

Table S1: SM templates defined by the *codeml* control file parameters values and summary of LRT comparisons.

PAML Parameters	Site Model						
	M0	M3	M1a	M2a	M7	M8	M8a
seqfile (*)	<i>automatic</i>						
treefile (*)	<i>automatic</i>						
outfile	R						
noisy	9						
verbose	1						
runmode	0						
seqtype	1						
CodonFreq	2 (F3x4)						
clock	0						
aaDist	0						
model	0						
Nssites (*)	0	3	1	2	7	8	8
icode (*)	<i>automatic</i>						
Mgene	0						
fix_kappa	0 (estimate)						
kappa (*)	0.2 ; 2 ; 5						
fix_omega	0 (estimate)						1 (fixed)
omega	0.4						1
fix_alpha	1						
alpha	0						
Malpha	0						
ncatG	(**)						4
getSE	0						
RateAncestor	0						
Small_Diff	0.5e-6						
cleandata	1						
fix_blength	1						
method	0						
Positive selection	None	Variation of ω among codons	None	Allows positively selected sites	None	Allows positively selected sites	False positive (relaxed purifying selection)
np	1	5	2	4	2	4	3
LRT	M0 vs. M3		M1a vs. M2a		M7 vs. M8		
df = np(H1) - np(H0)	4		2		M8a vs. M8		
					2		
					1		
BEB	No	No	No	Yes	No	Yes	No

NOTE: (*) These values are automatically changed by LMAP applications and must not be manually modified by users. Remaining values can and should be modified in respect to their requirements.

(**) Any values for this parameter are ignored when running site models in batch mode, whereas *codeml* employs default values. **Legend:** np – number of parameters; LRT – Likelihood Ratio Test; H0 – Null Hypothesis; H1 – Alternative Hypothesis; df – degrees of freedom; BEB – Bayes Empirical Bayes.

Table S2: BM templates defined by the *codeml* control file parameters values and summary of LRT comparisons.

PAML Parameters	Branch Model		
	M0	TrU	TrC
seqfile (*)		<i>automatic</i>	
treefile (*)		<i>automatic</i>	
outfile		R	
noisy		9	
verbose		1	
runmode		0	
seqtype		1	
CodonFreq		2 (F3x4)	
clock		0	
aaDist		0	
model	0		2
Nssites		0	
icode (*)		<i>automatic</i>	
Mgene		0	
fix_kappa		0 (estimate)	
kappa		2	
fix_omega		0 (estimate)	1 (fixed)
omega (*)		0.0 ; 0.1 ; 0.01 ; 0.001 ; 0.25 ; 0.5 ; 0.75 ; 1 ; 1.5 ; 2	1
fix_alpha		1	
alpha		0	
Malpha		0	
ncatG	2		4
getSE		0	
RateAncestor		0	
Small_Diff		0.5e-6	
cleandata		1	
fix_blength		1	
method		0	
Divergence	None ($\omega_F = \omega_B$)	Divergence ($\omega_F > 1$)	Relaxed selection ($\omega_F = 1$)
np	1	2	1
LRT	M0 vs. TrU		
		TrC vs. TrU	
df = np(H1) - np(H0)	1		
		1	
BEB	No	No	No

NOTE: (*) These values are automatically changed by LMAP applications and must not be manually modified by users. Remaining values can and should be modified in respect to their requirements.

Legend: ω_F – Foreground omega; ω_B – Background omega; np – number of parameters; LRT – Likelihood Ratio Test; H0 – Null Hypothesis; H1 – Alternative Hypothesis; df – degrees of freedom; BEB – Bayes Empirical Bayes.

Table S3: BSM templates defined by the *codeml* control file parameters values and summary of LRT comparisons.

PAML Parameters	Branch-Site Model	
	MA1	MA
seqfile (*)	<i>automatic</i>	
treefile (*)	<i>automatic</i>	
outfile	R	
noisy	9	
verbose	1	
runmode	0	
seqtype	1	
CodonFreq	2 (F3x4)	
clock	0	
aaDist	0	
model	2	
Nssites	2	
icode (*)	<i>automatic</i>	
Mgene	0	
fix_kappa	0 (estimate)	
kappa (*)	0.2 ; 2 ; 5	
fix_omega	1 (fixed)	0 (estimate)
omega	1	1.5
fix_alpha	1	
alpha	0	
Malpha	0	
ncatG	(**)	
getSE	0	
RateAncestor	0	
Small_Diff	0.5e-6	
cleandata	1	
fix_blength	1	
Method	0	
Positive selection	None ($\omega_F = \omega_B$)	Allows positive selected sites ($\omega_F > 1$)
np	1	2
LRT	MA1 vs. MA	
df = np(H1) - np(H0)	1	
BEB	No	Yes

NOTE: (*) These values are automatically changed by LMAP applications and must not be manually modified by users. Remaining values can and should be modified in respect to their requirements. (**) Any value in this parameter is ignored in both branch-site models A e B, whereas *codeml* employs default values. **Legend:** ω_F – Foreground omega; ω_B – Background omega; np – number of parameters; LRT – Likelihood Ratio Test; H0 – Null Hypothesis; H1 – Alternative Hypothesis; df – degrees of freedom; BEB – Bayes Empirical Bayes.

Table S4: CM templates defined by the *codeml* control file parameters values and summary of LRT comparisons.

PAML Parameters	Clade Model	
	M2a_rel	CmC
seqfile (*)	<i>user</i>	
treefile (*)	<i>user</i>	
outfile	R	
noisy	9	
verbose	1	
runmode	0	
seqtype	1	
CodonFreq	2 (F3x4)	
clock	0	
aaDist	0	
model	0	3
Nssites	22	2
icode (*)	<i>user</i>	
Mgene	0	
fix_kappa	0 (estimate)	
kappa	2	
fix_omega	0 (estimate)	
omega (*)	0.0 ; 0.1 ; 0.01 ; 0.001 ; 0.25 ; 0.5 ; 0.75 ; 1 ; 1.5 ; 2	
fix_alpha	1	
alpha	0	
Malpha	0	
ncatG	(**)	
getSE	0	
RateAncestor	0	
Small_Diff	0.5e-6	
cleandata	1	
fix_blength	1	
method	0	
Divergence	None ($\omega_F = \omega_B$)	Divergence ($\omega_F > 1$)
np	1	2
LRT	M2a_rel vs. CmC	
df = np(H1) - np(H0)	1	
BEB	No	Yes

NOTE: (*) These parameters are automatically changed by LMAP applications and must not be manually modified by users. Remaining parameters can and should be modified in respect to their requirements. (**) Any value in this parameter is ignored in both clade model C and M2a_rel models, whereas *codeml* employs default values. **Legend:** ω_F – Foreground omega; ω_B – Background omega; np – number of parameters; LRT – Likelihood Ratio Test; H0 – Null Hypothesis; H1 – Alternative Hypothesis; df – degrees of freedom; BEB – Bayes Empirical Bayes.