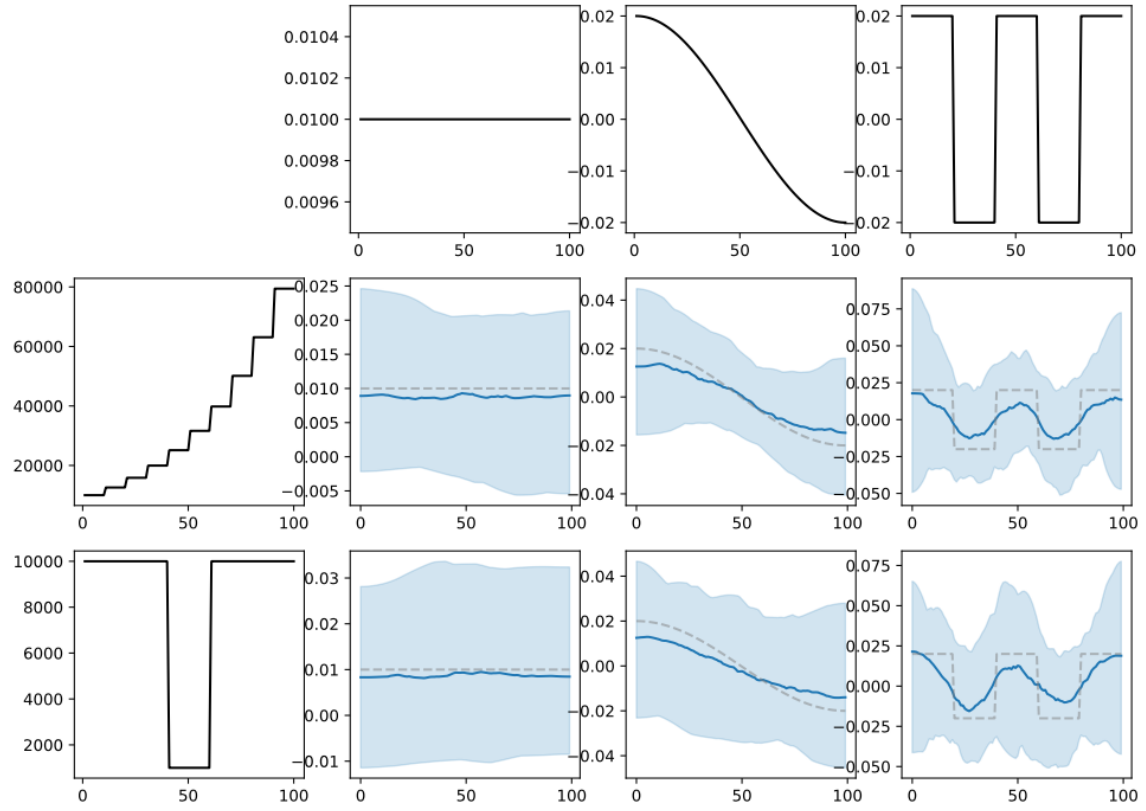




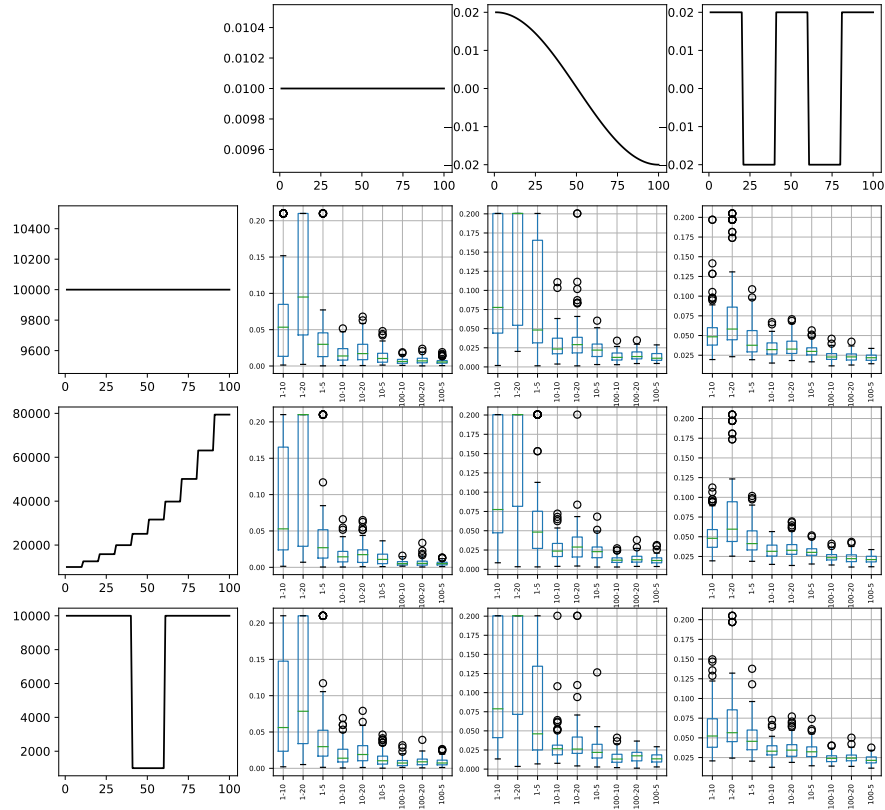
Supplemental Figure S1: Root mean squared bias, variance and total error as a function of $\log_{10}(\lambda)$ with uniform sampling of 100 chromosomes every 10 generations for different selective (columns) and effective population size (rows) trajectories.



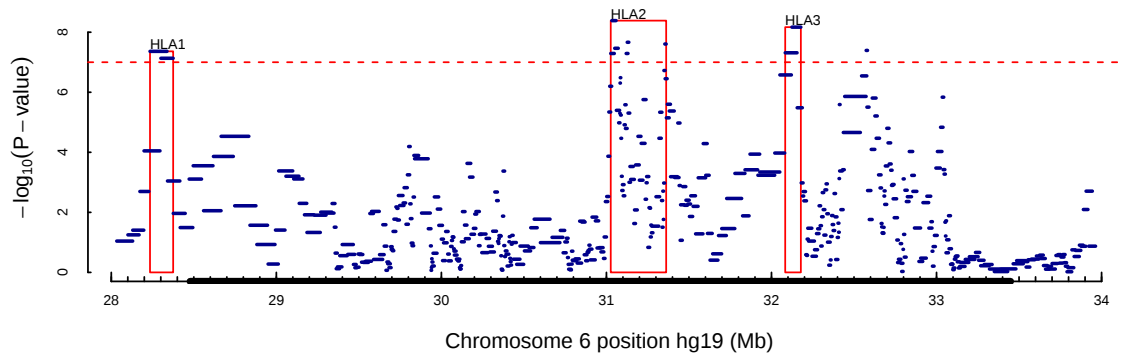
Supplemental Figure S2: Simulation results for different population size history with uniform sampling of 100 chromosomes (or haploid individual) every 10 generations. Each column represents a different selective trajectory and each row represents a different population size trajectory. Dashed lines: simulated selection coefficient. Solid blue lines: mean selection coefficient from 100 simulations. Light blue shaded areas: region containing point estimates from 95/100 simulations.



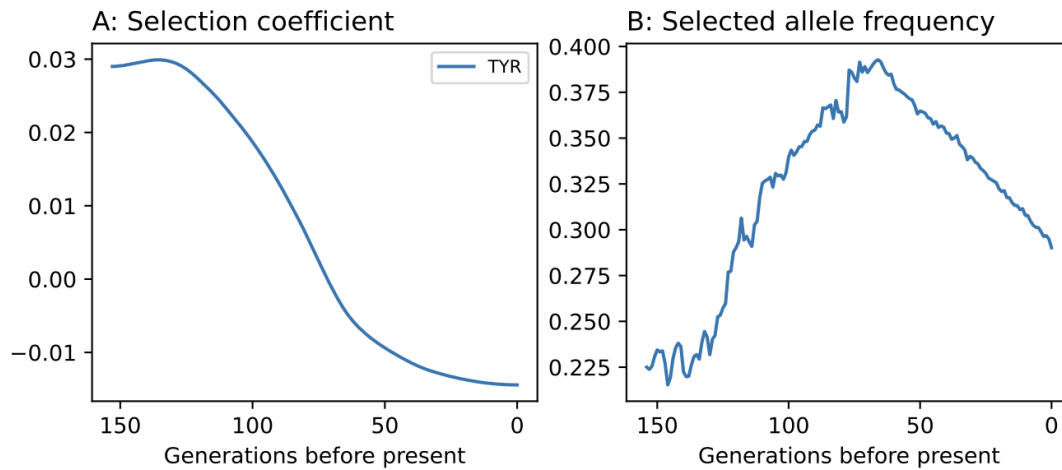
Supplemental Figure S3: Simulation results for different population size histories with uniform sampling of 100 chromosomes every 10 generations. As Fig. S2 but using a constant $N = 10^4$ in the model, instead of the correct effective population size. Dashed lines: simulated selection coefficient. Solid blue lines: mean selection coefficient from 100 simulations. Light blue shaded areas: region containing point estimates from 95/100 simulations.



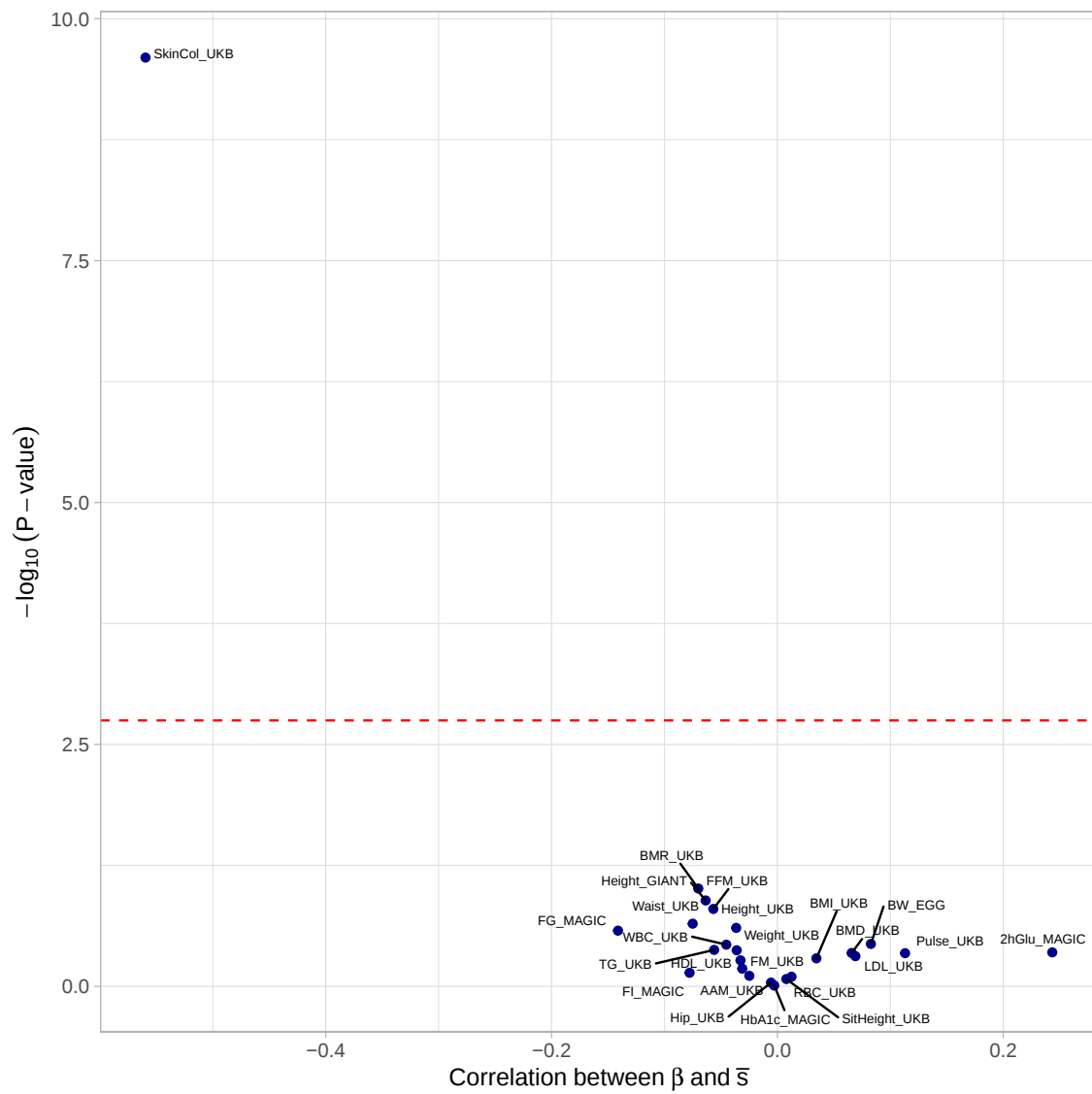
Supplemental Figure S4: Root mean squared error (RMSE) for different sampling schemes. Each column represents a different selective trajectory and each row represents a different population size trajectory as in Fig. S2. Each barplot shows the distribution of RMSE for 100 simulations based on a different sampling schemes. Sampling schemes are labeled "size-frequency", so for example "1-10" means that we sampled one chromosome every 10 generations.



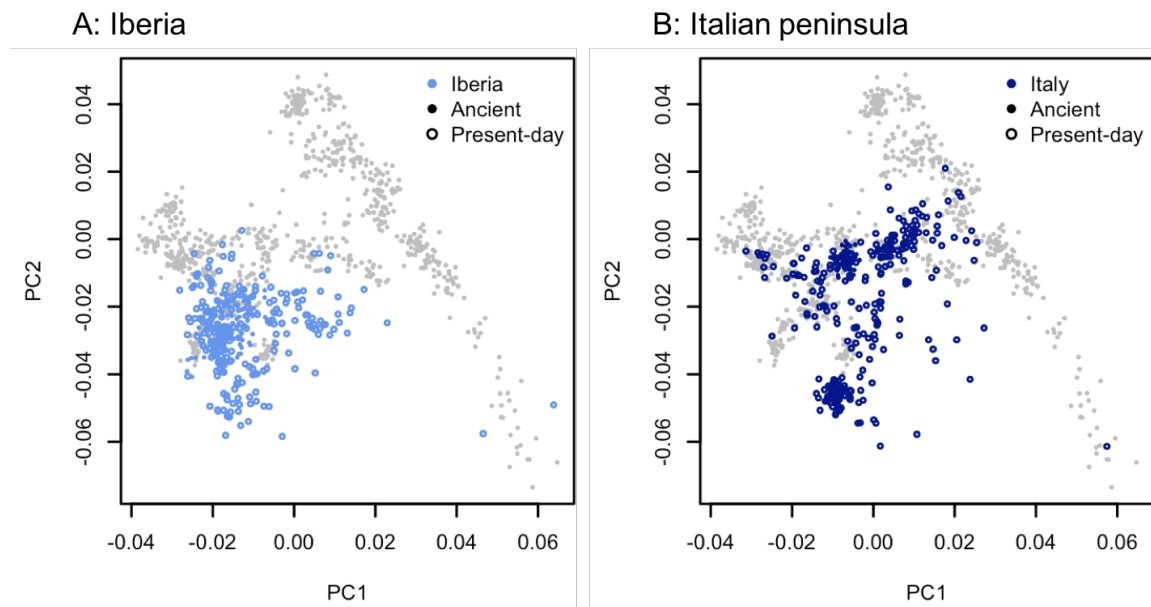
Supplemental Figure S5: Window-based P-values for the HLA region on Chromosome 6. The thick black x-axis shows the boundary of the HLA. Each blue bar represents a 20-SNP window. We highlight three regions with evidence of one or more significant signals.



Supplemental Figure S6: Estimated selection coefficient and frequency for the A allele of rs1042602 at the *TYR* locus.



Supplemental Figure S7: As Fig. 6 but restricting to SNPs with $P < 10^{-8}$, rather than $P < 10^{-4}$. Calcium does not appear on this plot because it has no SNPs with $P < 10^{-8}$.



Supplemental Figure S8: Projected principal components as in Fig. 2 but for ancient individuals from the past 4500 years in Iberia and the Italian peninsula, together with present-day individuals from the IBS and TSI populations of the 1000 Genomes Project. See [Lazaridis et al. \(2014\)](#) for details of the reference populations (grey points).