

**Table S3:** mutation rate estimates using different length cut-offs.

Minimum length (cM)	Proportion conflated	Estimate of $\mu$ ( $\times 10^{-8}$ bp per gen)
1	0.341 (0.325, 0.356)	1.312 (1.287, 1.337)
1.5	0.130 (0.105, 0.158)	1.345 (1.220, 1.482)
2	0.073 (0.0456, 0.106)	1.279 (1.138, 1.444)
2.5	0.064 (0.0311, 0.105)	1.267 (1.093, 1.470)

The median estimates across 1,000 simulated sets are presented, with 5<sup>th</sup> and 95<sup>th</sup> percentile values given in parenthesis. The mutation rate estimates become less inflated as the threshold for minimum length increases, though the confidence interval widens due to fewer and fewer segments available for analysis. Also note that for longer segments, one could use the core regions that are unlikely to be conflated for more accurate mutation rate estimation, which is not modeled here.