Supporting Information

Hussain *et al.* 10.1073/pnas.0803229106

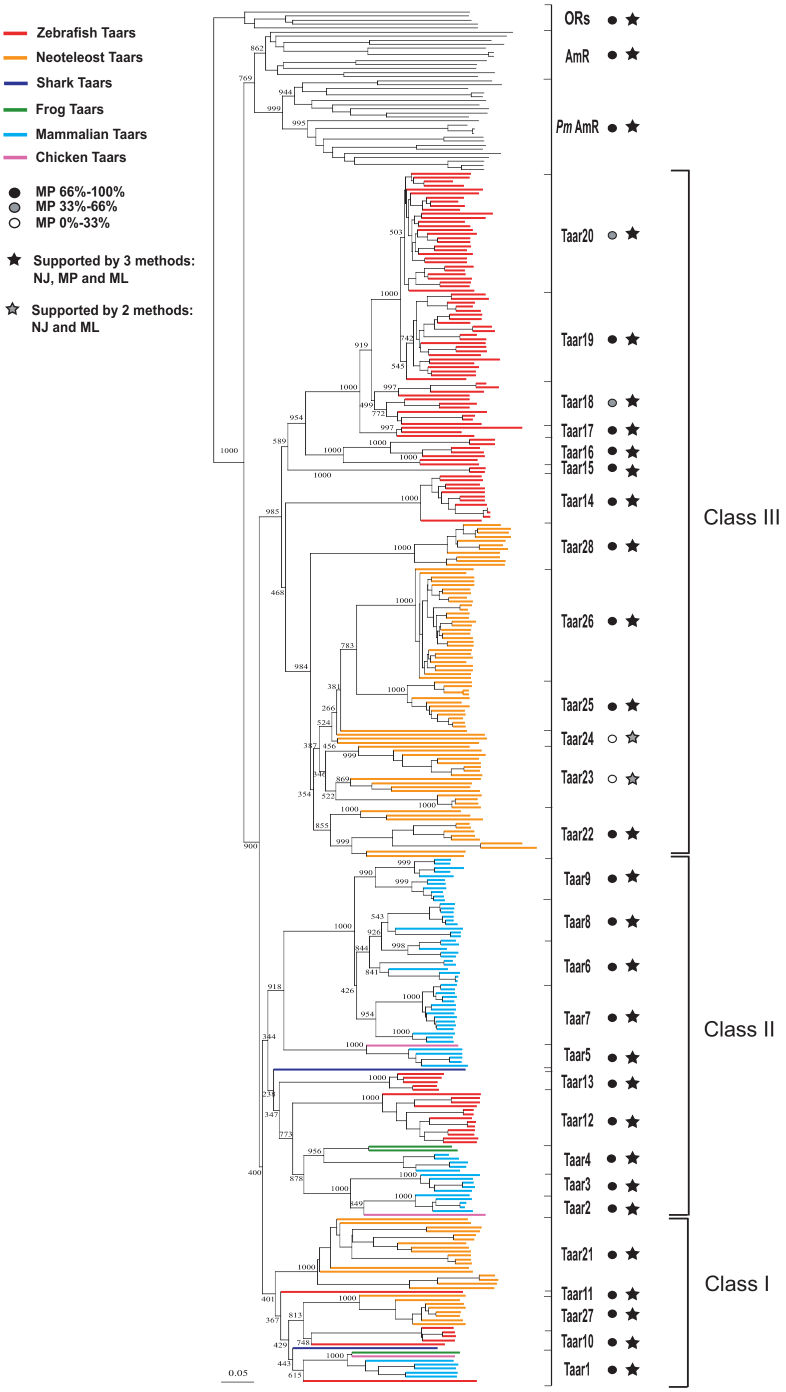

Fig. S1. Phylogenetic tree of the *taar* genes. The cladogram shown here corresponds to the unrooted tree in Fig. 1. The tree is constructed by using the neighbor-joining algorithm; bootstrap support at major nodes is indicated by numbers (1,000 cycles). All subfamilies are supported by all 3 tree algorithms used (neighbor joining; maximum parsimony, 100 bootstraps; maximum likelihood), except subfamilies 23 and 24 (supported by 2 methods). Red lines represent zebrafish *taar* genes; orange lines, neoteleost *taar* genes; dark blue, cartilaginous fish *taar* genes; green, amphibian *taar* genes; light-blue, mammalian *taar* genes; and black represents the outgroup (OR, odorant receptors; AmR, aminergic receptors; PmAmR, *Petromyzon marinus* (sea lamprey) aminergic receptors). Note the segregation in 3 clades, class I to III.

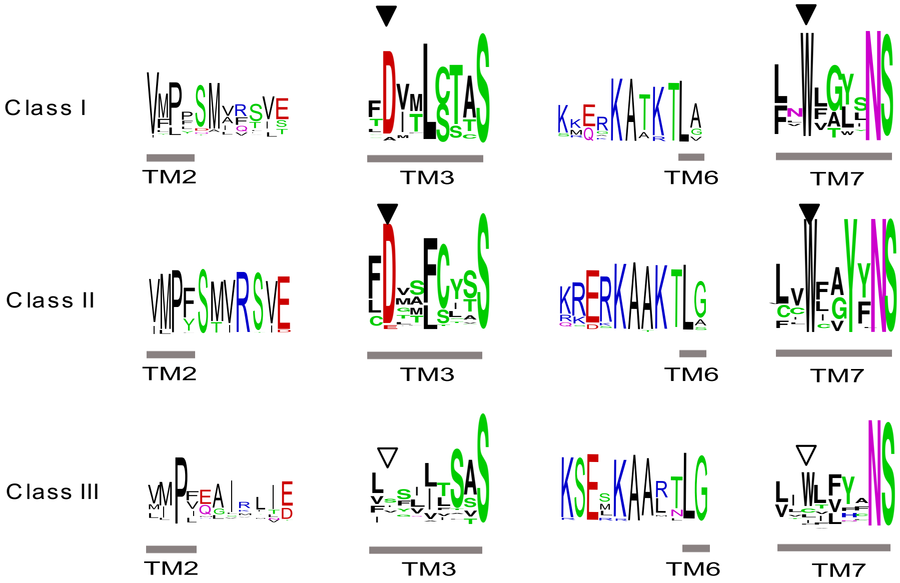

Fig. S2. Subclass-specific amino acid sequence conservation. Conservation is displayed as a sequence logo. Four motifs are shown (end of TM2, start of TM3, preceding TM6, and start of TM7, respectively) that distinguish among the 3 classes of TAARs. TM3 and TM7 contain the 2 amino acids (filled triangle) constituting the aminergic ligand motif (1). Note the absence of the motif (open triangle) in class III genes.

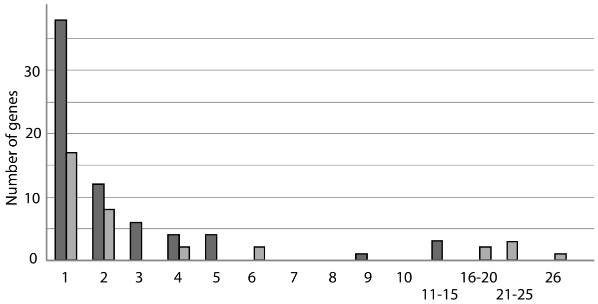

Fig. S3. Correlation of phylogenetic distance with physical distance in 2 zebrafish genomic clusters. For each gene within the clusters on chromosome 10 (dark gray bars) and chromosome 20 (light gray bars), the paralog with the highest homology was determined, and its position relative to the first gene was expressed as ordinal value, e.g., a value of 1 indicates a direct neighbor (most frequent case), and a value of 2 indicates 1 additional gene situated between the gene and its closest relative. Phylogenetic neighbors outside of the cluster occur only in 2 cases.

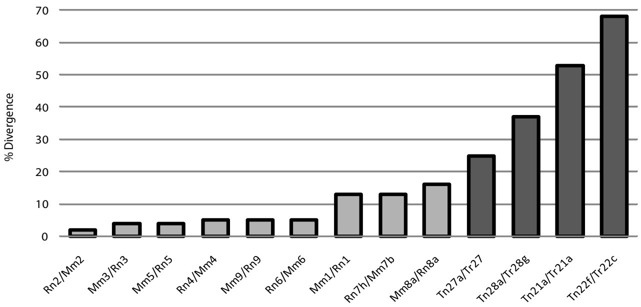

Fig. S4. Maximal divergence within rodent and pufferfish subfamilies. Bars show maximal divergence between ortholog genes in rat vs. mouse and tetraodon vs. fugu comparisons. Values are based on amino acid comparisons and ordered by size. Note that even the largest value for rodent comparisons is well below the smallest value for pufferfish comparisons.

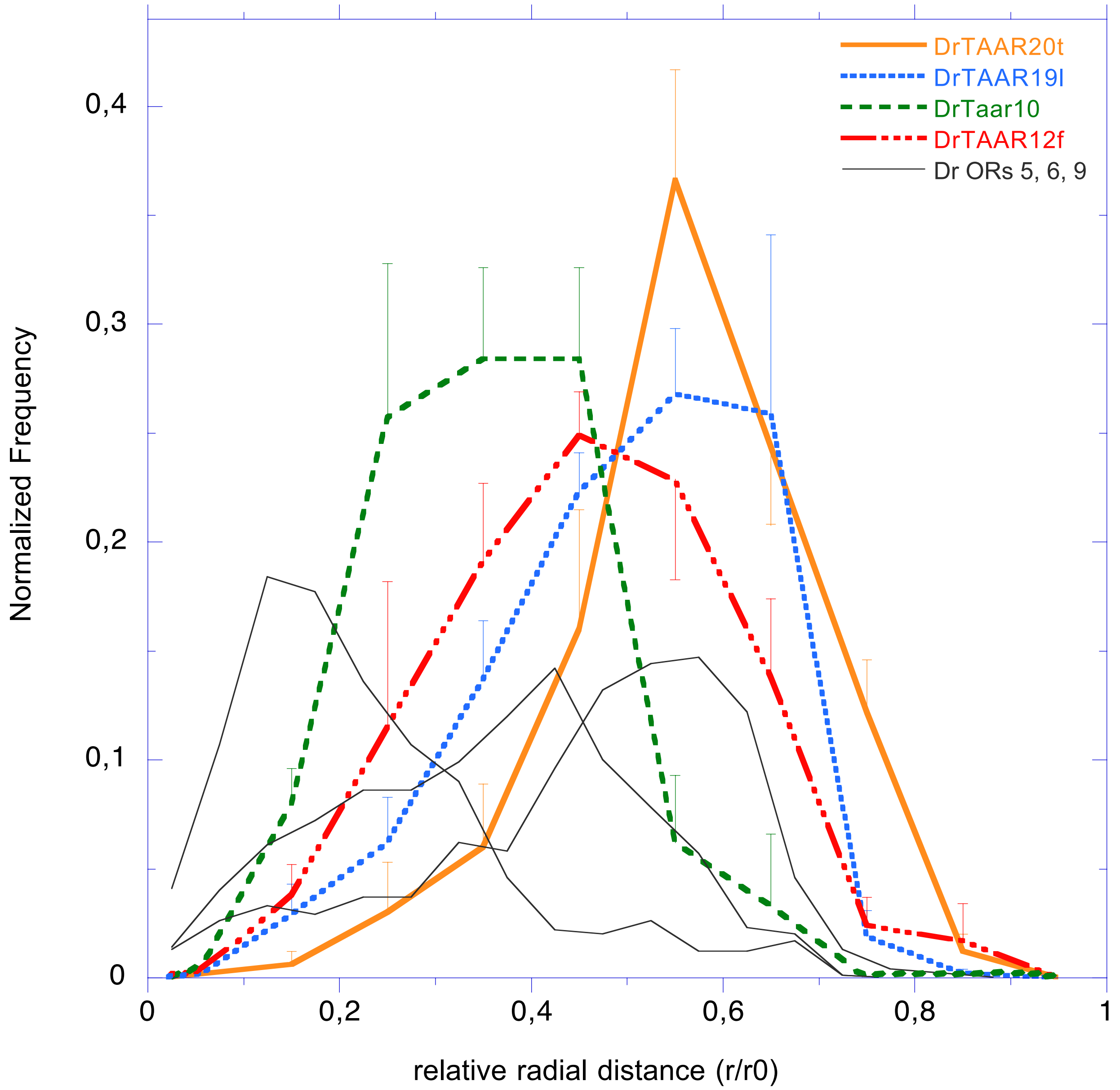

Fig. S5. Radial distribution of 4 TAAR genes. Positions of cells expressing particular TAAR genes were identified in horizontal sections of olfactory epithelia in the microscope and manually marked on printouts. Relative radial distance (r/r_0) of labeled cells was measured for each lamella separately as distance from the nadir of the sensory layer, closest to the median raphe, divided by the total length of the corresponding lamella. For each section, a histogram of the radial distribution was calculated for 10 equidistant bins, frequency values obtained for each bin were normalized and averaged for several sections. Values given represent mean ± SEM. Thick lines, TAAR genes; thin black lines, reference curves from left to right (peak values) for OR genes *zor6*, *zor9*, and *zor5*, respectively (data taken from ref. 2). Note the skewness of histogram curves for TAAR12f, 19l, 20t, similar to the skewness observed for zOR6 and zOR5. Peaks for TAAR distribution are found medially and distally, similar to the proximally, medially, and distally centered distributions described for ORs.

1. Huang ES (2003) Construction of a sequence motif characteristic of aminergic G protein-coupled receptors. *Protein Sci* 12:1360–1367.
2. Weth F, Nadler W, Korsching S (1996) Nested expression domains for odorant receptors in zebrafish olfactory epithelium. *Proc Natl Acad Sci USA* 93, 13321–13326.

Other Supporting Information Files

Table S1 (PDF)
Table S2 (PDF)
Table S3 (PDF)
Table S4 (PDF)
Table S5 (PDF)
Table S6 (PDF)