S6 Fig. Modeling of the 3D-structure of TAAR proteins. The same template, the B-chain of the turkey β1-adrenergic receptor (a: β1AR, PDB: 4AMJ), was selected by SWISS-MODEL (http://swissmodel.expasy.org; Arnold et al., 2006) for modeling protein structures of the human TAAR1 (b: NP_612200), elephant TAAR7a (c: XP_003404143), and mouse TAAR8a (d: NP_001010830) (all E-values < 0.001; their sequence similarities against β1AR, P07700, are 49.3%, 46.2%, and 43.9%, respectively). The 3D-structure of the 4AMJ (a) is color-coded based on the temperature factors (B-factors), ranging from 15.74 (blue) to 124.95 (red) (see color scale in the figure). The average B-factor is 45.52. The ligand for the β1AR, dobutamine, is shown with the stick model. Note that the template protein contains truncations at N-terminus, third intracellular loop, and C-terminus as well as some thermostabilizing point mutations to improve expression and to obtain crystals (Warne et al., 2012). None of these positions were, however, overlapped with those identified to be under positive selection (see S5 Fig for more details). Predicted protein structures of the human TAAR1 (b: yellow), elephant TAAR7a (c: cyan), and mouse TAAR8a (d: light blue) are superimposed with the template structure (gray) using PyMOL. The QMEAN4 Z-scores given by SWISS-MODEL were -8.27, -8.02, and -8.37 (raw scores: 0.234, 0.250, and 0.228), respectively. The overall root-mean-square deviations (RMSDs) given by PyMOL were 0.054 Å, 0.055Å, and 0.054 Å, respectively. The N-terminal 15, 25, 23 amino acids (aa) and the C-terminal 19, 16, and 16 aa, respectively, were excluded from the modeling due to insufficient sequence similarity. Positive-selection sites identified by our PAML analysis in elephant TAAR7a (c) and mouse TAAR8a (d) are indicated by red and purple (site models) and by green and brown (branch-site models). Position 184 in elephant TAAR7a was identified by both site and branch-site models. Sites identified with higher than 0.95 posterior probabilities are indicated with asterisks. See S3 and S4 Tables for details on PAML analysis. All amino acid sites corresponding to these positive-selection sites are also mapped on human TAAR1 by yellow spheres for comparison (b). All amino acid position numbers are according to the human TAAR1 sequence. The transmembrane (TM) and internal/external loop (IC1-3 and EC1-3) regions as well as the N-terminal (N) are labeled in each structure. The C-terminal is invisible locating behind TM1. See S5 Fig for the alignment and more detailed information on these sequences.

References: