

### Supplementary Table S3

Maximum likelihood estimates of  $d_N/d_S$  ratios ( $\omega$ ) for 88 mammalian HCA<sub>1</sub> and HCA<sub>2</sub> orthologs, for 5 ape HCA<sub>1</sub>, HCA<sub>2</sub> and HCA<sub>3</sub> orthologs and for 5 Hylobatidae HCA<sub>1</sub> and HCA<sub>2</sub> orthologs under different branch-specific models using PAML.

branch models	$p$	l	$\kappa$	Estimates of Parameters	hypothesis	$\chi^2$	P-Value
<b>HCA<sub>1</sub></b>							
<b>88 mammalian species</b>							
One ratio: $\omega_0$	142	-18285.29	4.08	$\omega_0 = 0.106$			
Two ratios: $\omega_0, \omega_{\text{Hominidae}}$	143	-18284.32	4.08	$\omega_0 = 0.105, \omega_{\text{Hominidae}} = 0.169$	$\omega_0 \neq \omega_{\text{Hominidae}}$	1.94	0.1637
Two ratios: $\omega_0, \omega_{\text{Hylobatidae}}$	143	-18284.04	4.08	$\omega_0 = 0.105, \omega_{\text{Hylobatidae}} = 0.233$	$\omega_0 \neq \omega_{\text{Hylobatidae}}$	2.51	0.1131
Two ratios: $\omega_0, \omega_{\text{Hominoidea}}$	143	-18282.81	4.09	$\omega_0 = 0.105, \omega_{\text{Hominoidea}} = 0.189$	$\omega_0 \neq \omega_{\text{Hominoidea}}$	4.97	0.0258
<b>HCA<sub>2</sub></b>							
<b>88 mammalian species</b>							
One ratio: $\omega_0$	142	-18378.75	3.43	$\omega_0 = 0.091$			
Two ratios: $\omega_0, \omega_{\text{Hominidae}}$	143	-18378.74	3.43	$\omega_0 = 0.091, \omega_{\text{Hominidae}} = 0.087$	$\omega_0 \neq \omega_{\text{Hominidae}}$	0.02	0.8875
Two ratios: $\omega_0, \omega_{\text{Hylobatidae}}$	143	-18378.73	3.43	$\omega_0 = 0.091, \omega_{\text{Hylobatidae}} = 0.099$	$\omega_0 \neq \omega_{\text{Hylobatidae}}$	0.05	0.8231
Two ratios: $\omega_0, \omega_{\text{Hominoidea}}$	143	-18378.69	3.43	$\omega_0 = 0.091, \omega_{\text{Hominoidea}} = 0.099$	$\omega_0 \neq \omega_{\text{Hominoidea}}$	0.13	0.7184
<b>HCA<sub>1</sub>-HCA<sub>2</sub>-HCA<sub>3</sub></b>							
<b>5 apes</b>							
<b>branch models</b>							
One ratio: $\omega_0$	29	-3047.70	2.32	$\omega_0 = 0.135$			
Two ratios: $\omega_{\text{HCA1}}, \omega_{\text{HCA2/HCA3}}$	30	-3045.26	2.36	$\omega_{\text{HCA1}} = 0.095, \omega_{\text{HCA2/HCA3}} = 0.184$	$\omega_{\text{HCA1}} \neq \omega_{\text{HCA2/HCA3}}$	4.88	0.0272
Two ratios: $\omega_{\text{HCA2}}, \omega_{\text{HCA1/HCA3}}$	30	-3047.70	2.32	$\omega_{\text{HCA2}} = 0.131, \omega_{\text{HCA1/HCA3}} = 0.137$	$\omega_{\text{HCA2}} \neq \omega_{\text{HCA1/HCA3}}$	0.01	0.9203
Two ratios: $\omega_{\text{HCA3}}, \omega_{\text{HCA1/HCA2}}$	30	-3043.99	2.36	$\omega_{\text{HCA3}} = 0.257, \omega_{\text{HCA1/HCA2}} = 0.103$	$\omega_{\text{HCA3}} \neq \omega_{\text{HCA1/HCA2}}$	7.43	0.0064
Two ratios: $\omega_{\text{HCA3}} = 1, \omega_{\text{HCA1/HCA2}}$	29	-3056.45	2.49	$\omega_{\text{HCA3}} = 1, \omega_{\text{HCA1/HCA2}} = 0.104$	$\omega_{\text{HCA3}} \neq 1$	24.92	0.0001
Two ratios:	30	-3045.02	2.33	$\omega_0 = 0.124, \omega_{\text{siamangHCA2/HCA3}} = 0.775$	$\omega_0 \neq \omega_{\text{siamangHCA2/HCA3}}$	5.36	0.0206

$\omega_0, \omega_{\text{siamangHCA2/HCA3}}$ Two ratios: $\omega_0, \omega_{\text{siamangHCA2/HCA3}} = 1$	29	-3045.07	2.33	$\omega_0 = 0.124, \omega_{\text{siamangHCA2/HCA3}} = 1$	$\omega_{\text{siamangHCA2/HCA3}} \neq 1$	0.09	0.7642
<b>HCA<sub>1</sub></b> <b>5 gibbons</b>							
One ratio: $\omega_0$	10	-1467.86	3.03	$\omega_0 = 0.207$			
Two ratios: $\omega_0, \omega_{\text{siamang}}$	11	-1467.40	3.03	$\omega_0 = 0.138, \omega_{\text{siamang}} = 0.415$	$\omega_0 \neq \omega_{\text{siamang}}$	0.93	0.3349
Two ratios: $\omega_0, \omega_{\text{siamang}} = 1$	10	-1467.82	3.17	$\omega_0 = 0.105, \omega_{\text{siamang}} = 1$	$\omega_{\text{siamang}} \neq 1$	0.84	0.3594
<b>HCA<sub>2</sub></b> <b>5 gibbons</b>							
One ratio: $\omega_0$	8	-1597.26	2.42	$\omega_0 = 0.114$			
Two ratios: $\omega_0, \omega_{\text{siamang}}$	9	-1593.68	2.42	$\omega_0 = 0.048, \omega_{\text{siamang}} = 0.643$	$\omega_0 \neq \omega_{\text{siamang}}$	7.16	0.0075
Two ratios: $\omega_0, \omega_{\text{siamang}} = 1$	8	-1593.81	2.46	$\omega_0 = 0.048, \omega_{\text{siamang}} = 1$	$\omega_{\text{siamang}} \neq 1$	0.26	0.6101

<sup>a</sup> LRT tests were performed between nested models.  $\omega$ ,  $d_N/d_S$  ratio;  $\omega_0$ , indicates  $\omega$  of all other branches (the ones that are not specifically labeled in a model).  $p$ , number of free parameters;  $\ell$ , Log likelihood;  $\kappa$ , transition to transversion rate ratio; \* indicates  $P > 0.95$ ; \*\* indicates  $P > 0.99$ ; corresponding tree in NEWICK notation: ((((((Hsapi3,Ptrog3),Ggori3),Ppygm3),Ssynd3),(((Hsapi2,Ptrog2),Ggori2),Ppygm2),Ssynd2)),(((Hsapi1,Ptrog1),Ggori1),Ppygm1),Ssynd1)); Hsapi: Homo sapiens, Ptrog: Pan troglodytes, Ggori: Gorilla gorilla, Ppygm: Pongo pygmaeus, Ssynd: Symphalangus syndactylus; corresponding tree in NEWICK notation: ((hoolock-gibbon1,silvery-gibbon1,(pileated-gibbon1)),siamang1,white-cheeked-gibbon1); ((hoolock-gibbon2,silvery-gibbon2,(pileated-gibbon2)),siamang2,white-cheeked-gibbon2);