

Table S1. The animal genomes used in this study.

Group/species	Order	Sources ^a	Coverage or version	Number of OR genes ^b	Number of TAAR genes ^b
[Euarchontoglires]					
<i>Homo sapiens</i>	Primate	NCBI (BUILD.37.2)	-	388 (414) ^c	6 (3)
<i>Mus musculus</i>	Rodentia	NCBI (BUILD.38.1)	-	1063 (328) ^c	15 (1)
<i>Rattus norvegicus</i>	Rodentia	NCBI (BUILD.4.1)	-	1259 (508) ^c	17 (2)
[Laurasiatheria]					
<i>Bos taurus</i>	Cetartiodactyla	BC	7.1×	970 (1159) ^c	21 (8)
<i>Tursiops truncatus</i>	Cetacea	BI	2.59×	26 ^c	0 (3)
<i>Equus caballus</i>	Perissodactyla	BI	6.79×	NA	11 (4)
<i>Canis familiaris</i>	Carnivora	BI	7.6×	822 (278) ^c	2 (2)
<i>Pteropus vampyrus</i>	Chiroptera	BI	2.63×	672 ^d	26 (10)
<i>Myotis lucifugus</i>	Chiroptera	BI	1.84×	659 ^d	6 (1)
<i>Sorex araneus</i>	Insectivora	BI	1.92×	NA	9 [1] (3)
<i>Erinaceus europaeus</i>	Insectivora	BI	1.86×	NA	6 [2] (4)
[Afrotheria]					
<i>Echinops telfairi</i>	Afrosoricida	BI	1.90×	NA	9 [1] (7)
<i>Loxodonta africana</i>	Proboscidea	BI	1.94×	NA	9 [3] (3)
[Xenarthra]					
<i>Dasyus novemcinctus</i>	Cingulata	WU	2.11×	NA	5 (4)
[Marsupialia]					
<i>Macropus eugenii</i>	Diprotodontia	Ens	2.0×	NA	18 [1] (3)
<i>Monodelphis domestica</i>	Didelphimorphia	BI	6.8×	1198 (294) ^c	22 (4)
[Prototheria]					
<i>Ornithorhynchus anatinus</i>	Monotremata	WU	6.0×	348 (370) ^c	4 (1)
[Sauropsida]					
<i>Gallus gallus</i>	Galliformes	WU	6.6×	211 [89] (133) ^c	4 (1)
<i>Taeniopygia guttata</i>	Passeriformes	WU	6.3×	NA	1 (0)
<i>Anolis carolinensis</i>	Squamata	BI	6.3×	112 [4] (30) ^c	3 (0)
[Amphibia]					
<i>Xenopus tropicalis</i>	Anura	JGI	7.65×	824 [200] (614) ^c	7 (0)
[Teleostei]					
<i>Takifugu rubripes</i>	Tetraodontiformes	IMC	8.7×	47 [39] (39) ^c	18 (1)
<i>Tetraodon nigroviridis</i>	Tetraodontiformes	Gen	8.2×	11 [4] (19) ^c	34 (3)
<i>Danio rerio</i>	Cypriniformes	-	-	154 [1] (21) ^c	110 (10) ^g
[Chondrichthyes]					
<i>Callorhynchus milii</i>	Chimaeriformes	IMC	1.4×	1 [1] (0) ^c	2 (3)
[Agnatha]					
<i>Petromyzon marinus</i>	Petromyzontiformes	UCSC	Ver.2	32 [8] (27) ^c	25 (3)
[Cephalochordata]					
<i>Branchiostoma floridae</i>	Amphioxiformes	JGI	8.1×	31 [3] (9) ^c	0
[Urochordata]					
<i>Ciona intestinalis</i>	Enterogona	JGI	11×	0 (0) ^c	0
<i>Ciona savignyi</i>	Enterogona	ASL (v2.1)	-	0 (0) ^c	0
[Cnidaria]					
<i>Nematostella vectensis</i>	Actiniaria	JGI	7.8×	45 ^f	0

^aData source abbreviations. ASL: the Arend Sidow Lab at Stanford University (<http://mendel.stanford.edu/sidowlab/ciona.html>), BC: Baylor College of Medicine Human Genome Sequencing Center (<http://www.hgsc.bcm.tmc.edu>), BI: Broad Institute at MIT (<http://www.broad.mit.edu>), Ens: Ensembl Genome Browser (<http://www.ensembl.org>), Gen: Genoscope (<http://www.genoscope.cns.fr>), IMC: the Institute of Molecular and Cellular Biology (<http://www.imcb.a-star.edu.sg>), JGI: the Joint Genome Institute (<http://www.jgi.doe.gov>), NCBI: National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov>), WU: the Genome Sequencing Center at Washington University School of Medicine (<http://genome.wustl.edu>), and UCSC the University of California-San Cruz (UCSC) Genome Browser (<http://genome.ucsc.edu>).

^bGene candidates are divided into three categories: intact, incomplete, and pseudogenes. See Table 1 for the details.

^{c-g}The numbers were taken from the following literatures: Nei et al. (2008)^c, Hayden et al. (2010)^d, Niimura (2009)^e, Churcher and Taylor (2011)^f, and Hashiguchi and Nishida (2007)^g.

NA: not available.