

Table 1. The number of TAAR genes identified in the thirteen primate and five other genomes.

Order (Group)/ Species name	Common name	Total number ^a	Number of TAAR subfamily genes ^b								
			T1	T2	T3	T4	T5	T6	T7	T8	T9
Primates (Haplorhini)											
[Simiiformes (Catarrhini)]											
<i>Homo sapiens</i>	Human	6 (3)	1	1	0 (1)	0 (1)	1	1	0 (1)	1	1
<i>Pan troglodytes</i>	Chimpanzee	3 (6)	1	0 (1)	0 (1)	0 (1)	1	1	0 (1)	0 (1)	0 (1)
<i>Pan paniscus</i>	Bonobo	2 (7)	1	0 (1)	0 (1)	0 (1)	1	0 (1)	0 (1)	0 (1)	0 (1)
<i>Gorilla gorilla</i>	Gorilla	3 (6)	1	1	0 (1)	0 (1)	1	0 (1)	0 (1)	0 (1)	0 (1)
<i>Pongo pygmaeus abelii</i>	Sumatran orangutan	4 (6)	1	0 (1)	0 (1)	1	1	0 (1)	0 (2)	0 (1)	1
<i>Nomascus leucogenys</i>	White-cheeked gibbon	1 (3)	1	0	0	0 (1)	0 (1)	0	0	0	0 (1)
<i>Macaca mulatta</i>	Rhesus macaque	6 (3)	1	1	1	1	1	1	0 (1)	0 (1)	0 (1)
<i>Papio hamadryas</i>	Hamadryas baboon	5 (3)	1	1	1	1	0 (1)	1	0	0 (1)	0 (1)
<i>Papio anubis</i>	Olive baboon	6 (2)	1	1	1	1	1	1	0	0 (1)	0 (1)
[Simiiformes (Platyrrhini)]											
<i>Callithrix jacchus</i>	Common marmoset	2 (6)	1	0 (1)	0 (1)	0 (1)	1	0 (1)	0	0 (1)	0 (1)
[Tarsiiformes]											
<i>Tarsius syrichta</i>	Philippine tarsier	5 (3)	1	1	1	1	0 (1)	0 (1)	0	0 (1)	1
Primates (Strepsirrhini)											
[Lemuriformes]											
<i>Microcebus murinus</i>	Grey mouse lemur	7 (1)	1	1	1	1	0 (1)	1	0	1	1
[Lorisiformes]											
<i>Otolemur garnettii</i>	Bushbaby	8 (0)	1	1	1	1	1	1	0	1	1
Dermoptera											
<i>Galeopterus variegatus</i>	Malayan colugo	8 (2)	0 (1)	1	1	1	1	1	0	2 (1)	1
Scandentia											
<i>Tupaia belangeri</i>	Northern treeshrew	10 [2] (5)	0 (1)	1	1	1	[1]	2 (2)	0	5 (2)	[1]
Rodentia											
<i>Mus musculus</i>	House mouse	15 (1) ^c	1	1	1	1	1	1	5 (1)	3	1
<i>Rattus norvegicus</i>	Norway rat	17 (2) ^c	1	1	1	1	1	1	7 (2)	3	1
Artiodactyla											
<i>Bos taurus</i>	cow	21 (8) ^c	1	1	1	1	1	5 (2)	7 (4)	3 (2)	1

^aTAAR 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 numbers of the "incomplete" genes due to contig ends and the pseudogenes due to premature stop codons or frame-shifting insertions or deletions are given in square brackets and in parentheses, respectively.

^bT1-T9 indicate TAAR1 to TAAR9.

^cThese numbers were taken from Eyun et al. (2016).