

**Table S3.** Estimated DFE parameters and rates of adaptive molecular evolution obtained when using ancestral repeats located within introns (excluding sites that may function as intronic splice sites, defined as the first and last 30bp of each intron) as a neutral standard.

<i>Site Class</i>	<i>N<sub>w</sub>S<sub>def</sub></i>	$\beta$	$\alpha$ (cas)	$\omega_a$ (cas)	$\alpha$ (fam)	$\omega_a$ (fam)	$\alpha$ (rat)	$\omega_a$ (rat)
Zero-fold	3.1e4	0.17 [0.16, 0.18]	0.46 [0.44, 0.48]	0.11 [0.10, 0.11]	0.56 [0.53, 0.58]	0.16 [0.15, 0.16]	0.45 [0.42, 0.27]	0.10 [0.092, 0.11]
Two-fold (nonsyn.)	5.4e6 [9.3e8, 3.4e5]	0.11 [0.079, 0.13]	0.45 [0.41, 0.49]	0.12 [0.11, 0.4]	0.55 [0.51, 0.58]	0.18 [0.17, 0.20]	0.49 [0.46, 0.53]	0.15 [0.14, 0.16]
UTRs	5.4e3 [9.8e3, 3.1e3]	0.05 [0.05, 0.05]	0.27 [0.24, 0.30]	0.20 [0.18, 0.23]	0.40 [0.37, 0.42]	0.37 [0.33, 0.40]	0.25 [0.23, 0.28]	[0.19 [0.17, 0.21]
CNEs	25 [27,24]	0.23 [0.22, 0.24]	0.39 [0.38, 0.40]	0.21 [0.20, 0.22]	0.51 [0.50, 0.52]	0.35 [0.34, 0.36]	0.32 [0.31, 0.33]	0.15 [0.15, 0.16]