

Supplementary Table3: Log-likelihood and parameter estimates generated from random-site models for RP genes. P = number of free parameters for each model, ℓ = log-likelihood value for each model.

RPL28:

Models	p	ℓ	Estimates of parameters
M0:one ratio	1	-14664.881	omega=0.223
M1a:nearly neutral	2	-15243.079	$p_0=0.0001, p_1=0.9999,$ omega ₀ =0.0001, omega ₁ =1.0000
M2a:positive selection	4	-15168.003	$p_0=0.0000, p_1=0.83519, p_2=0.16481$ omega ₀ =0, omega ₁ =1, omega ₂ =3.39940
M0, omega=1:fixed omega	4	-15848.007	None

RPL14:

Models	p	ℓ	Estimates of parameters
M0:one ratio	1	-11320.898	omega=0.348
M1a:nearly neutral	2	-10997.396	$p_0=0.7266, p_1=0.27331,$ omega ₀ =0.18668, omega ₁ =1.0000
M2a:positive selection	4	-10962.242	$p_0=0.71909, p_1=0.17451, p_2=0.10640$ omega ₀ =0.20926, omega ₁ =1, omega ₂ =2.54602
M0, omega=1:fixed omega	4	-12018.938	None

RPS16:

Models	p	ℓ	Estimates of parameters
M0:one ratio	1	-14320.835	omega=0.286
M1a:nearly neutral	2	-14134.842	$p_0=0.76, p_1=0.24,$ omega ₀ =0.226, omega ₁ =1
M2a:positive selection	4	-14646.878	$p_0=0, p_1=0.17451, p_2=0.10640$ omega ₀ =0, omega ₁ =1, omega ₂ =4.65
M0, omega=1:fixed omega	4	-15340.056	None

RPS18:

Models	p	ℓ	Estimates of parameters
M0:one ratio	1	-14320.835	omega=0.328
M1a:nearly neutral	2	-14134.842	$p_0=0.0001, p_1=0.9999,$ omega ₀ =0, omega ₁ =1.0000
M2a:positive selection	4	-14646.878	$p_0=0.8292, p_1=0.11455, p_2=0.05563$ omega ₀ =0.288, omega ₁ =1, omega ₂ =2.19489
M0, omega=1:fixed omega	4	-176000.284	None