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Cover photo: The exceptional genome architecture and genetic tools of *Tetrahymena thermophila* make it an ideal model system in which to study the rates and effects of mutation. The separation of germline and somatic functions in a single cell (in the small and large nuclei, respectively) allows for the accumulation of mutations in the germline genome, which is completely hidden from selection. The mating event shown here is part of a process of genomic exclusion, which leads to the expression of these newly accumulated mutations, allowing for their characterization, see Long *et al.* Genetics 195:527–540.

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