

Table S7. Estimated parameters under different codon substitution models for forkhead P sub-family genes¹.

	Model	dN/dS	Estimated parameters	Sites with $\omega > 1^2$	ℓ	P value
FOXP1	M1a: neutral	0.0731	$p_0 = 0.95618, (p_1 = 0.04382)$ $(\omega_0 = 0.03066), (\omega_1 = 1.00000)$		-13857.331728	1
	M2a: selection	0.0731	$p_0 = 0.95618, p_1 = 0.04382, (p_2 = 0.00000)$ $(\omega_0 = 0.03066), (\omega_1 = 1.00000), \omega_2 = 11.32611$		-13857.331728	
	M8a: β & $\omega=1$	0.0553	$p_0 = 0.99268, (p_1 = 0.00732), p = 0.15813$ $q = 2.81242, \omega = 1.00000$		-13799.608758	1
	M8: β & ω	0.0553	$p_0 = 0.99268, (p_1 = 0.00732), p = 0.15813,$ $q = 2.81243, \omega = 1.00000$		-13799.608758	
FOXP2	M1a: neutral	0.0615	$p_0 = 0.95735, (p_1 = 0.04265)$ $(\omega_0 = 0.01965), (\omega_1 = 1.00000)$		-12558.167089	0.9295
	M2a: selection	0.0628	$p_0 = 0.95601, p_1 = 0.01529, (p_2 = 0.02870)$ $(\omega_0 = 0.01965), (\omega_1 = 1.00000), \omega_2 = 1.00000$		-12558.093967	
	M8a: β & $\omega=1$	0.0458	$p_0 = 0.99999, (p_1 = 0.00001), p = 0.08897$ $q = 1.61951, \omega = 1.00000$		-12524.222980	1
	M8: β & ω	0.0455	$p_0 = 0.99999, (p_1 = 0.00001), p = 0.09061,$ $q = 1.66060, \omega = 1.00001$		-12524.233000	

¹ p_0 = proportion of sites where $\omega < 1$, p_1 = proportion of sites where $\omega = 1$, and p_2 = proportion of sites where $\omega > 1$ (selection models only), $\omega_0 < 1$ (negative selection), $\omega_1 = 1$ (neutral selection), and $\omega_2 > 1$ (positive selection), likelihood ratio tests were performed between neutral models (M1a - Nearly Neutral, and M7 - Beta) and models that identify positive selection (M2a - Selection, and M8 - Beta + Selection), the comparisons between M1 vs. M2 and M7 vs. M8 have 2 degrees of freedom. Parentheses indicate fixed parameters.

²Position and protein IUPAC code.

Table S7. Estimated parameters under different codon substitution models for forkhead P sub-family genes¹ (continued).

	Model	dN/dS	Estimated parameters	Sites with $\omega > 1^2$	ℓ	P value
FOXP3	M1a: neutral	0.1834	$p_0 = 0.89272$, ($p_1 = 0.10728$) ($\omega_0 = 0.08525$), ($\omega_1 = 1.00000$)		-12510.124897	1
	M2a: selection	0.1834	$p_0 = 0.89272$, $p_1 = 0.04720$, ($p_2 = 0.06008$) ($\omega_0 = 0.08525$), ($\omega_1 = 1.00000$), $\omega_2 = 1.00000$		-12510.124897	
	M8a: β & $\omega=1$	0.1518	$p_0 = 0.95683$, ($p_1 = 0.04317$), $p = 0.48347$ $q = 3.64447$, $\omega = 1.00000$		-12424.107542	0.9137
	M8: β & ω	0.1532	$p_0 = 0.96152$, ($p_1 = 0.03848$), $p = 0.47274$, $q = 3.45516$, $\omega = 1.06357$	183S, 184A, 194V, and 301V	-12424.017242	
FOXP4	M1a: neutral	0.0487	$p_0 = 0.97844$, ($p_1 = 0.02156$) ($\omega_0 = 0.02778$), ($\omega_1 = 1.00000$)		-18552.897747	1
	M2a: selection	0.0487	$p_0 = 0.97843$, $p_1 = 0.02157$, ($p_2 = 0.00000$) ($\omega_0 = 0.02778$), ($\omega_1 = 1.00000$), $\omega_2 = 6.24385$		-18552.897760	
	M8a: β & $\omega=1$	0.0384	$P_0 = 0.99789$, ($p_1 = 0.00211$), $p = 0.23183$ $q = 5.59727$, $\omega = 1.00000$		-18335.456738	1
	M8: β & ω	0.0392	$p_0 = 0.99999$, ($p_1 = 0.00001$), $p = 0.22328$ $q = 4.99479$, $\omega = 2.82598$		-18340.025059	

¹ p_0 = proportion of sites where $\omega < 1$, p_1 = proportion of sites where $\omega = 1$, and p_2 = proportion of sites where $\omega > 1$ (selection models only), $\omega_0 < 1$ (negative selection), $\omega_1 = 1$ (neutral selection), and $\omega_2 > 1$ (positive selection), likelihood ratio tests were performed between neutral models (M1a - Nearly Neutral, and M7 - Beta) and models that identify positive selection (M2a - Selection, and M8 - Beta + Selection), the comparisons between M1 vs. M2 and M7 vs. M8 have 2 degrees of freedom. Parentheses indicate fixed parameters.

²Position and protein IUPAC code.