

Table S5. Rejection of the clock with 100 neutral loci, $\mu = 0.001$, inferred allele frequencies

Cutoff	Biopsy size									
	1x1	2x2	3x3	4x4	5x5	6x6	7x7	8x8	9x9	10x10
10	0.028	0.064	0.052	0.050	0.064	0.048	0.066	0.060	0.060	0.060
20	0.028	0.064	0.052	0.062	0.084	0.058	0.070	0.062	0.084	0.086
30	0.028	0.044	0.054	0.054	0.066	0.072	0.076	0.088	0.086	0.078
40	0.028	0.040	0.052	0.066	0.066	0.068	0.070	0.072	0.048	0.080
50	0.028	0.040	0.038	0.056	0.056	0.064	0.046	0.044	0.054	0.060
60	0.028	0.066	0.062	0.074	0.074	0.080	0.064	0.066	0.100	0.082
70	0.028	0.070	0.098	0.106	0.100	0.084	0.090	0.090	0.098	0.086
80	0.028	0.102	0.116	0.104	0.122	0.104	0.108	0.104	0.094	0.080
90	0.028	0.102	0.106	0.108	0.098	0.092	0.080	0.074	0.084	0.089
100	0.028	0.102	0.106	0.114	0.082	0.085	0.069	0.055	0.047	0.043

μ , mutation rate per locus per generation

These data correspond to Supporting Figure S3.

A small proportion of runs could not be completed due to too many invariant biopsies, leading to sample sizes less than 500. For the last three entries in cutoff 90%, sample sizes were 499, 498, 497. For the last six entries in cutoff 100%, sample sizes were 497, 496, 494, 492, 492, 487.