Supplemental Table S10. Transition probability parameters used by the Viterbi algorithm implemented in HaploQA for the genotype imputation approach. Code provided in haplohmm.py available at https://github.com/TheJacksonLaboratory/GenomeMUSter and in **Supplemental Code**.

Transition probability parameters	Description
trans_prob = 0.001	the probability of transitioning from one haplotype to another in the space of a single SNP
hom_obs_probs = [0.97, 0.01,0.01, 0.01]	P(obs | homozygous read from hidden state) a numerical array with 4 entries 0) Probability the observation is homozygous and it matches the hidden state, (A -> A or B -> B) 1) Probability the observation is homozygous and the hidden state is homozygous but it does not match the observation, (A -> B or B -> A) 2) Probability the observation is homozygous but the hidden state is heterozygous, (A -> H or B -> H) 3) Probability the observation is homozygous but the hidden state is missing, e.g. (A -> N or B -> N)
het_obs_probs = [0.98, 0.01,0.01]	P(obs | heterozygous read from hidden state) a numerical array with 3 entries 0) Probability the observation is heterozygous and hidden state is heterozygous, (H -> H) 1) Probability the observation is heterozygous and the hidden state is homozygous, (H -> A or H -> B) 2) Probability the observation is heterozygous observation but the hidden state is missing, (H -> N)
n_obs_probs = [1/3, 1/3, 1/3]	P(obs | missing data from hidden state) a numerical array with 3 entries 0) Probability the observation is missing and the hidden state is missing, (N -> N) 1) Probability the observation is missing but the hidden state is homozygous, (N -> A or N -> B) 2) Probability the observation is missing but the hidden state is heterozygous, (N -> H)