

Table S2. Pairwise comparisons of the dosage response curves for androstenone with an F test

A. Pairwise comparisons between the hypothetical hominine ancestor and each synthetic mutant representing changes from the ancestor to various hominine species

	EC50	F (DFn, DFd)	P value	Function
hominine	0.69			
L17F	0.98	2.346 (1,12)	> 0.05	n
V26I	1.2	4.648 (1,12)	> 0.05	n
N84S	3.5	47.18 (1,12)	< 0.01**	d
S89I	1.7	20.94 (1,12)	< 0.01**	d
I160V	0.25	11.64 (1,12)	> 0.05	n
G171V	0.15	29.48 (1,12)	< 0.01**	i
R227G	3.7	51.33 (1,12)	< 0.01**	d
M228T	6.6	120.9 (1,12)	< 0.01**	d
E232K	0.30	6.504 (1,12)	> 0.05	n
M273T	1.7	24.09 (1,12)	< 0.01**	d

B. Pairwise comparison between the hypothetical Great Ape ancestor and each synthetic mutant representing changes from the ancestor to the hominine ancestor and to orangutan

	EC50	F (DFn, DFd)	P value	Function
Great Ape	0.23			
P58A	3.7	522.8 (1,12)	< 0.01**	d
M110L	0.58	116.2 (1,12)	< 0.01**	d
H128Y	0.22	0.04442 (1,12)	> 0.05	n
H131Q	0.30	12.19 (1,12)	> 0.05	n
I151V	0.23	0.01668 (1,12)	> 0.05	n
C179Y	>30	31.19 (1,12)	< 0.01**	d
E180V	>30	N/A	N/A	d
Q183R	2.1	451.3 (1,12)	< 0.01**	d
R189C	1.4	411.8 (1,12)	< 0.01**	d
Q220R	0.058	60.10 (1,12)	< 0.01**	i
T231P	0.22	0.2505 (1,12)	> 0.05	n
Y252N	>30	10.13 (1,12)	> 0.05	d
H266R	0.33	50.17 (1,12)	< 0.01**	d
M273T	0.38	48.19 (1,12)	< 0.01**	d

C. Pairwise comparison between the hypothetical catarrhine ancestor and each synthetic mutant representing changes from the ancestor to the Great Ape ancestor and to various Old World Monkey species

	EC50	F (DFn, DFd)	P value	Function
catarrhine	0.026			
L6Y	7.5E-05	23.27 (1,20)	< 0.01**	i

E11K	7.8E-04	9.192 (1,20)	> 0.05	n
D19G	1.7E-04	16.54 (1,20)	0.025*	i
D20A	4.3E-07	49.00 (1,20)	< 0.01**	i
P21S	1.9E-04	15.44 (1,20)	0.033*	i
P21_	0.052	1.243 (1,20)	> 0.05	n
E22Q	8.1E-07	48.54 (1,20)	< 0.01**	i
R88Q	0.52	55.77 (1,20)	< 0.01**	d
D91H	9.9E-04	9.944 (1,20)	> 0.05	n
M95V	2.6E-04	14.16 (1,20)	0.049*	i
G96R	0.088	5.190 (1,20)	> 0.05	n
G96W	0.18	14.45 (1,20)	0.045*	d
M110T	0.18	15.04 (1,20)	0.037*	d
N112T	3.0E-07	60.74 (1,20)	< 0.01**	i
A116T	0.033	0.1086 (1,20)	> 0.05	n
A116V	6.5E-04	9.007 (1,20)	> 0.05	n
R122W	>30	N/A	N/A	d
C139H	1.3E-06	57.84 (1,20)	< 0.01**	i
L143R	2.6E-05	31.13 (1,20)	< 0.01**	i
F153V	0.013	0.7381 (1,20)	> 0.05	n
V155F	3.0E-05	33.65 (1,20)	< 0.01**	i
I160L	4.0	112.8 (1,20)	< 0.01**	d
T167A	0.0043	4.272 (1,20)	> 0.05	n
T170I	0.019	0.1725 (1,20)	> 0.05	n
L181V	0.10	12.01 (1,20)	> 0.05	n
L181P	0.081	9.083 (1,20)	> 0.05	n
D191N	0.035	0.2046 (1,20)	> 0.05	n
L194_	2.7	132.3 (1,20)	< 0.01**	d
V198I	0.010	1.507 (1,20)	> 0.05	n
V211A	0.042	0.6602 (1,20)	> 0.05	n
F216I	0.13	14.54 (1,20)	0.045*	d
S219F	1.0E-04	30.61 (1,20)	< 0.01**	i
V222I	1.6E-05	61.17 (1,20)	< 0.01**	i
K236E	4.2	118.2 (1,20)	< 0.01**	d
T279A	0.0042	4.546 (1,20)	> 0.05	n
K295N	0.21	28.22 (1,20)	< 0.01**	d
G299A	>30	N/A	N/A	d
L301P	4.0	162.7 (1,20)	< 0.01**	d
G302E	0.10	10.81 (1,20)	> 0.05	n
A308T	0.021	0.1144 (1,20)	> 0.05	n
A309D	0.063	3.281 (1,20)	> 0.05	n

EC50 values for responses to androstenone are given in μM . An F test is used to compare the best-fit values of EC50 of the dosage response curves between each hypothetical ancestors and each synthetic mutant. (See Fig. S4 for the dosage response curves.) F value, DF_n, DF_d, and P value are shown for each synthetic mutant. A Bonferroni correction was applied to the F test. For A: Before correction: * P < 0.005, ** P < 0.001, *** P < 0.0001. For B: Before correction: * P < 0.0036, ** P < 0.00071, *** P < 0.000071. For C: Before correction: * P < 0.0012, ** P < 0.00024, *** P < 0.000024. After correction: * P < 0.05, ** P < 0.01. Asterisks shown represent

significance of P values after correction. Significant change in function is indicated as follows: i, increase in function; d, decrease in function; n, no change in function. DF_n, numerator degrees of freedom. DF_d, denominator degrees of freedom.