

**TABLE S4****PAML comparisons for *ran* and *ran* retrogenes**

Model	l	$p$	$\hat{w}_{ran}$	$\hat{w}_{ran-like}$	$\hat{w}_{ran-like\_dup}$	$\hat{w}_{Da\_ran-like}$	$\hat{w}_{Dg\_ran-like}$
One-ratio	-4610.4156	36	0.0571	0.0571	0.0571	0.0571	0.0571
Two-ratio	-4492.8616	37	0.0042	0.1793	0.1793	0.1793	0.1793
Four-ratio	-4452.4538	39	0.0043	0.3593	0.3593	0.0395	0.0349
Five-ratio	-4420.8830	40	0.0044	0.7023	0.0249	0.0408	0.0348
Five-ratio $\hat{w}_{ran-like}=\mathbf{1}$	-4422.9256	39	0.0044	1.0000	0.0250	0.0409	0.0350

Log likelihood values and parameters estimated under differing models of selection. l refers to log likelihood values. p is the number of parameters estimated in the model.  $\hat{w}_{ran}$  is  $K_A/K_S$  ratio for all ran genes.  $\hat{w}_{ran-like}$  is the  $K_A/K_S$  ratio for the melanogaster subgroup minus the branch immediately following duplication of *ran-like*.  $\hat{w}_{ran-like\_dup}$  is the  $K_A/K_S$  ratio for the branch immediately following duplication in the melanogaster subgroup.  $\hat{w}_{Da\_ran-like}$  and  $\hat{w}_{Dg\_ran-like}$  the  $K_A/K_S$  ratio for the retroposed sequence in *D. ananassae* and *D. grimshawi* respectively