R1	R2	2∆ <i>ln</i> L
[Test 1: TAAR1 (14) and TAAR3 ( $\omega_0$ $\omega_0$ TAAR7 $\omega_0$ $\omega_0$ TAAR3 $\omega_0 = 0.2012$	13) vs. TAAR7 (45)] $ \begin{array}{c}                                     $	46.2655 ( <b>&lt; 0.0001</b> )
[Test 2: TAAR1 (14) and TAAR3 ( $\omega_0$ $\omega_0$ TAAR8 $\omega_0$ $\omega_0$ TAAR3 $\omega_0$ $\omega_0$ TAAR3 $\omega_0$ = 0.1601	<b>13)</b> vs. TAAR8 (16)] $ \begin{array}{c} \omega_{1} & \text{TAAR8} \\ \hline \omega_{0} & \overline{\omega_{0}} & \text{TAAR3} \\ \hline \omega_{0} & = 0.1360, \ \omega_{1} = 0.2589 \end{array} $	8.7584 ( <b>0.0031</b> )
[Test 3: TAAR1 (14), TAAR3 (13), and TAAR7 (45) vs. TAAR8 (16)]		
$ \begin{array}{c}                                     $	$\omega_{0} \qquad \qquad$	1.3960 (0.2374)
[Test 4: TAAR1 (14), TAAR3 (13), and TAAR8 (16) vs. TAAR7 (45)]		
$\omega_{0} \qquad \omega_{0} \qquad \text{TAAR8}$ $\omega_{0} \qquad \text{TAAR7}$ $\omega_{0} \qquad \omega_{0} \qquad \text{TAAR3}$ $\omega_{0} = 0.2077$	$\omega_{0} \qquad \qquad$	36.4144 (< <b>0.0001</b> )
[Test 5: TAAR1 (14) and TAAR3 (13) <i>vs</i> . TAAR7 (45) and TAAR8 (16)]		
$\omega_{0} \qquad \omega_{0} \qquad \text{TAAR8} \\ \overline{\omega_{0}} \qquad \overline{\omega_{0}} \qquad \text{TAAR7} \\ \overline{\omega_{0}} \qquad \overline{\omega_{0}} \qquad \text{TAAR3} \\ \overline{\omega_{0}} \qquad \overline{\omega_{0}} \qquad \text{TAAR1} \\ \overline{\omega_{0}} = 0.2077$	$\omega_{1} \qquad \frac{\omega_{1}}{\omega_{0}} \qquad \frac{TAAR8}{TAAR7}$ $\omega_{0} \qquad \frac{\omega_{0}}{\omega_{0}} \qquad \frac{TAAR3}{TAAR1}$ $\omega_{0} = 0.1069, \ \omega_{1} = 0.3314$	47.7429 ( <b>&lt; 0.0001</b> )

S4 Fig. PAML branch-model tests between primary amine detecting TAARs (TAAR1 and TAAR3) and tertiary amine detecting TAARs (TAAR7 and TAAR8). All tests were performed comparing the two hypotheses: R1 (a single  $\omega$  for all branches) and R2 (two independent  $\omega$ 's:  $\omega_1$  for the red lineage and  $\omega_0$ for the black lineages). The number of the genes included in each TAAR subfamily is given in parentheses after the subfamily name. For the likelihood ratio test statistics,  $2\Delta lnL$ , *P*-values (shown in parentheses) are obtained based on a  $\chi^2$  distribution with d.f. = 1. Significant *P*-values (< 0.05) are shown in boldfaces.