

Supplemental Table S3. PAML analysis of human TRIM sequences: Base pairs 1-237

TRIM ^a dataset	ω_0 ^b	codon freq. ^c	M1a-M2a $2\Delta\ell$ ^d p-value	M7-M8 $2\Delta\ell$ ^d p-value	M8a-M8 $2\Delta\ell$ ^d p-value	tree length ^e	dN/dS (%) ^f	AA Positions of dN/dS>1 ^g * p>0.95 ** p>0.99			
TREE 3	0.4	f61	10.6	p = 0.005	17.1	p = 0.0002	10.9	p = 0.001	5.14	2.7 (27%)	I46*, P47*, F48*, V50**, E54**, E60**, H69**, L76*
	1.4	f61	10.6	p = 0.005	17.1	p = 0.0002	10.9	p = 0.001	5.14	2.7 (27%)	I46*, P47*, F48*, V50**, E54**, E60**, H69**, L76*
	0.4	f3x4	6.5	p = 0.04	10.4	p = 0.005	7.3	p = 0.007	4.96	2.7 (17%)	V50*, E54*, E60*, H69*
	1.4	f3x4	6.5	p = 0.04	10.4	p = 0.005	7.3	p = 0.007	4.96	2.7 (17%)	V50*, E54*, E60*, H69*
TREE 4 (node collapsed)	0.4	f61	10.0	p = 0.007	15.4	p = 0.0004	10.4	p = 0.001	5.11	2.7 (25%)	F48*, V50**, E54**, E60**, H69**
	1.4	f61	10.0	p = 0.007	15.4	p = 0.0004	10.4	p = 0.001	5.11	2.7 (25%)	F48*, V50**, E54**, E60**, H69**
	0.4	f3x4	6.1	p = 0.047	9.3	p = 0.01	6.9	p = 0.009	4.94	2.7 (16%)	H69*
	1.4	f3x4	6.1	p = 0.047	9.3	p = 0.01	6.9	p = 0.009	4.94	2.7 (16%)	H69*

PAML analysis of human TRIM sequences: Base pairs 238-1356

TRIM ^a dataset	ω_0 ^b	codon freq. ^c	M1a-M2a $2\Delta\ell$ ^d p-value	M7-M8 $2\Delta\ell$ ^d p-value	M8a-M8 $2\Delta\ell$ ^d p-value	tree length ^e	dN/dS (%) ^f	AA Positions of dN/dS>1 ^g * p>0.95 ** p>0.99			
TREE 1	0.4	f61	16.8	p = 0.0002	30.2	p < 0.0001	10.9	p = 0.001	4.96	2.2 (18%)	R166*, C167*, R222*, Y320*, A323*
	1.4	f61	16.8	p = 0.0002	30.2	p < 0.0001	18.7	p < 0.0001	4.96	2.2 (18%)	R166*, C167*, R222*, Y320*, A323*
	0.4	f3x4	17.0	p = 0.0002	29.4	p < 0.0001	17.7	p < 0.0001	4.77	2.1 (18%)	R166*, C167*, Y320*, A323*
	1.4	f3x4	17.0	p = 0.0002	29.4	p < 0.0001	17.7	p < 0.0001	4.77	2.1 (18%)	R166*, C167*, Y320*, A323*
TREE 2 (node collapsed)	0.4	f61	15.8	p = 0.0004	28.8	p < 0.0001	17.9	p < 0.0001	5.01	2.1 (19%)	R166*, C167*, R222*, Y320*, A323*
	1.4	f61	15.8	p = 0.0004	28.8	p < 0.0001	17.9	p < 0.0001	5.01	2.1 (19%)	R166*, C167*, R222*, Y320*, A323*
	0.4	f3x4	16.3	p = 0.0003	28.1	p < 0.0001	17.1	p < 0.0001	4.82	2.1 (18%)	R166*, C167*, Y320*, A323*
	1.4	f3x4	16.3	p = 0.0003	28.1	p < 0.0001	17.1	p < 0.0001	4.82	2.1 (18%)	R166*, C167*, Y320*, A323*

^a Dataset consisted of the 15 aligned human sequences: B1, B2, B5, F1, F2, F3, A1, A2, C1, C2, C6, C8, H1, H2, G1

^b Initial seed value for ω (dN/dS) used in the maximum likelihood simulation

^c Model of codon usage frequency

^d Twice the difference in the natural logs of the likelihoods ($\Delta\ell \times 2$) of the two models being compared. This value is used in a likelihood ratio test along with the degrees of freedom. In all cases (M1a-M2a), (M7-M8), (M8a-M8), a model that allows positive selection is compared to a null model. The p-value indicates the confidence with which the null model can be rejected.

^e The tree length is the number of substitutions per site along all branches in the phylogeny. It is calculated as the sum of the branch lengths, and is a representation of total diversity in the dataset

^f dN/dS value of the class of codons evolving under positive selection in M8, and the percent of codons assigned to that class.

^g Amino acid positions identified in the class of codons evolving under positive selection in M8 with a posterior probability >0.95 by Naive Empirical Bayes (NEB). Coordinates correspond to the TRIM49(F1) protein.