

Table S4. PAML branch model and Clade model tests between Haplorhini TAARs and Strepsirrhini TAARs.

Genes ^a	Models ^b	ω_0	ω_1	ω_2	$\ln L^c$	$2\Delta\ln L^d$ (<i>P</i> -values)
TAAR1 (13)						
	R1	0.2726	-	-	-2951.441	0.0575
	R2	0.2838	0.2669	-	-2951.412	(<i>P</i> =0.8105)
	M2a_rel	0.127 (76%)	1 (17%)	0.127 (7%)	-2914.836	43.672
	CmC	0.125 (76%)	1 (17%)	0.323 (7%)	-2936.672	(<i>P</i> <0.0001)
TAAR2 (8)						
	R1	0.158	-	-	-2621.087	9.4838
	R2	0.0906	0.2081	-	-2616.345	(<i>P</i> =0.0021)
	M2a_rel	0.263 (51%)	1 (2.2%)	0.00 (47%)	-2511.988	196.28
	CmC	0.06 (62.5%)	1 (6.5%)	0.488 (31%)	-2610.127	(<i>P</i> <0.0001)
TAAR3 (6)						
	R1	0.1195	-	-	-3742.381	15.065
	R2	0.0541	0.2001	-	-3734.848	(<i>P</i> =0.0001)
	M2a_rel	0.12 (100%)	1 (0.0%)	0.00 (0.0%)	-3738.445	15.717
	CmC	0.002 (5%)	1 (5%)	0.16 (90%)	-3730.587	(<i>P</i> <0.0001)
TAAR4 (7)						
	R1	0.2915	-	-	-2761.761	7.7626
	R2	0.1739	0.3783	-	-2757.879	(<i>P</i> =0.0053)
	M2a_rel	0.00 (16%)	1 (27%)	0.105 (57%)	-2715.469	42.742
	CmC	0.023 (61%)	1 (18%)	1.414 (21%)	-2736.840	(<i>P</i> <0.0001)
TAAR5 (9)						
	R1	0.261	-	-	-2246.589	1.6229
	R2	0.0001	0.307	-	-2245.777	(<i>P</i> =0.2027)
	M2a_rel	0.145 (87%)	1 (0.0%)	1.157 (13%)	-2220.218	42.742
	CmC	0.123 (81%)	1 (11%)	1.580 (8%)	-2241.946	(<i>P</i> <0.0001)
TAAR6 (7)						
	R1	0.2592	-	-	-2399.209	7.1162
	R2	0.1949	0.4498	-	-2395.651	(<i>P</i> =0.0076)
	M2a_rel	0.096 (63%)	1 (20%)	0.096 (17%)	-2391.598	8.568
	CmC	0.090 (79%)	1 (6.7%)	1.390 (15%)	-2389.314	(<i>P</i> =0.0034)
TAAR8 (3)						
	R1	0.314	-	-	-2161.239	3.0658
	R2	0.3927	0.0001	-	-2159.706	(<i>P</i> =0.08)
	M2a_rel	0.76 (46%)	1 (0.0%)	0.00 (54%)	-2156.412	2.51
	CmC	0.00 (53%)	1 (0.0%)	0.00 (47%)	-2155.746	(<i>P</i> =0.1131)
TAAR9 (5)						
	R1	0.1485	-	-	-2552.026	10.7164
	R2	0.0799	0.2169	-	-2546.668	(<i>P</i> =0.0011)
	M2a_rel	0.09 (72%)	1 (5%)	0.09 (23%)	-2285.187	510.53
	CmC	0.08 (87%)	1 (0.0%)	1.286 (13%)	-2540.453	(<i>P</i> <0.0001)

^aThe number of the genes included in each TAAR subfamily is given in parentheses after the subfamily name.

^bAll tests were performed comparing two hypotheses: R1 (a single ω for all branches) vs. R2 (two independent ω 's: ω_0 for the Strepsirrhini lineages and ω_1 for the Haplorhini lineages) and M2a_rel vs. Clade model C (CmC).

^cThe natural logarithm of the likelihood value.

^dFor the likelihood ratio test statistics, $2\ln L$ (P -values shown in parentheses) are obtained based on a χ^2 distribution with d.f. = 1. Significant P -values (< 0.01) are shown in boldfaces.