Table 3. Comparisons of mutation rates per cell division

Organism	Base substitution		Small insertion/ deletion		Nu microsatellite		Nu homopolymer	
	Nu	Mt	Nu	Mt	10 rpt	25 rpt	5 bp	15 bp
S. cerevisiae	0.33	12.23	0.02	7.48	0.70	18.86	4.07	104.07
C. elegans	1.07	11.58	1.16	6.51	0.31	6.82	0.04	10.75
D. melanogaster	0.16	0.38	0.04	—	0.56	2.02	—	—
Homo sapiens	0.10	2.09	0.01	—	4.78	52.30	27.39	483.62

Data are in units of 10^{-9} per germ-line cell division for base substitutions and small insertion/deletions, and as 10^{-6} per germ-line cell division for repetitive DNAs. Small insertion/deletions are 1–3 bp in length. C. elegans: mutation rate estimates (5–7, 23); assumes 8.5 germ-line cell divisions per generation (51). D. melanogaster: mutation rate estimates (8, 52–55); assumes 36 germ-line cell divisions per generation (56). H. sapiens: mutation rate estimates (22, 54, 56–58); rates for homopolymeric runs assume an average 35 times inflation over that for microsatellites of the same size (the observed inflation in yeast); assumes 200 germ-line cell divisions per generation (3). The rates for homopolymers in yeast are derived from the regression involving ML estimates, and reduce to 0.01 and 1.64 if the regression involving large loci is relied on.