

Figure S1: Read depth and allelic balance distributions and the effect of varying the allelic balance cut-off on rate estimates. Related to Figure 1. **A**, read depth and allelic balance distributions for all unfiltered Mendelian violations (MVs) in the 30 owl monkey individuals. The cut-offs used to filter MVs are indicated by the vertical dotted grey lines. **B**, read depth and allelic balance distributions for all SNP sites in the 30 owl monkey individuals. Filtering cut-offs are again indicated by the vertical dashed grey lines for comparison. **C**, mutation rate estimates for the 14 owl monkey trios when using a less stringent allelic balance cut-off to 0.3 and 0.7 (purple dots). A linear regression still shows a correlation with father's age (solid purple line; $R^2=0.15$, d.f.=12 $P=0.10$) that is not significantly different from our model's prediction (dashed purple line; $F=1.0$, d.f.=13, $P=1.0$). Mutations at CpG sites (blue dots) are not correlated with father's age (blue line). The grey dotted line indicates age of puberty for owl monkeys.

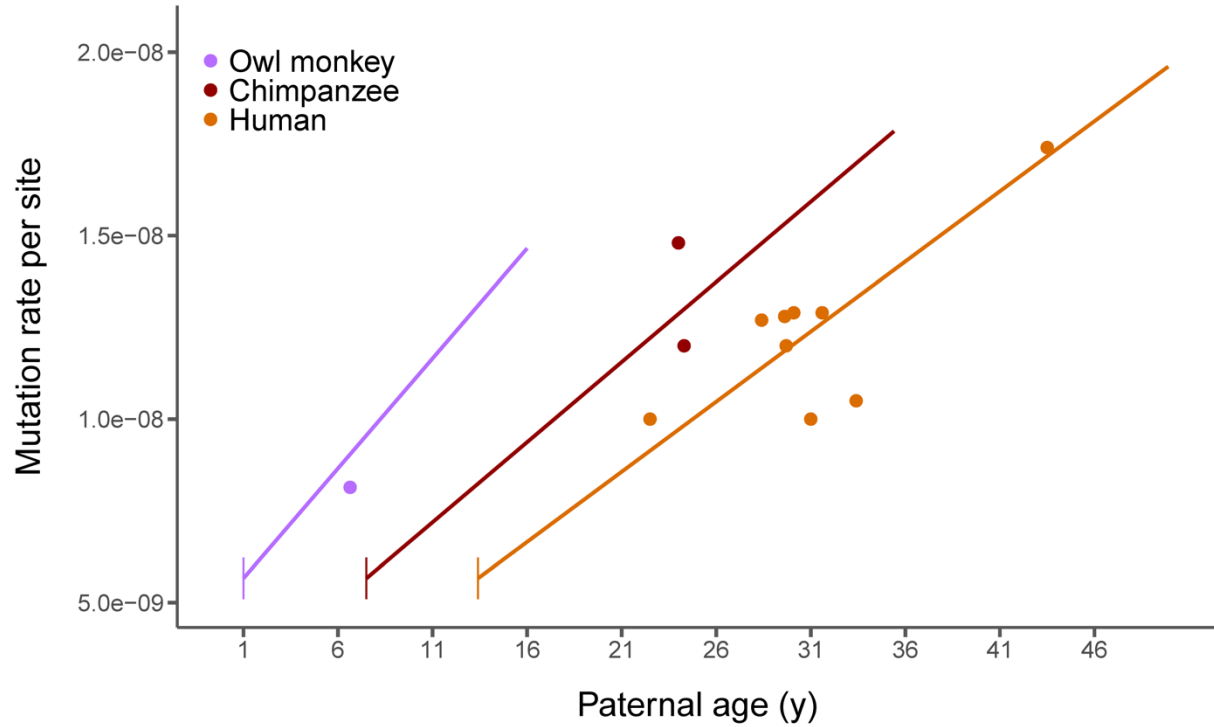


Figure S2: Mutational function predictions using species specific rates of spermatogenesis. Related to Figure 3. Using species specific rates for the three species with high-quality mutation estimates when making predictions from our model of reproductive longevity (lines; equations 3-8 in Methods) does not greatly affect the fit of the model to published estimates of mutation rates (points; see Data S1D for references). Vertical line segments represent the age of puberty for each species. In this figure we used $t_{sc}^{Owl\ monkey} = 10.2$ [S1], $t_{sc}^{Chimp} = 14$ [S2], $t_{sc}^{Human} = 16$ [S3].

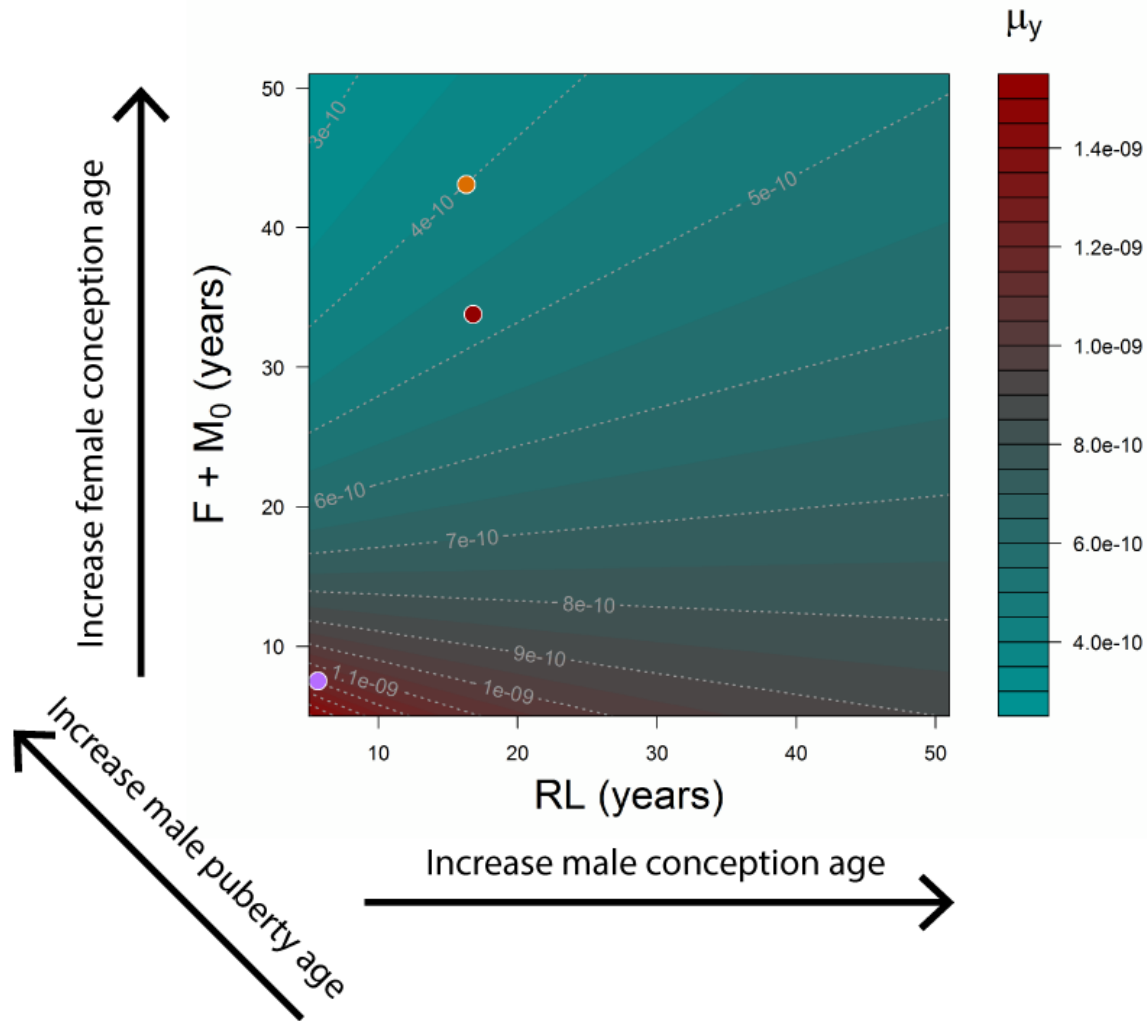


Figure S3: Modeling mutation rate per year over various parental ages at reproduction and puberty. Related to STAR Methods. Mutation rates per year (μ_y) are a function of the length of all three life stages of the mammalian germline: Female (F), males before puberty (M_0), and males after puberty (RL). Increasing F consistently decreases μ_y , while increasing M_0 by increasing the age of puberty in males tends to increase μ_y (note that the y-axis plots the sum of these two parameters). Increasing the length of RL either by decreasing the age of puberty or increasing the average age of conception in males has varying effects based on the length of the other two stages. Points are the predicted mutation rates per year for humans (orange), chimpanzees (red), and owl monkeys (purple).

Supplemental References

- S1. Derooij, D.G., Vanalphen, M.M.A., and Vandekant, H.J.G. (1986). Duration of the cycle of the seminiferous epithelium and its stages in the rhesus-monkey (*Macaca mulatta*). *Biology of Reproduction* 35, 587-591.
- S2. Smithwick, E.B., Young, L.G., and Gould, K.G. (1996). Duration of spermatogenesis and relative frequency of each stage in the seminiferous epithelial cycle of the chimpanzee. *Tissue Cell* 28, 357-366.
- S3. Heller, C.G., and Clermont, Y. (1963). Spermatogenesis in man: an estimate of its duration. *Science* 140, 184-186.