

TABLE S2**PAML comparisons for *Dntf-2* and *Dntf-2r* retrogenes**

Model	l	p	\hat{W}_{Dntf-2}	$\hat{W}_{Dntf-2r}$	$\hat{W}_{Dntf-2r_dup}$	\hat{W}_{Dn_Ntf-2r}	\hat{W}_{Dg_Ntf-2r}
One-ratio	-2570.8689	34	0.0533	0.0533	0.0533	0.0533	0.0533
Two-ratio	-2531.7282	35	0.0243	0.2657	0.2657	0.2657	0.2657
Four-ratio	-2522.3422	37	0.0247	0.5311	0.5311	0.3309	0.0754
Five-ratio	-2522.0333	38	0.0247	0.6235	0.3655	0.3310	0.0754
Four-ratio $\hat{W}_{Dntf-2r} = \mathbf{1}$	-2524.2914	36	0.0248	1.0000	1.0000	0.3328	0.0758
Four-ratio $\hat{W}_{Da_Ntf-2r} = 1$	-2527.5541	36	0.0239	0.5362	0.5362	1.0000	0.0762

Log likelihood values and estimates of K_A/K_S ratios are shown. p is the number of parameters estimated in the model. \hat{W}_{Dntf-2} is K_A/K_S ratio for all *Dntf-2* genes. $\hat{W}_{Dntf-2r}$ is the K_A/K_S ratio for the melanogaster subgroup minus the branch immediately following duplication of *Dntf-2r*. $\hat{W}_{Dntf-2r_dup}$ is the K_A/K_S ratio for the branch immediately following duplication in the melanogaster subgroup. \hat{W}_{Da_Ntf-2r} and \hat{W}_{Dg_Ntf-2r} the K_A/K_S ratio for the retroposed sequence in *D. ananassae* and *D. grimshawi* respectively.