Appendix 1. PAML summary results for TRIM5α

A. PAML (1) Analysis of Entire Data Set (hominids+OWM+NWM)

1. Log Likelihood Scores and Parameter Estimates for Four Models of Variable ω's Among Sites Assuming the F3x4 Model of Codon Frequencies.

Model	**Parameter Estimates**	**Sites* with $\omega > 1$**	ℓ
M0: one ratio	Average dN/dS for each branch = 1.160 S = 1.55260		–5772.38
Site models			
M1: neutral	$(\omega_0 = 0)$ f_0= 0.354	Not allowed	–5,725.00
	$(\omega_1 = 1)$ $(f_1 = 0.646)$		
	Average dN/dS for each branch = 0.646 S = 1.56259		
M2: selection	$(\omega_0 = 0)$ $f_0 = 0.281$ $(\omega_1 = 1)$ $f_1 = 0.566$ **$\omega_2 = 4.624$ ($f_2 = 0.153$)** Average dN/dS for each branch = 1.273 S = 1.62074	**(47–51: gaps)** 175 Q 0.9958** 213 S 0.9635* 215 T 0.9955** 228 L 0.9942** 310 C 0.9924** 311 A 0.9603* 317 K 0.9757* 324 K 0.9995** 325 P 0.9933** **(326-338: gaps)** 339 F 0.9994** 340 V 0.9999** **(385-386: gaps)** 389 K 0.9953** 407 G 0.9974** 418 F 0.9997** 421 P 0.9769* 423 V 0.9633* 471 Q 0.9535*	–5,667.01

Model	**Parameter Estimates**	**Sites* with $\omega > 1$**	ℓ
		483 G 0.9936**	
M3:discrete	$\omega_0 = 0.342$ $f_0 = 0.662$ **$\omega_1 = 2.575$ ($f_1 = 0.305$)** **$\omega_2 = 7.922$ ($f_2 = 0.033$)** Average dN/dS for each branch = 1.273 S = 1.63377	Too many to list. Note: M3 vs. M0 is a test of heterogeneity among sites and not an explicit test of positive selection.	–5,664.25
M7:β	$p = 0.02830$ $q = 0.01638$ Average dN/dS for each branch = 0.6160 S = 1.55777	Not allowed	–5,724.62
M8:β and ω	$p = 0.2299$ $q = 0.14801$ $f_0 = 0.829$ **$\omega_1 = 4.308$ ($f_1 = 0.171$)** Average dN/dS for each branch = 1.2426 S = 1.62038	**(47-51: gaps)** 139 Q 0.9534* 175 Q 0.9967** 213 S 0.9739* 215 T 0.9966** 228 L 0.9958** 257 T 0.9511* 310 C 0.9943** 311 A 0.9717* 317 K 0.9830* 324 K 0.9996** 325 P 0.9946** **(326-338: gaps)** 339 F 0.9995** 340 V 0.9999** 384 D 0.9539* **(385-386: gaps)** 389 K 0.9964** 390 N 0.9611* 407 G 0.9979** 418 F 0.9998** 421 P 0.9830* 423 V 0.9737*	–5,666.71

Model	Parameter Estimates	Sites* with ω > 1	ℓ
		471 Q 0.9670* 483 G 0.9952**	

p and *q* are parameters of the β distribution. *f* is the proportion of sites assigned to an individual ω (= dN/dS) category or to a β distribution with shape parameters *p* and *q*. The proportion $f_{1,2}$ in parentheses is not a free parameter. Sites assigned to $\omega_{1,2}$ are those with posterior probabilities (*P*) > 0.95 , and those with *P* > 0.99 are in bold. Analyses were conducted using κ as a free parameter. S = tree length.

*Sites assigned to $\omega > 1$ are those with posterior probabilities $P > 0.95$ (*) or $P > 0.99$ (**).

2. Log Likelihood Scores and Parameter Estimates for Four Models of Variable ω's Among Sites Assuming the F61 Model of Codon Frequencies.

Model	Parameter estimates	Sites* with ω > 1	ℓ
M0: one ratio	Average dN/dS for each branch = 1.144 S = 1.55005		–5,748.06
Site models			
M1: neutral	$(\omega_0 = 0)\ f_0 = 0.359$	Not allowed	–5,696.78
	$(\omega_1 = 1)\ (f_1 = 0.641)$		
	Average dN/dS for each branch = 0.641 S = 1.56922		
M2: selection	$(\omega_0 = 0)\ f_0 = 0.291$ $(\omega_1 = 1)\ f_1 = 0.551$ **$\omega_2 = 4.451$ ($f_2 = 0.158$)** Average dN/dS for each branch = 1.2545 S = 1.62398	**(47-51: gaps)** 175 Q 0.9954** 213 S 0.9544* 215 T 0.9970** 228 L 0.9957** 310 C 0.9930** 311 A 0.9669* 317 K 0.9736* 324 K 0.9994** 325 P 0.9903**	–5,641.84

Model	**Parameter estimates**	**Sites* with $\omega > 1$**	ℓ
		(326-338: gaps) 339 F 0.9987** 340 V 0.9999** **(385-386: gaps)** 389 K 0.9935** 407 G 0.9958** 411 S 0.9536* 418 F 0.9994** 421 P 0.9784* 423 V 0.9680* 483 G 0.9909**	
M3:discrete	$\omega_0 = 0.301$ $f_0 = 0.631$ **$\omega_1 = 2.379$ ($f_1 = 0.328$)** **$\omega_2 = 7.224$ ($f_2 = 0.041$)** Average dN/dS for each branch = 1.2692 S = 1.63693	Too many to list. Note: M3 vs. M0 is a test of heterogeneity among sites and not an explicit test of positive selection.	–5,639.09
M7:β	$p = 0.029$ $q = 0.0167$	Not allowed	–5,696.39
	Average dN/dS for each branch = 0.6144 S = 1.56601		
M8:β and ω	$p = 0.16877$ $q = 0.11056$ $f_0 = 0.825$ **$\omega_1 = 4.190$ ($f_1 = 0.175$)** Average dN/dS for each branch = 1.2331 S = 1.62300	**(47-51: gaps)** 139 Q 0.9532* 175 Q 0.9963** 213 S 0.9659* 215 T 0.9975** 228 L 0.9967** 257 T 0.9607* 310 C 0.9945** 311 A 0.9749* 317 K 0.9805* 324 K 0.9995** 325 P 0.9920** **(326-338: gaps)** 339 F 0.9989** 340 V 0.9999** **(385-386: gaps)**	–5,641.64

Model	**Parameter estimates**	**Sites* with ω > 1**	ℓ
		389 K 0.9949** 390 N 0.9587* 407 G 0.9966** 411 S 0.9653* 418 F 0.9995** 421 P 0.9832* 423 V 0.9756* 471 Q 0.9570* 483 G 0.9929**	

p and *q* are parameters of the β distribution. *f* is the proportion of sites assigned to an individual ω (= dN/dS) category or to a β distribution with shape parameters *p* and *q*. The proportion $f_{1,2}$ in parentheses is not a free parameter. Sites assigned to $\omega_{1,2}$ are those with posterior probabilities $P > 0.95$; those with $P > 0.99$ are in bold. Analyses were conducted by using κ as a free parameter. S = tree length.

*Sites assigned to $\omega > 1$ are those with posterior probabilities $P > 0.95$ (*) or $P > 0.99$ (**).

3. Likelihood Ratio Test Statistics (2δ) for Models of Variable Selective Pressure Among Sites.

	2δ	**df**	***P* value**
Model 0 (one dN/dS ratio for all branches)			
F3x4			
One ratio vs. M3 ($k = 3$)	216.26	4	$P < 0.0001$
M1 vs. M2	115.98	2	$P < 0.0001$
M7 vs. M8	115.82	2	$P < 0.0001$
F61			
One ratio vs. M3 ($k = 3$)	217.94	4	$P < 0.0001$
M1 vs. M2	109.88	2	$P < 0.0001$
M7 vs. M8	109.50	2	$P < 0.0001$

4. Likelihood Ratio Test Statistics (2δ) for Models of Variable Selective Pressure Along Branches.

	ℓ	**2δ**	**df***	***P* value**
TRIM5				
Model 0 (same dN/dS ratio for all branches)	–5,784.326			
Model 1 (different dN/dS ratio for each branch)	–5,755.534	57.584	37	$P < 0.02$
Apobec3G[†]				
Model 0 (same dN/dS ratio for all branches)	–4,209.048			
Model 1 (different dN/dS ratio for each branch)	–4,201.337	15.422	20	$P > 0.75$ (N.S.)

*df denotes degrees of freedom that is equal to one less than the total number of branches in the phylogeny. For a 20-taxa tree like in TRIM5, the total number of branches is 38, so df =37. N.S., not significant.

[†] Sawyer, S. L., Emerman, M. & Malik, H. S. (2004) *PLoS Biol.* **2,** e275.

5. Likelihood Ratio Test Statistics for Models of Selection Along the Human and Gibbon Lineages (OWM + hominids only).

	ω (dN/dS) (human or gibbon branch)	**ω (dN/dS) (remainder of tree)**	ℓ	**2δ**	**df***	***P* value**
Human						
Model 0 (two-ratio, human ω =1)	1.00	1.132	–5,748.233			
Model 1 [two-ratio, human ω >1 (estimated by PAML; ref. 1)]	2.985	1.133	–5,747.543	1.38	1	0.24 (N.S)
Gibbon						
Model 0 (two-ratio, gibbon ω =1)	1.00	1.087	–5,748.718			
Model 1 [two-ratio, gibbon ω >1 (estimated by PAML; ref. 1)]	5.594	1.091	–5,744.345	8.746	1	0.0031

df denotes degrees of freedom; here, $df = 1$.

6. *P* Value Statistics for Positive Selection Along the Human and Gibbon Lineages, Based on Monte Carlo Simulation.

	Confidence ancestral sequence (0-1) per site	**ω (dN/dS)**	***P* value**
Human vs. Ancestral Node	0.99971	3.6	$P < 10^{-4}$
Gibbon vs. Ancestral Node	0.99633	6.5	$P < 10^{-4}$

B. PAML (1) Analysis of Partial Data Set (hominids+OWM)

1. Log Likelihood Scores and Parameter Estimates for Four Models of Variable ω's Among Sites Assuming the F3x4 Model of Codon Frequencies.

Model	**Parameter estimates**	**Sites* with ω > 1**	ℓ
M0: one ratio	Average dN/dS for each branch = 1.1923		**–3,519.244**
Site models			
M1: neutral	$(\omega_0 = 0)\ f_0 = 0.307$	Not allowed	**–3,513.813**
	$(\omega_1 = 1)\ (f_1 = 0.693)$		
	Average dN/dS for each branch = 0.693		
M2: selection	$(\omega_0 = 0)\ f_0 = 0.185$ $(\omega_1 = 1)\ f_1 = 0.783$ **$\omega_2 = 11.283\ (f_2 = 0.032)$** Average dN/dS for each branch = 1.1429	**330 G 0.9960**** **332 R 0.9929**** **335 R 0.9890*** **337 Q 0.9981**** **340 V 0.9993****	**–3,492.320**
M3:discrete	ω_0 0.00001 $f_0 = 0.380$ **$\omega_1 = 1.667\ (f_1 = 0.601)$** **$\omega_2 = 16.866\ (f_2 = 0.019)$** average dN/dS for each branch = 1.3219	Too many to list. Note: M3 vs. M0 is a test of heterogeneity among sites and not an explicit test of positive selection.	**–3,490.526**
M7:β	$p = 0.00592$ $q = 0.00273$ Average dN/dS for each branch = 0.7	Not allowed	**–3,513.818**

Model	Parameter estimates	Sites* with $\omega > 1$	ℓ
M8:β and ω	$p = 0.01037$ $q = 0.00248$ $f_0 = 0.968$ **$\omega_1 = 11.191$ ($f_1 = 0.032$)** Average dN/dS for each branch = 1.1308	**330 G 0.9959**** **332 R 0.9927**** **335 R 0.9888*** **337 Q 0.9980**** **340 V 0.9992****	**–3,492.324**

p and *q* are parameters of the β distribution. *f* is the proportion of sites assigned to an individual ω (= dN/dS) category or to a β distribution with shape parameters *p* and *q*. The proportion $f_{1,2}$ in parentheses is not a free parameter. Sites assigned to $\omega_{1,2}$ are those with posterior probabilities $P > 0.95$; those with $P > 0.99$ are in bold. Analyses were conducted using κ as a free parameter. S = tree length.

*Sites assigned to $\omega > 1$ are those with posterior probabilities $P > 0.95$ (*) or $P > 0.99$ (**).

2. Log Likelihood Scores and Parameter Estimates for Four Models of Variable ω's Among Sites Assuming the F61 Model of Codon Frequencies

Model	Parameter estimates	Sites* with $\omega > 1$	ℓ
M0: one ratio	Average dN/dS for each branch = 1.1375		–**3,469.858**
Site models			
M1: neutral	($\omega_0 = 0$) $f_0 = 0.331$	Not allowed	**–3,462.818**
	($\omega_1 = 1$) ($f_1 = 0.669$)		
	Average dN/dS for each branch = 0.669		
M2: selection	($\omega_0 = 0$) $f_0 = 0.215$ ($\omega_1 = 1$) $f_1 = 0.749$ **$\omega_2 = 10.019$ ($f_2 = 0.036$)** Average dN/dS for each branch = 1.1057	**330 G 0.9914**** **332 R 0.9934**** **335 R 0.9840*** **337 Q 0.9984**** **338 T 0.6807** **340 V 0.9993****	**–3,443.237**
M3:discrete	$\omega_0 = 0.00001$ $f_0 = 0.415$ **$\omega_1 = 1.761$ ($f_1 = 0.568$)**	Too many to list. Note: M3 vs. M0 is a test	**–3,441.147**

Model	**Parameter estimates**	**Sites* with $\omega > 1$**	ℓ
	$\omega_2 = 17.069$ ($f_2 = 0.017$) Average dN/dS for each branch = 1.2835	of heterogeneity among sites and not an explicit test of positive selection.	
M7:β	$p = 0.00484$ $q = 0.00310$	Not allowed	**–3,463.372**
	Average dN/dS for each branch = 0.6		
M8:β and ω	$p = 0.00553$ $q = 0.00144$ $f_0 = 0.964$ **$\omega_1 = 10.263$ ($f_1 = 0.036$)** Average dN/dS for each branch = 1.2368	**330 G 0.9919**** **332 R 0.9938**** **335 R 0.9849*** **337 Q 0.9985**** **340 V 0.9994****	**–3,443.266**

p and *q* are parameters of the β distribution. *f* is the proportion of sites assigned to an individual ω (= dN/dS) category or to a β distribution with shape parameters *p* and *q*. The proportion $f_{1,2}$ in parentheses is not a free parameter. Sites assigned to $\omega_{1,2}$ are those with posterior probabilities $P > 0.95$; those with $P > 0.99$ are in bold. Analyses were conducted using κ as a free parameter. S = tree length.

* Sites assigned to $\omega > 1$ are those with posterior probabilities $P > 0.95$ (*) or $P > 0.99$ (**).

3. Likelihood Ratio Test Statistics (2δ) for Models of Variable Selective Pressure Among Sites.

	2δ	**df**	***P* value**
Model 0 (one ω for all branches)			
F3x4			
One ratio vs. M3 ($k = 3$)	57.436	4	$P < 0.0001$
M1 vs. M2	42.986	2	$P < 0.0001$
M7 vs. M8	42.988	2	$P < 0.0001$
F61			
One ratio vs. M3 ($k = 3$)	57.422	4	$P < 0.0001$
M1 vs. M2	39.162	2	$P < 0.0001$
M7 vs. M8	40.212	2	$P < 0.0001$

1. Yang, Z. (1997) *Comput. Appl. Biosci.* **13,** 555–556.