Table 1: Positive selection parameter estimates obtained by analysis of the uSFS for simulated poplations.

Divergence [a]	γ_a Simulated	γ_a Estimated	p_a Simulated	p_a Estimated	$\gamma_a p_a$	Prop. Significant [b]
+	10	11.2 [5.60 - 20.0]	0.010000	0.00856 [0.00440 - 0.0199]	0.0954 [0.0838 - 0.115]	1.00
-	10	3.97 [1.13 - 27.2]	0.010000	0.0201 [0.00472 - 0.0706]	0.0828 [0.0616 - 0.155]	1.00
+	20	16.6 [9.20 - 37.4]	0.005000	0.00568 [0.00241 - 0.0107]	0.0949 [0.0822 - 0.108]	1.00
-	20	19.9 [2.90 - 37.4]	0.005000	0.00532 [0.00289 - 0.0207]	0.106 [0.0454 - 0.193]	0.97
+	50	37.4 [21.6 - 41.8]	0.002000	0.00257 [0.00202 - 0.00467]	0.0951 [0.0809 - 0.106]	1.00
-	50	37.3 [1.87 - 65.5]	0.002000	0.00266 [0.00125 - 0.0146]	0.0717 [0.0112 - 0.145]	0.86
+	100	37.43 [37.4 - 1530]	0.001000	0.00249 [0.0000738 - 0.00283]	0.0938 [0.0795 - 0.107]	1.00
-	100	0.323 [0.0371 - 1.25]	0.001000	0.00259 [0.000525 - 0.0941]	0.00102 [0.0000620 - 0.0137]	0.00
+	200	37.4 [37.4 - 1,700]	0.000500	0.00251 [0.000220 - 0.00283]	0.0947 [0.0738 - 0.106]	1.00
-	200	0.272 [0.00546 - 1.911]	0.000500	0.0122 [0.000690 - 0.138]	0.00310 [0.000104 - 0.0294]	0.07
+	400	37.4 [32.7 - 37.4]	0.000250	0.00245 [0.00199 - 0.00283]	0.0919 [0.0776 - 0.102]	1.00
-	400	12.3 [0.287 - 66.6]	0.000250	0.00212 [0.000783 - 0.0104]	0.0338 [0.000250 - 0.0984]	0.22
+	800	37.4 [32.9 - 37.4]	0.000125	0.00222 [0.00186 - 0.00264]	0.0831 [0.0701 - 0.0936]	1.00
-	800	1.75 [0.111 - 43.0]	0.000125	0.00240 [0.000343 - 0.0293]	0.0134 [0.0000515 - 0.0649]	0.12

[a] +/- indicates whether or not divergence was included when analysing the uSFS
[b] The proportion of bootstrap replicates where a full DFE gave a significantly better fit than a model containing just deleterious mutations

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