

**S4 Table. The results of PAML branch-site model analysis.<sup>a</sup>**

TAAR subfamily <sup>b</sup>	Foreground branch	$2\Delta\ln L^c$	Proportion of site class	$\omega$	Positively selected sites <sup>d</sup>
TAAR7 (45)	flying fox TAAR7c	3.9934 (0.0457)	0: 0.68747, 1: 0.29542, 2a: 0.01197, 2b: 0.00514	$\omega_0=0.11593$ , $\omega_1=1$ , $\omega_2=140.19823$	A162 (0.657), I184 (0.599)
TAAR7 (45)	tenrec- elephant TAAR7	<b>7.2427</b> <b>(0.0071)</b>	0: 0.69211, 1: 0.29130, 2a: 0.01167, 2b: 0.00491	$\omega_0=0.11524$ , $\omega_1=1$ , $\omega_2=169.33093$	S161 (0.581), S177 (0.522), <b>S188<sup>5,36</sup> (0.973)</b>
TAAR8 (16)	mouse TAAR8a	6.0053 (0.0142)	0: 0.82235, 1: 0.17302, 2a: 0.00383, 2b: 0.00081	$\omega_0=0.14625$ , $\omega_1=1$ , $\omega_2=777.9954$	F190 <sup>5,38</sup> (0.935)

<sup>a</sup>Only the results where the given foreground branch having positive selection is supported significantly are listed. These branches are indicated with red color and arrows in Fig 2.

<sup>b</sup>The number of the TAAR subfamily genes tested is given in parentheses.

<sup>c</sup>Likelihood-ratio test statistics. *P*-values (shown in parentheses) are obtained based on a  $\chi^2$  distribution with d.f. = 1. *P*-values smaller than 0.01 are shown in boldfaces.

<sup>d</sup>Positively selected amino acid sites using the Bayes Empirical Bayes inference. Posterior probabilities are shown in parentheses, in boldfaces when *P* > 0.95. The position numbers are based on the alignment in S5 Fig. The numbering of the Ballesteros-Weinstein scheme (Ballesteros and Weinstein 1995) is shown in superscripts.

#### References:

Ballesteros JA, Weinstein H. 1995. Integrated methods for the construction of three-dimensional models and computational probing of structure-function relations in G protein-coupled receptors. In: CS Stuart, editor. Receptor Molecular Biology: Academic Press. p. 366-428.