

eKINDS Project Paper

The Uniqueness of Humans Is Clearly Demonstrated by the Gene-Content Statistical Baraminology Method

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Abstract

The Creation Research Society's eKINDS (examination of kinds in natural diversification and speciation) research project has been working with a newly developed statistical baraminology tool, the gene-content method. In this paper we apply this method to several vertebrate taxa: humans, simians (monkeys and apes), two other mammalian taxa (Felidae, or cats, and Muridae—mice and rats), and two avian taxa (Galliformes, or chicken-like birds; and Anseriformes—ducks, geese, and swans). Three of the four non-primate taxa have good hybridization data, allowing us to compare our findings here to other lines of evidence. The results were largely consistent with what would be expected based on previous studies and current taxonomy, with one exception: humans are clearly distinct from all other taxa, including simians; the great apes more naturally fit in with the monkeys. These findings conflict with the popular-level evolutionary narrative that humans are closely related to the great apes. Instead, the results are in keeping with the biblical narrative that God created creatures according to their kinds, with humans being created separate from all other animals.

Introduction

A realistic understanding of biological relationships requires an accurate framework for interpreting data. While the evolutionary worldview assumes that

all life is related by universal common descent, the Bible makes it clear that plant and animal life were created “according to their kinds” (Genesis 1:11–12, 20–22, 24–25). Humans were created

separately from all other animals, and in the image of God, with unique traits appropriate to our role of ruling the earth (Genesis 1:26–28).

The field of baraminology, or the study of created kinds, involves identifying which groups of plants and animals known today are truly related, in that they belong to a single created kind, or *baramin*. There are many examples

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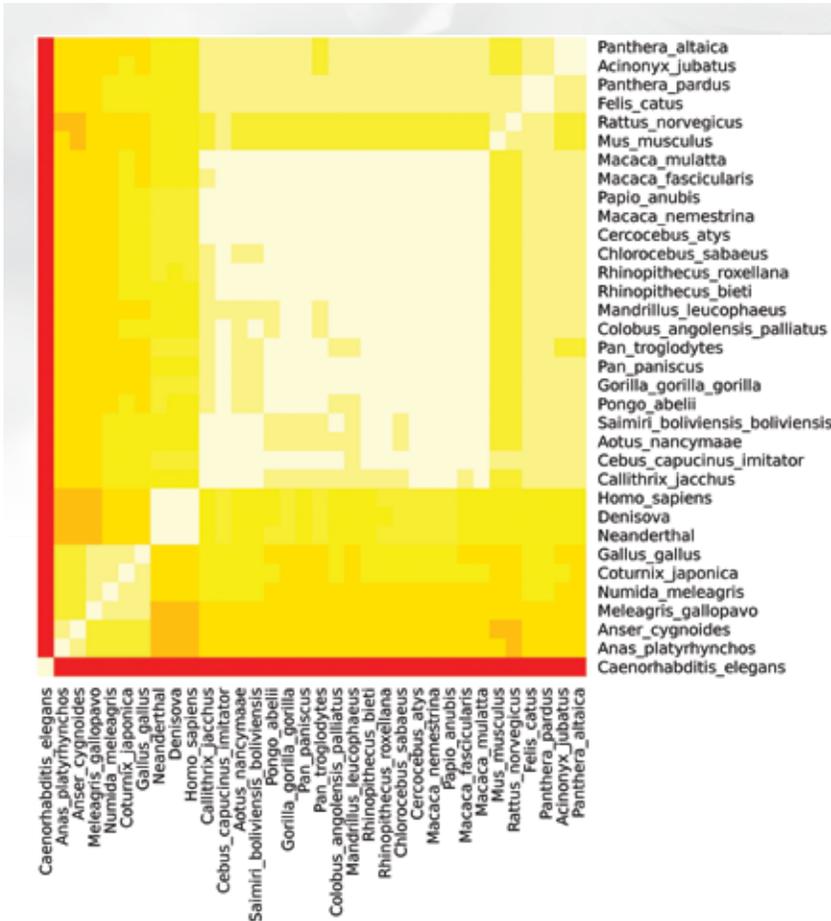


Figure 1 (left). A heat map visually representing the relative similarity (and dissimilarity) within clusters and between clusters. Lighter colors represent greater similarity; darker colors, and especially the red, indicate greater dissimilarity. Every species listed down on the right side is also listed across the bottom. The white “stair step” pattern from the lower left to the upper right of the figure is where each species is compared to itself.

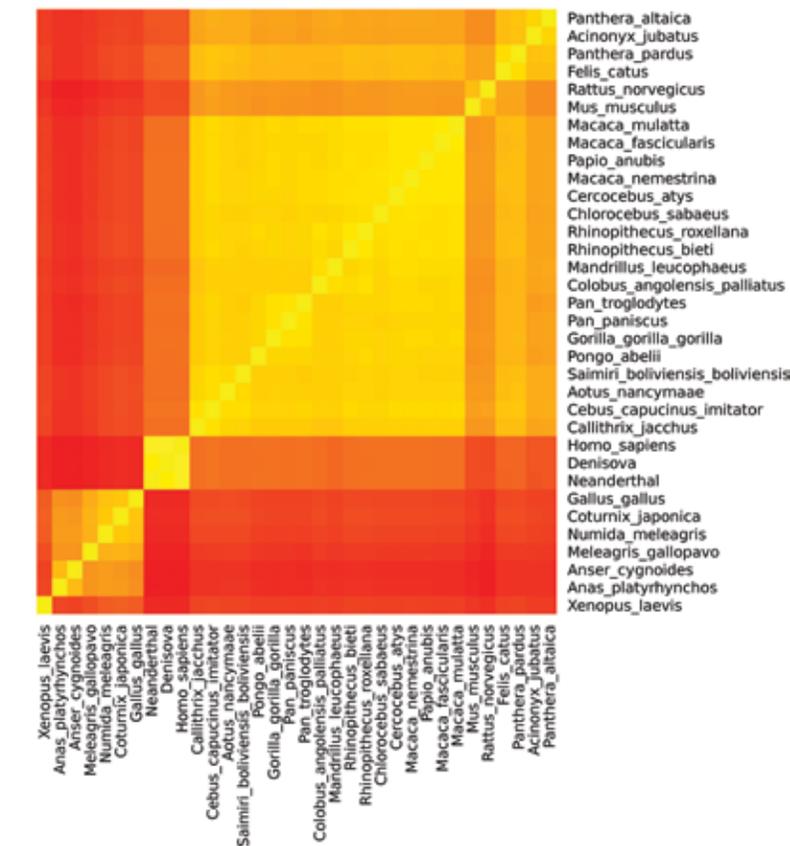


Figure 2 (below). This heat map uses a similar color scheme as Figure 1, but substitutes a vertebrate outgroup species (*Xenopus laevis*) for the invertebrate one (*Caenorhabditis elegans*) used in the previous heat map.

of animals from different species that can reproduce together to produce viable offspring. This hybridization is considered, by most creationists, a clear indication that these species are from the same baramin. The underlying rationale is that reproduction is an enormously complex process, requiring compatibility on multiple levels. This suggests that reproduction could not occur between two organisms unless they were specifically designed for this possibility, as would be the case if they were from the same baramin (Wood et al., 2003; Lightner et al., 2011).

It is important to recognize that the level of the baramin does not necessarily correspond to any particular taxonomic rank in our current classification system. This was pointed out over a century ago based on morphological data (Wasmann, 1910, pp. 291–292). It was repeated by Marsh (1964), who discussed hybridization data. So, depending on the group under consideration, the level of the kind could be at the order, the family,

the genus, or somewhere else. In Felidae (cats), hybridization data indicates the kind is at least at the family level; in Galiformes (chicken-like birds), it is at least at the order. When it comes to humans, which are currently placed in the same family as the great apes (Hominidae), the kind is not at the level of the family (Lightner, 2012, 2013).

At one time great apes were placed in the family Pongidae, separate from humans (Lightner, 2012). Anatomical differences that separate us from the great apes include a big toe that is not opposable, a unique position of the larynx and associated structures that allows for speech, skeletal differences associated with our upright posture, different organization of the brain that supports superior cognitive function, and hands designed for greater dexterity. Despite our profound anatomical and cognitive differences, evolutionary philosophy—that overemphasizes our genetic similarity (see Tomkins, 2018)—seems to be the motive for placing humans in the same family as the great apes.

Since (for a variety of reasons) hybridization data between different species of interest is not always available, other tools have been developed to aid in identifying baramins (Wood et al., 2003; Lightner et al., 2011). As part of the Creation Research Society (CRS) eKINDS (examination of kinds in natural diversification and speciation) project we have developed a comparative statistical tool. As explained by O’Micks (2017), this tool compares all catalogued expressed proteins for a species that belong to known orthology groups and clusters these species based on similarities. In this current study, we applied this technique to protein sequence data from humans, great apes, Old World and New World monkeys, and several other mammalian and avian taxa. Our results show clear clusters, consistent with creationist expectations. More profoundly, we show further evidence of discontinuity between humans

Table 1. A species list showing current classification of the species in the order they appear on the heat maps.

Species List	
(in the order they appear on the heat maps)	
Class Mammalia	
Order Carnivora; Family Felidae	
<i>Panthera altaica</i>	Siberian tiger
<i>Acinonyx jubatus</i>	cheetah
<i>Panthera pardus</i>	leopard
<i>Felis catus</i>	domestic cat
Order Rodentia; Family Muridae	
<i>Rattus norvegicus</i>	brown rat
<i>Mus musculus</i>	house mouse
Order Primates	
Family Cercopithecidae (Old World monkeys)	
<i>Macaca mulatta</i>	Rhesus macaque*
<i>Macaca fascicularis</i>	crab-eating macaque*
<i>Papio Anubis</i>	olive baboon*
<i>Macaca nemestrina</i>	Southern pig-tailed macaque*
<i>Cercocebus atys</i>	sooty mangabey*
<i>Chlorocebus sabaues</i>	green monkey
<i>Rhinopithecus roxellana</i>	golden snub-nosed monkey
<i>Rhinopithecus bieti</i>	black snub-nosed monkey
<i>Mandrillus leucophaeus</i>	drill*
<i>Colobus angolensis palliatus</i>	Peter’s Angolan colobus
Family Hominidae (Great apes)	
<i>Pan troglodytes</i>	common chimpanzee
<i>Pan paniscus</i>	bonobo
<i>Gorilla gorilla gorilla</i>	western lowland gorilla
<i>Pongo abelii</i>	Sumatran orangutan
Families Cebidae, Aotidae, and Callitrichidae (New World monkeys)	
<i>Saimiri boliviensis boliviensis</i>	Bolivian squirrel monkey
<i>Aotus nancymae</i>	Nancy Ma’s night monkey
<i>Cebus capucinus imitator</i>	white-headed capuchin
<i>Callithrix jacchus</i>	common marmoset
Family Hominidae (Humans)	
<i>Homo sapiens</i>	modern humans
Denisova	extinct human (people group)
Neanderthal	extinct human (people group)
Class Aves	
Order Galliformes; Families Phasianidae and Numididae	
<i>Gallus gallus</i>	red junglefowl/domestic chicken
<i>Coturnix japonica</i>	Japanese quail
<i>Numida meleagris</i>	helmeted guineafowl
<i>Meleagris gallopavo</i>	turkey
Order Anseriformes; Family Anatidae	
<i>Anser cygnoides</i>	swan goose
<i>Anas platyrhynchos</i>	mallard
Class Chromadorea (outgroup species, heat map 1, from Phylum Nematoda)	
Order Rhabditida; Family Rhabditidae	
<i>Caenorhabditis elegans</i>	
Class Amphibia (outgroup species, heat map 2, from Phylum Chordata)	
Order Anura; Family Pipidae	
<i>Xenopus laevis</i>	African clawed frog
* monkey species that are known to be related based on hybridization data	

and great apes, with the latter showing far more similarity to monkeys than to humans.

Materials and Methods

Only species with at least 20,000 cataloged proteins were used in this study, as previous experience shows that strong clusters may not be formed unless a complete representative proteome is used (discussed in Lightner and Anderson, 2018). We selected species from the following taxa: humans (3), simian primates (18), Felidae (4), Muridae (2), Galliformes (4), and Anseriformes (2), with *Caenorhabditis elegans* (1) as an outgroup species.

All RefSeq protein sequences for each of the 34 species were downloaded from NCBI (Table 1). Since the Neanderthal and Denisovan did not have a complete proteome, protein sequences were predicted using the gene prediction method Augustus (Stanke et al., 2006). The whole genome sequences for Neanderthal and Denisovan are available at <http://golgi.unmc.edu/HumanMotifomeData/> (Cserhati et al., 2018).

The proteome data for each species was analyzed with the statistical tool's default parameters (at the OrthoMCL website at <http://orthomcl.org/orthomcl/>) (Chen et al., 2006) to find orthologous groups. After the initial run, we substituted *Xenopus laevis* (a frog) for *Caenorhabditis elegans* (a worm) to compare the difference between using a more similar outgroup species. OrthoMCL results for *X. laevis* were calculated on the Galaxy server at <https://eupathdb.globusgenomics.org/>. The number of RefSeq proteins and the number of found orthologous groups can be found in Table I of the Appendix, and also on github at <https://github.com/csmaty/humanUniqueness>.

Statistical analysis was done using the k-means clustering algorithm as part of the gene-content method for determination of species clusters. This analysis

was performed for 5, 6, 7, and 8 clusters. Groupings and their associated p-values were obtained.

The gene-content method was used on the list of species and their orthologous gene groups to define species clusters (O'Micks, 2017). The heat map depicting the relationships between the 34 species (Figures 1 and 2) was produced by the R script, which implements the gene-content method. On the heat map, lighter colors represent species pairs with a highly similar gene content (JCV closer to 1), whereas darker colors represent species pairs with less similar gene content (JCV closer to 0). The cluster membership for each k-value is found in Table II of the Appendix. The number of species in each cluster, as well as the minimum, mean, maximum JCV value and p-value, are recorded in Table III of the Appendix. A matrix containing the JCV values for all species pairs can be seen in the Supplementary Data file (available at <https://github.com/csmaty/humanUniqueness>).

Results

The heat maps (Figures 1 and 2) provide a visual representation of the groups to which each species belongs based on orthologous protein comparisons. Every species listed along the right of the heat map is also listed along the bottom. This results in a diagonal of light-colored squares from the bottom left corner to the upper right, as each species compared to itself has 100% similarity (JCV = 1). Light areas (white or light yellow) correspond to high similarity; darker (redder) colors indicate less similarity. Note that the outgroup species, the nematode *Caenorhabditis elegans*, shows the greatest dissimilarity compared to all other species, except itself (Figure 1). It shows a red streak with all other species, indicating low common protein content. Figure 2 uses a different color palette than Figure 1 (making it somewhat darker), but with

a vertebrate outgroup species, *Xenopus laevis*, (African clawed frog).

Table 1 lists the species in this study in the order they appear in the heat maps (from top to bottom along the right side). Note that with the exception of humans, all species cluster where we would expect based on their current taxonomic classification. Identifying clusters can be somewhat subjective. For example, are all simians (apes and monkeys) one group, or are they three groups? Are all the birds one group, or are they two? Our analysis helps to address these questions, with resulting groupings and associated p-values listed in Table 2.

Discussion

The top right group depicted on the heat map is comprised of the four species of Felidae included in this study ($p = 1.52 \times 10^{-7}$). Visual inspection of the heat map almost hints that the group might be divided, but that would divide two species from the same genus, *Panthera*. Based on morphology and hybridization data, all members of the cat family are recognized as belonging to the same baramin (Lightner, 2012). It is only when the clusters are taken down to five ($k = 5$) that the cat spuriously clusters with the rat and mouse (Muridae), which are from a different order. While it is possible that the level of the kind could sometimes be above the order, it seems precluded here due to significant discontinuity between Carnivora and Rodentia (Lightner, 2012). The distinction between the felids and the murids is best seen on the heat map using a vertebrate outgroup species, *Xenopus laevis*, the African clawed frog (Figure 2).

The second cluster consists of the brown (or Norwegian) rat and the house mouse. Since this group consists of only two species, the t-test cannot be performed between the JCV values of these two species and all other species to calculate a p-value. There is no hybrid data connecting these two species,

Table 2. The clusters revealed statistically by specifying 5 (k= 5), 6 (k=6), 7 (k=7), and 8 (k=8) clusters, along with the associated p-values for each cluster.

k = 5		
Group	number of species	p-value
Felidae + Muridae	6	9.97×10^{-06}
OW + NW monkeys + apes	18	8.02×10^{-94}
humans	3	1.91×10^{-30}
Galliformes	4	4.86×10^{-09}
Anatidae	2	*
k = 6		
Group	number of species	p-value
Felidae	4	1.52×10^{-07}
Muridae	2	*
OW monkeys	10	9.56×10^{-46}
Great apes + NW monkeys	8	2.84×10^{-28}
humans	3	1.91×10^{-30}
Galliformes + Anatidae	6	9.25×10^{-14}
k = 7		
Group	number of species	p-value
Felidae	4	1.52×10^{-07}
Muridae	2	*
OW monkeys	10	9.56×10^{-46}
Great apes	4	2.45×10^{-15}
NW monkeys	4	1.61×10^{-16}
humans	3	1.91×10^{-30}
Galliformes + Anatidae	6	9.25×10^{-14}
k = 8		
Group	number of species	p-value
Felidae	4	1.52×10^{-07}
Muridae	2	*
OW monkeys	10	9.56×10^{-46}
Great apes	4	2.45×10^{-15}
NW monkeys	4	1.61×10^{-16}
humans	3	1.91×10^{-30}
Galliformes	4	4.86×10^{-09}
Anatidae	2	*

* When a group consists of 2 species, the t-test cannot be performed between the JCV values of the 2 species and all other species to calculate a p-value.

which are both from the largest rodent family, Muridae. Previous work suggests that they are likely related (Lightner, 2012), and the results here are consistent with that hypothesis. More species in this order should be evaluated when more complete protein sequence data becomes available.

The next group we come to are the simians (apes and monkeys). On the heat map, it looks like they could easily be a single cluster. When eight clusters are specified, the Old World (OW) monkeys, great apes, and New World (NW) monkeys are distinctly separated (see Table 2). Interestingly, when six clusters are specified, the great apes cluster with the New World monkeys with a lower p-value than when they are separate 2.84×10^{-28} vs. 2.45×10^{-15} . This is rather surprising, as great apes are supposed to be more closely related to Old World monkeys. When five clusters are specified, a highly significant cluster with all simians is formed ($p=8.02 \times 10^{-94}$). Division into the three groups identified statistically is somewhat discernable on the heat map shown in Figure 1 but less discernable in Figure 2.

In previous work the great apes and different families of New World monkeys were tentatively considered separate kinds (Lightner, 2012). However, the results of this study suggest the hypothesis that all simian primates, but not humans, may belong to a single baramin. In support of the latter, the average person is not likely to be able to readily distinguish between Old World and New World monkeys upon observing them in an exhibit in the zoo (unless they read the signage). Further, if one is not familiar with the separate status of great apes, most people would naturally tend to group them in with monkeys (tailless monkeys). Thus, there is a strong cognitum, or natural grouping, based on human cognitive senses, for simians, which explains why the word "simian" exists. If it is, in fact, the case that they are related, the differences between Old

World and New World monkeys would be from an early split in the lineage after the ancestral simian pair disembarked from the ark.

Certainly, there are other taxa where the apparent level of the baramin is well above the family level based on hybridization data (e.g., Galliformes and Passeriformes; Lightner, 2013). However, for several reasons, caution should be exercised before concluding all simians are related. First, statistically the three simian groups were separate when a larger number of clusters were specified. They fell into a single cluster only when $k = 5$, which also spuriously grouped the felids (cats) with the murids (the rats and mice). This spurious grouping could result of the small sample sizes for some of these animals. Further, hybrid data in simians only unites one subfamily of the two comprising Cercopithecidae, or Old World monkeys. Thus, it might be informative to look at the traits taxonomists use to distinguish these three groups of simians.

Old World monkeys display considerable diversity in facial features, coloration (especially in males), and in the habitats where they live, yet they retain the ability to hybridize across several of the genera. Thus, their inclusion in the same cluster is expected based on hybridization data (Lightner, 2012). However, the differences within this family are considered superficial by taxonomists. According to Fleagle (1999), Old World monkeys are remarkably uniform, due partly to a recent adaptive radiation. This is why they are placed in a single family, while New World monkeys comprise several.

New World monkeys, or platyrrhines, dwell in Central and South America. They can be distinguished by their broad, flat nose, as compared to Old World monkeys, which have narrow nostrils. Furthermore, New World Monkeys usually have three premolars as opposed to two in Old World monkeys. They lack hypoconulids on their first two lower

molars. In the skull, their tympanic ring is fused to the side of the auditory bulla and does not extend laterally like a bony tube as in Old World monkeys. In New World monkeys the zygomatic bone is connected to the parietal bone, whereas in Old World monkeys, the frontal and sphenoid bones are connected with each other (Fleagle, 1999, pp. 136–137, 185).

Great apes are characterized by relatively broad palates and nasal regions, large brains, a reduced lumbar region, an extended sacral region, and the absence of a tail. Furthermore, they have a relatively broad thorax, with a dorsally positioned scapula, and relatively long upper limbs (Fleagle, 1999, p. 235).

Creationists still debate if the differences between these three simian groups are created differences, or if they developed because God designed these creatures to be able to undergo such changes as they reproduced and filled the earth. If simians indeed comprise three baramins, there is a tremendous amount of designed similarity in the proteins they express.

The humans included in the next cluster ($p = 1.91 \times 10^{-30}$) are remarkably similar in expressed proteins among themselves and strikingly different from all other animals, including the simian primates included in this study. This supports the humanity of Neanderthals and Denisovans, as much as it contradicts evolutionary narratives about common descent between humans and apes. In conjunction with other lines of evidence of human morphological, cognitive, and genetic (including non-protein coding regions) distinctiveness, it clearly demonstrates that the evolutionary ideas on the origin of man have no plausible scientific foundation (Tomkins, 2013, 2014, 2016, 2018).

The last cluster(s) is (are) comprised of the birds included in this study. When 5 or 8 clusters were designated, the Galliform (chicken-like) birds ($p = 4.86 \times 10^{-09}$) were in a separate cluster from the duck and goose (Anseriformes). Again,

regarding the latter, when only two species are in a single cluster, no p-value can be assigned because t-test cannot be run. Interestingly, when 6 or 7 clusters were designated, all birds fell in a single cluster ($p = 9.25 \times 10^{-14}$).

Based on morphological and hybridization data, the order Galliformes is considered a baramin (Lightner, 2013). There are hybrids connecting ducks, geese, and swans with each other, but no hybrids that bridge the gap to the galliform (chicken-like) birds. The division between these two orders (Galliformes and Anseriformes) has been relatively noncontroversial, suggesting they are separate kinds. Thus, it is more consistent with current creationist expectations that these two groups comprise two baramins. Nevertheless, more detailed creationist work is needed to come to a stronger conclusion.

Based on these observations, we can suggest the following regarding the gene-content methodology: First, it is desirable to select taxa for study where at least three species would be expected to land in any given cluster. This way there is enough data for the t-test to be performed. It may also help decrease spurious clustering, such as was seen in this study with the felids and murids. While strong clusters should, in theory, be at the level of the baramin, at times there seems to be some semblance of clusters above or below that. So, caution and multiple lines of evidence should always be used when interpreting the results of this or any other statistical baraminology technique. Further, we know from previous unpublished results in insects (mentioned in Lightner and Anderson, 2018) that only taxa with nearly complete, high-quality representative proteomes that yield $\gg 6000$ orthologues should be used, or they often will not cluster well.

While the gene-content method seems to hold promise as a tool to help identify baramins, one of the biggest current challenges is finding taxa with

complete, high-quality proteome data for numerous species. In this study, simians were well represented, but the felids, murids, and birds were less so. With the accumulation of more species' protein data, this challenge should lessen over time.

Conclusion

The results of this study yield another striking confirmation of the biblical narrative. First, animals cluster together in groups consistent with the biblical history that they were created according to their kinds. Even more profoundly, humans are clearly distinct from all other animals, including apes. The great apes land in the middle of a simian cluster, between the Old World and New World monkeys. As expected from previous creationist works, the cats form a distinct group, as do the rodents included in this study. It is not quite as clear if the chicken-like birds are distinct from ducks and geese as generally believed by creationists, but further analyses when more proteomes become available should clarify that point.

The gene-content statistical baraminology method appears to be a valuable tool for creationists when complete proteome data is available for a taxon of interest. As we continue to use it, we should continue to learn helpful strategies to use it more effectively. We currently recognize the need for good quality proteomes (> 20,000 proteins) and at least three species for any group likely to form a cluster. Further, some caution is necessary when interpreting

the results because weaker clusters are often detected above or below more obvious ones. For this reason, other lines of evidence should always be considered as conclusions are drawn.

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Appendix: Supplementary Data

Table I. Species included in this study.

Species	Refseq proteins	Orthologues
<i>Acinonyx jubatus</i>	27284	13973
<i>Anas platyrhynchos</i>	30500	11127
<i>Anser cygnoides</i>	31811	11244
<i>Aotus nancymae</i>	47568	14622
<i>Caenorhabditis elegans</i>	38541	13059
<i>Callithrix jacchus</i>	45275	14620
<i>Cebus capucinus imitator</i>	53173	14801
<i>Cercocebus atys</i>	65950	14953
<i>Chlorocebus sabaeus</i>	61809	14953
<i>Colobus angolensis palliatus</i>	38654	14660
<i>Coturnix japonica</i>	39111	12027
<i>Denisova</i>	32733	13306
<i>Felis catus</i>	54767	29796
<i>Gallus gallus</i>	46485	12248
<i>Gorilla gorilla gorilla</i>	46456	14987
<i>Homo sapiens</i>	44006	13404
<i>Macaca fascicularis</i>	63105	14890
<i>Macaca mulatta</i>	55775	15010
<i>Macaca nemestrina</i>	66586	14958
<i>Mandrillus leucophaeus</i>	38430	14779
<i>Meleagris gallopavo</i>	33325	11942
<i>Mus musculus</i>	78425	15436
<i>Neanderthal</i>	33049	13363
<i>Numida meleagris</i>	43240	11997
<i>Pan paniscus</i>	50092	14990
<i>Pan troglodytes</i>	91838	14014
<i>Panthera altaica</i>	29462	14898
<i>Panthera pardus</i>	57954	15204
<i>Papio anubis</i>	66688	14973
<i>Pongo abelii</i>	49906	14951
<i>Rattus norvegicus</i>	72948	30302
<i>Rhinopithecus bieti</i>	49617	14826
<i>Rhinopithecus roxellana</i>	37319	14834
<i>Saimiri boliviensis boliviensis</i>	36216	14528
<i>Xenopus laevis</i>	42878	32497

Table II. Clusters identified in this study.

Species	Taxon	k=5	k=6	k=7	k=8
Anas_platyrhynchos	Anseriformes	3	5	7	1
Anser_cygnoides	Anseriformes	3	5	7	1
Gorilla_gorilla_gorilla	Hominidae	4	4	2	2
Pan_paniscus	Hominidae	4	4	2	2
Pan_troglodytes	Hominidae	4	4	2	2
Pongo_abelii	Hominidae	4	4	2	2
Aotus_nancymae	NW monkey	4	4	6	3
Callithrix_jacchus	NW monkey	4	4	6	3
Cebus_capucinus_imitator	NW monkey	4	4	6	3
Saimiri_boliviensis_boliviensis	NW monkey	4	4	6	3
Mus_musculus	Muridae	2	3	3	4
Rattus_norvegicus	Muridae	2	3	3	4
Denisova	Human	5	1	1	5
Homo_sapiens	Human	5	1	1	5
Neanderthal	Human	5	1	1	5
Acinonyx_jubatus	Felidae	2	6	5	6
Felis_catus	Felidae	2	6	5	6
Panthera_altaica	Felidae	2	6	5	6
Panthera_pardus	Felidae	2	6	5	6
Cercocebus_atys	OW Monkey	4	2	4	7
Chlorocebus_sabaeus	OW Monkey	4	2	4	7
Colobus_angolensis_palliatus	OW Monkey	4	2	4	7
Macaca_fascicularis	OW monkey	4	2	4	7
Macaca_mulatta	OW monkey	4	2	4	7
Macaca_nemestrina	OW monkey	4	2	4	7
Mandrillus_leucophaeus	OW Monkey	4	2	4	7
Papio_anubis	OW Monkey	4	2	4	7
Rhinopithecus_bieti	OW Monkey	4	2	4	7
Rhinopithecus_roxellana	OW Monkey	4	2	4	7
Coturnix_japonica	Galliformes	1	5	7	8
Gallus_gallus	Galliformes	1	5	7	8
Meleagris_gallopavo	Galliformes	1	5	7	8
Numida_meleagris	Galliformes	1	5	7	8

Table III. Statistics

k=5							
baramin	species	mean	stdev	min	max	p-value	group name
1	4	0.903	0.016	0.883	0.922	4.86E-09	Galliformes
2	6	0.887	0.037	0.84	0.951	9.97E-06	Muridae and Felidae
4	18	0.942	0.01	0.92	0.969	8.02E-94	great apes, OW and NW monkeys
5	3	0.979	0.005	0.974	0.984	1.91E-30	human
k=6							
baramin	species	mean	stdev	min	max	p-value	group name
1	3	0.979	0.005	0.974	0.984	1.91E-30	human
2	10	0.953	0.008	0.938	0.969	9.56E-46	OW monkey
4	8	0.938	0.01	0.924	0.96	2.84E-28	great apes and NW monkey
5	6	0.876	0.028	0.841	0.922	9.25E-14	Anseriformes and Galliformes
6	4	0.923	0.018	0.909	0.951	1.52E-07	Felidae
k=7							
baramin	species	mean	stdev	min	max	p-value	group name
1	3	0.979	0.005	0.974	0.984	1.91E-30	human
2	4	0.948	0.009	0.94	0.96	2.45E-15	great apes
4	10	0.953	0.008	0.938	0.969	9.56E-46	OW monkey
5	4	0.923	0.018	0.909	0.951	1.52E-07	Felidae
6	4	0.947	0.007	0.938	0.955	1.61E-16	NW monkey
7	6	0.876	0.028	0.841	0.922	9.25E-14	Anseriformes and Galliformes
k=8							
baramin	species	mean	stdev	min	max	p-value	group name
2	4	0.948	0.009	0.94	0.96	2.45E-15	Great apes
3	4	0.947	0.007	0.938	0.955	1.61E-16	NW monkey
5	3	0.979	0.005	0.974	0.984	1.91E-30	human
6	4	0.923	0.018	0.909	0.951	1.52E-07	Felidae
7	10	0.953	0.008	0.938	0.969	9.56E-46	OW monkey
8	4	0.903	0.016	0.883	0.922	4.86E-09	Galliformes