



CHROMOSOME NUMBER CHANGES WITHIN TERRESTRIAL MAMMALIAN FAMILIES

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ABSTRACT

This study comprehensively surveys diploid chromosome numbers across terrestrial mammal families using Wilson and Reeder's classification. The data are organized around families, subfamilies, tribes, and genera to determine the extent of and identify trends and patterns in diploid number changes. A preliminary survey of nine established baramins revealed approximately 75% with significantly variable diploid numbers. An extensive compilation of chromosome numbers across 113 families that contain more than one species shows similar distribution with 75% variability using a strict definition of stability. There are many factors to examine such as speciose groups, high reproductive rates, and identifying parameters for defining stability. However, karyotype form diversity was found to be prevalent in spite of these considerations. Assuming that the rank of family approximates a baramin and using looser parameters to define constancy in diploid numbers, 62 families exhibit relative karyotype stability, 19 families with more extensive variation might be explained by multiple centric fusions and the remaining 48 families have unusual karyotype deviations.

INTRODUCTION

Chromosomal speciation, or chromosomal variability within lineages, continues to perplex scientists and numerous models have been put forth to explain the proliferation of karyotype changes seen within taxonomic groups. Tracing these karyotype changes helps to establish pathways of speciation. Take for example family Canidae. To trace the karyotype speciation from the consensus ancestral carnivore of $2n=42$, as proposed by Murphy, *et al.* (cited by Graphodatsky, *et al.*, 2008), could have given rise to the proposed Canidae ancestral karyotype of $2n=82$ by way of at least 42 fissions and 25 fusions – a total of at minimum 67 chromosomal rearrangements. They suggest this took place over the past 45-50 million years prior to the modern Canidae lineage. Considering that fissions and fusions are not well understood and that the rearrangements mentioned above only reflect gross morphology, this represents a continual challenge from a naturalistic worldview. For the creationist, attempting to trace a lineage with chromosome variability, such as Canidae, who range from $2n=34$ to $2n=78$, back to two mating pairs aboard the Ark holds similar challenges, though on a smaller scale.

Multiple studies have shown that the currently identified mono and holobaramins (designations for biblical created kinds) contain a very wide range of varying diploid numbers of chromosomes (Hennigan, 2009; Lightner, 2006; Bedinger, 2012). For example, family Canidae members, identified as a monobaramin (Wood, 2008), include fox, wolves, jackals, dogs, dholes, and coyotes. Diploid numbers (pairs of chromosomes) of $2n = 34, 36, 38, 40, 42, 48, 50, 54, 56, 60, 64, 66, 72, 74, 76,$ and 78 are represented in this family. The general creation model of diversity easily explains variation of phenotypes within kind through Mendelian genetics such as the variety in dogs but not so easily the diversity of karyotypic changes as seen in family Canidae. If these genera are all descendants from one mating pair of the dog kind on board the Ark, there must be a mechanism to explain the diverse range in chromosome numbers.

Mechanisms that change diploid number include centric fusions, also known as a Robertsonian translocation (Rb), and centric fissions. A fusion reduces the number of chromosomes while a fission increases it. An Rb results when a long arm of an acrocentric chromosome (centromere near the end) fuses with another, losing both short arms in the process and becomes a metacentric chromosome (centromere in the middle of two long arms). A fission starts as a metacentric and ends as two non-homologous acrocentric or telocentric (centromere at the end of an arm) chromosomes. Both processes can produce unbalanced gametes that segregate abnormally at meiosis but fusions seem to be more tolerated than fissions (see below). Other chromosome rearrangements, where the karyotype differs from the normal presentation, involve inversions and reciprocal translocations. These produce gross morphological changes but not diploid number differences. This paper does not address these kinds of alterations.

A few studies have shown that centric fusions found as polymorphisms are well tolerated in a population with minimal reduction in fitness but may be species specific (Baker & Bickham, 1986; Eaker, *et al.* 2001; O'Toole, 1998; Pardo-Manuel de Villena & Sapienza, 2001; Wallace & Searle, 1994). These studies support the presence of designed mechanisms that reduce the potential deleterious effects of such arrangements. However, more complicated rearrangements such as multiple chromosomes involved in centric fusions, monobrachial centric fusion (two independent fusions in conspecific organisms where one arm of the new metacentric chromosome is homologous and the other is not), and centric fission result in high incidents of sterility, birth defects and death (Baker & Bickham, 1986; Imai, *et al.*, 1988; Lespinasse, *et al.*, 2003; O'Toole; 1998; Perry, *et al.*, 2005;). The wide variation of diploid numbers within baramins must be explained within this paradox. Another possibility may be that the diploid diverse families contain more than one baramin. In either case, refinement reflecting one or both alternatives is necessary to account for the data.

An initial survey of nine established baramins revealed that 78% had considerable variation in chromosome numbers and only 22% exhibited stability. Diploid numbers spanned a minimum of a 14-point range and a maximum of a 44-point range. For example, Canidae has a range of $2n=34-78$ which is a 44-point spread between the lowest and the highest diploid numbers

represented in that family. The conclusion, given the data presented, seems to point to diploid number changes being the rule within a baramin and stasis the exception (Bedinger, 2012). Therefore a larger data set is needed to confirm or refute this generalization. Following Wood's lead (2011) of approximating terrestrial mammalian baramins to be at the level of the family or subfamily, this study provides a comprehensive survey of 129 families (Wilson & Reeder, 2005a) to determine the extent of their diploid number diversity.

RESULTS

Secondary to the large volume of data, the results have been consolidated into tables for ease in reviewing. These tables are contained in Appendix 1. Table A1 contains data for families with only one genus. Tables A2-A8 divide the data into sections in increments of five, ten, twenty-five, fifty, and greater than 100 genera. Less than 5% of mammals have been described as having B chromosomes, therefore Bs have been left out of the dataset for better comparison of diploid numbers. B chromosomes are composed of heterochromatin and segregate abnormally during meiosis (Pardo-Manuel de Villena, 2005). Families, subfamilies or genera found to be extinct were eliminated from the dataset. Because of the overwhelming numbers, family Muridae, with its 148 genera, 732 species, and a diploid number spread of $2n=16-76$, was eliminated from this study to be considered separately at a later date. Some families have a scarcity of genetic information while others are well studied. To reflect the amount of data uncovered within a family, the number of species found with well-documented karyotypes versus those without information is shown as a percentage of the total number of species in that family. There are three families without any karyotype information and they were excluded from the original 132 total.

Various aspects of the data were examined. Of the 129 families with available data, 44 or 34% show no diploid diversity following a strict definition of variability. Of those 44 families, 16 contain single-species. Removing these 16 from the mix, as there is very low probability of diploid variation given only one species, reduces the number of families with good potential for variability to 28 out of 113, or 25% with stable chromosome numbers (Figures 1 and 2). Within the 41 single-genus families including single-species, 25 or 61% are stable and 39% are variable. Surprisingly, even with one genus, the range of diploid numbers can be great within a family, anywhere from a difference of two points up to a 34-point spread. 44% of the single-genus families with karyotype variability have diploid variations with greater than a 22-point spread. Within this group the greatest disparity is found within Cuniculidae where its two species have diploid numbers of 42 and 74. Unless otherwise stated the remaining analyses are done excluding single-specie families.

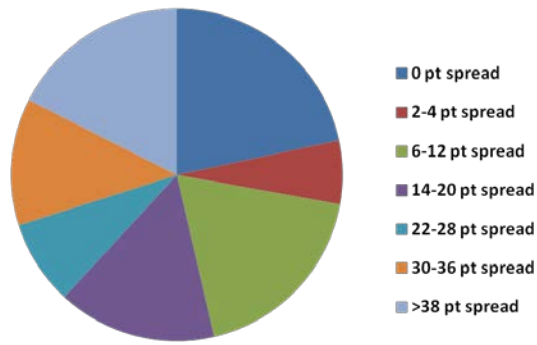


Figure 1. Diploid spread of all families with more than two species.

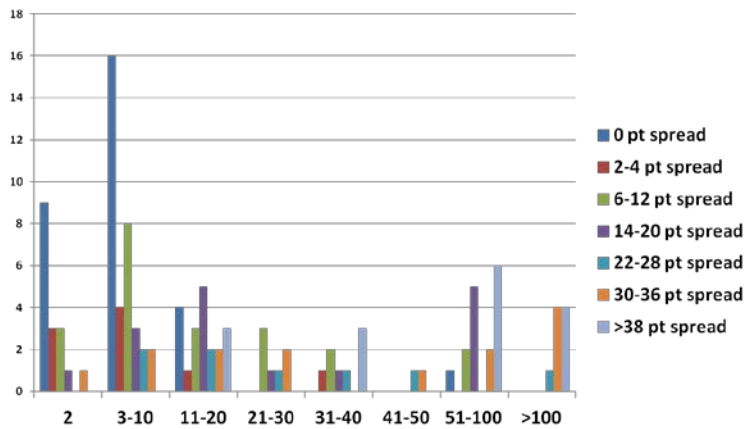


Figure 2. Comparison of number of species and their diploid number range.

Over three-quarters of the total families studied have less than 50 species and half of this total contains 10 species or less (Figure 3). Given this, 29 of the 88 families with less than 50 species, or 33%, have stable karyotypes leaving 67% with variable diploid numbers. Of those remaining 59 families, 32, or 54% have diploid number ranges of greater than a 14-point spread, 21 with a range greater than 22 points or 36%, 15 or 25% with greater than a 30-point spread and 7, or 12%, greater than a 38-point spread. The largest spread for this group belongs to Octodontidae with a 64-point spread among 13 species and includes six karyotype variations.

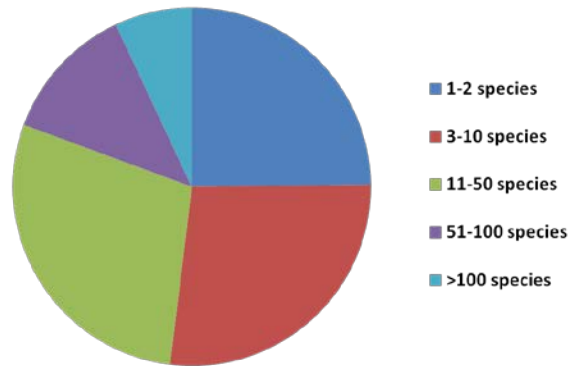


Figure 3. Families and the number of species found within them.

Breaking it down further to those with 2-10 species, 49%, or 25 of the 51 remaining families contain chromosome number differences (Figure 4). Of those 25, nine families or 36% are significantly altered with a 14-point or greater spread, five are greater than 22 and three are greater than a 30-point spread in diploid numbers. The largest spread for this group belongs to Equidae with a 34-point spread across nine species representing 9-11 karyotype variations (male/female difference in two karyotypes).

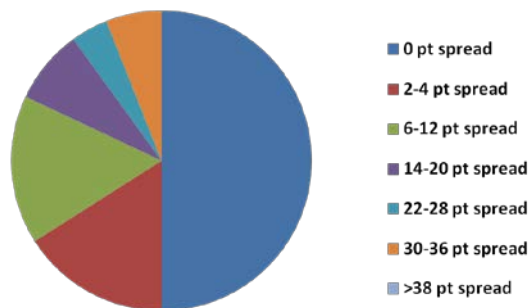


Figure 4. Diploid spreads in families with 2-10 species.

Omitting the five most speciose families (Muridae, 732 species; Cricetidae, 683 species; Vespertilionidae, 407 species; Soricidae, 375 species; Sciuridae, 279 species) from the dataset to get a sense of variability without extreme family groups shows the following: 51% still exhibit ranges greater than 14-point spreads in diploid numbers, 35% with greater than 22-point spreads, 26% greater than a 30-point spread, and 15% greater than a 38-point spread (Figure 5). The largest spread for this group belongs to Echimyidae with 84 species, a range of diploid numbers from $2n=28$ to $2n=118$ for a 90-point difference and 18 different chromosome numbers documented. Family Cervidae, with 51 species, also has an impressive spread of 64 points from $2n=6$ to $2n=70$ with 25 different diploid numbers studied. Four of the five most speciose groups

are from order Rodentia. Examining the 16 families with greater than 50 species shows that two-thirds have a diploid number range of a 30-point spread or higher.

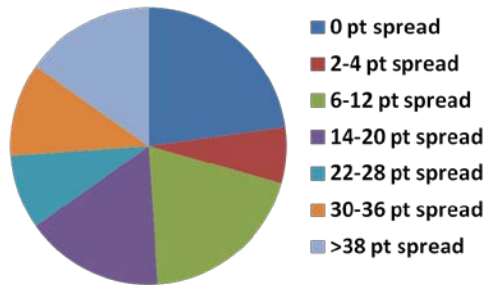


Figure 5. Diploid spread of all families with >2 species, omitting the five most speciose families.

The number of karyotype variations warrant investigation. Dividing the families into groups by common number of species gives the following percentages of diploid number variations: 2-10 species – 49% stable, 45% with two to five variations and 6% between 6 and 15 variations; 11-50 species – 10% stable, 51% with two to five variations, 33% with 6-10 variations and 10% over 11 variations including one at 24 rearrangements; 51-100 species – no stability, 33% with two to five variations, 33% with 6-10 variations and 33% over 11 variations; >100 species – no stability, 33% with 11-15 variations, 22% between 16 and 25 rearrangements and 33% with greater than 25 variations. Looking at the large group between 2-50 species the numbers are consistent with 32% stable, 48% with the majority of variability between two and five changes, and 22% with over 6 rearrangements.

Families have been broken down into subfamilies, tribes, and genera to see at what taxonomic level their chromosome numbers become stable. In this study, for analysis purposes only, a family is considered stable if it has a diploid spread of six points or less as this may represent a few centric fusions that may be well tolerated. A review of the literature, especially of FISH or G-Banding analysis would provide more detailed data for resolution of a family but for ease in determining which families to look more closely at and which are easily explainable by centric fusion six was chosen as the cut-off for stability. A detailed analysis of this section has been omitted secondary to the large number of variables and will be dealt with in a subsequent study. 19 families that fall outside of the six-point $2n$ spread criterion exhibited karyotype variation (progressed by 2's) such that they still may (or may not) easily resolve by an explanation of centric fusion and would benefit from closer examination. 47 families exhibited an unusual presentation in their diploid numbers that are more difficult to explain by centric fusion alone and definitely need closer examination.

To determine if karyotype variability is biased towards small rodent-like animals, 31 families representing order Rodentia were compared to 93 non-rodent families. Percentages were calculated for each diploid range spread and for the number of karyotype forms represented in each family for their respective groups, non-rodent or rodent, and then compared.

32% of Rodentia demonstrated diploid ranges of greater than a 36 point spread while only 5% of non-Rodentia exceeded that limit. On the opposite end, 23% of Rodentia had very stable karyotypes versus 42% in non-Rodentia. Using the criteria for stability of a six-point spread or less in diploid range resulted in 36% of Rodentia and 53% non-Rodentia demonstrating relative stability. Regarding number of karyotype forms, Rodentia contained 55% families with zero to four forms while non-Rodentia families had 67% of their karyotypes within that range. Non-Rodentia families did not exceed 28 different diploid number forms while 7% of Rodentia families had between 29-36 different forms.

DISCUSSION

The results of this 129-family study at first glance seem to mirror the initial survey of nine established baramins and point to diploid number variability as the norm and stability the exception. The first study discovered that 78% of the published terrestrial mammalian baramins showed considerable variation in chromosome numbers. The current comprehensive study found the similar proportions with 75% variable and only 25% stable of those families with two or more species (potential for variability). When including the 16 single-species families back in the mix, 66% of the total 129 families had variable karyotypes and 34% exhibited stability. However there are many factors to consider before arriving at conclusions that will be useful or have implications for creation diversity studies.

Concern over statistical problems associated with karyotypic diversity such that “a speciose group may appear to have high karyotypic diversity simply because of the high number of species” (Prescott, 1972, p.45) has been addressed in this study. Wood (2011) referred to this as the power law distribution where two quantities, in this case species and karyotype variation, increase in size proportionally to the number of variation or species already in the mix. Restating his findings for the occurrence of speciation, the likelihood is higher for a larger genus than a smaller genus “simply by virtue of the greater number of species” (p. 4). To mitigate the effects of a power law distribution, the five most speciose groups of 278-730 species (Wood, 2011), four of which are from order Rodentia, were removed to find diploid number diversity without these large family groups. Half of the families still showed extreme karyotype diversity of over a 14-point spread and a full quarter of the group exceeded a 30-point diploid number spread. Adding back in those with over a six-point spread represents two-thirds of the total families with significant diversity. This supports widespread karyotype diversity at the level of the family.

Relating this study to a recent article on speciation, Wood (2011) referred to the most speciose terrestrial mammal families as small-bodied animals with an implied high reproductive rate. This also suggests a highly variable diploid number. To test this assumption the families were divided into two groups, Rodentia and non-Rodentia. Indeed, Rodentia did show great diversity with two-thirds of the families having a range of greater than six in their diploid numbers and a third of those showed greater than a 36-point spread. However, the remaining third exhibited very little diversity. In contrast, the non-rodent group dropped to a little over half of the families with diversity and just under a half being stable. Those with diversity of over a 36-point spread represented a small minority. Thus, small-bodied mammals, specifically rodents, have a higher diploid diversity than their counterparts. However, high variability remains in more than half of non-Rodentia families.

To determine if speciose families of any kind follow a high diversity pattern, those with greater than 50 species were evaluated. The results showed that 96% of the 25 families had highly diverse karyotype forms. This is in contrast to 56% of the 87 families with less than 50 species exhibiting diversity. Wood (2011) found that the median family size contains eight species. Of the 50 families having between two and ten species, only 34% had diverse karyotypes. Because of the sharp distinction in numbers of karyotype forms between those families with greater than or less than 50 species, this division line was used in further comparisons.

The extreme contrast between families with greater than 50 species and those with less continues when considering the number of variations in diploid numbers. For example, the chromosome numbers listed in the introduction for Canidae contains 16 different diploid numbers. The data reveals 79% of those families with less than 50 species had five or less variations in contrast with 21% of those with over 50 species. Canidae falls within the 6% bracket of families with less than 50 species for having over 11 variations. Interestingly, half of the families with less than 50 species have between 2-5 variations in their diploid number. In other words, having variation at the family level is typical, especially when considering both groups together at 75% with two or more forms.

Comparing karyotype forms of Rodentia and non-rodent mammals shows essentially the same distribution when looking at zero to four variations in diploid number. Significant differences appear when looking at 13 karyotype forms and higher. Very few, in fact only 5% of non-rodent type mammals, have greater than 13 different diploid numbers in contrast with 24% of rodent families. This supports the hypothesis of a bias towards small, highly reproductive mammals having greater karyotype diversity.

Using karyotype variability to test the assumption that the level of family or subfamily approximates a baramin (Wood, 2011), families were divided into taxonomic levels down to genera and examined to see at what point, if any, the karyotype became stable. Bickham and Baker (1979, p. 76, 77) found that chromosomal variation at the generic level in most families showed “consistent stability” but “considerable variation among genera” in the bat families.

They further state that Robertsonian translocations (fusions) were found within families but more extreme mechanisms of rearrangements were needed to explain karyotype differences between families, particularly in Phyllostomatidae, Molossidae, and Vespertilionidae. Their conclusions support the concept of a family approximating a baramin. This current study confirms that, at the level of genus, most karyotypes are fairly stable. At the family level, using a looser definition of stability of a six-point spread in diploid numbers, 62 families displayed stability (Table 1). This raises the statistical picture to 48% with low variability and 52% with variability. Further research and correlation with previous work on baramins would be needed to confirm and establish if these were mono or holobaramins. The groups that require more in-depth study and may be especially useful for examining mechanisms that allow significant karyotype variability are shown in Tables 2 and 3. Families that fall outside of the six-point 2n spread criterion in diploid number but whose karyotype variation may (or may not) easily resolve by an explanation of centric fusion (their 2n numbers progress by twos) are listed in Table 2. Table 3 delineates families with unusual presentations in diploid numbers that warrant a closer look at either the mechanism for karyotype variation or a baramin boundary refinement different from the level of the family.

Table 1. Families with relatively stable diploid numbers of a six-point spread or less. Heading Key: A= # of Genera; B= # of Species;

Classification Level	Common Name	A	B	Classification Level	Common Name	A	B
F-Ornithorhynchidae	Platypus	1	1	F-Hypsiprymno- dontidae	Rat kangaroo	1	1
F-Myrmecobiidae	Numbat	1	1	F-Phascolarctidae	Koala	1	1
F-Tarsipedidae	Honey pos	1	1	F-Miobatheriidae	M. del M.	1	1
F-Orycteropodidae	Aardvark	1	1	F-Cyclopedidae	Pygmy anteater	1	1
F-Aplodontiidae	Mt. beaver	1	1	F-Daubentoniidae	Aye-aye	1	1
F-Dinomyidae	Pacarana	1	1	F-Petromuridae	Dassie rat	1	1
F-Nandiniidae	A. palm civet	1	1	F-Myocastoridae	Nutria	1	1
F-Antilocapridae	Pronghorn	1	1	F-Myzopodidae	Sucker-ft bat	1	1
F-Ailuridae	Red panda	1	1	F-Mystacinidae	NZ sh. tail bat	1	2
F-Thylacomyidae	Bilby	1	2	F-Noctilionidae	Bulldog bat	1	2
F-Thryonomyidae	Cane rat	1	2	F-Notoryctidae	Mar. mole	1	2
F-Megalonychidae	2-toed sloth	1	2	F-Solenodontidae	Solendon	1	4
F-Solenodontidae	Solendon	1	4	F-Bradypodidae	3-toed sloth	1	4
F-Bradypodidae	3-toed sloth	1	4	F-Tarsidae	Tarsier	1	7
F-Moschidae	S. musk deer	1	7	F-Manidae	Pangolin	1	8
F-Nycteridae	Slit faced bat	1	16	F-Acrobatidae	Pygmy glider	2	2
F-Cynocephalidae	Flying Lemur	2	2	F-Platacanthomyidae	Spiny dormice	2	2
F-Pedetidae	Spring hare	2	2	F-Furipteridae	Smokey bat	2	2
F-Hippopotamidae	Hippopotamus	2	2	F-Vombatidae	Wombat	2	3
F-Elephantidae	Elephant	2	3	F-Tachygossidae	Echidna	2	4
F-Burramyidae	Pygmy pos	2	5	F-Abrocomidae	Chinchilla rat	2	10
F-Mormoopidae	Mustached bat	2	10	F-Dasyproctidae	Agouti	2	13
F-Procaviidae	Hyrax	3	4	F-Hyaenidae	Hyena	3	4
F-Caenolestidae	Shrew op	3	6	F-Hominidae	Gorilla, chimp	3	6
F-Camelidae	Camel	3	6	F-Natalidae	Funnel-ear bat	3	7
F-Tragulidae	A. mouse deer	3	8	F-Petauridae	Gliding pos	3	11

F-Hystricidae	OW porcupine	3	11	F-Rhinocerotidae	Rhinoceros	4	5
F-Ctenodactylidae	Gundi	4	5	F-Suidae	Pig	5	19
F-Procyonidae	Raccoon	6	17	F-Peramelidae	Bandicoot	6	18
F-Eupleridae	Fossa	7	8	F-Octodontidae	Rock rat	8	13
F-Felidae	Cat	14	40	F-Dasyuridae	Marsupials	21	69

Table 2. Families that fall outside of the six-point 2n spread criterion in diploid number but whose karyotype variation may (or may not) easily resolve by an explanation of centric fusion; Heading Key: A= # of Genera; B= #of Species; C=2n range; D= # of 2n Variations; E= Mode of 2n; F= Diploid Numbers (2n); Abbreviation key: F=Family. Diploid numbers are written in stem-leaf format where “1-2446” means diploid numbers of 12, 14, 14, 16; not all diploid numbers are available in the literature.

Classification Level	Common Name	A	B	C	D	E	F
F-Aotidae	Nght monkey	1	8	46-58	11	-	4-6789, 5-0012234468
F-Macrosclididae	El. shrew	4	16	26-34	4	26	2-66666888, 3-004
F-Lemuridae	Lemur	5	19	44-60	8	-	4-4688, 5-0468, 6-000
F-Pseudocheiridae	Ring-tail p.	6	17	10-22	6	-	1-022668, 2-022
F-Spalacidae	Subterranean rat	6	36	38-64	13	60	38, 4-048889, 5-000244466, 58x3, 6-0000022224
F-Cebidae	NW Monkey	6	57	44-54	5	44x10 46x10	44x10, 46x10, 48, 5-2222444
F-Heteromyidae	Kangaroo rat	6	60	34-74	19	60	3-4688, 4-0222244466, 48x5, 50x4, 56x6, 5-22244448, 60x12, 6-24444, 7-00222224
F-Geomyidae	Pocket gopher	6	40	36-88	24	-	3-688, 40x8, 42x5, 4-4446666888, 5-022446666, 58x5, 6-008, 70x4, 74x4, 7-22266888, 8-02468
F-Chrysochloridae	Golden mole	9	21	26-36	5	30	2-68, 3-000000046
F-Gliridae	Dormouse	9	28	44-62	4	-	4-4688, 62
F-Erinaceidae	Hedgehog	10	24	40-48	2	48	40, 48x9
F-Leporidae	Rabbit, hare	11	52	38-52	6	48	3-88, 4-222224446, 48x15, 52
F-Macropodidae	Wallaby	11	67	10-24	8	16x13 22x12	16x13, 1-0000244488, 22x12
F-Talpidae	Mole	17	39	32-42	5	34	34x14, 3-26666688, 42
F-Mustelidae	Erm, mk wsl	22	59	30-44	7	38	3-026, 38x22, 4-0000222244
F-Soricidae	Shrew	26	375	20-68	35	36x18 38x17 40x17 42x14 50x16	22x4, 24x3, 26x3, 28x5, 2-0013355799, 30x7, 34x7, 36x18, 38x17, 3-2222335557, 40x17, 42x14, 4-4444666888, 50x16, 52x13, 54x5, 5-3566888, 60x3, 6-2224466688
F-Vespertilionidae	Evening bat	48	407	20-52	15	44	2-022266, 28x7, 30x9, 36x21, 3-2222444488, 42x8, 44x54, 4-00666666, 50x13, 52
F-Sciuridae	Squirrels	52	279	30-62	13	38	30, 32x11, 34x4, 36x13, 38x35, 40x14, 42x7, 4-666668, 5-000468, 62
F-Phyllostomidae	NW Leaf-nosed bat	55	155	13-46	20	30x19 32x18	1-36668, 20/21x3, 2-01222444, 26x7, 28x11, 30/31x11, 30x19, 32x18, 3-444466888, 4-0002466

Table 3. Families with unusual presentations in diploid numbers that warrant a closer look at either the mechanism for karyotype variation or a baramin boundary refinement different from the level of the family

Heading Key: A= # of Genera; B= # of Species; C = 2n range; D= # of 2n Variations; E= Mode of 2n; F= Diploid Numbers (2n);

Abbreviation key: F=Family

Diploid numbers are written in stem-leaf format where “1-2446” means diploid numbers of 12, 14, 14, 16; not all diploid numbers are available in the literature

Classification Level	Common Name	A	B	C	D	E	F
F-Castoridae	Beaver	1	2	40-48	2	-	4-08
F-Cuniculidae	Paca	1	2	42-74	2	-	42, 74
F-Thyropteridae	Disc-wg bat	1	3	32-40	2	-	32, 40
F-Rhinopomatidae	Mouse tl bat	1	4	36-42	2	-	36, 42
F-Tapiridae	Tapir	1	4	52-80	3	80	52, 76, 8-00
F-Lepilemuridae	Sport. Lemur	1	8	20-34	3	-	2-006, 34
F-Calomyscidae	M-lk hamster	1	8	30-52	7	44	3-027, 4-44448, 5-002
F-Equidae	Horse	1	9	32-66	11	-	32, 4-4456, 5-2456, 6-2446
F-Ochotonidae	Pika	1	30	38-68	7	-	38, 4-02, 50, 6-022888
F-Ctenomyid	Tuco-tuco	1	60	26-56	13	48x5 26x4	10, 2-6666, 3-46, 4-456688888, 5-02456
F-Rhinolophidae	Horseshoe bat	1	76	28-62	7	58	28, 3-66, 44, 5-2666, 58x9, 6-22222
F-Giraffidae	Giraffe	2	2	30-46	3	-	30, 4-56
F-Myrmecophagidae	Anteater	2	3	54-60	2	-	54, 60
F-Tayassuidae	Peccary	3	3	20-30	3	-	2-06, 30
F-Chinchillidae	Chinchilla	3	7	56-64	2	64	56, 6-444
F-Indridae	Sifaka	3	18	40-70	5	70	4-0222248888, 7-00000000
F-Galagidae	Galago	3	19	38-62	4	-	3-688, 40, 6-22
F-Megadermatidae	False V. Bat	4	5	0	0	62	62
F-Potoroidae	Variety	4	10	12-32	4	22	1-2, 2-2224, 3-2
F-Mephitidae	Skunk	4	12	46-64	6	-	4-68, 5-008, 6-04
F-Hylobatidae	Gibbon	4	14	38-52	4	44	38, 4-4444, 5-02
F-Tupalidae	Tree shrew	4	19	44-68	6	-	44, 52, 6-00268
F-Pitheciidae	Titi	4	40	16-54	9	-	16, 20, 4-245666888, 5-0000444
F-Ursidae	Bear	5	8	42-74	3	74	42, 52, 74x6
F-Lorisidae	Loris	5	9	50-62	3	-	5-00022, 6-22
F-Bathyergidae	Mole rat	5	16	40-78	10	-	40, 5-04444688, 6-0028, 7-488
F-Atelidae	NW monkey	5	25	32-62	11	-	3-244444, 4-245789, 5-0002222, 62
F-Caviidae	Guinea pig	6	18	52-68	5	64	52, 6-22444444468
F-Phalangeridae	-	6	28	12-20	3	20	1-244, 2-000
F-Capromyidae	Hutia	6	16	40-88	2	-	40, 88
F-Octodontidae	Rock rat	8	13	38-102	6	58	38, 5-4668888, 78, 102
F-Dasyopodidae	Armadillo	9	21	38-64	6	64	38, 5-0088, 6-0222444444
F-Hipposideridae	OW L.ns bat	9	81	32-52	5	32	32x12, 3-006, 5-022

F-Tenrecidae	Tenrec	10	31	14-56	7	30x5 32x5 38x4	1-4, 30x5, 3-22222888 4-00, 5-46
F-Canidae	Dog, fox, jackal...	12	37	34-78	16	78x8 74x5	3-46888, 4-028, 5-00046, 6-046, 7-02, 74x5, 78x8
F-Emballonouridae	Sac wing bat	13	50	22-44	7	-	2-24668, 3-222, 4-22224
F-Herpestidae	Mongoose	14	33	35-44	5 (8)	35/36x 736x7	35/36x7, 36x7, 39/40, 41/42, 43/44
F-Viverridae	Civet, Genet	15	35	34-54	9	38x4 42x5	3-468888, 4-02222244, 5-00244
F-Dipodidae	Jerboas	16	51	18-72	14	-	1-89, 2-0446, 3-226, 58, 4-02246888, 72
F-Molossidae	Free-tl bat	16	100	34-48	4	48	3-444, 4-02, 48x25
F-Didelphidae	Opossum	17	90	14-22	3	14	1-4x31, 1-8x7, 2-2x8
F-Echimyidae	Spiny rat	18	84	14- 118	19	-	1-46, 2-2488, 3-0000244, 4-0268, 5-022, 6-0222224, 98, 118
F-Cervidae	Deer	19	51	6-70	25	68x11, 70x-11	0-6678889, 1-24, 3-67789, 4-046689, 5-0066668, 6-0245666, 68x11, 70x-11
F-Cercopithecidae	Old World Monkey	21	133	42-84	11	42 x17 44x11	42x17, 44x11, 4-88, 5-4488, 60x5, 64, 66x5, 7-022, 84
F-Nesomyidae	Rat/mouse	21	61	32-76	8	-	32, 48, 5-28, 60, 7-4456
F-Pteropodidae	Fruit bat	42	186	24-48	8	36x16 38x15	2-46, 34x8, 35, 36x16, 38x15, 4-088
F-Bovidae	Bovid	50	143	30-60	21	60	30/31x2, 32/31x3, 32/33x2, 34/33, 34/35, 56/55, 3-0002388, 4-00246669, 48x8, 50x4, 52x7, 53, 54x5, 56x9, 58x16, 60x24
F-Cricetidae	Vole, hamster	129	683	9-92	36	48x36 52x30 56x25 54x20 50x18	0-99, 1-445667778, 22x7, 24x5, 2-00066, 28x9, 30x4, 32x4, 34x7, 3- 666667, 38x13, 40x9, 42x9, 44x9, 4-366666, 48x36, 50x18, 52x30, 54x22, 56x25, 5-8888, 60x9, 62x8, 64x8, 6-6668, 7-00, 80x6, 82, 9-22

Studies on specific baramins not easily resolved at the chromosome level will be important going forward. Technology such as zoo-FISH or chromosome painting has significantly enhanced our vision into the genome however it often generates more questions than answers. According to multiple studies (Graphodatsky, *et al.* 2008; Wienberg 2004; Yang, *et al.* 1999; Yang, *et al.* 2000), Canidae, classified as a monobaramin, has one of the most rearranged karyotypes. In the preliminary survey of nine baramins (Bedinger, 2012), the following was reported:

All red fox probes painted on corsac fox chromosomes split into multiple segments, including one that split into eight pieces, with not a single autosome shared between them even though they are considered to be from the same genus per Graphodatsky, *et al.* (2008). They further show the complexities of family unity with the following findings: Raccoon dogs and gray fox do not resolve well in phylogenetic analyses and remain so

despite current technology; corsac fox and arctic fox lineages are isolated from red fox...hybridization data separates *Canis* from *Vulpes* (Gray 1972) and zoo-FISH does not resolve the family.

Trends in the chromosome patterns show that at the genus level *Canis*, *Cuon*, *Lycaon*, *Chrysocyon*, *Atelocynus*, *Lycalopex*, *Speothos*, *Cerdocyon*, and *Otocyon*, all cluster around the karyotype forms of $2n=70, 72, 74, 76$ and 78 . *Urocyon* (grey fox) stands isolated at $2n=66$. *Nyctereutes* (raccoon dog) and *Vulpes* (true fox) have similar patterns to each other in they are highly diversified within their respective genus. The former with $2n=38, 42, 54, 56$ and the latter with $2n=34, 36, 38, 40, 50, 60, 64$. An in-depth review of family Canidae (Pendragon, 2011) contends that they have the taxonomic status of a basic type, capable of hybridization. Given their significant karyotype variability, further study into this group will be invaluable for understanding designed mechanisms in karyotype rearrangements and speciation, and possible further baramin refinement.

The data on karyotype diversity collected for this study represents the most comprehensive compilation found in the literature to date. This dataset could be used not only to add another element to the holistic view of a baramin but also as a starting point for determining which families warrant further study, especially those with significant variability. Fundamental arm number or number of chromosome types (e.g., metacentrics or acrocentric) could be added to further round out the picture for deeper analysis, especially on unusual presentations such as seen in Canidae. A copy of the full dataset which includes diploid numbers for each species is available on request and represents a work in progress.

CONCLUSIONS

Chromosome number diversity is widespread across families. At first glance, roughly three-quarters of all terrestrial mammal families contain members with variability in their karyotype form. Speciose families with greater than 50 members are just shy of 100% for significant karyotype diversity. Those with less than 50 species drop to a little over 50% for diversity. This number is also consistent with removing members of order Rodentia from the dataset, implicating high reproduction rates with high karyotype diversification rates. Based on the assumption that a taxonomic family approximates a baramin and using a looser definition of stability (a six-point spread or less), 62 baramins can be identified by their karyotypes with relatively few discrepancies in their diploid numbers. Using this new definition brings the total to 48% of all families are relatively stable and 52% have significant variability. The dataset provided represents the most comprehensive compilation found in the literature to date.

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APPENDIX

Table A1. Diploid numbers of families with only one genus. Diploid numbers are written in stem-leaf format where “1-2446” means diploid numbers of 12, 14, 16; not all diploid numbers are available in the literature. Heading Key: A= # of Genera; B= # of Species; C= # Karyotyped species used in dataset; D= % 2n known; E=2n range; F=#of 2n Variations; G= Mode of 2n; H= Diploid Numbers (2n); I= Reference. Abbreviation key: F=Family.

Classification Level	Common Name	A	B	C	D	E	F	G	H	I
F-Ornithorhynchidae	Platypus	1	1	1	100	0	0	52	52	1
F-Mirobatheriidae	M. del M.	1	1	1	100	0	0	14	14	15
F-Myrmecobiidae	Numbat	1	1	1	100	0	0	14	14	3
F-Phascolarctidae	Koala	1	1	1	100	0	0	16	16	1
F-Tarsipedidae	Honey pos	1	1	1	100	0	0	24	24	1
F-Hypsiprymnodontidae	Rat kangaroo	1	1	1	100	0	0	22	22	12
F-Orycteropodidae	Aardvark	1	1	1	100	0	0	20	20	1
F-Cyclopedidae	Pygmy anteater	1	1	1	100	0	0	64	64	1
F-Ptilocercidae	Tree shrew	1	1	0	0	-	-	-	-	-
F-Daubentoniidae	Aye-aye	1	1	1	100	0	0	30	30	1
F-Aplodontiidae	Mt. beaver	1	1	1	100	0	0	46	46	1
F-Petromuridae	Dassie rat	1	1	1	100	0	0	56	56	72
F-Dinomyidae	Pacarana	1	1	1	100	0	0	58	58	1
F-Myocastoridae	Nutria	1	1	1	100	0	0	42	42	1
F-Craseonycteridae	K. hog nose bat	1	1	0	0	-	-	-	-	-
F-Myzopodidae	Sucker-foot bat	1	1	1	100	0	0	26	26	82
F-Nandiniidae	A. palm civet	1	1	1	100	0	0	38	38	40
F-Ailuridae	Red panda	1	1	1	100	0	0	36	36	1
F-Antilocapridae	Pronghorn	1	1	1	100	56-58	2	-	5-68	1, 40
F-Noctilionidae	Bulldog bat	1	2	2	100	0	0	34	34	1, 6
F-Mystacinidae	NZ sh. tail bat	1	2	1	50	0	0	36	36	1
F-Notoryctidae	Mar. mole	1	2	1	50	0	0	20	20	1, 11
F-Thylacomyidae	Bilby	1	2	1	50	0	0	18	18	1
F-Megalonychidae	2-toed sloth	1	2	2	100	50-53	2	-	50, 53	1
F-Castoridae	Beaver	1	2	2	100	40-48	2	-	4-08	1
F-Thryonomyidae	Cane rat	1	2	2	100	40-44	2	-	4-04	59, 62
F-Cuniculidae	Paca	1	2	2	100	42-74	2	-	42, 74	71
F-Thyropteridae	Disc-wing bat	1	3	2	67	32-40	2	-	32, 40	40
F-Bradypodidae	3-toed sloth	1	4	1	25	0	0	54	54	6
F-Solenodontidae	Solendon	1	4	1	25	0	0	34	34	1
F-Rhinopomatidae	Mouse tail bat	1	4	2	50	36-42	2	-	36, 42	1, 40

F-Tapiridae	Tapir	1	4	4	100	52-80	3	80	52, 76, 8-00	1
F-Tarsidae	Tarsier	1	7	2	29	0	0	80	80	1, 30
F-Moschidae	S. musk deer	1	7	7	100	0	0	58	58	94, 95
F-Lepilemuridae	Sport. Lemur	1	8	4	50	20-34	3	-	2-006, 34	1, 6
F-Aotidae	Night monkey	1	8	5	63	46-58	11	-	4-6789 5- 0012234468	1, 31, 32, 33
F-Calomyscidae	Mouse-like hamster	1	8	6	75	30-52	7	44	3-027, 4-44448, 5- 002	1, 48
F-Manidae	Pangolin	1	8	2	25	36-42	4	-	3-688, 4-02	1
F-Equidae	Horse	1	9	9	100	32-66	11	-	32, 4-4456, 5-2456, 6- 2446	1, 40, 90
F-Nycteridae	Slit faced bat	1	16	2	13	0	0	42	42	40, 81
F-Ochotonidae	Pika	1	30	10	33	38-68	7	-	38, 4-02, 50, 6-022888	1, 40
F-Ctenomyid	Tuco-tuco	1	60	18	30	26-56	13	48x 5 26x 4	10, 2-6666, 3-46, 4- 456688888, 5-02456	1, 6, 69
F-Rhinolophidae	Horseshoe bat	1	76	19	25	28-62	7	58	28, 3-66, 44, 5-2666, 58x9, 6- 22222	1, 6, 40, 78, 80

Table A2. Diploid numbers of families with two to five genera. Diploid numbers are written in stem-leaf format where “1-2446” means diploid numbers of 12, 14, 14, 16; not all diploid numbers are available in the literature. Alternating gray areas separate families for easier comparison; Heading Key: A= # of Genera; B= # of Species; C= # Karyotyped species used in dataset; D= % 2n known; E=2n range; F=#of 2n Variations; G= Mode of 2n; H= Diploid Numbers (2n); I= Reference. Abbreviation key: F=Family, SF=Subfamily, T=Tribe, G=Genus, SG=Subgenus; “OW” = Old World; “NW” = New World.

Classification Level	Common Name	A	B	C	D	E	F	G	H	I
F-Acrobatidae	Pygmy glider	2	2	2	100	0	0	14	14	1, 16
F-Cynocephalidae	Flying Lemur	2	2	1	50	0	0	38	38	1
F-Platacanthomyidae	Spiny dormice	2	2	1	50	0	0	38	38	43
F-Pedetidae	Spring hare	2	2	2	100	38-40	2	-	38, 40	1
F-Furipteridae	Smokey bat	2	2	1	50	0	0	34	34	40
F-Hippopotamidae	Hippopotamus	2	2	1	50	0	0	36	36	1
F-Giraffidae	Giraffe	2	2	2	100	30-46	3	-	30, 4-56	1
G-G. <i>Giraffa</i>	Giraffe	-	1	1	100	0	0	30	30	1
G-G. <i>Okapia</i>	Okapi	-	1	1	100	45-46	2	-	4-56	1
F-Vombatidae	Wombat	2	3	2	50	0	0	14	14	1
F-Elephantidae	Elephant	2	3	2	67	0	0	56	56	1
F-Myrmecophagidae	Anteater	2	3	2	67	54-60	2	-	54, 60	1
G-M. <i>Myrmecophaga</i>	Giant A.	-	1	1	100	0	0	60	60	1
G-M. <i>Tamandua</i>	Tamandua	-	2	1	50	0	0	54	54	1
F-Tachygossidae	Echidna	2	4	2	50	0	0	64	64	1
F-Burramyidae	Pygmy pos	2	5	4	80	0	0	14	14	1, 6, 12, 15
F-Abrocomidae	Chinchilla rat	2	10	2	20	0	0	64	64	1
F-Mormoopidae	Mustached bat	2	10	7	70	0	0	38	38	1, 40
F-Dasyproctidae	Agouti	2	13	5	39	0	0	64	64	69, 70
F-Tayassuidae	Peccary	3	3	3	100	20-30	3	-	2-06, 30	1, 40
G-T. <i>Catagonus</i>	Tagua peccary	-	1	1	100	0	0	20	20	1
G-T. <i>Pecari</i>	Collared p.	-	1	1	100	0	0	26	26	1
G-T. <i>Tayassus</i>	White-lipped p.	-	1	1	100	0	0	30	30	1, 40
F-Procaviidae	Hyrax	3	4	1	25	0	0	54	54	1
F-Hyaenidae	Hyena	3	4	3	75	0	0	40	40	1, 40
F-Caenolestidae	Shrew op	3	6	4	67	0	0	14	14	1, 10,

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F-Hominidae	Gorilla, chimp	3	6	5	83	0	0	48	48	1
F-Camelidae	Camel	3	6	6	100	72-74	2	74	7-2244444	1, 40
F-Anomaluridae	Scaly tail squir.	3	7	0	0	-	-	-	-	-
F-Natalidae	Funnel-ear bat	3	7	3	43	0	0	36	36	1, 40
F-Chinchillidae	Chinchilla	3	7	4	57	56-64	2	64	56, 6-444	1, 6, 64
<i>G-C.Chinchilla</i>	Chinchilla	-	2	2	100	0	0	64	64	6, 64
<i>G-C.Lagidium</i>	Viscacha	-	3	1	33	0	0	64	64	64
<i>G-C.Lagostomus</i>	Chinchilla	-	2	1	50	0	0	56	56	1
F-Tragulidae	A. mouse deer	3	8	2	25	0	0	32	32	1, 92
F-Hystricidae	OW porcupine	3	11	3	27	60-66	2	60	6-006	59, 60, 61
F-Petauridae	Gliding pos	3	11	5	46	18-22	2	22	1-88 2-222	1, 15, 16
<i>G-P.Dactylopsila</i>	Triok	-	4	2	50	0	0	18	18	15, 16
<i>G-P.Gymnobelideus</i>	Possum	-	1	1	100	0	0	22	22	15
<i>G-P.Petaurus</i>	Gliders	-	6	2	33	0	0	22	22	1, 15
F-Indridae	Sifaka	3	18	18	100	40-70	5	70	4- 0222248888 7-00000000	1, 23
<i>G-I.Avahi</i>	Woolly lemur	-	8	8	100	0	0	70	70	23
<i>G-I.Indri</i>	Babakoto	-	1	1	100	0	0	40	40	23
<i>G-I.Propithecus</i>	Sifika	-	9	9	100	42-48	3	-	4-2224888	1, 23
F-Galagidae	Galago	3	19	5	26	38-62	4	-	3-688, 40 6-22	1, 6, 25, 31
<i>G-G.Galago</i>	Bushbaby	-	14	3	21	36-40	3	-	3-688, 40	1, 6, 25
<i>G-G.Otolemur</i>	Greater gal.	-	3	2	67	0	0	62	62	1, 31
F-Ctenodactylidae	Gundi	4	5	4	80	36-40	2	40	36, 4-000	1
F-Megadermatidae	False vamp. Bat	4	5	2	40	38-54	2	-	38, 54	1
<i>G-M.Megaderma</i>		-	2	2	100	38-54	2	-	38, 54	1
F-Rhinocerotidae	Rhinoceros	4	5	4	80	82-84	2	82	8-2224	1, 91

F-Potoroidae	Variety	4	10	6	60	12-32	4	22	1-2 2-2224 3-2	1, 12, 14, 15
G- <i>P.Aepyprymnus</i>	R. rat kang	-	1	1	100	0	0	32	32	14
G-P. <i>Bettongia</i>	Bettong	-	4	3	75	0	0	22	22	12, 15
G-P. <i>Potorous</i>	Potoroo	-	4	2	50	12-24	2	-	12 24	1, 12, 15
F-Mephitidae	Skunk	4	12	6	50	46-64	6	-	4-68, 5-008, 6-04	1, 40, 87
G-M. <i>Conepatus</i>	Hog-nose sk.	-	4	1	25	0	0	46	46	87
G-M. <i>Mephitis</i>	Skunk	-	2	2	100	0	0	50	50	40, 87
G-M. <i>Mydaus</i>	Stink skunk	-	2	0	0	-	-	-	-	-
G-M. <i>Spilogale</i>	Spotted skunk	-	4	3	75	48-64	3	-	48, 6-04	1, 87
F-Hylobatidae	Gibbon	4	14	5	36	38-52	4	44	38, 4-4444, 5-02	1, 6, 31
G- <i>H.Bunopithecus</i>	Hoolock G.	-	1	1	100	38-44	2	-	38, 44	31
G-H. <i>Hylobates</i>	Gibbon	-	7	3	43	0	0	44	44	1, 31
G-H. <i>Nomascus</i>	Gibbon	-	5	1	20	0	0	52	52	1
G- <i>H.Symphalangus</i>	Siamang	-	1	1	100	0	0	50	50	1
F-Macroscolididae	Elephant shrew	4	16	9	60	26-34	4	26	2-66666888 3-004	19, 40
F-Tupalidae	Tree shrew	4	19	7	37	44-68	6	-	44, 52, 6-00268	1, 21
G-T. <i>Tupaia</i>	Tree shrew	-	15	6	40	52-68	5	-	52, 6-00268	1, 21
G-T. <i>Urogale</i>	Tree shrew	-	1	1	100	0	0	44	44	21
F-Pitheciidae	Titi	4	40	15	38	16-54	9	-	16, 20 4-245666888 5-0000444	1, 6, 31, 32, 33
SF-P. <i>Callicebinae</i>	Titi	1	28	8	29	16-50	6	50	16, 20, 4-268 5-0000	1, 6, 31, 32, 33
SG- <i>P.C.C. Callicebus</i>	Titi	-	22	6	27	42-50	4	50	4-268 5-0000	1, 31, 32, 33
SG-P.C.C <i>Torquatus</i>	Collared titi	-	5	2	40	16-20	2	-	16, 20	6
SF-P.Pitheciinae	variety	3	12	7	59	44-54	5	-	4-456688 5-444	1, 31, 33
G-P.P. <i>Cacajao</i>	Uakari	-	2	2	100	44-46	3	-	4-456	1, 31,

										33
G-P.P. <i>Chiropotes</i>	Saki	-	5	3	60	0	0	54	54	32, 33
G-P.P. <i>Pithecia</i>	Saki	-	5	2	40	46-48	2	-	4-68	31, 32
F-Ursidae	Bear	5	8	8	100	42-74	3	74	42, 52, 74x6	40
G-U. <i>Ailuropoda</i>	Giant panda	-	1	1	100	0	0	42	42	40
G-U. <i>Tremarctos</i>	Spectacled bear	-	1	1	100	0	0	52	52	40
F-Lorisidae	Loris	5	9	4	44	50-62	3	-	5-00022 6-22	1, 6, 28
G-L. <i>Arctocebus</i>	Gold. Pottos	-	2	1	50	0	0	52	52	28
G-L. <i>Loris</i>	Slender loris	-	2	1	50	0	0	62	62	1
G-L. <i>Nycticebus</i>	Slow loris	-	3	3	100	50-52	2	50	5-0002	1, 28
G-L. <i>Perodicticus</i>	Potto	-	1	1	100	0	0	62	62	6
F-Bathyergidae	Mole rat	5	16	13	81	40-78	10	-	40, 5-04444688, 6-0028, 7- 488	1, 6, 57, 62
SF- B.Bathyerginae	Mole rat	4	15	6	40	40-78	10	-	40, 5-04444688, 6-028 7-488	1, 6, 62
G- B.B. <i>Bathyergus</i>		-	2	2	100	54-56	2	-	5-46	1, 6
G-B.B. <i>Crytomys</i>		-	11	8	73	40-78	6		40, 5-04, 68, 7-488	1, 6, 62
G-B.B. <i>Georychus</i>		-	1	1	100	0	0	54	54	1
G- B.B. <i>Heliophobius</i>		-	1	1	100	60-62	2	-	6-02	57
SF- B.Hetrocephalinae	Naked mole rat	1	1	1	100	0	0	60	60	57
F-Cheirogaleidae	Mouse lemur	5	16	16	100	46-66	2	66	66x12 46x4	1, 22
G-C. <i>Phaner</i>		-	4	4	100	0	0	46	46	22
F-Erethizontidae	NW porcupine	5	16	10	63	42-74	4	42	4-2222, 52, 7-2444, 62	58, 63, 65
SF- E.Chaetomyinae	Bristle spine rat	1	1	1	100	0	0	52	52	58
SF- E.Erthizontinae	Porcupine	4	15	9	60	42-74	3	42x 4, 74x 3	4-2222, 62, 7-2444	58, 63, 65
G-E.E. <i>Coendou</i>	Prehensile tail porcupine	-	4	3	75	0	0	74	7-444	58, 63
G-E.E. <i>Erethizon</i>	Common p.	-	1	1	100	0	0	42	42	58

G-E.E. <i>Sphiggurus</i>	Porcupine	-	9	6	68	42-72	3	42	4-222, 62, 72	58, 63, 65
F-Lemuridae	Lemur	5	19	10	53	44-60	8	-	4-4688, 5-0468, 6-000	1, 6
G-L. <i>Eulemur</i>	True lemur	-	11	6	55	44-60	5	-	4-4688, 50, 6-00	1, 6
G-L. <i>Hapalemur</i>	Gentle l	-	4	2	50	54-58	2	58	5-488	6
G-L. <i>Lemur</i>	Ring tail l	-	1	1	100	0	0	56	56	6
G-L. <i>Prolemur</i>	G. bamboo l	-	1	1	100	0	0	60	60	6
F-Suidae	Pig	5	19	10	53	32-38	4	34x 5 38x 4	3-24444468888	1, 40
SF-S.Suinae	Babirusa	5	19	10	53	32-38	4	34x 5 38x 4	3-24444468888	1, 40
T-S.S.Suini	Pig	1	10	4	40	34-38	3	38	3-46888	1, 40
T-S.S.Babyrousiini	Babirusa	1	4	1	25	0	0	38	38	1
T-S.S.Potamochoerini	Hog	3	5	5	100	32-34	2	34	3-24444	1, 40
F-Atelidae	NW monkey	5	25	12	48	32-62	11	-	3-244444, 4-245789, 5-0002222, 62	1, 6, 31, 33
SF-A.Alouattinae	Howler mon	1	11	5	46	44-52	7	50x 4 52x 4	4-45789, 5-00002222	1, 6, 33
Sp-A.A. <i>Alouatta seniculus</i>	Red Howler	-	1	1	100	44-52	7	-	4-45789, 5-02	1, 33
SF-A.Atelinae	Spider/wool	4	14	6	43	32-62	3	34	3-2244444, 62	6, 31, 33
G-A.A. <i>Lagothrix</i>	Woolly mon	-	4	1	25	0	0	62	62	6

Table A3. Diploid numbers of families with six to 10 genera. Diploid numbers are written in stem-leaf format where “1-2446” means diploid numbers of 12, 14, 14, 16; not all diploid numbers are available in the literature. Alternating gray areas separate families for easier comparison; Heading Key: A= # of Genera; B= # of Species; C= # Karyotyped species used in dataset; D= % 2n known; E=2n range; F=#of 2n Variations; G= Mode of 2n; H= Diploid Numbers (2n); I= Reference. Abbreviation key: F=Family, SF=Subfamily, T=Tribe, G=Genus, SG=Subgenus; “OW” = Old World; “NW” = New World.

Classification Level	Common Name	A	B	C	D	E	F	G	H	I
F-Procyonidae	Raccoon	6	17	8	57	0	0	38	38	1, 40, 89
F-Pseudocheiridae	Ring-tail p.	6	17	10	59	10-22	6	-	1-022668, 2-022	1, 15, 16
SF-P.Hemibelideinae	Variety	2	2	2	100	20-22	2	22	2-022	1, 15
G-P.H.Hemibelideus	Lemuroid	-	1	1	100	20-22	2	-	2-02	1, 15
G-P.H.Petauroides	Glider	-	1	1	100	0	1	22	22	15
SF-P.Pseudocheirinae	Ring-tail p.	3	10	5	50	12-20	4	-	1-2268, 2-0	1, 15, 16
G-P.P.Petropseudes	Rock pos	-	1	1	100	0	0	16	16	1
G-P.P.Pseudocheirus	Ring tail pos	-	1	1	100	0	0	20	20	1
G-P.P.Pseudochirulus	Ringtail pos	-	8	3	38	12-18	2	12	1-228	15, 16
SF-P.Pseudochiropsinae	Ringtail pos	1	5	3	60	10-16	2	16	1-066	15, 16
F-Peramelidae	Bandicoot	6	18	8	44	0	0	14	1-44444444	1, 12, 15, 16
F-Caviidae	Guinea pig	6	18	11	61	52-68	5	64	52, 6-22444444468	1, 6, 7, 66, 67, 68, 69
SF-C.Caviinae	Guinea pig	3	12	8	67	62-68	3	64	6-224444448	1, 6, 7, 66, 67, 68
G-C.C.Cavia	Guinea pig	-	6	6	100	62-64	2	64	6-2244444	7, 66, 68
G-C.C.Galea	Yellow tooth c.	-	3	2	67	64-68	2	-	6-48	6, 67
G-C.C.Microcavia	Mountain cavy	-	3	0	0	-	-	-	-	-
SF-C.Dolichotinae	Paantagon.hare	1	2	2	50	0	0	64	64	6
SF-C.Hydrochoeris	Capybara, rock cavy	2	4	2	50	52-66	2	-	52, 66	1, 69

G-C.H. <i>Hydrochoeris</i>	Capybara	-	2	1	50	0	0	66	66	1
G-C.H. <i>kerodon</i>	Rock cavy	-	2	1	50	0	0	52	52	69
F-Phalangeridae	-	6	28	6	21	12-20	3	20	1-244 2-000	1, 12, 15, 16
SF-P. <i>Ailuropinae</i>	Cuscus	1	2	0	0	-	-	-	-	-
SF-P. <i>Phalangerinae</i>	-	5	25	6	24	12-20	3	20	1-244 2-000	15
T-P.P. <i>Phalangerini</i>	Cuscus	2	17	2	11	0	0	14	14	15
T-P.P. <i>Trichosurini</i>	Possum	3	8	4	50	12-20	2	20	1-2 2-000	1, 12, 16
G-P.P.T. <i>Strigocuscus</i>	Cuscus	-	2	1	50	0	0	12	12	16
G-P.P.T. <i>Trichosurus</i>	Brush tail possum	-	5	3	60	0	0	20	20	1, 12, 16
F-Spalacidae	Subterranean rat	6	36	15	42	38-64	13	60	38, 4- 048889, 5- 000244466, 58x3, 6- 0000022224	1, 45, 46, 47, 48, 49, 52
SF-S. <i>Myospalacinae</i>	Zoker	2	6	6	100	44-64	5	62	44, 58, 6- 02224	48, 49
G-S.M. <i>Esopalax</i>	Zoker	-	3	3	100	58-62	3	62	58, 6-022	48, 49
G-S.M. <i>Myosplalax</i>	Zoker	-	3	3	100	44-64	3		44, 6-24	48
SF-S. <i>Rhizomyinae</i>	Bamboo rat	2	4	0	0	-	-	-	-	-
SF-S. <i>Spalacinae</i>	Blind mole rat	1	15	6	40	38-62	11	-	38, 4-089, 5- 00244466888 , 6-00002	45, 46, 47
G-S.S. <i>Spalax</i>	Blind mole rat	-	15	6	40	38-62	11	-	38, 4-089, 5- 00244466888 , 6-00002	45, 46, 47
SF-S. <i>Tachyoryctinae</i>	Mole rat	1	13	3	23	48-50	2	48	4-88, 50	1, 52
F-Cebidae	NW Monkey	6	57	13	23	44-54	5	44x 10 46x 10	44x10, 46x10, 48, 5-2222444	1, 6, 32, 33
SF-C.Marmoset	Marmoset	4	43	19	44	44-48	3	44x 9	44x9, 46x10, 48	1, 32, 33

								46x 10		
SF-C.Cebinae	Capuchin	1	9	5	57	52-54	2	52x 4 54x 3	5-2222444	1, 6, 33
SF-C.Saimiriinae	Squir mon	1	5	1	20	0	0	44	44	1
F-Heteromyidae	Kangaroo rat	6	60	50	83	34-74	19	60	3-4688, 4- 0222244466, 48x5, 50x4, 56x6, 5-22244448, 60x12, 6-24444, 7-00222224	1, 6, 36, 37, 38, 39, 40
SF-H. Dipodomyinae	Kangaroo rat	2	21	19	91	40-74	10	-	4-02, 5-224, 6- 0000024444, 7-00222224	1, 6, 39, 40
G-H.H. <i>Dipodomys</i>	Kangaroo rat	-	19	17	90	52-74	8	60x 5 72x 5	5-224, 6- 0000024444, 7-00222224	1, 6, 39, 40
G-H.H. <i>Micro- podipops</i>	Kang. Mouse	-	2	2	100	40-42	2	-	4-02	39
SF- H.Heteromyinae	Pocket mouse	2	13	13	100	40-60	6	60	4-2888, 5-6668, 6-0000000	6, 36, 37, 38, 39, 40
G- H.H. <i>Heteromys</i>	Spiny pocket mouse	-	8	7	88	42-60	3	60	42, 56, 6- 00000	6, 36, 37, 38, 39
G-H.H.. <i>Liomys</i>	Sp. Pocket m.	-	5	5	100	48-60	4	-	4-88, 5-668, 60	38, 40
SF- H.Perognathinae	Pocket mouse	2	26	17	65	34-56	11	-	3-4688, 4- 224446688, 5- 00002444666	39, 40
G- H.P. <i>Chaetodipus</i>	Pocket mouse	-	17	9	53	34-56	11	-	3-4688, 4- 2244466688, 5-0246	39, 40
G- H.P. <i>Perognathus</i>	Pocket mouse	-	9	8	89	44-56	4	50x 4 54x 3 56x	44, 5- 0000444666	39, 40

								3		
F-Geomyidae	Pocket gopher	6	40	19	48	36-88	24	-	3-688, 40x8, 42x5, 4-4446666888, 5-022446666, 58x5, 6-008, 70x4, 74x4, 7-22266888, 8-02468	1, 39, 40
G-G. <i>Geomys</i>	Eastern pocket gopher	-	9	6	67	38-74	5	-	3-88, 4-22, 68, 7-000022244	39, 40
G- <i>G.Orthogeomys</i>	Giant pocket g.	-	11	3	27	44-58	3	-	44, 5-28	39
G- <i>G.Pappogeomys</i>	Pocket gopher	-	2	2	100	36-58	5	40	36, 4-000026, 58	39
G-G. <i>Thomomys</i>	Small toothed pocket gopher	-	13	12	92	40-88	19	-	4-0002244666, 48x3, 56x4, 5-0244888, 6-00, 7-4466888, 8-02468	1, 39, 40
SG- <i>G.T.Thomomys</i>	Southern pocket gopher	-	5	5	100	40-60	11	-	4-0002244666, 48x3, 5-02446666888 6-00	40
SG- <i>G.T.Megascapheus</i>	Northern and Western pocket gopher	-	4	4	100	74-88	8	76	7-4466888, 8-022468 (76x17 subspecies)	39, 40
G-G. <i>Zygogeomys</i>	Pocket gopher	-	1	1	100	0	0	40	40	39
F-Capromyidae	Hutia	6	16	2	13	40-88	2	-	40, 88	71
SF- <i>C.Capromyinae</i>	Hutia	4	13	2	15	40-88	2	-	40, 88	71
G-C.C. <i>Capromys</i>	Desmarest's h.	-	2	1	50	0	0	40	40	71
G-C.C. <i>Geocapromys</i>	Hutia	-	2	1	50	0	0	88	88	71
F-Eupleridae	Fossa	7	8	3	38	42-44	2	42	4-224	1
SF-Euplerinae	M. civet	3	3	2	67	0	0	42	42	1
SF-Galidiinae	Mongoose	4	5	1	20	0	0	44	44	1

F-Octodontidae	Rock rat	8	13	10	77	38-102	6	58	38, 5-4668888, 78, 102	1, 6
G-O. <i>Aconaemys</i>	Rock rat	-	3	3	100	54-58	3	-	5-468	1
G-O. <i>Octodon</i>	Degu	-	4	3	75	58-78	2	58	5-88, 78	1, 6
G-O. <i>Octodontomys</i>	Mountain degu	-	1	1	100	0	0	38	38	6
G-O. <i>Octomys</i>	Mt Viscacha	-	1	1	100	0	0	56	56	6
G-O. <i>Spalacopus</i>	Coruro	-	1	1	100	0	0	58	58	1
G-O. <i>Tympanoctomys</i>	Red Viscacha	-	1	1	100	0	0	102	102	1
F-Chrysochloridae	Golden mole	9	21	11	53	26-36	5	30	2-68 3-000000046	1, 18
SF-C.Chrysochlorinae	G. Mole	6	11	6	55	26-30	2	30	26, 3-00000	1, 18
SF-C.Amblysominae	G. Mole	3	10	5	50	28-36	4	-	28, 3-0046	18
F-Dasypodidae	Armadillo	9	21	14	67	38-64	6	64	38, 5-0088 6-0222444444	1, 6
SF-D.Dasypodinae	9-banded A	1	7	6	86	0	0	64	6-444444	1, 6
SF-D.Euphractinae	6-banded A	5	7	4	57	58-62	3	-	5-8 6-022	1, 6
SF-D.Tolypeutinae	Variety	3	7	4	57	38-62	3	-	38, 5-00, 62	1, 6
G-D.T. <i>Cabassous</i>	Naked tail A	-	4	2	50	50-62	2	-	50, 62	1
G-D.T. <i>Priodontes</i>	Giant A	-	1	1	100	0	0	50	50	6
G-D.T. <i>Tolypeutes</i>	3-banded A	-	2	1	50	0	0	38	38	1
F-Gliridae	Dormouse	9	28	5	18	44-62	4	-	4-4688, 62	1
SF-G.Graphiurinae	Afr. Dormouse	1	14	0	0	-	-	-	-	-
SF-G.Leithiinae	Dormouse	6	12	4	33	44-48	3	-	4-4688	1
SF-G.Glirinae	Edible d.	2	2	1	50	0	0	62	62	1
F-Hipposideridae	OW Leaf nosed bat	9	81	15	19	32-52	5	32	32x12, 3-006, 5-022	1, 20, 40, 81
G-H. <i>Asellia</i>	Trident leaf n.	-	2	1	50	0	0	50	50	40
G-H. <i>Aselliscus</i>	Trident leaf n.	-	2	1	50	0	0	30	30	80
G-H. <i>Hipposideros</i>	Round leaf bat	-	67	13	19	32-52	2	32	32x11, 5-22	1, 6, 40, 81
F-Erinaceidae	Hedgehog	10	24	10	42	40-48	2	48	40, 48x9	1, 40

SF-E.Erinaceinae	Hedgehog	5	16	9	56	0	0	48	48	1, 40
SF-E.Galericinae	Moonrat	5	8	1	13	0	0	40	40	1
F-Tenrecidae	Tenrec	10	31	20	65	14-56	7	30x 5 32x 5 38x 4	1-4, 30x5, 3-222228888 4-00, 5-46	1, 14, 17, 40
SF-T.Geogalinae	Large-ear T	1	1	1	100	0	0	14	14	14
SF- T.Oryzoricinae	Variety	3	21	12	57	30-56	6	30x 5 32x 5	3- 00000222228 5-46	17, 40
G-T.O. <i>Microgale</i>	Shrew tenrec	-	18	12	67	30-56	6	30x 5 32x 4	3- 00000222228 5-46	17
G- T.O. <i>Oryzorictes</i>	Rice tenrec	-	2	1	50	0	0	32	32	17
SF- T.Potamogalinae	Otter shrew	2	3	2	67	38-40	2	-	38, 40	17, 40
SF-T.Tenrecinae	Hedgehog Tenrec	4	5	5	100	38-40	2	-	3-888 4-00	1, 17, 40

Table A4. Diploid numbers of families with 11 to 15 genera. Diploid numbers are written in stem-leaf format where “1-2446” means diploid numbers of 12, 14, 14, 16; not all diploid numbers are available in the literature. Alternating gray areas separate families for easier comparison; Heading Key: A= # of Genera; B= # of Species; C= # Karyotyped species used in dataset; D= % 2n known; E=2n range; F=#of 2n Variations; G= Mode of 2n; H= Diploid Numbers (2n); I= Reference. Abbreviation key: F=Family, SF=Subfamily, T=Tribe, G=Genus, SG=Subgenus; “OW” = Old World; “NW” = New World.

Classification Level	Common Name	A	B	C	D	E	F	G	H	I
F-Leporidae	Rabbit, hare	11	52	25	48	38-52	6	48	3-88, 4- 222224446, 48x15, 52	1, 40
G-L. <i>Brachylagus</i>	Pygmy rabbit	-	1	1	100	0	0	44	44	1
G-L. <i>Bunolagus</i>	Riverine rabbit	-	1	1	100	0	0	44	44	1
G-L. <i>Lepus</i>	Antelope jack r	-	32	13	41	0	0	48	48x13	1, 40
G-L. <i>Sylvilagus</i>	Cottontail	-	17	7	41	38-52	5	42	3-88, 4-2222268, 52	1, 40
F-Macropodidae	Wallaby	11	67	36	54	10-24	8	16x 13 22x 12	16x13, 1-024488 22x12, 1- 0004	1, 12, 15, 16
SF-M.Sthenurinae	B-hare wallaby	1	1	1	100	0	0	24	24	15
SF-M.Macropodinae	Variety	10	66	35	53	10-22	7	16x 13 22x 12	16x13, 1-024488 1-000, 22x12	1, 12, 15, 16
G-M.M. <i>Dendrolagus</i>	Tree kang	-	12	3	25	12-14	2	14	1-244	15, 16
G-M.M. <i>Dorcopsis</i>	Greater d	-	4	1	25	0	0	22	22	16
G-M.M. <i>Dorcopsulus</i>	Lesser d	-	2	1	50	0	0	18	18	15
G-MM. <i>Lagorchestes</i>	Hare-wallabies	-	4	2	50	16-22	3	-	16 2-02	12, 15
G-M.M. <i>Macropus</i>	Kangaroos Wallaroos	-	14	12	86	16-20	2	16	1- 66666666666 2-0	1, 12, 15, 16,
G-MM. <i>Onychogalea</i>	Nail tail w	-	3	2	67	18-20	2	-	18, 20	12, 15
G-M.M. <i>Petrogale</i>	Rock-wal	-	16	7	44	16-22	3	22	16, 2-022222	1, 12
G-M.M. <i>Setonix</i>	Quokka	-	1	1	100	0	0	22	22	12
G-M.M. <i>Thylogale</i>	Pademelons	-	7	4	57	0	0	22	22	1, 12, 16
G-M.M. <i>Wallabia</i>	Swamp wal		1	1	100	0	0	10	10	1
F-Canidae	Dog, wolf,	12	37	25	68	34-78	16	78x	3-46888,	1, 40,

	fox, jackal...							8 74x 5	4-028, 5-00046, 6-046, 7-02, 74x5, 78x8	86
G-C. <i>Canis</i>	Dog, wolf	-	9	7	78	0	0	78	78	1, 40
G-C. <i>Cuon</i>	Dhole	-	1	1	100	0	0	78	78	40
G-C. <i>Lycaon</i>	Af. Wild dog	-	1	1	100	0	0	78	78	40
G-C. <i>Chrysocyon</i>	Maned wolf	-	1	1	100	0	0	76	76	1
G-C. <i>Atelocynus</i>	Short ear zorro	-	1	1	100	0	0	74	74	1
G-C. <i>Lycalopex</i>	Zorro	-	6	3	50	0	0	74	74	86
G-C. <i>Speothos</i>	Bush dog	-	1	1	100	0	0	74	74	40
G-C. <i>Cerdocyon</i>	Crab-eating fox	-	1	1	100	70-75	2	-	70, 74	1, 40
G-C. <i>Otocyon</i>	Bat eared dog	-	1	1	100	0	0	72	72	40
G-C. <i>Urocyon</i>	Grey fox		2	1	50	0	0	66	66	1
G-C. <i>Nyctereutes</i>	Raccoon dog	-	3	3	100	38-56	4	-	3-88, 42, 54, 56	1, 40
G-C. <i>Vulpes</i>	True fox	-	12	8	67	34-64	7	50	3-468, 40, 5-000, 6-04	1, 40
F- Emballonouridae	Sac wing bat	13	50	14	28	22-44	7	-	2-24668, 3-222, 4- 22224	1, 40
SF-Taphozoinae	Tomb bat	2	18	5	28	42-44	2	42	4-22224	1, 40
SF- Emballonurinae	Sac wing bat	11	32	9	28	22-32	5		2-224668, 3-222	40
G-E.E. <i>Balan- tiodpteryx</i>	Sac wing bat	-	3	1	33	0	0	32	32	40
G-E.E. <i>Comura</i>	Chestnut s.w	-	1	1	100	0	0	22	22	40
G- E.E. <i>Saccopteryx</i>	Sac wing bat	-	5	3	60	24-28	3	-	2-468	40
F-Herpestidae	Mongoose	14	33	17	49	35-44	5 (8)	35/3 6x7 36x 7	35/36x7, 36x7, 39/40, 41/42, 43/44	1, 40
F-Felidae	Cat	14	40	30	75	36-38	2	38	36x4, 38x27	1, 6, 40
SF-F.Felinae	Sm-med cats	11	34	24	71	36-38	2	38	36x4, 38x21	1, 6, 40
SF-F.Pantherinae	Big cats	3	6	6	100	0	0	38	38	1, 40
F-Viverridae	Civet, Genet	15	35	15	43	34-54	9	38x 4 42x 5	3-468888, 4-02222244 5-00244	1, 40, 84, 85
SF- V.Paradoxurinae	Binturong	5	7	4	57	40-44	3	42	4-02224	1, 40

SF-V.Hemigalinae	Civet	4	4	2	50	0	0	42	42	1, 40
SF-V.Prionodontinae	Lingsang	1	2	1	50	0	0	34	34	1
SF-V.Viverrinae	Genet, Civet	5	22	8	36	36-54	5	38	3-68888, 5-00244	1, 40, 84, 85
G-V.V. <i>Genetta</i>	Genet	-	14	4	29	50-54	3	-	5-00244	1, 40, 85
G-V.V. <i>Viverra</i>	Civet	-	4	3	75	0	0	38	38	84

Table A5. Diploid numbers of families with 16-25 genera. Diploid numbers are written in stem-leaf format where “1-2446” means diploid numbers of 12, 14, 14, 16; not all diploid numbers are available in the literature. Alternating gray areas separate families for easier comparison; Heading Key: A= # of Genera; B= # of Species; C= # Karyotyped species used in dataset; D= % 2n known; E=2n range; F=#of 2n Variations; G= Mode of 2n; H= Diploid Numbers (2n); I= Reference. Abbreviation key: F=Family, SF=Subfamily, T=Tribe, G=Genus, SG=Subgenus; “OW” = Old World; “NW” = New World.

Classification Level	Common Name	A	B	C	D	E	F	G	H	I
F-Dipodidae	Jerboas	16	51	20	39	18-72	14	-	1-89, 2-0446, 3-226, 58, 4-02246888, 72	1, 41, 42, 44
SF-D.Allactaginae	Fat tail, 4-5 toe	3	16	6	38	0	0	48	48	41
SF-D.Cardiocraniinae	Pygmy jerboa	3	7	1	14	0	0	46	46	1
SF-D.Dipodinae	3-toed jerboa	5	9	3	33	48-58	2	-	4-88, 58	1, 44
G-D.D. <i>Jaculus</i>	Jerboa	-	3	2	67	0	0	48	4-88	44
G-D.D. <i>Stylodipus</i>	3-toed jerboa	-	3	1	33	0	0	58	58	1
SF-D.Euchoreutinae	Long-eared j.	1	1	0	0	-	-	-	-	-
SF-D.Sicistinae	Birch mouse	1	13	9	69	18-44	10	-	1-89, 2-0446, 3-226, 4-0224	1, 42
G-D.S. <i>Sicista</i>	Birch mouse	-	13	9	69	18-44	10	-	1-89, 2-0446, 3-226, 4-0224	1, 42
SF-D.Zapodinae	Jumping mouse	3	5	1	20	0	0	72	72	1
F-Molossidae	Free-tail bat	16	100	28	28	34-48	4	48	3-444, 4-02, 48x25	1, 40
SF-M.Tomopeatinae	Blunt-eared bat	1	1	0	0	-	-	-	-	-
SF-M.Molossinae	Free-tail bat	15	99	28	28	34-48	4	48	3-444, 4-02, 48x25	1, 40
G-M.M. <i>Cynomops</i>	Dog-faced bat	-	5	2	40	0	0	34	34	40
G-M.M. <i>Eumops</i>	Mastiff bat	-	10	4	40	40-48	3	48	4-0288	1, 40
G-M.M. <i>Nyctinomops</i>	Free-tailed bat	-	4	4	100	0	0	48	4-8888	1, 40
F-Talpidae	Mole	17	39	23	59	32-42	5	34	34x14, 3-26666688, 42	40, 74
SF-T.Scalopinae	NW mole	5	7	4	57	0	0	34	34	40
T-T.S.Condylurini	Star-nosed m.	1	1	1	100	0	0	34	34	40
T-T.S.Scalopini	Mole	4	6	3	50	0	0	34	34	40
SF-T.Talpinae	Old World	11	28	18	64	32-42	5	34	3-	40, 74

	Talpid								226666688, 34x10, 42	
T-T.T.Desmanini	Desman	2	2	2	100	32-42	2	-	32, 42	40
G-T.T.D. <i>Desmana</i>		-	1	1	100	0	0	32	32	40
G-T.T.D. <i>Galemys</i>		-	1	1	100	0	0	42	42	40
T-T.D.Neurotrichini	Am. Shrew m.	1	1	1	100	0	0	38	38	40
T-T.T.Scaptonychini	Short faced m.	1	1	1	100	0	0	34	34	74
T-T.T.Talpini	Mole	5	22	12	55	32-38	4	34	34x8, 3-2666668	40
G-T.T.T. <i>Mogera</i>		-	5	4	80	32-36	2	36	3-2666	40
G-T.T.T. <i>Talpa</i>		-	9	6	67	34-38	3	34	3-444468	1, 6, 40
T-T.T.Urotrichini	J. shrew mole	2	2	2	100	0	0	34	34	40, 74
SF-T.Uropsilinae	Shrew-like m.	1	4	1	25	0	0	34	34	74
F- Didelphidae	Opossum	17	90	48	53	14-22	3	14	1-4x31 1-8x7 2-2x8	1, 2, 3, 5, 6, 8, 9, 12, 15
SF-D. Caluromyinae	Wooly op.	3	5	4	4	14-18	2	14	1-4448	1, 2, 3, 5, 12, 15
G-D.C. <i>Caluromys</i>	Wooly op.	-	3	3	100	0	0	14	14	1, 2, 5, 12, 15
G-D.C. <i>Glironia</i>	Bushy tail	-	1	1	100	0	0	18	18	3
SF-D. Didelphinae	American opppssum	14	82	44	54	14-22	3	14	14 x 27 18x7 22x10	1, 2, 3, 4, 6, 9,
G-D.D. <i>Chironectes</i>	Water op	-	1	1	100	0	0	22	22	2, 9
G-D.D. <i>Didelphis</i>	Large Am	-	6	4	67	0	0	22	22	1, 2, 6, 9
G-D.D. <i>Gracilinanus</i>	Mouse op	-	9	3	33	0	0	14	14	2, 6, 9
G-D.D. <i>Lestodelphis</i>	Patagon.op	-	1	1	100	0	0	14	14	9
G-D.D. <i>Lutreolina</i>	Thick tail	-	1	1	100	0	0	22	22	2, 9
G-D.D. <i>Marmosa</i>	Mouse op	-	12	6	50	14-22	2	14	1-44444 22	1, 2, 9
G-D.D. <i>Marmosops</i>	Variety	-	14	4	30	0	0	14	14	1, 4, 9, 13
G-D.D. <i>Metachirus</i>	Br 4-eyed	-	1	1	100	0	0	14	14	1, 9
G-D.D.	Wooly m	-	6	3	50	0	0	14	14	1, 2,

<i>Micoureus</i>										4, 9
G-D.D. <i>Monodelphis</i>	Variety	-	18	7	39	0	0	18	18	1, 2, 3, 6, 9
G-D.D. <i>Philander</i>	Gr 4-eyed	-	4	3	75	0	0	22	22	1, 2, 9
G-D.D. <i>Thylamys</i>	Variety	-	10	10	100	0	0	14	14	1, 8, 9
F-Echimyidae	Spiny rat	18	84	33	39	14-118	19	-	1-46, 2-2488, 3-0000244, 4-0268, 5-022, 6-0222224, 98, 118	1, 6, 58, 69
SF-E. <i>Dactylomyinae</i>	Bamboo rat	3	6	2	33	96-118	2	-	98, 118	1, 58
G-E.D. <i>Dactylomys</i>	Coro-coro	-	3	2	67	96-118	2	-	98, 118	1, 58
SF-E.Echimyinae	Spiny rat	6	29	14	48	22-52	3	-	22, 28, 50, 52	1, 58, 69
G-E.E. <i>Callistomys</i>	Painted tree rat	-	1	1	100	0	0	42	42	73
G-E.E. <i>Echimys</i>	Arboreal sp. Rat	-	3	2	67	90-94	3	-	9-024	73
G-E.E. <i>Isothrix</i>	Toro	-	4	4	100	22-60	3	-	2-28, 6-00	1, 73
G-E.E. <i>Makalata</i>	Tree rat	-	6	2	33	66-70	2	-	66, 70	73
G-E.E. <i>Phyllomys</i>	Tree rat	-	12	5	42	52-96	5	-	5-02, 7-22, 80, 96	58, 69, 73
SF-E.Eumysopinae	Primitive spiny rat	9	49	17	35	14-64	15	-	1-46, 2-48, 3-0000244, 4-0268, 52, 6-0222224	1, 6, 58, 69
G-E.E. <i>Clyomys</i>	Spiny rat	-	3	2	67	34-46	2	-	34, 46	69
G-E.E. <i>Lonchothrix</i>	Tuft tail sp. Rat	-	1	1	100	0	0	62	62	1
G-E.Eproechimyss	Spiny rat	-	25	11	44	14-62	11	-	1-46, 2-48, 3-00024, 4-228, 52, 6-222	1, 6, 58, 69
G-E.E. <i>Trinomys</i>	Punare'	-	11	1	9	60-64	3	-	6-024	69
F-Cervidae	Deer	19	51	37	73	6-70	25	68x11, 70x-11	0-6678889, 1-24, 3-67789, 4-046689, 5-0066668, 6-0245666, 68x11, 70x-11	1, 40, 96, 97, 98, 99, 100, 101
SF-C.Capreolinae	New World deer	9	22	16	73	36-70	11	70x10	3-67789, 4-049, 5-006, 6-8888,	1, 40, 96, 97,

									70x10	98, 99
G-C.C. <i>Mazama</i>		-	9	5	56	36-70	11	-	3-67789, 4-049, 5-006, 68, 7-00	40, 96, 97, 98, 99
SF-C.Cervinae	Old World deer	9	28	20	71	6-68	16	68	0-6678889, 1-24, 4-668, 5-668, 68x7, 6-0245666,	1, 40, 100, 101
G-C.C. <i>Muntiacus</i>	Muntjac	-	11	6	55	6-46	7	8	0-6678889, 1-24, 46	1, 40
SF-Hydroptinae	Ch. Water deer	1	1	1	100	0	0	70	70	40
F-Dasyuridae	Marsupials	21	69	15	22	0	0	14	14	1, 12, 15, 16
SF D. Dasyurinae	Variety	17	39	10	26	0	0	14	14	1, 12, 15, 16
T-D.D.Dasyurini	Quoll +	10	22	7	33	0	0	14	14	1, 16
T.D.D. Phascogali	Wambenger	7	17	3	18	0	0	14	14	16
SF-D.Sminthopsinae	Variety	4	30	5	17	0	0	14	14	1, 12, 15
T.D.S.Sminthopsini	Dunnart	3	25	3	12	0	0	14	14	1, 12
T.D.S Planigalini	Planigale	1	5	2	40	0	0	14	14	1, 15
F-Cercopithecidae	Old World Monkey	21	13 3	46	35	42-84	11	42 x17 44x 11	42x17, 44x11, 4-88, 5-4488, 60x5, 64, 66x5 7-022, 84	1, 6, 31, 32, 34, 35,
SF-C.Cercopithecinae	Macaque, baboon, vervet.	11	73	34	47	42-84	9	42	42x17, 48, 5-4488, 6-000066666, 7-022, 84	1, 6, 31, 34
G-C.C. <i>Allenopithecus</i>	A. swamp mon.	-	1	1	100	0	0	48	48	1
G-C.C. <i>Cerocebus</i>	Mangabey	-	6	2	33	0	0	42	42	1
G-C.C. <i>Cercopithecus</i>	Guenon	-	25	10	40	58-72	5	66	5-88, 7-022 6-066666,	1, 6, 31
G-C.C. <i>Chlorocebus</i>	Vervet	-	6	4	67	60-84	2	60	6-0000, 84	1, 6
G-C.C. <i>Macaca</i>	Macaque	-	21	9	43	0	0	42	42x9	1, 6
G-C.C. <i>Papio</i>	Baboon	-	5	4	80	0	0	42	42x4	1, 31
G-C.C. <i>Erythrocebus</i>	Patas monkey	-	1	1	100	0	0	54	54	1
SF-C.Colobinae	Colobus,	10	60	13	22	44-64	3	44	44x11, 48, 64	1, 6,

	proboscis, langur monkey									31, 32, 35
G-C.C. <i>Colobus</i>	Colobus	-	5	3	60	0	0	44	44x3	1, 6
G-C.C. <i>Nasalis</i>	Proboscis m.	-	1	1	100	0	0	48	48	1
G-C.C. <i>Rhinopithecus</i>	Snub nose m.	-	4	1	25	0	0	64	64	34
F-Nesomyidae	Rat/mouse	21	61	7	12	32-76	8	-	32, 48, 5-28, 60, 7-4456	18, 51, 52, 53, 55
SF- N.Cricetomyinae	Pouched rat	3	8	1	13	0	0	52	52	18, 51
SF- N.Delanymyinae	Delaney mouse	1	1	0	0	-	-	-	-	-
SF- N.Dendromurinae	Climbing m.	6	24	1	4	0	0	48	48	52
SF- N.Mystromyinae	White-tail m.	1	1	1	100	0	0	32	32	53
SF- N.Nesomyinae	Malagasy rat	9	23	4	17	58-76	5	-	58, 60, 7- 4456	55
G-N.N. <i>Eliurus</i>	Tufted tail rat	-	10	3	30	58-76	4	-	58, 7-4456	55
G-N.N. <i>Nesomys</i>	Nesomys	-	3	1	33	0	0	60	60	55
SF- N.Petromyscinae	African rock m.	1	4	0	0	-	-	-	-	-
F-Mustelidae	Ermine, mink weasel, stoat	22	59	32	54	30-44	7	38	3-026, 38x22, 4- 0000222244	1, 40
SF-M.Lutrinae	Otter	7	13	6	46	36-40	3	38	3-688888, 40	1, 40
SF-M.Mustelinae	Wolverine, mink, weasel	15	46	26	57	30-44	6	38	3-02, 38x17, 4- 0002222444	1, 40
G-M.M. <i>Neovison</i>	Mink	-	2	1	50	0	0	30	30	1
G-M.M. <i>Taxidea</i>	Badger	-	1	1	100	0	0	32	32	1
G-M.M. <i>Martes</i>	Marten	-	8	6	75	38-40	2	38	3-888888, 40	1, 40

Table A6. Diploid numbers of families with 26-50 genera. Diploid numbers are written in stem-leaf format where “1-2446” means diploid numbers of 12, 14, 14, 16; not all diploid numbers are available in the literature. Alternating gray areas separate families for easier comparison; Heading Key: A= # of Genera; B= # of Species; C= # Karyotyped species used in dataset; D= % 2n known; E=2n range; F=#of 2n Variations; G= Mode of 2n; H= Diploid Numbers (2n); I= Reference. Abbreviation key: F=Family, SF=Subfamily, T=Tribe, G=Genus, SG=Subgenus; “OW” = Old World; “NW” = New World.

Classification Level	Common Name	A	B	C	D	E	F	G	H	I
F-Soricidae	Shrew	26	375	98	26	20-68	35	36x 18 38x 17 40x 17 42x 14 50x 16	22x4, 24x3, 26x3, 28x5, 2- 0013355799 30x7, 34x7, 36x18,38x17, 3- 2222335557, 40x17, 42x14, 4- 4444666888, 50x16, 52x13, 54x5, 5-3566888, 60x3, 6- 2224466688	1, 6, 40, 73, 74, 75, 76,
SF-S.Crocidurinae	White-tooth shrew	9	210	55	26	22-68	21	36x 14 38x 12 40x 13 50x 12	2-2266888, 30x5, 36x14, 38x12, 3- 224444557, 40x13, 42x5, 4-4446688, 50x12, 5-22222268, 6-08	1, 40, 73, 75, 76,
G-S.C. <i>Crocidura</i>	Musk shrew	-	172	51	30	22-68	21	36x 13 40x 12 50x 12	2-2266888, 30x3, 36x13, 38x9, 3-24444557, 40x12, 42x4, 4-44668, 50x12, 5-22222268, 6-08	1, 40, 73, 75, 76,
G-S.C. <i>Diplo-</i> <i>mesodon</i>	Pie-bald shrew	-	1	1	100	0	0	44	44	40
G-S.C. <i>Suncus</i>	shrew	-	18	3	17	30-48	6	-	3-025, 4-028	40, 76
G-S.C. <i>Sylvisorex</i>	Forest shrew	-	12	6	50	30-38	3	38	3-06888	76

SF-S. <i>Myosoricinae</i>	African w.t.s	3	18	4	22	38-42	3	-	3-88, 4-02	76
SF-S. <i>Soricinae</i>	Red-tooth shrew	14	147	50	34	20-68	34	42	2-001223344455678899, 34x3, 36x4, 3-0022335888, 42x8, 4-0004688, 50x4, 52x7, 5-3444445688, 6-00222446668	1, 6, 40, 74, 76
T-S.S. <i>Anourosoricini</i>	Asian mole s.	1	4	1	25	48-50	2	-	48, 50	6, 40
T-S.S. <i>Blarinellini</i>	Short tailed s.	1	3	0	0	-	-	-	-	-
T.S.S. <i>Blarinini</i>	Sh. t/small ear	2	34	5	15	46-52	4	-	4-68, 5-000222	1, 40
T-S.S. <i>Nectogalini</i>	OW water shrew	7	25	7	32	44-64	4	52	44, 5-2228, 64	40, 74, 76
G-S.S.N. <i>Chimarrogale</i>	Asiatic water s.	-	6	1	17	0	0	52	52	40
G-S.S.N. <i>Chodsigoa</i>	-	-	8	1	13	0	0	44	44	76
G-S.S.N. <i>Episoriculus</i>	Brown toothed	-	4	2	50	58-60	2	-	58, 60	74, 76
G-S.S.N. <i>Neomys</i>	Water shre	-	3	3	100	0	0	52	52	40. 76
T-S.S. <i>Notiosoricini</i>	Gray/Mexican	2	5	2	40	62-68	2	62	6-228	40, 76
T-S.S. <i>Soricini</i>	Common shrew	1	76	35	46	20-66	29	42	2-001223344455678899, 34x3, 36x4, 3-0022335888, 4-000, 42x8, 5-2344444568, 6-0024666	1, 6, 40, 74, 76
F- Pteropodidae	Fruit bat	42	186	40	22	24-48	8	36x16 38x15	2-46, 34x8, 35, 36x16, 38x15,, 4-088	1,40, 77
G-P. <i>Balionycteris</i>	Spotted-wing	-	1	1	100	0	0	24	24	40
G-P. <i>Megaerops</i>	Tailless fruit b.	-	4	1	25	0	0	26	26	40
G-P. <i>Otopteropus</i>	Luzon fruit	-	1	1	100	0	0	48	48	1

	bat									
G-P. <i>Penthetor</i>	Dusky fruit bat	-	1	1	100	0	0	48	48	40
G-P. <i>Pteropus</i>	Flying fox	-	65	7	11	38-40	2	38	3-888888, 40	1, 40
G-P. <i>Macroglossus</i>	Long tongue	-	2	2	100	0	0	34	34	40
F-Vespertilionidae	Evening bat	48	407	12 6	31	20-52	15	44	2-022266, 28x7, 30x9, 36x21, 3- 2222444488, 42x8, 44x54, 4-00666666, 50x13, 52	1, 6, 20, 40, 79, 81, 82, 84
SF-V.Vesper-tilioninae	Vesper bat	38	237	73	31	22-52	13	36	2-22266, 28x7, 30x9, 36x21, 3- 222244448, 42x8, 44x9, 4-0666, 50x13, 52	1, 6, 20, 40, 79
T-V.V.Eptesicini	Pipistrelle	3	32	12	38	32-50	2	50	32, 50x11	1, 6, 40
G-V.V.E. <i>Eptesicus</i>	House bat	-	22	11	50	0	0	50	50	1, 6, 40
G-V.V.E. <i>Hesperopterus</i>	False serotine	-	5	1	20	0	0	32	32	1
T-V.V.Lasiurini	Hairy tail bat	1	17	8	47	22-28	3	28	2-26888888	1, 6, 40
T-V.V.Nycticeini	Evening bat	8	37	13	35	30-52	8	36	36x6, 3-000244, 4-222446, 52	1, 20, 40
G-V.V.N. <i>Scotophilus</i>	Yellow bat	-	12	5	42	0	0	36	36	1, 40
G-V.V.N. <i>Rhogeessa</i>	Rhogeessa bat	-	10	4	40	30-52	6	-	3-024, 4- 2244, 52	6, 40
T-V.V.Pipistrellini	-	4	42	18	43	26-46	9	-	2-68, 3-00024666, 4-22224446	1, 40
G-V.V.P. <i>Nyctalus</i>	Noctule bat	-	8	5	63	42-46	3	42	4-22246	40
G-V.V.N. <i>Pipistrellus</i>	Pipistrelle bat	-	31	12	39	26-44	8	-	2-68, 3- 0024666, 4- 244	1, 40
G-V.V.N. <i>Scotozous</i>	Dormer's bat	-	1	1	100	0	0	30	30	1
T-V.V.Picotini	Big eared bat	6	16	8	50	30-32	2	32	3-00222222	1, 6,

										40
T-V.V.Vesper- tilionini	-	14	81	14	17	22-50	11	44	2-22, 3- 02468, 4- 0244446, 50	1, 20, 40, 79, 81
G-V.V.V. <i>Glaucocy- nycteris</i>	Butterfly bat	-	12	2	17	0	0	22	22	81
G-V.V.V. <i>Falsi- strellus</i>	Pipistrelle	-	5	3	60	34-44	3	-	3-46, 44	1, 40
G-V.V.V. <i>Tylo- nycteris</i>	Bamboo bat	-	2	2	100	32-46	2	-	32. 46	1
SF- V.Antrozoinae	Pallid bat	2	2	1	50	0	0	46	46	84
SF-V.Myotinae	Wing-gland bat	3	107	43	40	20-46	3	44	20, 44x41, 46	1, 6, 40
G-V.M. <i>Laio- nycteris</i>	Silver haired b.	-	1	1	100	0	0	20	20	40
SF- V.Miniopterinae	Bent-winged bat	1	19	3	16	0	0	46	46	6, 79, 82
SF-V.Murininae	Tube nosed bat	2	19	5	26	40-44	2	44	4-04444	1, 40
SF-Kerivoulinae	Painted bat	2	23	1	4	0	0	38	38	40
F-Bovidae	Bovid	50	143	86	60	30-60	21	60	30/31x2, 32/31x3, 32/33x2, 34/33, 34/35, 56/55, 3-0002388, 4-00246669, 48x8, 50x4, 52x7, 53, 54x5, 56x9, 58x16, 60x24	1, 40, 93
SF- B.Aepycerotinae	Impala	1	1	1	100	58-60	2	-	58, 60	1
SF- B.Alcelaphinae	Wildebeest	4	10	6	60	36-58	6	-	3-689, 4-04, 5-88	1, 40
G- B.A. <i>Alcelaphus</i>	Hartebeest	-	3	1	33	39-40	2	-	39, 40	1, 40
G-B.A. <i>Beatragus</i>	Hirola	-	1	1	100	0	0	44	44	1
G-B.A. <i>Conno- chaetes</i>	Wildebeest	-	2	2	100	0	0	58	58	1
G- B.A. <i>Damaliscus</i>	Korrigum	-	4	2	50	36-38	2	-	3-68	1
SF-B.Antilopinae	True antelope	15	38	21	55	30-60	20	-	30/31x2, 32/31, 32/33x2, 34/35, 3- 0038,	1, 40

									4-066889, 5-02266888, 6-000	
G-B.A. <i>Antelope</i>	Blackbuck	-	1	1	100	30-33	2	-	30, 33	1
G-B.A. <i>Eudorcas</i>	Gazelle	-	3	2	67	0	0	58	58	1
G-B.A. <i>Gazella</i>	Gazelle	-	10	7	70	30-52	10	-	3- 0112223345, 4-69, 5-23	1, 40
G-B.A. <i>Lithocranius</i>	Gerenuk	-	1	1	100	0	0	60	60	1
G-B.A. <i>Madoqua</i>	Dik-dik	-	3	3	100	46-50	3	48	4-688, 50	1
G-B.A. <i>Nanger</i>	Gazelle	-	3	3	100	30-40	6	-	3-01489, 40	1
SF-B.Bovinae	Bison, cattle	9	24	18	75	31-60	17	60	32/31x2, 34/33x2, 56/55, 3-028, 4-688, 5- 024688, 6-0000,	1, 40
G-B.B. <i>Bos</i>	Cattle, yak	-	5	4	80	58-60	2	60	5-88, 6-000	1
G-B.B. <i>Boselaphus</i>	Blue bull	-	1	1	100	0	0	46	46	1
G-B.B. <i>Bubalis</i>	Water buffalo	-	4	2	50	48-50	2	48	4-88, 50	1
G-B.B. <i>Syncerus</i>	African buffalo	-	1	1	100	52-56	3	-	5-246	1, 40
G-B.B. <i>Taurotragus</i>	Eland	-	2	2	100	31-32	2	32/3 1	32/31	1
G-B.B. <i>Tetracerus</i>	4-horn antelope	-	1	1	100	0	0	38	38	40
G-B.B. <i>Tragelaphus</i>	Kudu	-	7	6	86	30-56	7	-	3-0233448, 56/57	1, 40
SF-B.Caprinae	Goat-antelope	12	35	20	57	42-60	8	60	4-2888, 5- 0222444666, 58x3, 60x6	1, 40
G-B.C. <i>capra</i>	ibex, goat	-	8	6	75	0	0	60	60	1, 40
G-B.C. <i>Oreamnos</i>	Rocky Mt goat	-	1	1	100	0	0	42	42	1
G-B.C. <i>Ovibos</i>	Musk ox	-	1	1	100	0	0	48	48	1
G-B.C. <i>Ovis</i>	Sheep	-	5	4	80	52-58	4	54	5-2244468	1, 40, 93
SF-B.Cephalophinae	Duiker	3	18	9	50	58-60	2	60	58, 60x8	1, 40
SF-B.Hippotraginae	Grazing antel.	3	8	6	75	56-60	3	58	5-668888, 6- 00	1, 40
SF-B.Reduncinae	Antelope	3	9	5	56	48-56	6	-	48, 5-02346	1

Table A7. Diploid numbers of families with 51-100 genera. Diploid numbers are written in stem-leaf format where “1-2446” means diploid numbers of 12, 14, 14, 16; not all diploid numbers are available in the literature. Alternating gray areas separate families for easier comparison; Heading Key: A= # of Genera; B= # of Species; C= # Karyotyped species used in dataset; D= % 2n known; E=2n range; F=#of 2n Variations; G= Mode of 2n; H= Diploid Numbers (2n); I= Reference. Abbreviation key: F=Family, SF=Subfamily, T=Tribe, G=Genus, SG=Subgenus; “OW” = Old World; “NW” = New World.

Classification Level	Common Name	A	B	C	D	E	F	G	H	I
F-Sciuridae	Squirrels	52	279	93	33	30-62	13	38	30, 32x11, 34x4, 36x13, 38x35, 40x14, 42x7, 4-666668 5-000468, 62	1, 40
SF-S.Ratufinae	Giant tree sq.	2	5	0	0	-	-	-	-	-
SF-S.Sciurillinae	Squirrel	21	82	11	13	38-46	4	40	38, 40x8 4-26	1, 40
T-S.S.Sciurini	Squirrel	5	37	10	27	40-46	3	40	40x8, 4-26	40
T-S.S.Pteromyini	Flying squirrel	15	44	1	2	0	0	38	38	1
SF-Callosciurinae	Asiatic squirrel	14	64	8	13	38-62	7	-	3-888, 4-00668, 5-46, 62	1, 40
SF-S.Xerinae	Squirrel	15	128	74	58	32-50	8	38	32x11, 34x4, 36x13, 38x31, 40x4, 42x6, 4-66 5-000	1, 40
T-S.X.Xerini	Long clawed s.	3	6	0	0	-	-	-	-	-
T-S.X.Protoxeri	African tree s.	6	30	1	3	0	0	46	46	40
T-S.X.Marmotini	Marmot, Chipmunk, Prairie dog	6	92	73	79	32-50	8	38	32x11, 34x4, 36x13, 38x31, 4-00002222226 5-000	1, 40
G-SXMAmmospermophilus	Antelope squirrel	-	5	4	80	0	0	32	32	40
G-S.X.M.Cynomys	Prairie dog	-	5	4	80	40-50	2	50	40, 5-000	40
G-S.X.M.Marmota	Marmot	-	14	13	93	38-42	3	38	38x8, 4-00222	40
G-S.X.M.Spermophilus	Ground squirrel	-	41	32	78	32-46	8	36	32x7, 36x13, 3-044448888, 4-0226	1, 40
G-S.X.M.Tamias	Chipmunk	-	25	19	76	0	0	38	38	1, 40

G-S.X.M. <i>Sciuro-tamias</i>	Rock squirrel	-	2	0	0	-	-	-	-	-
F-Phyllostomidae	NW Leaf-nosed bat	55	155	74	48	13-46	20	30/31 x11, 30x 19, 32x 18	1-36668, 20/21x3, 2-01222444, 26x7, 28x11, 30/31x11, 30x19, 32x18, 3- 444466888, 4-0002466	1, 6, 40
SF-P.Desmodontinae	Vampire bat	3	3	3	100	28-32	2	32	28, 3-22	1
SF-P.Brachyphyllinae	Fruit eating bat	1	2	2	100	0	0	32	32	40
SF-P.Phyllostomycterinae	Flower bat	2	5	5	100	0	0	32	32	1, 40
SF-P.Glossophaginae	Long tongue bat	13	32	14	44	16-32	6	32x 5 30x 4	1-66, 2-0488, 3-000022222	1, 6, 40
T-P.G.Glossophagini	Long tongue bat	10	23	11	48	16-32	5	30x 3 32x 4	1-66, 2-04, 3-0002222	1, 6, 40
G-P.G. <i>Anoura</i>	Long nosed bat		5	3	60	0	0	30	3-000	1, 6
G-P.G. <i>Choeronycteris</i>	Long tail bat	-	1	1	100	0	0	16	16	1
G-P.G. <i>Hylonycteris</i>	Long tongued	-	1	1	100	0	0	16	16	1
G-P.G. <i>Lichonycteris</i>	Dark lg tongue	-	1	1	100	0	0	24	24	1
G-P.G. <i>Monophyllus</i>	Single leaf bat	-	2	1	50	0	0	32	32	1
T-P.G.Lonchophyllini	Long tongue bat	3	9	3	33	28-32	3	28	2-88, 3-02	1, 40
SF-P.Phyllostominae	Big-eared bat	16	46	29	69	16-46	10	30x 6 32x 9	16, 28x6, 2- 26, 30x6, 32x9, 3-448, 4- 00066	1, 6
G-P.P. <i>Lophostoma</i>	Round ear bat	-	5	4	80	26-34	4	-	2-68, 3-04	40
G-P.P. <i>Macrotis</i>	Big ear bat	-	2	2	100	40-46	2	-	4-06	1, 40
G-P.P. <i>Micronycteris</i>	Little big ear	-	9	4	44	28-40	4	-	2-88, 3-08, 40	1, 40
G-P.P. <i>Mimon</i>	Spear nose bat	-	4	3	75	30-34	3	-	3-024	1, 6, 40

G-P.P. <i>Tonatia</i>	Round ear bat	-	2	1	50	0	0	16	16	1
SF-P. <i>Carollinae</i>	Short-tail leaf nose bat	2	9	6	67	20-36	5	-	20/21x3, 22, 3-446	1, 40
G-P.C. <i>Carollia</i>	Sht tail leaf bat	-	6	4	67	20-22	3	20/21	2-0001112	1, 40
G-P.C. <i>Rhinophylla</i>	Little fruit bat	-	3	2	67	34-36	2	34	3-446	1, 40
SF-P. <i>Stenodermatinae</i>	Fruit bat	18	67	39	58	13-44	13	30/31x11, 30x9	1-38, 26x6, 2-124488, 30/31x11, 30x9, 3-688, 4-24	1, 6, 40
T-P.S. <i>Sturnira</i>	Yellow sh. bat	1	14	7	50	0	0	30	30	1, 6, 40
T-P.S. <i>Stenodermatini</i>	Tent making b.	17	53	32	60	13-44	13	30/31x11, 30x8	1-38, 26x6, 2-124488, 30/31x11, 30x8, 3-688, 4-24	1, 6, 40
G-P.S.S. <i>Artibeus</i>	Fruit eating bat	-	18	8	42	30-31	2	30	30x8, 31x5	1, 6, 40
G-P.S.S. <i>Chiroderma</i>	Big eyed bat	-	5	4	80	0	0	26	26	1, 40
G-P.S.S. <i>Mesophylla</i>	MacConnell's	-	1	1	100	21-22	2	22/21	22/21	40
G-P.S.S. <i>Sphaeronycteris</i>	Visored bat	-	1	1	100	0	0	28	28	1
G-P.S.S. <i>Uroderma</i>	Tent making b.	-	6	5	83	13-26	4	-	1-38, 2-4466	1, 6, 40

Table A8. Diploid numbers of families with >100 genera. Diploid numbers are written in stem-leaf format where “1-2446” means diploid numbers of 12, 14, 14, 16; not all diploid numbers are available in the literature. Alternating gray areas separate families for easier comparison; Heading Key: A= # of Genera; B= #of Species; C= # Karyotyped species used in dataset; D= % 2n known; E=2n range; F=#of 2n Variations; G= Mode of 2n; H= Diploid Numbers (2n); I= Reference. Abbreviation key: F=Family, SF=Subfamily, T=Tribe, G=Genus, SG=Subgenus; “OW” = Old World; “NW” = New World.

Classification Level	Common Name	A	B	C	D	E	F	G	H	I
F-Cricetidae	Vole, hamster	12 9	683	25 2	37	9-92	36	48x 36 52x 30 56x 25 54x 20 50x 18	0-99, 1- 445667778, 22x7, 24x5, 2-00066, 28x9, 30x4, 32x4, 34x7, 3-666667, 38x13, 40x9, 42x9, 44x9, 4-366666, 48x36, 50x18. 52x30, 54x22, 56x25, 5- 8888, 60x9, 62x8, 64x8, 6- 6668, 7-00, 80x6, 82, 9-22	1, 6, 40, 54, 69
SF-Arvicolinae	Vole, muskrat, lemming	27	152	60	40	17-62	19	50x 7, 54x 13, 56x 12	1-778, 22 3-0006668, 4-02466688, 50x7, 54x13, 5-222238, 56x13, 6-022	1
SF-Cricetinae	Hamster	7	20	17	85	20-44	9	-	20x3, 22x3, 2-44, 28x3, 3-48, 4-244	1,56
SF-Lophiomyinae	Crested rat	1	1	0	0	-	-	-	-	-
SF-Neotominae	New World rat	16	124	54	44	40-58	9	48	4-0026, 48x31, 52x13, 5-004688,	1, 40
SF-Sigmodontinae	NW rat, mouse	74	377	11 7	31	9-92	35	38	0-99, 1-445667, 2-2224446, 28x6, 34x6, 3-02222667,	1, 6, 40, 54

									38x11, 40x6, 42x5 44x6, 4-3688, 50x8. 52x12, 54x8, 56x11, 5-88, 60x8, 64x8, 6-22226668, 7-00, 80x6, 82, 9-22	
SF-Tylomyinae	Vesper, climbing rat	4	10	4	40	42-52	4	-	42, 48, 50, 52	40

Reference key for tables 1-8: 1. O'Brien *et al.*, 2006; 2. Carvalho and Mattevi, 2000; 3. Fantin and da Silva, 2011; 4. Pereira *et al.*, 2008; 5. Casartelli *et al.*, 1986; 6. Gregory, 2010; 7. Gava *et al.*, 2012; 8. Carvalho *et al.*, 2009; 9. Voss and Jansa, 2003; 10. Svartman, 2009; 11. Calaby *et al.*, 1974; 13. Carvalho *et al.*, 2002; 14. Rens *et al.*, 2003; 15. Rens and Ferguson-Smith, 2010; 16. Westerman *et al.*, 2010; 17. Gilbert *et al.*, 2007; 18. Hubert, 1978; 19. Smit, *et al.*, 2008; 20. Bronner *et al.*, 2003; 21. Arrighi *et al.*, 1969; 22. Swindler, 1998; 23. Rimpler *et al.*, 2011; 25. Stanyon *et al.*, 2002; 28. Boer, 1973; 30. Fridman, 2002; 31. Ankel-Simons, 2007; 32. Chiarelli *et al.*, 1979; 33. Dumas and Sineo, 2004; 34. Haipeng *et al.*, 2002; 35. Chaveerach *et al.*, 2007; 36. Schmidt *et al.*, 1989; 38. Anderson *et al.*, 2006; 39. Hafner and Hafner, 1982; 40. Diploid numbers, 2000. 41. Arslan and Zima, 2009; 42. Baskevich, 1996; 43. Abramov *et al.*, 2012; 44. Faleh *et al.*, 2010; 45. Nevo *et al.*, 1994; 46. Sozen *et al.*, 2011; 48. Shahabi *et al.*, 2010; 49. Li and Chen, 1987; 52. Matthey, 1967; 53. Srivastava *et al.*, 1974; 54. Andrades-Miranda *et al.*, 2001; 55. Solano *et al.*, 2011; 56. Ross, 1995; 57. Deuve *et al.*, 2008; 58. Vileta *et al.*, 2009; 59. George, 2008; 60. Arsian, 2006; 61. Tanomtong, 2008; 62. Deuve, 2008; 63. Bonvicino *et al.*, 2000; 65. Voss, 2011; 66. Gava *et al.*, 1998a; 67. Dunnun and Salazar-Bravo, 2010b; 68. Dunnun and Salazar-Bravo, 2009; 69. Kasahara and Yonenaga-Yassuda, 1984; 70. Souza *et al.*, 2007; 71. Henriques-Gil *et al.*, 1996; 72. Wilson and Reeder, 2005a; 73. Ventura *et al.*, 2008; 74. Motokawa *et al.*, 2009; 75. Bannikova *et al.*, 2005; 76. Wilson and Reeder, 2005b; 77. Haiduk, 1983; 78. Mao *et al.*, 2007; 79. Ao *et al.*, 2006; 80. Ao *et al.*, 2007; 81. Porter, 2010; 82. Matsuda, 2010; 84. Tanomtong *et al.*, 2006; 85. Gaubert *et al.*, 2004; 86. Solar and Rau, 2004; 87. Perelman *et al.*, 2008; 89. Castro *et al.*, 2011; 90. Musilova *et al.*, 2009; 91. Houck *et al.*, 1995; 92. Bunjongrat *et al.*, 2009; 93. Huang *et al.*, 2005; 94. Studies on the Cytogenetics, 2012; 95. Groves, 2011; 96. Resende *et al.*, 2011; 97. Bello *et al.*, 2008; 98. Abril and Duarte, 2008; 99. Giannoni *et al.*, 1991; 100. Idris and Moin, 2009; 101. Meijaard and Groves, 2003.