



**Figure S11:** The effect of possible confounders on the admixture test. (A) The effect of a variable population size. We simulated a simple two-size population history, with ancestral population size  $N_a$  until  $T = 50$  generations ago, followed by population size of  $N_c = 10000$  until present.  $N_a$  varied between 1000 and 20000, such that both expansions and contractions were studied. We simulated two scenarios: one without admixture and one with admixture taking place  $G_a = 5$  generations ago, replacing a proportion  $1 - \alpha = 0.3$  of the population. We then ran the admixture test as described in the main text and in Figure S10 (with 100 simulated constant-size populations). The results demonstrate that for all values of  $N_a$  tested, while for the no-admixture case, the test always resulted in an insignificant P-value, for the admixture case, the P-value was always below 0.05. We note, however, that it might be that a more extreme or complex demographic history will confound the admixture test; but at least for the parameters investigated here, the admixture test is robust. (B) The effect of IBD detection errors. We simulated populations of constant size  $N$  and dropped each detected IBD segment with probability  $\epsilon = 0.2$  (as in the error model of *The total sharing distribution and an error model* section of the main text). Again, we simulated two scenarios: with and without admixture (same parameters as in (A)). We then ran the admixture test, and as in (A), the resulting P-values were significant only for the truly admixed populations.