

Table S3 Summary statistics of the MK table for mitochondrially encoded OXPHOS complexes in *D. melanogaster*

Species	Gene set ^a	NI ^b	NI_{TG} ^c	Z ^b	P_{FET} ^d
<i>D. melanogaster</i> – <i>D. yakuba</i> (more inclusive)	Complex I	1.731	1.59 (0.94, 3.17)	-0.238	0.070
	Complex IV	0.556	0.55 (0, 1.30)	0.255	0.750
	Complex V	9.923	9.64 (undefined)	-0.997	0.007
<i>D. melanogaster</i> – <i>D. yakuba</i> (less inclusive)	Complex I	2.221	2.06 (0.98, 5.38)	-0.346	0.019
	Complex IV	0.499	0.50 (0, 1.43)	0.302	1.000
	Complex V	12.000	13.5 (undefined)	-1.079	0.002
<i>D. melanogaster</i> – <i>D. simulans</i> (more inclusive)	Complex I	2.313	2.00 (1.17, 4.04)	-0.364	0.006
	Complex IV	0.470	0.45 (0, 0.69)	0.328	0.539
	Complex V	13.000	10.4 (undefined)	-1.114	0.005
<i>D. melanogaster</i> – <i>D. simulans</i> (less inclusive)	Complex I	2.722	2.39 (1.18, 5.25)	-0.435	0.004
	Complex IV	0.335	0.31 (0, 0.79)	0.475	0.474
	Complex V	10.800	9.25 (undefined)	-1.033	0.006

^a Complex I, ND, seven loci; Complex IV, CO, three loci; Complex V, ATPase, two overlapping loci. Complex II is nuclear encoded and Complex III has only a single mitochondrial locus, *Cyt-b*.

^b $NI = \frac{D_S P_N}{D_N P_S}$ and $Z = \text{Log}_{10} \left(\frac{D_N P_S}{D_S P_N} \right)$ were calculated using counts of P_N , P_S , D_N and D_S summed across genes within gene sets.

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

^d P -value for Fisher's Exact Test of the MK table containing counts of P_N , P_S , D_N and D_S summed across genes within gene sets.