SI Text

1. Analysis Parameters for 1.4 Mb data set including all taxa.

Maximum Likelihood Settings and Results in PAUP* Analysis:

Heuristic search settings:
Optimality criterion = likelihood
Likelihood settings:
User-specified substitution rate matrix =

-	1.578600	4.270300	1.035200
1.578600	-	1.335800	7.055100
4.270300	1.335800	-	1.000000
1.035200	7.055100	1.000000	-

Assumed nucleotide frequencies (set by user):
A=0.27630 C=0.24200 G=0.25440 T=0.22730
Among-site rate variation:
Assumed proportion of invariable sites = 0.3082
Distribution of rates at variable sites = gamma (discrete approximation)
Shape parameter (alpha) = 0.6954
Number of rate categories = 4
Representation of average rate for each category = mean
These settings correspond to the GTR+G+I model
Number of distinct data patterns under this model = 129151
Molecular clock not enforced
Starting branch lengths obtained using Rogers-Swofford approximation method
Trees with approximate likelihoods 5% or further from the target score are rejected without additional iteration
Branch-length optimization = one-dimensional Newton-Raphson with pass limit=20, delta=1e-06
-ln L (unconstrained) = unavailable due to missing-data and/or ambiguities
Starting tree(s) obtained via stepwise addition
Addition sequence: random
Number of replicates = 10
Starting seed = 107388993
Number of trees held at each step during stepwise addition = 1
Branch-swapping algorithm: tree-bisection-reconnection (TBR)
Steepest descent option not in effect
Initial 'MaxTrees' setting = 100 (will be auto-increased by 100)
Branches collapsed (creating polytomies) if branch length is less than or equal to 1e-08
'MulTrees' option in effect

```
  Topological constraints not enforced
  Trees are unrooted

Heuristic search completed
   Total number of rearrangements tried = 864
   Score of best tree(s) found = 7238023.8075
   Number of trees retained = 1
   Time used = 17:27:16 (CPU time = 17:22:22.5)
]
        Translate
                1 human,
                2 chimp,
                3 macac,
                4 mouse,
                5 rat,
                6 rabbi,
                7 dog,
                8 cow,
                9 armad,
                10 eleph,
                11 tenre,
                12 chick,
                13 oposs,
                14 xenop
                ;
tree PAUP_1 = [&U]
(((((((1:0.003866,2:0.005885):0.008017,3:0.019001):0.026805,((4:0.024971,5:0.027735):0.064416,6:
0.070669):0.007313):0.004378,(7:0.039901,8:0.053906):0.008360):0.006063,(9:0.069935,(10:0.05348
0,11:0.082869):0.012225):0.004323):0.060321,13:0.113324):0.065272,12:0.138760):0.315434,14:0);
End;
```

Maximum Likelihood Settings and Results using PhyML:

```
Sequence file : mam
. Data set : #1
. Random init tree : #6
. Tree search : SPRs. Initial tree : random tree
. Model of nucleotides substitution : GTR
. Number of taxa : 14
. Log-likelihood : -7240210.13026
. Discrete gamma model : Yes
  - Number of categories : 4
  - Gamma shape parameter : 0.509
. Proportion of invariant : 0.238
. Nucleotides frequencies :
  - f(A)= 0.27787
```

- f(C)= 0.23831
- f(G)= 0.25616
- f(T)= 0.22766

. GTR relative rate parameters :

A <-> C 1.59449
A <-> G 4.25481
A <-> T 1.03899
C <-> G 1.35391
C <-> T 7.12648
G <-> T 1.0 (fixed)

. Instantaneous rate matrix :

[A---------C---------G---------T------]			
-0.85171	0.18965	0.54400	0.11806
0.22114	-1.20401	0.17310	0.80976
0.59011	0.16104	-0.86477	0.11363
0.14410	0.84765	0.12786	-1.11960

eg., the instantaneous rate of change from 'C' to 'A' is 0.27787 x 1.59449 = 0.22114

```
Best tree:
(chick:0.137602,xenop:0.312338,(oposs:0.112620,((armad:0.069778,(elep
h:0.053398,tenre:0.082550)0.000000:0.012258)1.000000:0.004339,((dog:0
.039896,cow:0.053829)0.022000:0.008402,((macac:0.019032,(human:0.0038
80,chimp:0.005904)1.000000:0.008052)1.000000:0.026849,(rabbi:0.070415
,(mouse:0.025000,rat:0.027752)1.000000:0.064160)0.000000:0.007399)1.0
00000:0.004417)0.850000:0.006130)0.000000:0.060095)0.997000:0.064592)
;
```

Maximum Parsimony Settings and Results using PAUP*:

Character-exclusion status changed:
  481275 characters excluded
  Total number of characters now excluded = 481275
  Number of included characters = 962550

Heuristic search settings:
  Optimality criterion = parsimony
    Character-status summary:
      481275 characters are excluded
      Of the remaining 962550 included characters:

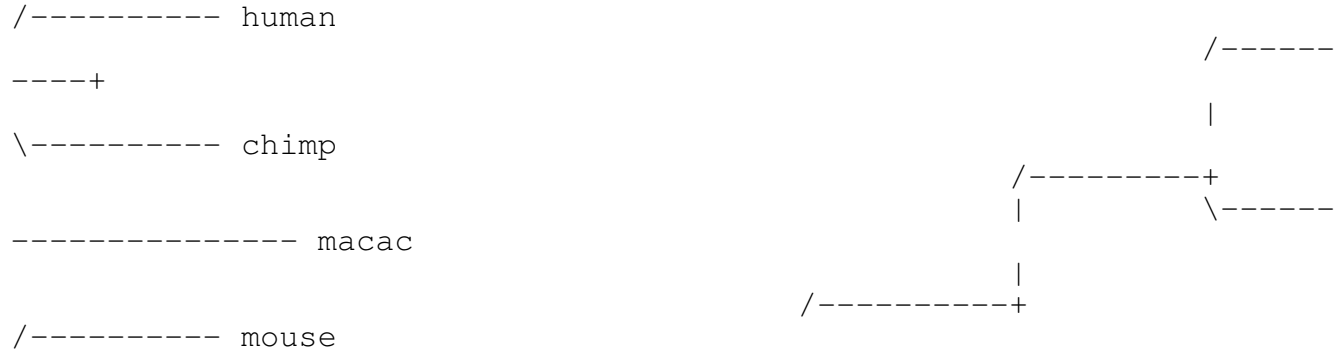
All characters are of type 'unord'
All characters have equal weight
779508 characters are constant
118838 variable characters are parsimony-uninformative
Number of (included) parsimony-informative characters = 64204
Gaps are treated as "missing"
Multistate taxa interpreted as uncertainty
Starting tree(s) obtained via stepwise addition
Addition sequence: random
Number of replicates = 100
Starting seed = 187994677
Number of trees held at each step during stepwise addition = 1
Branch-swapping algorithm: tree-bisection-reconnection (TBR)
Steepest descent option not in effect
Initial 'MaxTrees' setting = 100
Branches collapsed (creating polytomies) if maximum branch length is zero
'MulTrees' option in effect
Topological constraints not enforced
Trees are unrooted

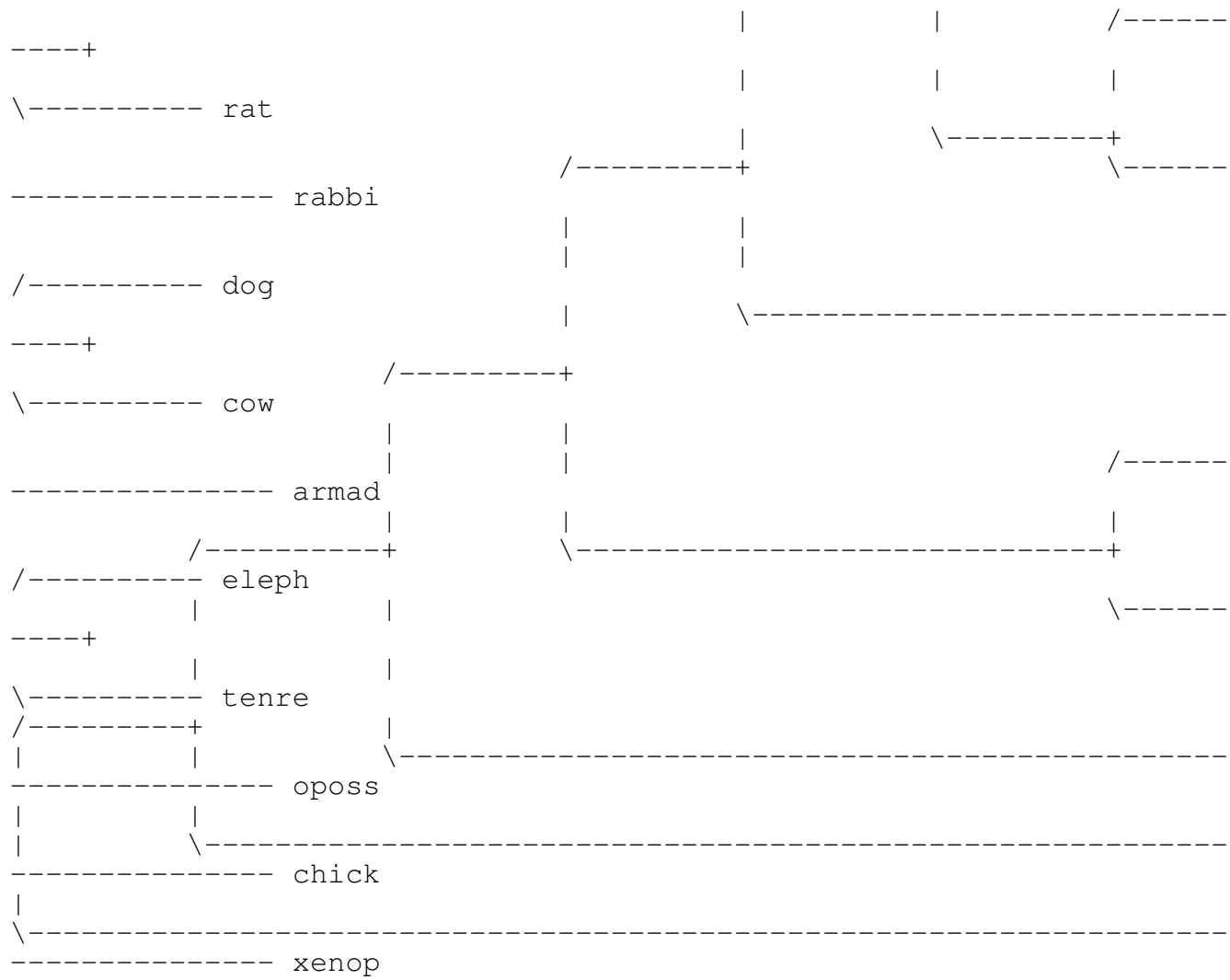
Heuristic search completed
Total number of rearrangements tried = 76731
Score of best tree(s) found = 267158
Number of trees retained = 1
Time used = 52.50 sec

Tree-island profile:

Island	Size	First tree	Last tree	Score	First replicate	Times hit
1	1	1	1	267158	1	100

Tree number 1 (rooted using user-specified outgroup)



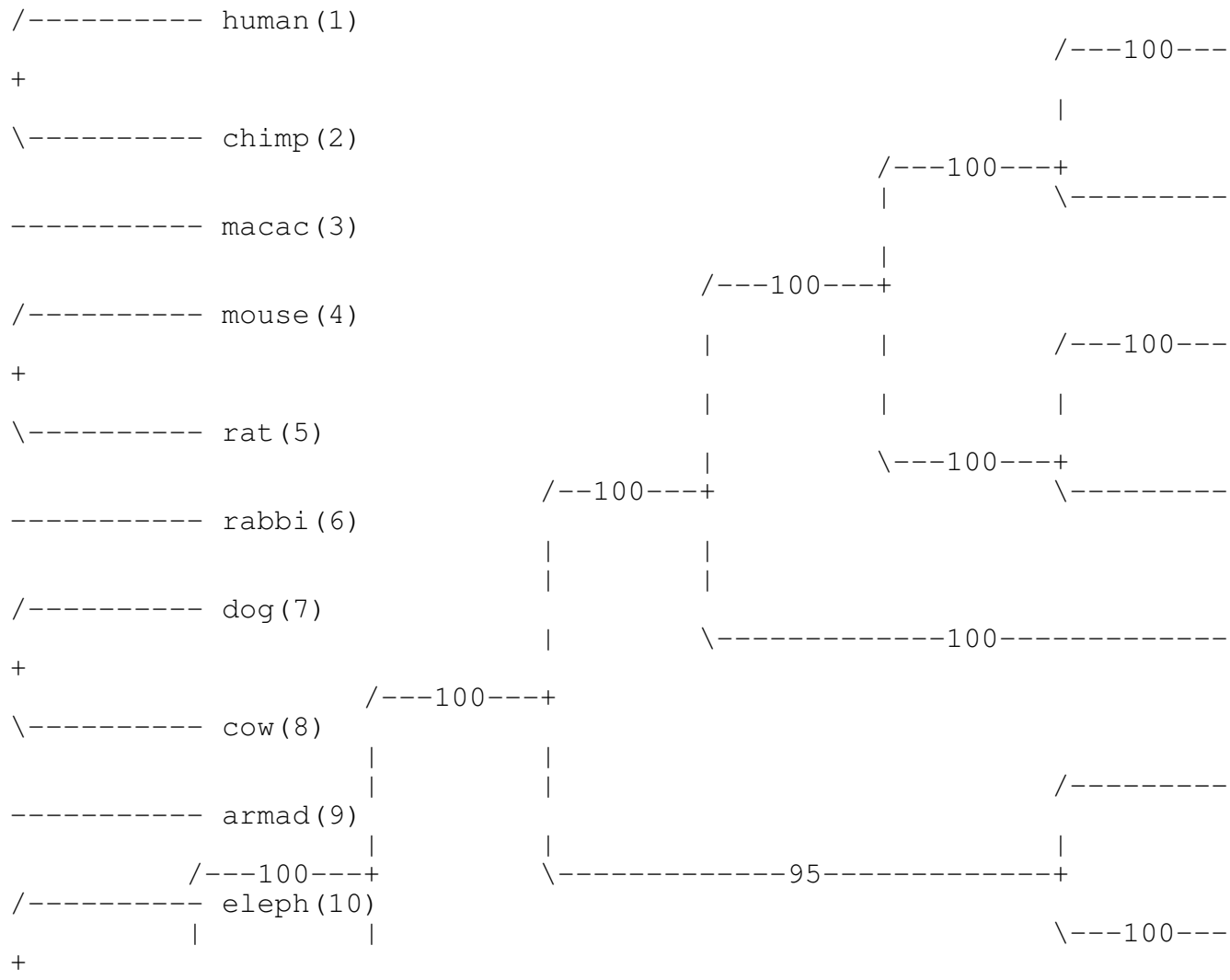


Bootstrap method with heuristic search:
  Number of bootstrap replicates = 1000
  Starting seed = 819785654
  Optimality criterion = parsimony
    Character-status summary:
      481275 characters are excluded
      Of the remaining 962550 included characters:
        All characters are of type 'unord'
        All characters have equal weight
        779508 characters are constant
        118838 variable characters are parsimony-uninformative
        Number of (included) parsimony-informative characters = 64204
    Gaps are treated as "missing"
    Multistate taxa interpreted as uncertainty
  Starting tree(s) obtained via stepwise addition
  Addition sequence: random

Number of replicates = 10
Starting seed = 927659101
Number of trees held at each step during stepwise addition = 1
Branch-swapping algorithm: tree-bisection-reconnection (TBR)
Steepest descent option not in effect
Initial 'MaxTrees' setting = 100
Branches collapsed (creating polytomies) if maximum branch length is zero
'MulTrees' option in effect
Topological constraints not enforced
Trees are unrooted

1000 bootstrap replicates completed
Time used = 02:36:34.5

Bootstrap 50% majority-rule consensus tree



```
          |         |
\---------- tenre(11)
/---------+         |
|         |         \-----------------------------------------------
---------- oposs(13)
|         |
|         \-------------------------------------------------------------
---------- chick(12)
|
\-------------------------------------------------------------------------
---------- xenop(14)

Bipartitions found in one or more trees and frequency of occurrence
(bootstrap support
values):

         1   1
12345678901234      Freq      %
-----------------------------
..........*.*      1000 100.0%
..........***      1000 100.0%
.........**...      1000 100.0%
...**.........      1000 100.0%
........******      1000 100.0%
......**......      1000 100.0%
......********      1000 100.0%
...***........      1000 100.0%
...**********      1000 100.0%
..**********       1000 100.0%
........***...       953  95.3%
```

Bayesian Analysis Settings

Parameters were set according to the MrBayes manual. We used the following command block to direct the MrBayes analysis:

begin mrbayes;

set autoclose=yes nowarn=yes;

lset nst=6 rates=invgamma; prset revmatpr=dirichlet (1,1,1,1,1,1)

statefreqpr=dirichlet(1,1,1,1) shapepr=uniform(0.1,50)

pinvarpr=uniform(0,1);

mcmc ngen=1000000 samplefreq=1000 nchains=4 savebrlens=yes file=mammals.nxs;

end;

2. Additional Analyses

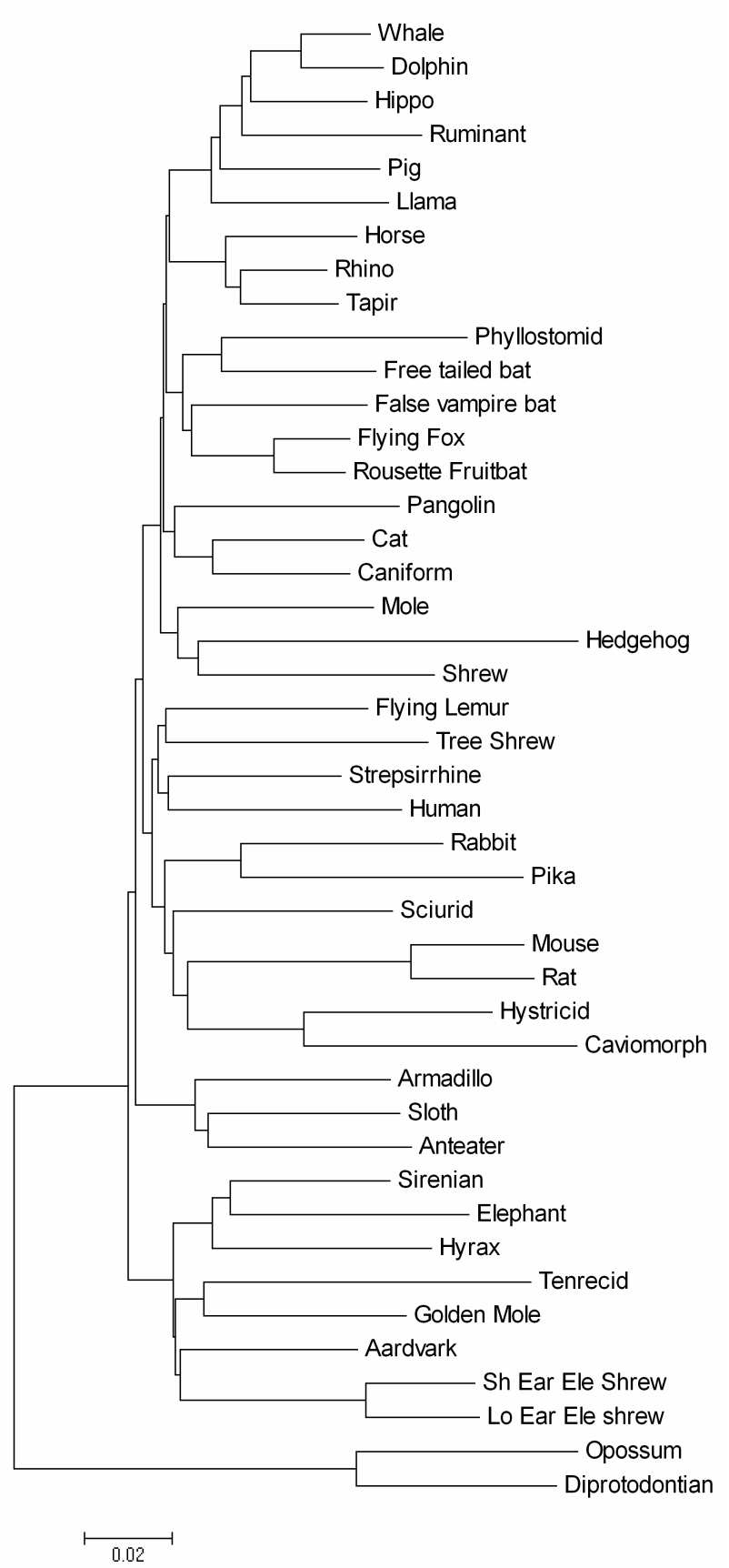

Whale
Dolphin
Hippo
Ruminant
Pig
Llama
Horse
Rhino
Tapir
Phyllostomid
Free tailed bat
False vampire bat
Flying Fox
Rousette Fruitbat
Pangolin
Cat
Caniform
Mole
Hedgehog
Shrew
Flying Lemur
Tree Shrew
Strepsirrhine
Human
Rabbit
Pika
Sciurid
Mouse
Rat
Hystricid
Caviomorph
Armadillo
Sloth
Anteater
Sirenian
Elephant
Hyrax
Tenrecid
Golden Mole
Aardvark
Sh Ear Ele Shrew
Lo Ear Ele shrew
Opossum
Diprotodontian
0.02

Figure S1. Evolutionary relationships of 44 taxa using the Murphy et al. dataset [1].

The evolutionary history was inferred using the Neighbor-Joining method [2]. The optimal tree with the sum of branch length = 2.22771052 is shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [3] and are in the units of the number of base substitutions per site. Codon positions included were 1st+2nd+3rd. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 3180 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 [4].

1. Murphy WJ, Eizirik E, O'Brien SJ, Madsen O, Scally M, Douady CJ, Teeling E, Ryder OA, Stanhope MJ, de Jong WW, Springer MS (2001) Resolution of the early placental mammal radiation using Bayesian phylogenetics. Science 294:2348-2351.

2. Saitou N & Nei M (1987) The neighbor-joining method: A new method for reconstructing phylogenetic trees. Molecular Biology and Evolution 4:406-425.

3. Tamura, K., Nei, M. & Kumar S. (2004) Prospects for inferring very large phylogenies by using the neighbor-joining method. PNAS 101:11030-11035.

4. Tamura K, Dudley J, Nei M & Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Molecular Biology and Evolution 10.1093/molbev/msm092.

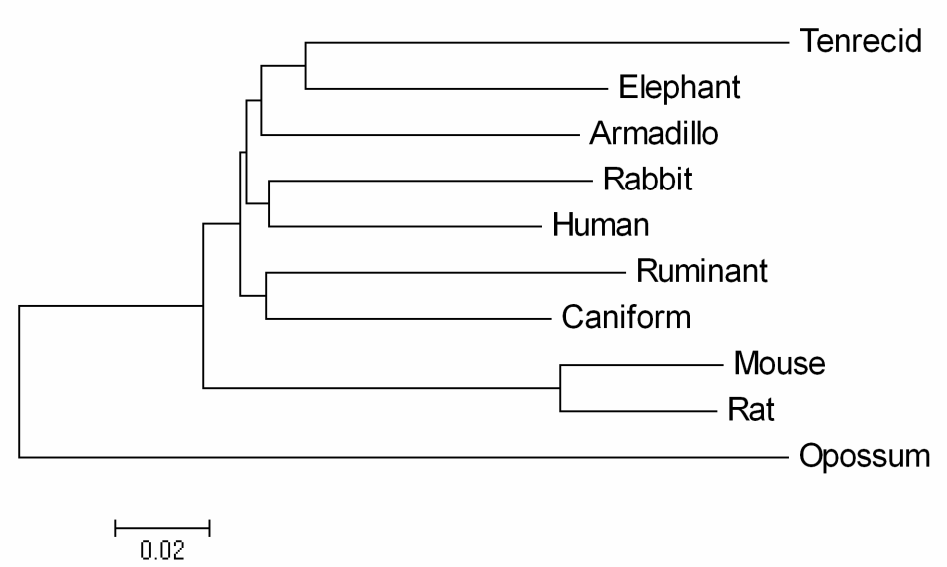


Figure S2. Evolutionary relationships of the 10 taxa from the Murphy et al [1] dataset that are also represented in this study.

The evolutionary history was inferred using the Neighbor-Joining method [2]. The optimal tree with the sum of branch length = 0.87295519 is shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [3] and are in the units of the number of base substitutions per site. Codon positions included were 1st+2nd+3rd. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 10190 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 [4].

1. Murphy WJ, Eizirik E, O'Brien SJ, Madsen O, Scally M, Douady CJ, Teeling E, Ryder OA, Stanhope MJ, de Jong WW, Springer MS (2001) Resolution of the early placental mammal radiation using Bayesian phylogenetics. Science 294:2348-2351.

2. Saitou N & Nei M (1987) The neighbor-joining method: A new method for reconstructing phylogenetic trees. Molecular Biology and Evolution 4:406-425.

3. Tamura, K., Nei, M. & Kumar S. (2004) Prospects for inferring very large phylogenies by using the neighbor-joining method. PNAS 101:11030-11035.

4. Tamura K, Dudley J, Nei M & Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Molecular Biology and Evolution 10.1093/molbev/msm092.

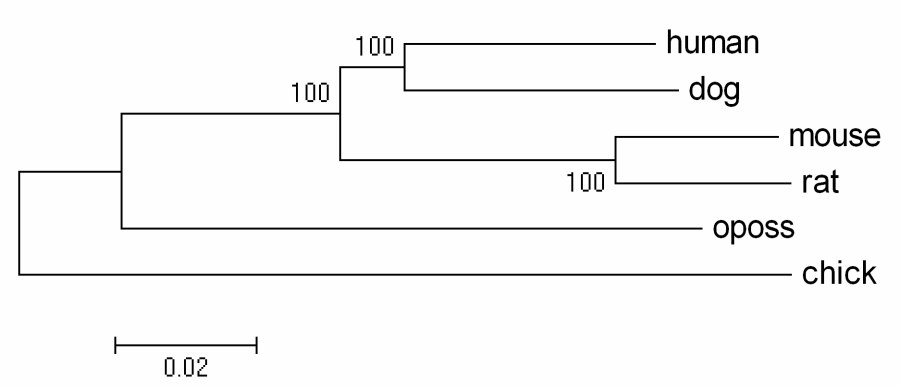


Figure S3. Evolutionary relationships of the 6 taxa from the current study's dataset that overlap with those of Huttley et al [1], inferred using the Neighbor-Joining method [2].

The optimal tree with the sum of branch length = 0.40734661 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [4] and are in the units of the number of base substitutions per site. Codon positions included were 1st+2nd+3rd. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 1340243 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 [5].

1. Huttley GA, Wakefield MJ, Easteal S. (2007) Rates of Genome Evolution and Branching Order from Whole Genome Analysis. Molecular Biology and Evolution. May 9; [Epub ahead of print].

2. Saitou N & Nei M (1987) The neighbor-joining method: A new method for reconstructing phylogenetic trees. Molecular Biology and Evolution 4:406-425.

3. Felsenstein J (1985) Confidence limits on phylogenies: An approach using the bootstrap. Evolution 39:783-791.

4. Tamura, K., Nei, M. & Kumar S. (2004) Prospects for inferring very large phylogenies by using the neighbor-joining method. PNAS 101:11030-11035.

5. Tamura K, Dudley J, Nei M & Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Molecular Biology and Evolution 10.1093/molbev/msm092.

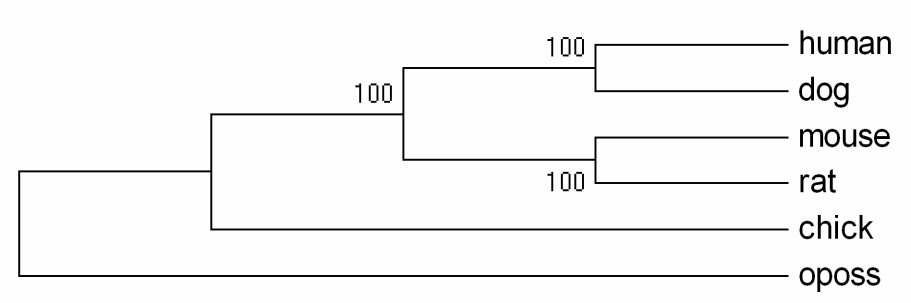


Figure S4. Evolutionary relationships of the 6 taxa from the current study's dataset that overlap with those of Huttley et al [1], inferred using the Maximum Parsimony method [2].

The most parsimonious tree with length = 104247 is shown. The consistency index is (0.751765), the retention index is (0.691242), and the composite index is 0.626678 (0.519652) for all sites and parsimony-informative sites (in parentheses). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. The MP tree was obtained using the Close-Neighbor-Interchange algorithm [4, pg. 128] with search level 3 [3, 4] in which the initial trees were obtained with the random addition of sequences (10 replicates). The codon positions included were 1st+2nd. All positions containing gaps and missing data were eliminated from the dataset (Complete Deletion option). There were a total of 893526 positions in the final dataset, out of which 26717 were parsimony informative. Phylogenetic analyses were conducted in MEGA4 [5].

1. Huttley GA, Wakefield MJ, Easteal S. (2007) Rates of Genome Evolution and Branching Order from Whole Genome Analysis. Molecular Biology and Evolution. May 9; [Epub ahead of print].

2. Eck RV & Dayhoff MO (1966) Atlas of Protein Sequence and Structure. National Biomedical Research Foundation, Silver Springs, Maryland.

3. Felsenstein J (1985) Confidence limits on phylogenies: An approach using the bootstrap. Evolution 39:783-791.

4. Nei M & Kumar S (2000) Molecular Evolution and Phylogenetics. Oxford University Press, New York.

5. Tamura K, Dudley J, Nei M & Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Molecular Biology and Evolution 10.1093/molbev/msm092.

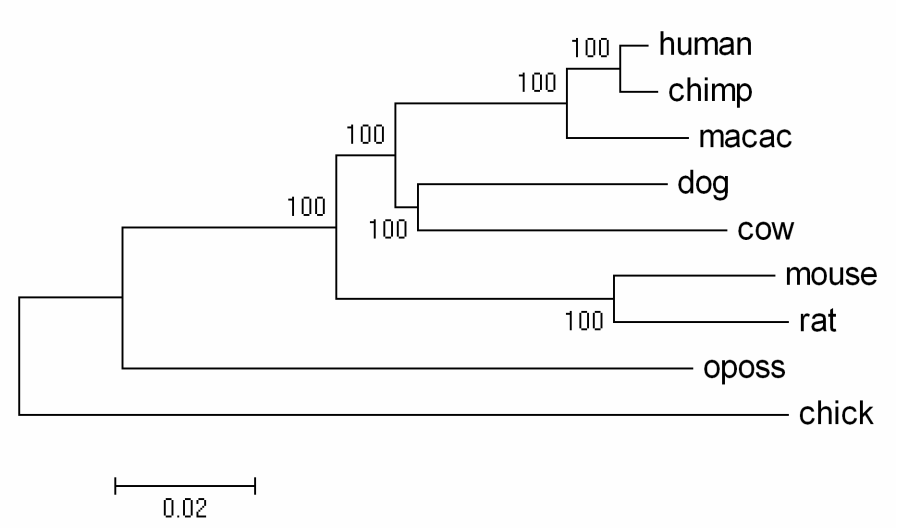


Figure S5. Evolutionary history of the 9 taxa from the current study's dataset that overlap with those of Canarrozzi et al [1], inferred using the Neighbor-Joining method [2].

The optimal tree with the sum of branch length = 0.47458168 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [4] and are in the units of the number of base substitutions per site. Codon positions included were 1st+2nd+3rd. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 1309972 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 [5].

1. Cannarozzi G, Schneider A, Gonnet G (2007) A phylogenomic study of human, dog, and mouse. PLoS Computational Biology. 2007 Jan 5;3(1):e2.

2. Saitou N & Nei M (1987) The neighbor-joining method: A new method for reconstructing phylogenetic trees. Molecular Biology and Evolution 4:406-425.

3. Felsenstein J (1985) Confidence limits on phylogenies: An approach using the bootstrap. Evolution 39:783-791.

4. Tamura, K., Nei, M. & Kumar S. (2004) Prospects for inferring very large phylogenies by using the neighbor-joining method. PNAS 101:11030-11035.

5. Tamura K, Dudley J, Nei M & Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Molecular Biology and Evolution 10.1093/molbev/msm092.

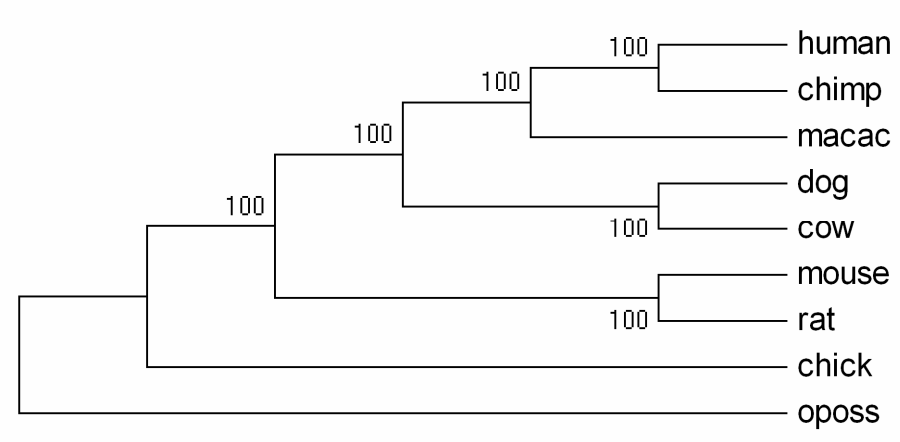


Figure S6. Evolutionary relationships of the 9 taxa from the current study's dataset that overlap with those of Canarrozzi et al [1], inferred using the Maximum Parsimony method [2].

The most parsimonious tree with length = 123325 is shown. The consistency index is (0.706188), the retention index is (0.684586), and the composite index is 0.596452 (0.483447) for all sites and parsimony-informative sites (in parentheses). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. The MP tree was obtained using the Close-Neighbor-Interchange algorithm [4, pg. 128] with search level 3 [3, 4] in which the initial trees were obtained with the random addition of sequences (10 replicates). The codon positions included were 1st+2nd. All positions containing gaps and missing data were eliminated from the dataset (Complete Deletion option). There were a total of 873346 positions in the final dataset, out of which 33696 were parsimony informative. Phylogenetic analyses were conducted in MEGA4 [5].

1. Cannarozzi G, Schneider A, Gonnet G (2007) A phylogenomic study of human, dog, and mouse. PLoS Computational Biology, 2007 Jan 5;3(1):e2.

2. Eck RV & Dayhoff MO (1966) Atlas of Protein Sequence and Structure. National Biomedical Research Foundation, Silver Springs, Maryland.

3. Felsenstein J (1985) Confidence limits on phylogenies: An approach using the bootstrap. Evolution 39:783-791.

4. Nei M & Kumar S (2000) Molecular Evolution and Phylogenetics. Oxford University Press, New York.

5. Tamura K, Dudley J, Nei M & Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Molecular Biology and Evolution 10.1093/molbev/msm092.