

**TABLE S3**

**Estimates of the distribution of fitness effects and the fraction of adaptive substitutions using the Eyre-Walker and Keightley method on the dataset restricted to the two-thirds of loci with the highest  $K_A/K_S$  values**

	$N2/N1$	Shape parameter ( $b$ )	Location parameter (mean/ $b$ )	Proportion of mutations in different $N_{es}$ categories:				$\alpha$ (fraction adaptive)
				0 – 0.5	0.5 – 5	5 – 50	50 – Inf	
<b>X</b>								
<i>mir</i>	8.79	0.090	-1.1 x 10 <sup>9</sup>	0.102	0.023	0.029	0.847	0.122
	(0.1/10)	(0.033/99.999)		(0.000/0.459)	(0.000/0.389)	(0.022/1.000)	(0.000/0.891)	(-3.014/1.000)
<i>pse</i>	10	0.221	-5997.851	0.036	0.024	0.040	0.901	0.697
	(3.07/10)	(0.100/1.034)		(0.003/0.071)	(0.010/0.067)	(0.014/0.316)	(0.621/0.946)	(0.358/0.972)
<b>A</b>								
<i>mir</i>	2.79	0.229	-74.315	0.122	0.085	0.143	0.650	-0.361

	(0.1/10)	(0.060/99.999)		(0.000/0.213)	(0.016/0.790)	(0.021/0.958)	(0.000/0.885)	(-1.938/1.000)
<i>pse</i>	10	0.407	-111.884	0.016	0.024	0.062	0.899	0.833
	(3.07/10)	(0.105/0.992)		(0.002/0.074)	(0.010/0.047)	(0.015/0.188)	(0.762/0.946)	(0.10/0.981)

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95% confidence intervals in parentheses.

mir / pse refer to data for *D. miranda* and *D. pseudoobscura*, respectively.

$N2/N1$  = estimated demographic model (relative difference between current and ancestral population size)