

**Table 1. The number of TAAR genes identified in the 30 animal genomes.**

Group/Species name	Common name	Total number <sup>a</sup>	Number of TAAR subfamily genes <sup>b</sup>																	
			T1	T2	T3	T4	T5	T6	T7	T8	T9	TE1	TM1	TM2	TM3	TFI	TFII	TFIII	TL	TV
<b>[Euarchontoglires]</b>																				
<i>Homo sapiens</i>	human	6 (3)	1	1	0 (1)	0 (1)	1	1	0 (1)	1	1	0	0	0	0	0	0	0	0	0
<i>Mus musculus</i>	house mouse	15 (1)	1	1	1	1	1	1	5 (1)	3	1	0	0	0	0	0	0	0	0	0
<i>Rattus norvegicus</i>	Norway rat	17 (2)	1	1	1	1	1	1	7 (2)	3	1	0	0	0	0	0	0	0	0	0
<b>[Laurasiatheria]</b>																				
<i>Bos taurus</i>	cow	21 (8)	1	1 <sup>c</sup>	1	1	1	5 (2)	7 (4)	3 (2)	1	0	0	0	0	0	0	0	0	0
<i>Tursiops truncatus</i>	bottlenosed dolphin	0 (3)	0 (2)	0	0	0	0	0	0	0	0 (1)	0	0	0	0	0	0	0	0	0
<i>Equus caballus</i>	horse	11 (4)	1	1	1	1	2	1	1 (1)	2 (1)	1 (1)	0 (1)	0	0	0	0	0	0	0	0
<i>Canis familiaris</i>	dog	2 (2)	0 (1)	0 (1)	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Pteropus vampyrus</i>	Malayan flying fox	26 (10)	1	1 <sup>c</sup>	0 (1)	1	1	4 (6)	16	1 (3)	1	0	0	0	0	0	0	0	0	0
<i>Myotis lucifugus</i>	little brown bat	6 (1)	1	1 <sup>c</sup>	1	1	1	0 (1)	0	0	1	0	0	0	0	0	0	0	0	0
<i>Sorex araneus</i>	common shrew	9 [1] (3)	1	[1] (1)	1	1 (1)	1	3	2	0	0 (1)	2	0	0	0	0	0	0	0	0
<i>Erinaceus europaeus</i>	hedgehog	6 [2] (4)	[1] (1)	1 <sup>c</sup>	1	0 (2)	0 (1)	[1]	2	0	1	1	0	0	0	0	0	0	0	0
<b>[Afrotheria]</b>																				
<i>Echinops telfairi</i>	lesser hedgehog tenrec	9 [1] (7)	1 (1)	1 <sup>c</sup> (2)	1	1	0	0 (1)	2 (1)	1	[1]	2 (2)	0	0	0	0	0	0	0	0
<i>Loxodonta africana</i>	African elephant	9 [3] (3)	[1]	1 <sup>c</sup>	[1]	1 [1]	1	1	2	2 (3)	0	1	0	0	0	0	0	0	0	0
<b>[Xenarthra]</b>																				
<i>Dasyurus novemcinctus</i>	nine-banded armadillo	5 (4)	1	1 <sup>c</sup>	1	0	1	0	1 (1)	0 (2)	0 (1)	0	0	0	0	0	0	0	0	0
<b>[Marsupialia]</b>																				
<i>Macropus eugenii</i>	tammar wallaby	18 [1] (3)	(1)	[1]	1	1	1	0	0	0	1	0	1 (1)	9 (1)	4	0	0	0	0	0
<i>Monodelphis domestica</i>	opossum	22 (4)	1	1 <sup>c</sup>	1	3 (1)	1	0	0	0	7 (1)	0	1	2 (1)	5 (1)	0	0	0	0	0
<b>[Prototheria]</b>																				
<i>Ornithorhynchus anatinus</i>	platypus	4 (1)	1	1 <sup>c</sup>	1	1 (1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<b>[Sauropsida]</b>																				
<i>Gallus gallus</i>	chicken	4 (1)	1	2 <sup>c</sup>	0	0	1 (1)	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Taeniopygia guttata</i>	zebra finch	1 (0)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Anolis carolinensis</i>	Carolina anole	3 (0)	1	1 <sup>c</sup>	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

<b>[Amphibia]</b>																			
<i>Xenopus tropicalis</i>	pipid frog	7 (0)	1	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	1
<b>[Teleostei]</b>																			
<i>Takifugu rubripes</i>	fugu (Japanese pufferfish)	18 (1)	0	0	0	0	0	0	0	0	0	0	0	0	14 (1)	0	3	0	1
<i>Tetraodon nigroviridis</i>	spotted green pufferfish	34 (3)	0	0	0	0	0	0	0	0	0	0	0	0	12 (3)	0	21	0	1
<i>Danio rerio</i>	zebrafish	110 (10) <sup>d</sup>	1	0	0	0	0	0	0	0	0	0	0	0	92 (8)	11	6 (2)	0	1
<b>[Chondrichthyes]</b>																			
<i>Callorhynchus milii</i>	elephant shark	2 (3)	1 (1)	0	0	1 (2) <sup>e</sup>	0	0	0	0	0	0	0	0	0	0	0	0	0
<b>[Agnatha]</b>																			
<i>Petromyzon marinus</i>	sea lamprey	25 (3)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	25 (3)	0
<b>[Cephalochordata]</b>																			
<i>Branchiostoma floridae</i>	amphioxus	0																	
<b>[Urochordata]</b>																			
<i>Ciona intestinalis</i>	vase tunicate	0																	
<i>Ciona savignyi</i>	tunicate	0																	
<b>[Cnidaria]</b>																			
<i>Nematostella vectensis</i>	sea anemone	0																	

<sup>a</sup>TAAR gene candidates are divided into three categories: intact, incomplete, and pseudogenes. The first number shown is that of "intact" genes, which contain full-length open reading frames with seven complete transmembrane regions. The number of "incomplete" genes due to incomplete genome sequences (*e.g.*, long ambiguous sequences such as a run of N's or contig ends) or incompletely identified exons (*e.g.*, TAAR2, see below) is given in square brackets. The number in parentheses is that of possible pseudogenes, which contain premature stop codons or frame-shifting insertions or deletions.

<sup>b</sup>T1-T9, TE1, TM1-TM3, TFI-III, TL, and TV indicate TAAR1-9, TAAR E1, TAAR M1-M3, fish-specific TAAR I-III, lamprey TAAR-like genes, and TAAR V, respectively. The group names of fish-specific TAAR I-III and TAAR V are given by Hashiguchi and Nishida [26].

<sup>c</sup>Only the exon2 sequences (coding 304 to 331 amino acids) were identified from these TAAR2 genes. The exon1 (coding 8 to 20 amino acids) can be located more than 6000 bp upstream.

<sup>d</sup>The sequences are from Hashiguchi and Nishida [26]. We classified them into five subfamilies.

<sup>e</sup>These three shark sequences (S2a, S2bP, and S2cP) are most similar to TAAR4. However, as we described, these shark TAARs may have diverged from the ancestral TAARs before the divergence of TAAR2-4 (see also phylogenies in Figures 2 and 3, and S1).