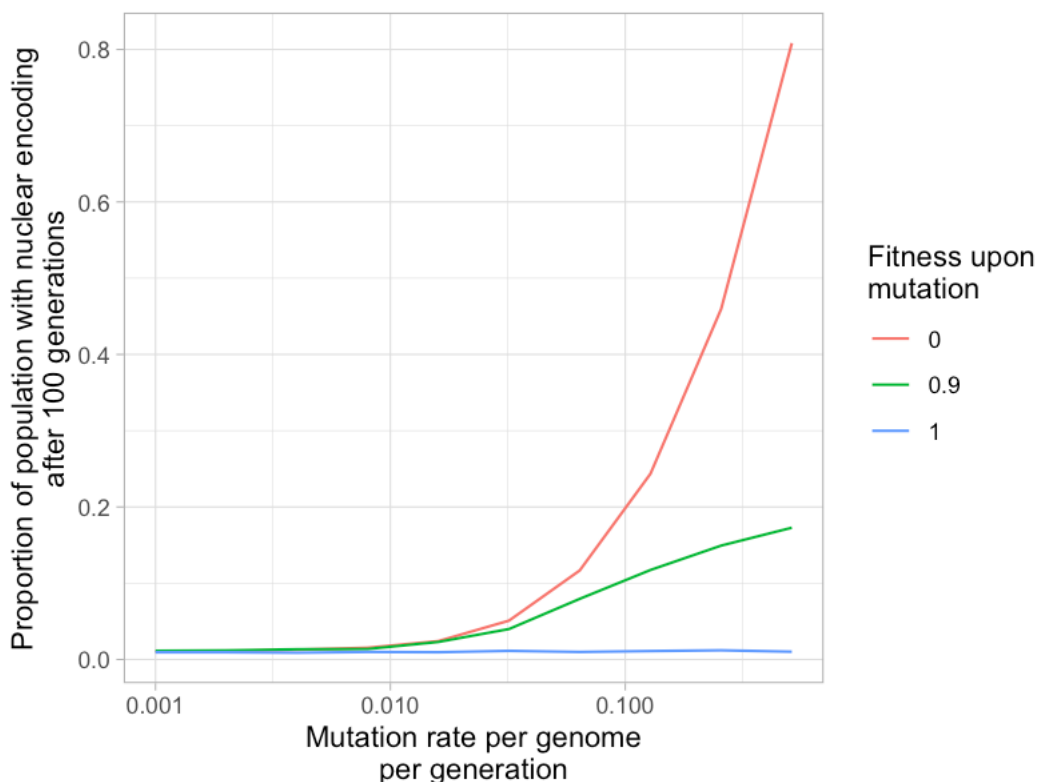


Supplementary Information

To demonstrate how mutational hazard can stabilise transfer of genes to the nucleus, we consider a simple toy model. We simulate a population of N organisms evolving through non-overlapping, asexual generations. A single gene determines fitness. It can be encoded in the mitochondrion or in the nucleus. If in the mitochondrion, it experiences a loss of function mutation with probability μ per genome per generation, which leads to a reduction in fitness. If in the nucleus, it never mutates. The simulation begins with a single individual with nuclear encoding and $N-1$ with organelle encoding. Roulette wheel selection is used to construct a new generation given the fitnesses of the previous generation, and the proportion of individuals with the gene encoded in the nucleus is reported after $t = 100$ generations. Supp. Fig. 1 shows the results for $N=100$ with different fitness effects of the mutated gene, and 10^4 instances of each parameterisation. As μ increases, the proportion of nuclear-encoding individuals increases above the neutral case of $1/N$ towards unity. There is no contribution of mutation rate to the fitness function: it suffices that a lineage prone to mutation is more likely to die out. Code to reproduce this analysis is freely available at <https://github.com/StochasticBiology/mt-gene-stats>.



Supplementary Figure 1. Nuclear encoding of a gene is preferred under higher organelle mutation rates as individuals harbouring deleterious mutations are removed from the population.