

Supplementary Material

Table S1. Paternal mutation rate estimates from multigenerational pedigrees in Kong et al. (2012). Direct computation of *de novo*, per-site, paternal mutation rates for each of the five trios for which the parental origin of mutations could be inferred. Assuming a Poisson distribution for the number of mutations, we obtain confidence intervals for the expected number of *de novo* mutations using the R function `poisson.test`. We then divide by the total number of tested sites (2.63 billion) to calculate the corresponding per-site mutation rates.

Trio	Paternal age (years)	Number of <i>de novo</i> paternal mutations	Paternal mutation rate per year	
			Point estimate	(95% CI)
Trio 1	21.8	39	6.80×10^{-10}	$4.84 \times 10^{-10} - 9.30 \times 10^{-10}$
Trio 2	22.7	43	7.20×10^{-10}	$5.21 \times 10^{-10} - 9.70 \times 10^{-10}$
Trio 3	25	51	7.76×10^{-10}	$5.78 \times 10^{-10} - 10.20 \times 10^{-10}$
Trio 4	36.2	53	5.57×10^{-10}	$4.17 \times 10^{-10} - 7.28 \times 10^{-10}$
Trio 5	40	91	8.65×10^{-10}	$6.96 \times 10^{-10} - 10.62 \times 10^{-10}$