(A)

Mean: 125.1
Standard deviation: 4.5

Observed (26, $P = 4.37\mathrm{e}{-}109$)

Frequency

Number of shared nucleotide haplotypes

(B)

Mean: 101.8
Standard deviation: 3.9

Observed (30, $P = 8.89\mathrm{e}{-}76$)
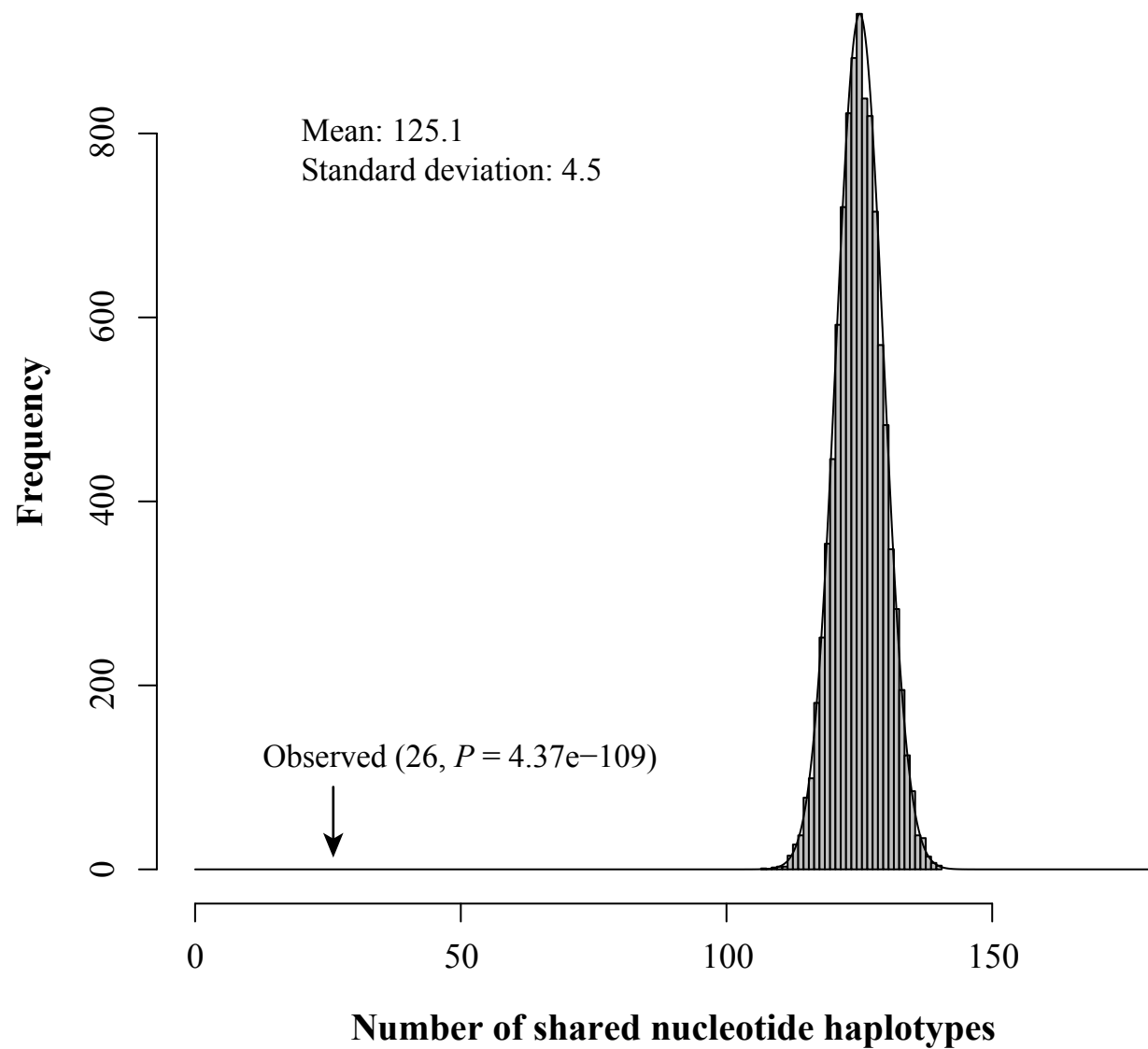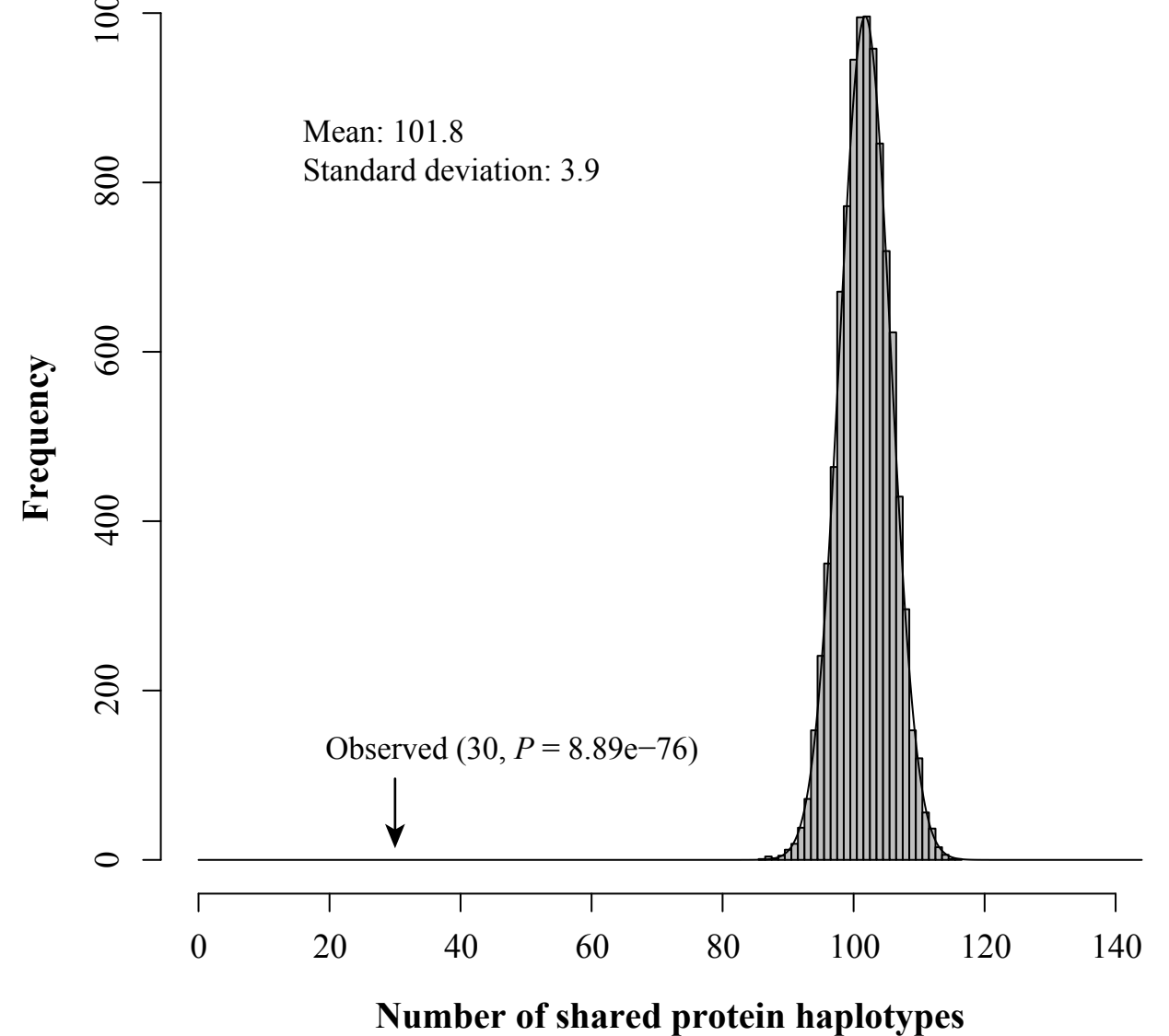
Frequency

Number of shared protein haplotypes

Figure S2. Monte Carlo simulations to reconstruct the haplotype distribution. A histogram shows simulated distribution of a total expected number of shared haplotypes between western and eastern chimpanzees in the 28 c*TAS2R*s, assuming no differentiation of the 2 populations, given the sampling number of chromosomes (92 and 20, respectively) and the observed haplotypes with mean frequencies for the total metapopulation in each c*TAS2R* under 10,000 replicates. The probability that shared haplotypes were sampled in the observed number or less was estimated based on a fitted Gaussian distribution shown as a line graph. (A) Nucleotide haplotypes. (B) Protein haplotypes.