

Table S1. Observed numbers of convergent and parallel sites and the corresponding numbers expected under various neutral models of amino acid substitution. Results presented are for the two exterior branches leading to *D. yakuba* and *D. melanogaster*, respectively, in Fig. 2A.

Type of sites	Number of sites examined	Observed number of sites	Expected number of sites		R^a	P-value ^b
			Substitution model	Number of sites		
Convergent sites						
	2,028,428	12	JTT- f_{gene}	4.1	2.93	0.0011
	2,028,428	12	JTT- f_{site}	12.1	0.99	0.56
	780,615	2	JTT-CAT	3.5	0.57	0.32
Parallel sites						
	2,028,428	479	JTT- f_{gene}	128.9	3.72	1.7E-123
	2,028,428	479	JTT- f_{site}	620.6	0.77	1.9E-09
	780,615	142	JTT-CAT	73.1	1.94	6.4E-13

^aRatio between the observed number and expected number.

^bA statistical test is conducted under the assumption that the number of convergent (or parallel) sites follows a Poisson distribution with the mean equal to the expected number. When the observed number is smaller than the expected, the lower tail probability is given; when the observed number is larger than the expected, the upper tail probability is given.