

Table S2 *D. melanogaster* MK tables calculated using different methods

A. Changes along the *D. melanogaster* branch^a

Gene	P_N	P_S	D_N	D_S	NI^b	Z^{*c}	P_{FET}^d
<i>ATPase6</i>	5	1	2	10	25.000	-1.041	0.013
<i>ATPase8</i>	1	0	0	5	12.000	-1.079	0.167
<i>COI</i>	0	12	3	23	0.462	0.336	0.538
<i>COII</i>	0	3	2	11	1.000	0.000	1.000
<i>COIII</i>	1	6	3	13	0.722	0.000	1.000
<i>Cyt-b</i>	2	2	1	18	18.000	-0.978	0.067
<i>ND1</i>	1	3	1	13	4.333	-0.544	0.405
<i>ND2</i>	3	3	3	8	2.667	-0.352	0.600
<i>ND3</i>	1	0	0	6	14.000	-1.146	0.143
<i>ND4</i>	6	5	4	11	3.300	-0.447	0.228
<i>ND4L</i>	2	1	1	4	8.000	-0.574	0.464
<i>ND5</i>	4	8	9	32	1.778	-0.263	0.459
<i>ND6</i>	0	2	3	3	0.333	0.477	0.464
Sum	26	46	32	157	2.773	-0.439	0.001
NI_{TG}^e	2.57 (1.27, 5.08)						
		mt v. nuc ^f	mt v. X ^f	mt v. auto ^f			
NI		0.045	0.011	0.054			
Z^*		0.037	0.01	0.043			

B. *D. melanogaster-D. simulans* (less inclusive)^g

C. *D. melanogaster-D. simulans* (more inclusive)^g

Gene	P_N	P_S	D_N	D_S	NI^b	Z^{*c}	P_{FET}^d	P_N	P_S	D_N	D_S	NI^b	Z^{*c}	P_{FET}^d
<i>ATPase6</i>	5	3	4	18	7.500	-0.756	0.032	5	2	5	17	8.500	-0.778	0.030
<i>ATPase8</i>	1	0	1	9	10.000	-1.000	0.182	1	0	1	9	10.000	-1.000	0.154
<i>COI</i>	0	13	4	78	1.130	-0.053	1.000	0	16	6	77	0.655	0.183	1.000
<i>COII</i>	0	5	6	23	0.570	0.243	0.558	1	5	6.5	22.5	0.692	-0.019	1.000
<i>COIII</i>	1	7	6	33	0.786	-0.084	1.000	1	9	6.5	34.5	0.590	0.024	1.000
<i>Cyt-b</i>	2	4	1	48	24.000	-1.167	0.029	2	5	2	47	9.400	-0.903	0.072
<i>ND1</i>	3	3	4	31	7.750	-0.806	0.050	3	3	5	33	6.600	-0.753	0.063
<i>ND2</i>	3	4	11	29	1.977	-0.301	0.657	6	5	15	29	2.320	-0.340	0.300
<i>ND3</i>	1	0	1	16	17.000	-1.230	0.111	1	1	1	17	17.000	-0.954	0.195
<i>ND4</i>	6	5	10	38	4.560	-0.617	0.054	7	7	13	40	3.077	-0.467	0.099
<i>ND4L</i>	2	1	1	9	18.000	-0.875	0.108	2	1	1	9	18.000	-0.875	0.108
<i>ND5</i>	4	10	19	59	1.242	-0.135	0.744	4	10	26.5	59.5	0.898	0.000	1.000
<i>ND6</i>	0	3	5	8	0.375	0.426	0.509	2	4	7	9	0.643	0.125	1.000
Sum	28	58	73	399	2.640	-0.424	0.0004	35	68	95.5	403.5	2.170	-0.340	0.002
NI_{TG}^e	2.39 (1.30, 4.39)							2.02 (1.22,3.58)						
		mt v. nuc ^f	mt v. X ^f	mt v. auto ^f				mt v. nuc ^f	mt v. X ^f	mt v. auto ^f				
NI		0.039	0.009	0.05				0.075	0.018	0.089				
Z^*		0.02	0.005	0.02				0.028	0.009	0.033				

D. D. melanogaster-D. yakuba (less inclusive) ^g								E. D. melanogaster-D. yakuba (more inclusive) ^g						
Gene	P _N	P _S	D _N	D _S	NI ^b	Z* ^c	P _{FET} ^d	P _N	P _S	D _N	D _S	NI ^b	Z* ^c	P _{FET} ^d
ATPase6	5	3	6	40	11.111	-0.944	0.006	5	2	11	35	7.955	-0.778	0.021
ATPase8	1	0	2	8	6.000	-0.778	0.273	1	0	2	8	6.000	-0.778	0.273
COI	0	13	5	98	1.180	-0.071	1.000	0	16	8	101	0.667	0.176	0.595
COII	0	5	5	39	1.110	-0.046	1.000	1	5	6	39	1.300	-0.280	1.000
COIII	1	7	5	50	1.429	-0.327	0.573	1	9	8.5	47.5	0.621	-0.009	1.000
Cyt-b	2	4	12	73	3.042	-0.533	0.229	2	5	17.5	67.5	1.543	-0.267	0.641
ND1	3	3	9	45	5.000	-0.663	0.088	3	3	11	45	4.091	-0.584	0.122
ND2	3	4	15	45	2.250	-0.362	0.375	6	5	25	41	1.968	-0.275	0.334
ND3	1	0	4	21	8.800	-0.944	0.192	1	1	5	22	4.400	-0.584	0.377
ND4	6	5	15	65	5.200	-0.682	0.016	7	7	24	63	2.625	-0.408	0.120
ND4L	2	1	1	7	14.000	-0.778	0.152	2	1	1	7	14.000	-0.778	0.152
ND5	4	10	45	109	0.969	-0.036	1.000	4	10	55.83	107.17	0.768	0.063	0.775
ND6	0	3	14	21	0.367	0.436	0.283	2	4	21.5	22.5	0.523	0.203	0.669
Sum	28	58	138	621	2.172	-0.342	0.004	35	68	196.3	605.67	1.588	-0.205	0.041
NI _{TG} ^e	2.29 (1.26, 4.71)							1.67 (1.05, 2.86)						
	mt v. nuc ^f		mt v. X ^f		mt v. auto ^f		mt v. nuc ^f		mt v. X ^f		mt v. auto ^f			
NI	0.038		0.007		0.047		0.277		0.065		0.325			
Z*	0.01		0.002		0.012		0.087		0.019		0.104			

^a Changes were assigned to the *D. melanogaster* branch using *D. simulans* as the close outgroup and *D. yakuba* as the distant outgroup. Codons with missing data and mitochondrial genome SRX022291 were omitted from the analysis.

^b A count of one was added to each cell in order to calculate $NI = \frac{D_S P_N}{D_N P_S}$ when any single cell had a count of zero.

^c $Z^* = \text{Log}_{10} \left(\frac{(D_N+1)(P_S+1)}{(D_S+1)(P_N+1)} \right)$, as in Presgraves (2005).

^d P-value from Fisher's Exact Test of the MK table.

^e $NI_{TG} = \frac{\sum D_{Si} P_{Ni} / (P_{Si} + D_{Si})}{\sum P_{Si} D_{Ni} / (P_{Si} + D_{Si})}$ with confidence intervals from 5000 bootstrap samples (Stoletzki and Eyre-Walker 2011).

^f P-values from Mann Whitney U tests contrasting statistics between the mitochondrial gene set and either the entire nuclear (nuc), X chromosome (X), or autosomal (A) gene sets.

^g Divergence was estimated between *D. melanogaster* and *D. simulans* or between *D. melanogaster* and *D. yakuba*. The less inclusive analysis omitted codons with missing data in any genome, did not include mitochondrial genome SRX022291, and used a conservative criterion that minimized D_N for codons with multiple substitutions. The more inclusive analysis did not omit codons with missing data, included mitochondrial genome SRX022291, and averaged across all possible mutational paths between codons with multiple substitutions.