

Table S8. Branch site model for *FOXP* genes.

		Model Clade D (free-ratio model, admit selection)			M1a (neutral)		Probability	
		Proportion	Clade 1 ^b	Clade 2 ^f	LogL	Proportion	LogL	M1a vs. Clade
FOXP1 ²	Mammals ^f vs. non-mammals ^b	P ₀ = 0.70045	ω ₀ = 0.00176	ω ₀ = 0.00176	−15531.277393	P ₀ = 0.93230	−15594.616874	1
		P ₁ = 0.24561	ω ₁ = 0.13116	ω ₁ = 0.13116		P ₁ = 0.06770		
		P ₂ = 0.05394	ω ₂ = 0.68705	ω ₂ = 0.60693		ω ₀ = 0.03010		
						ω ₁ = 1.00000		
FOXP4	Mammals ^f vs. non-mammals ^b	P ₀ = 0.70046	ω ₀ = 0.00627	ω ₀ = 0.00627	−22189.482510	P ₀ = 0.95450	−22463.434676	<0.001
		P ₁ = 0.25887	ω ₁ = 0.11160	ω ₁ = 0.11160		P ₁ = 0.04550		
		P ₂ = 0.04067	ω ₂ = 0.18012	ω ₂ = 0.66102		ω ₀ = 0.03293		
						ω ₁ = 1.00000		

¹P = Proportion of codons in each ω class, where ω = dN/dS (non-synonymous/synonymous rate ratio), two degrees of freedom were considered.

²For such analysis in *FOXP1*, *Xenopus sp.* was excluded. Mammals and primates are respective to Clade 2.

^f = foreground clade, ^b = background