

Supplementary Information

Dataset S1 (the manually edited multiple sequence alignment for 39TaxonSet in nexus format), and **all topologies** obtained under every model tested are available for download from: [doi:10.5061/dryad.vh49j](https://doi.org/10.5061/dryad.vh49j)

Fig S1. Posterior predictive simulations in P4.

Bar graphs **(A)**, **(C)**, **(E)**, **(G)** and **(I)** represent the posterior predictive simulations of homogeneous models JTT+I+4 Γ and 1GTR+1C+4 Γ for 66TaxonSet, and JTT+4 Γ and 1GTR+1C+4 Γ for 39TaxonSet. Bar graphs **(B)**, **(D)**, **(F)**, **(H)** and **(J)** represent the posterior predictive simulations of the heterogeneous models of best fit. The arrows in all cases represent the χ^2 -position for the actual dataset (66TaxonSet **(A)** – **(D)** and 39TaxonSet **(E)** – **(J)**).

Table S1. Test for compositional heterogeneity using P4.

The results of the χ^2 -test for compositional homogeneity and the Model Fit Test are shown for 66TaxonSet and 39TaxonSet. In all tests shown “+” denotes composition fits the homogeneous model while “-” denotes that this species or entire dataset does not fit the homogeneous model. All numbers shown are the Posterior Probability scores for the fit of the data to the compositionally homogeneous model.

Table S2. Description of Models applied to 66TaxonSet and 39TaxonSet using P4.

Details of the model codes used in this study and the associated number of GTR/JTT rate matrices, number of composition vectors, proportion of invariable sites (+I), and the gamma distributed associated rate variation (+ Γ) for each model. The total number of free parameters estimated for each model are also given. v = variable parameters, f = fixed parameters.

Table S3. Comparison of models applied through P4 using BF.

All models applied to 66TaxonSet and 39TaxonSet in P4 are depicted as follows: Model 1 is on the top row and Model 2 is given on the left most column. The results of $2\ln(\text{Model 1} - \text{Model 2})$ are shown in the intersect. $2(\ln\text{BF})$ were carried out using

the Kass and Raftery table (shown in inset) as a guide. $2(\ln\text{BF}) > 10$ strongly support the more parameter rich model.

Table S4. Testing alternative rooting hypotheses

The $2(\ln\text{BF})$ are shown for the comparison of topologies generated under the heterogeneous model of best fit for each dataset and the alternative rooting hypotheses (for the 66TaxonSet this comparison was also carried out between the original topology published and the model of best fit). $2(\ln\text{BF})$ are not calculated for 39TaxonSet_aa against competing hypotheses as it failed the posterior predictive sampling test.

Table S5. Details of the data used in the analysis

(A) Details the taxa names along with genome version and coverages used. (B) lists the unique identifiers for the 27 genes identified as 1:1 orthologs across the 39 species for the Ensembl database (for all taxa except Polar Bear) and the BGI polar bear genome project. (C) Shows the GC% by lineage and by gene. (D) Summarizes the results of the test of lineage-specific compositionally homogeneity, a p-value < 0.05 indicates compositional heterogeneity.

Table S6. Testing the fit of 66TaxonSet and 39TaxonSet to the model in PhyloBayes.

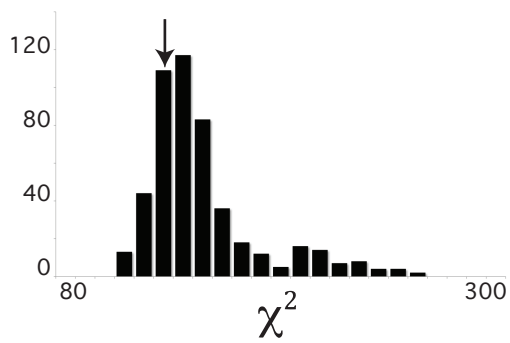
Posterior predictive simulations were conducted under CAT, GTR, JTT and CAT-GTR on 66TaxonSet and 39TaxonSet in PhyloBayes v3.2. Z-scores exceeding 2.00 denote compositionally heterogeneous taxa (in bold). The global fitness test describes the overall fit of the data to the model tested, again a value > 2.00 indicates compositional heterogeneity.

Table S7. Cross Validation (CV) of models in PhyloBayes

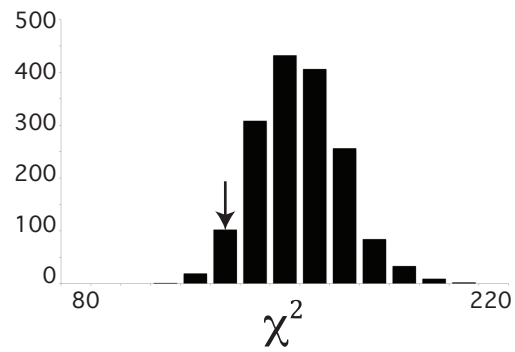
The average of the CV log-likelihood scores compared across all models in PhyloBayes are shown “+/-“ the standard deviation between the CV scores. The reference model is shown on the horizontal and the test model is shown on the vertical. A positive score indicates that the tested model is better than the reference model.

Supplementary Figure S1

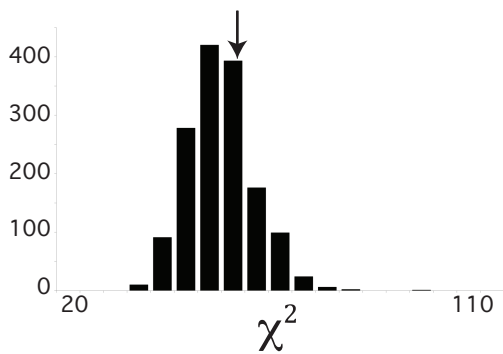
(A) 66TaxonSet_aa (1JTT+I+4 Γ)



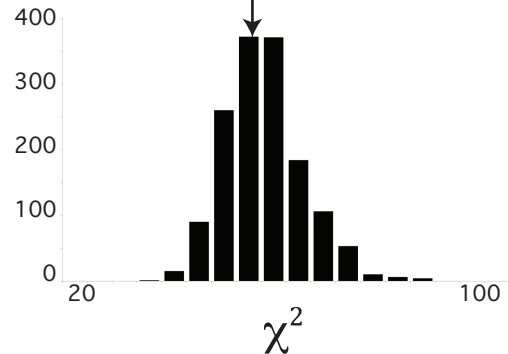
(B) 66TaxonSet_aa (1JTT+4C+I+4 Γ)



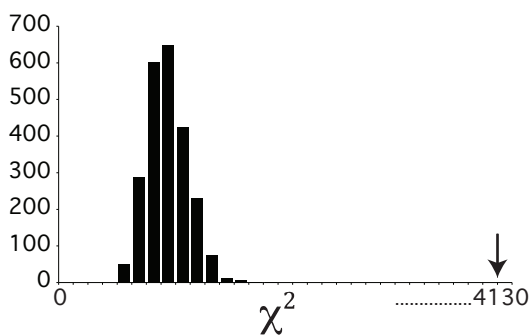
(C) 66TaxonSet_day (1GTR+1C+I+4 Γ)



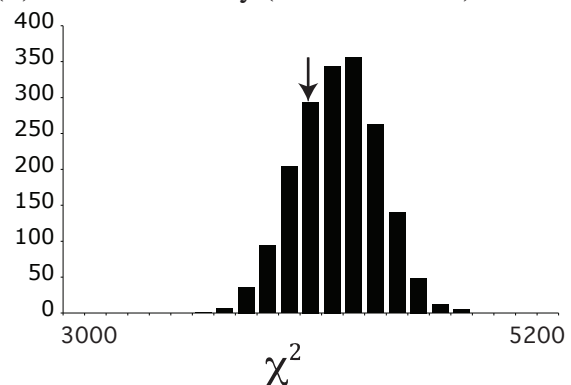
(D) 66TaxonSet_day (5GTR+2C+I+4 Γ)



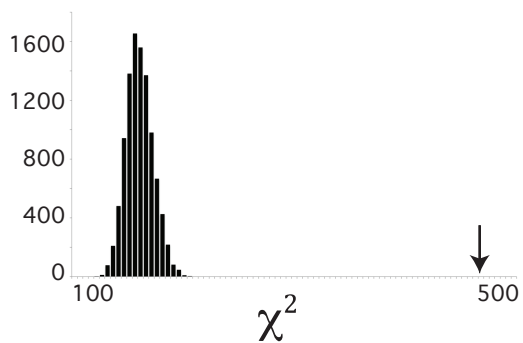
(E) 39TaxonSet_nuc (1GTR+1C+4 Γ)



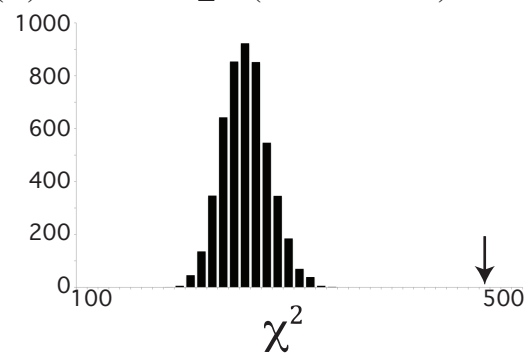
(F) 39TaxonSet_day (2GTR+4C+4 Γ)



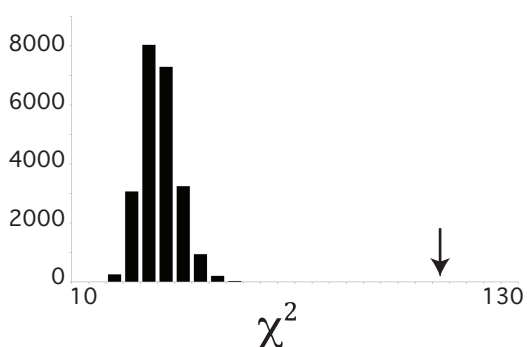
(G) 39TaxonSet_aa (1JTT+4 Γ)



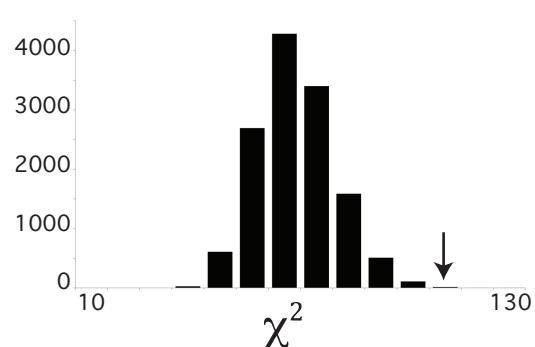
(H) 39TaxonSet_aa (1JTT+5C+4 Γ)



(I) 39TaxonSet_day (1GTR+1C+4 Γ)



(J) 39TaxonSet_day (2GTR+4C+4 Γ)



Supplementary Table 1

	66TaxonSet_nuc		66TaxonSet_aa		66TaxonSet_day	
χ^2 -test for compositional homogeneity	-	0.00	+	1.00	+	1.00
Model Fit Test						
Overall Simulations Fit	+	1.00	+	0.42	+	0.75
Aardvark	-	0.00	-	0.00	+	0.80
Anteater	+	1.00	-	0.00	+	0.19
Antelope	+	1.00	+	1.00	+	0.74
Big_hairy_armadillo	+	1.00	-	0.00	+	0.98
Black_gibbon	+	1.00	-	0.00	+	0.70
Black_headed_spirder_monkey	-	0.02	-	0.00	+	0.20
Brown_bear	+	1.00	+	1.00	+	0.49
Capybara	-	0.00	-	0.00	+	0.44
Cat	+	1.00	-	0.00	+	0.64
Chinese_Pangolin	+	1.00	-	0.00	+	0.91
Chinese_hamster	+	1.00	+	1.00	+	0.75
Chipmunk	-	0.00	-	0.00	+	0.66
Colugo	+	1.00	-	0.00	+	0.89
Common_shrew	+	1.00	-	0.00	+	0.46
Cotton_tailed_rabbit	+	1.00	-	0.00	+	0.8
Coypu	+	1.00	+	1.00	+	0.36
Dog	+	1.00	+	1.00	+	0.77
Dolphin	+	1.00	-	0.00	+	0.81
Egyptian_slit_nosed_bat	+	1.00	+	1.00	+	0.75
Elephant	-	0.00	-	0.00	+	0.58
Forest_giraffe	+	1.00	-	0.00	+	0.96
Giant_Anteater	+	1.00	-	0.00	+	0.46
Goeldis_marmoset	-	0.00	-	0.00	+	0.34
Hazel_Dormouse	+	1.00	-	0.00	+	0.56
Hippo	+	1.00	-	0.00	+	0.64
Hoffmanns_two_toed_Sloth	+	1.00	-	0.00	+	0.91
Horse	+	1.00	-	0.00	+	0.83
Human	-	0.00	-	0.00	+	0.22

Humpback_Whale	+	1.00	-	0.00	+	0.77
Indian_flying_fox	+	1.00	-	0.00	+	0.47
Jaguar	+	1.00	-	0.00	+	0.62
Jamaican_fruit_bat	+	0.41	-	0.00	+	0.62
Kangaroo_Rat	+	1.00	+	0.61	+	0.55
Lesser_Hedgehog_Tenrec	+	1.00	+	1.00	+	0.89
Linnaeus_two_toed_sloth	+	1.00	+	1.00	+	0.88
Llama	+	1.00	+	1.00	+	0.68
Long_haired_rousette	-	0.00	-	0.00	+	0.25
Macaque	-	0.00	-	0.00	+	0.38
Malayan_Porcupine	+	1.00	-	0.00	+	0.70
Malayan_Tapir	+	1.00	-	0.00	+	0.80
Manatee	-	0.00	-	0.00	+	0.48
Montane_guinea_pig	+	1.00	-	0.00	+	0.74
Mountain_paca	+	1.00	-	0.00	+	0.90
Mouse	-	0.00	-	0.00	+	0.64
Naked_mole_rat	+	1.00	-	0.00	+	0.95
North_american_beaver	-	0.00	-	0.00	+	0.39
North_american_porcupine	+	1.00	-	0.00	+	0.69
Northern_pika	+	1.00	-	0.00	+	0.62
Ocelot	+	1.00	-	0.00	+	0.60
Opossum	+	1.00	+	1.00	+	0.81
Pacarana	+	1.00	+	1.00	+	0.65
Pig	+	1.00	-	0.00	+	0.74
Pygmy_treeshrew	+	1.00	-	0.00	+	0.70
Rat	+	1.00	-	0.00	+	0.58
Ring_tailed_lemur	+	0.38	-	0.00	+	0.34
Rock_Hyrax	+	1.00	+	1.00	+	0.73
Rufous_elephant_shrew	+	1.00	-	0.00	+	0.43
Short_eared_elephant_shrew	+	1.00	+	1.00	+	0.54
Siberian_mole	+	1.00	+	1.00	+	0.72
Six_banded_armadillo	+	1.00	-	0.00	+	0.92
Springhare	+	1.00	+	1.00	+	0.45
Star_nosed_mole	+	1.00	-	0.00	+	0.83

Tammar_wallaby	+	1.00	+	1.00	+	0.98
Tarsier	+	1.00	+	1.00	+	0.54
White_Rhinoceros	-	0.00	-	0.00	+	0.65
Southern_white_breasted_hedgehog	+	1.00	+	1.00	+	0.92
		39TaxonSet_nuc		39TaxonSet_aa		39TaxonSet_day
χ^2-test for compositional homogeneity	-	0.00	+	1.00	+	1.00
Model Fit Test						
Overall Simulations Fit	-	0.00	-	0.00	+	1.00
Alpaca	+	1.00	-	0.00	+	1.00
Armadillo	+	1.00	+	1.00	+	1.00
Bushbaby	+	1.00	-	0.00	+	1.00
Cat	+	1.00	+	1.00	-	1.00
Chicken	-	0.00	-	0.00	-	0.00
Chimp	-	0.00	-	0.00	-	0.00
Common shrew	+	1.00	+	1.00	+	1.00
Cow	-	0.00	-	0.00	-	0.00
Dog	-	0.00	-	0.00	-	0.00
Dolphin	-	0.00	-	0.00	+	1.00
Elephant	-	0.00	-	0.00	-	0.00
Giant_panda	-	0.00	-	0.00	-	0.00
Gorilla	-	0.00	-	0.00	-	0.00
Guineapig	+	1.00	-	0.00	-	1.00
Hedgehog	+	1.00	-	0.00	+	1.00
Horse	-	0.00	-	0.00	-	0.00
Human	-	0.00	-	0.00	-	0.00
Kangaroo_rat	+	1.00	-	0.00	-	1.00
Macaque	-	0.00	-	0.00	-	0.00
Marmoset	-	0.00	-	0.00	-	0.00
Megabat	-	0.00	-	0.00	+	0.07
Microbat	+	1.00	-	0.00	+	1.00
Mouse	-	0.00	-	0.00	-	0.01
Mouse_lemur	+	1.00	-	0.00	-	1.00
Opossum	-	0.00	-	0.00	-	0.00

Orangutan	-	0.00	-	0.00	+	0.16
Pig	+	1.00	-	0.00	-	1.00
Pika	+	1.00	-	0.00	-	1.00
Platypus	+	1.00	-	0.00	+	1.00
Polar_bear	-	0.00	-	0.00	-	0.00
Rabbit	+	1.00	-	0.00	+	1.00
Rat	+	1.00	-	0.00	+	1.00
Rock Hyrax	+	1.00	-	0.00	+	1.00
Sloth	+	1.00	+	1.00	+	1.00
Squirrel	+	1.00	-	0.00	+	1.00
Tarsier	+	1.00	-	0.00	+	1.00
Tenrec	+	1.00	-	0.00	-	1.00
Treeshrew	+	1.00	-	0.00	+	1.00
Wallaby	+	1.00	-	0.00	+	1.00

Supplementary Table S2

Model	Rates	Comp	pInvar	+ Γ	Parameters
66TaxonSet_aa					
1JTT+I+4 Γ	1JTT(f)	1JTT(f)	0.3(v)	0.7(v)	2
1JTT+1C+I+4 Γ	1JTT(f)	1Estimate(v)	0.3(v)	0.7(v)	22
1JTT+2C+I+4 Γ	1JTT(f)	2Estimate(v)	0.3(v)	0.7(v)	42
1JTT+3C+I+4 Γ	1JTT(f)	3Estimate(v)	0.3(v)	0.7(v)	62
1JTT+4C+I+4 Γ	1JTT(f)	4Estimate(v)	0.3(v)	0.7(v)	82
1JTT+5C+I+4 Γ	1JTT(f)	5Estimate(v)	0.3(v)	0.7(v)	102
1JTT+6C+I+4 Γ	1JTT(f)	6Estimate(v)	0.3(v)	0.7(v)	122
1JTT+7C+I+4 Γ	1JTT(f)	7Estimate(v)	0.3(v)	0.7(v)	142
66TaxonSet_day					
1GTR+1C+I+4 Γ	1GTR(v)	1Estimate(v)	0.3(v)	0.7(v)	23
2GTR+1C+I+4 Γ	2GTR(v)	1Estimate(v)	0.3(v)	0.7(v)	38
3GTR+1C+I+4 Γ	3GTR(v)	1Estimate(v)	0.3(v)	0.7(v)	53
4GTR+1C+I+4 Γ	4GTR(v)	1Estimate(v)	0.3(v)	0.7(v)	68
5GTR+1C+I+4 Γ	5GTR(v)	1Estimate(v)	0.3(v)	0.7(v)	83
6GTR+1C+I+4 Γ	6GTR(v)	1Estimate(v)	0.3(v)	0.7(v)	98
1GTR+2C+I+4 Γ	1GTR(v)	2Estimate(v)	0.3(v)	0.7(v)	29
1GTR+3C+I+4 Γ	1GTR(v)	3Estimate(v)	0.3(v)	0.7(v)	35
1GTR+4C+I+4 Γ	1GTR(v)	4Estimate(v)	0.3(v)	0.7(v)	41
1GTR+5C+I+4 Γ	1GTR(v)	5Estimate(v)	0.3(v)	0.7(v)	47
1GTR+6C+I+4 Γ	1GTR(v)	6Estimate(v)	0.3(v)	0.7(v)	53
1GTR+7C+I+4 Γ	1GTR(v)	7Estimate(v)	0.3(v)	0.7(v)	59
5GTR+2C+I+4 Γ	5GTR(v)	2Estimate(v)	0.3(v)	0.7(v)	89
5GTR+3C+I+4 Γ	5GTR(v)	3Estimate(v)	0.3(v)	0.7(v)	95
5GTR+4C+I+4 Γ	5GTR(v)	4Estimate(v)	0.3(v)	0.7(v)	101
39TaxonSet_nuc					
1GTR+1C+4 Γ	1GTR(v)	1Estimate(v)	0.0(f)	1.00(f)	10
2GTR+1C+4 Γ	2GTR(v)	1Estimate(v)	0.0(f)	1.00(f)	16
3GTR+1C+4 Γ	3GTR(v)	1Estimate(v)	0.0(f)	1.00(f)	22
4GTR+1C+4 Γ	4GTR(v)	1Estimate(v)	0.0(f)	1.00(f)	28
5GTR+1C+4 Γ	5GTR(v)	1Estimate(v)	0.0(f)	1.00(f)	34
6GTR+1C+4 Γ	6GTR(v)	1Estimate(v)	0.0(f)	1.00(f)	40
1GTR+2C+4 Γ	1GTR(v)	2Estimate(v)	0.0(f)	1.00(f)	14
1GTR+3C+4 Γ	1GTR(v)	3Estimate(v)	0.0(f)	1.00(f)	18
1GTR+4C+4 Γ	1GTR(v)	4Estimate(v)	0.0(f)	1.00(f)	22
1GTR+5C+4 Γ	1GTR(v)	5Estimate(v)	0.0(f)	1.00(f)	26
1GTR+6C+4 Γ	1GTR(v)	6Estimate(v)	0.0(f)	1.00(f)	30
2GTR+4C+4 Γ	2GTR(v)	4Estimate(v)	0.0(f)	1.00(f)	28
39TaxonSet_aa					
1JTT+4 Γ	1JTT(f)	1Estimate(f)	0.0(f)	0.62(f)	0
1JTT+1C+4 Γ	1JTT(f)	1Estimate(v)	0.0(f)	0.62(f)	20
1JTT+2C+4 Γ	1JTT(f)	2Estimate(v)	0.0(f)	0.62(f)	40
1JTT+3C+4 Γ	1JTT(f)	3Estimate(v)	0.0(f)	0.62(f)	60
1JTT+4C+4 Γ	1JTT(f)	4Estimate(v)	0.0(f)	0.62(f)	80
1JTT+5C+4 Γ	1JTT(f)	5Estimate(v)	0.0(f)	0.62(f)	100
1JTT+6C+4 Γ	1JTT(f)	6Estimate(v)	0.0(f)	0.62(f)	120

1JTT+7C+4Γ	1JTT(f)	7Estimate(v)	0.0(f)	0.62(f)	140
1JTT+8C+4Γ	1JTT(f)	8Estimate(v)	0.0(f)	0.62(f)	160
39TaxonSet_day					
1GTR+1C+4Γ	1GTR(v)	1Estimate(v)	0.0(f)	0.62(f)	21
2GTR+1C+4Γ	2GTR(v)	1Estimate(v)	0.0(f)	0.62(f)	36
3GTR+1C+4Γ	3GTR(v)	1Estimate(v)	0.0(f)	0.62(f)	51
4GTR+1C+4Γ	4GTR(v)	1Estimate(v)	0.0(f)	0.62(f)	66
5GTR+1C+4Γ	5GTR(v)	1Estimate(v)	0.0(f)	0.62(f)	81
1GTR+2C+4Γ	1GTR(v)	2Estimate(v)	0.0(f)	0.62(f)	27
1GTR+3C+4Γ	1GTR(v)	3Estimate(v)	0.0(f)	0.62(f)	33
1GTR+4C+4Γ	1GTR(v)	4Estimate(v)	0.0(f)	0.62(f)	39
1GTR+5C+4Γ	1GTR(v)	5Estimate(v)	0.0(f)	0.62(f)	45
2GTR+4C+4Γ	2GTR(v)	4Estimate(v)	0.0(f)	0.62(f)	53
3GTR+4C+4Γ	3GTR(v)	4Estimate(v)	0.0(f)	0.62(f)	69
4GTR+4C+4Γ	4GTR(v)	4Estimate(v)	0.0(f)	0.62(f)	84
5GTR+4C+4Γ	5GTR(v)	4Estimate(v)	0.0(f)	0.62(f)	99

Supplementary Table S3

Bayes Factor (BF) Comparisons

2ln(BF)	Evidence in favor of Model 2
<0	Negative
0-2.2	Not noteworthy
2.2-6	Positive
6-10	Strong
>10	Very Strong

66TaxonSet_nuc	
2GTR+1C+4F	113.77
3GTR+1C+4F	176.77
4GTR+1C+4F	201.56
5GTR+1C+4F	216.36
6GTR+1C+4F	232.85
1GTR+2C+4F	727.73
1GTR+3C+4F	879.13
1GTR+4C+4F	904.72
1GTR+5C+4F	937.86
1GTR+6C+4F	950.55
1GTR+7C+4F	956.41
2GTR+5C+4F	1068.96
3GTR+5C+4F	1097.11
4GTR+5C+4F	1118.31
2GTR+1C+4F	57.35
3GTR+1C+4F	82.15
4GTR+1C+4F	14.53
5GTR+1C+4F	29.33
6GTR+1C+4F	45.82
1GTR+2C+4F	540.7
1GTR+3C+4F	692.09
1GTR+4C+4F	717.69
1GTR+5C+4F	750.82
1GTR+6C+4F	717.69
1GTR+7C+4F	769.38
2GTR+5C+4F	881.93
3GTR+5C+4F	910.07
4GTR+5C+4F	902.9
4GTR+1C+4F	0.95
5GTR+1C+4F	-7.61
6GTR+1C+4F	17.44
1GTR+2C+4F	481.43
1GTR+3C+4F	632.82
1GTR+4C+4F	658.42
1GTR+5C+4F	697.4
1GTR+6C+4F	710.09
1GTR+7C+4F	715.95
2GTR+5C+4F	828.5
3GTR+5C+4F	856.64
4GTR+5C+4F	872
1GTR+2C+4F	140.91
1GTR+3C+4F	166.51
1GTR+4C+4F	17.74
1GTR+5C+4F	50.87
1GTR+6C+4F	36.57
1GTR+7C+4F	69.43
2GTR+5C+4F	181.98
3GTR+5C+4F	210.12
4GTR+5C+4F	231.32
1GTR+2C+4F	199.64
1GTR+3C+4F	212.34
1GTR+4C+4F	36.81
1GTR+5C+4F	10.94
1GTR+6C+4F	-17.98
1GTR+7C+4F	79.7
2GTR+5C+4F	123.49
3GTR+5C+4F	122.72
4GTR+5C+4F	129.04
2GTR+5C+4F	11.53
3GTR+5C+4F	3.17

66TaxonSet_aa	
LJTT+1C+4F	217.3
LJTT+2C+4F	283.3
LJTT+3C+4F	326.6
LJTT+4C+4F	369.4
LJTT+1C+4F	63.1
LJTT+2C+4F	106.5
LJTT+3C+4F	31.6
LJTT+4C+4F	74.4
LJTT+1C+4F	31.6
LJTT+2C+4F	39.8

66TaxonSet_day	
2GTR+1C+4F	67
3GTR+1C+4F	102.7
4GTR+1C+4F	121.9
5GTR+1C+4F	152.3
6GTR+1C+4F	171
1GTR+2C+4F	16.4
1GTR+3C+4F	28.9
1GTR+4C+4F	44.8
1GTR+5C+4F	55.7
1GTR+6C+4F	64.2
1GTR+7C+4F	71.5
5GTR+2C+4F	169.3
5GTR+3C+4F	184.5
5GTR+4C+4F	199.8
2GTR+1C+4F	29.4
3GTR+1C+4F	8.4
4GTR+1C+4F	16.7
5GTR+1C+4F	7.9
6GTR+1C+4F	57.4
1GTR+2C+4F	-97.1
1GTR+3C+4F	-84.7
1GTR+4C+4F	-28.6
1GTR+5C+4F	-17.6
1GTR+6C+4F	-9.1
1GTR+7C+4F	-1.9
5GTR+2C+4F	96
5GTR+3C+4F	111.1
5GTR+4C+4F	126.5
3GTR+1C+4F	49.3
4GTR+1C+4F	35.4
5GTR+1C+4F	7.1
6GTR+1C+4F	-147.5
1GTR+2C+4F	-165.3
1GTR+3C+4F	9
1GTR+4C+4F	8.9
1GTR+5C+4F	6.3
1GTR+6C+4F	1
1GTR+7C+4F	8.3
5GTR+2C+4F	119.9
5GTR+3C+4F	133.4
5GTR+4C+4F	148.6
1GTR+2C+4F	35.9
1GTR+3C+4F	-126
1GTR+4C+4F	35.9
1GTR+5C+4F	44.4
1GTR+6C+4F	22.1
1GTR+7C+4F	22.1
5GTR+2C+4F	106.1
5GTR+3C+4F	121.3
5GTR+4C+4F	136.6
1GTR+2C+4F	19.8
1GTR+3C+4F	151.63
1GTR+4C+4F	122.72
1GTR+5C+4F	107.84
1GTR+6C+4F	111.4
1GTR+7C+4F	103.5
5GTR+2C+4F	1.6
5GTR+3C+4F	-7.8

39TaxonSet_nuc	
2GTR+1C+4F	204.4
3GTR+1C+4F	251.6
4GTR+1C+4F	210.2
5GTR+1C+4F	438.1
6GTR+1C+4F	487.2
1GTR+2C+4F	5163.4
1GTR+3C+4F	5664.5
1GTR+4C+4F	5817.7
1GTR+5C+4F	5884.2
1GTR+6C+4F	5954.4
2GTR+1C+4F	6092.4
2GTR+1C+4F	0.8
3GTR+1C+4F	169.7
4GTR+1C+4F	187.3
5GTR+1C+4F	187.3
6GTR+1C+4F	236.4
1GTR+2C+4F	4912.6
1GTR+3C+4F	5413.7
1GTR+4C+4F	5566.9
1GTR+5C+4F	5842
1GTR+6C+4F	5954.4
2GTR+1C+4F	5841.6
3GTR+1C+4F	49.3
4GTR+1C+4F	66.9
5GTR+1C+4F	48.0
6GTR+1C+4F	39.3
1GTR+2C+4F	4636.9
1GTR+3C+4F	5137.9
1GTR+4C+4F	5330.8
1GTR+5C+4F	5357.7
1GTR+6C+4F	5393.4
2GTR+1C+4F	5654.4
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	690.8
1GTR+6C+4F	761.0
2GTR+1C+4F	899.0
3GTR+1C+4F	518.0
4GTR+1C+4F	518.0
5GTR+1C+4F	5330.8
6GTR+1C+4F	5256.8
1GTR+2C+4F	471.1
1GTR+3C+4F	624.3
1GTR+4C+4F	96.5
1GTR+5C+4F	

Supplementary Table S4

	Model of Best Fit (Model 2)	Alternative Rooting Hypotheses (Model 1)		
66TaxonSet_nuc	Atlantogenata (3GTR+5C+I+4Γ)	Xenarthra	Afrotheria	66TaxonSet Original
2ln(BF)	-----	6.20	6.98	3.48
66TaxonSet_aa	Xenarthra (1JTT+4C+I+4Γ)	Atlantogenata	Afrotheria	66TaxonSet Original
2ln(BF)	-----	8.44	7.64	23.24
66TaxonSet_day	Xenarthra (5GTR+2C+I+4Γ)	Atlantogenata	Afrotheria	66TaxonSet Original
2ln(BF)	-----	1.96	5.24	0.24
39TaxonSet_nuc	Atlantogenata (2GTR+4C+4Γ)	Afrotheria	Xenarthra	
2ln(BF)	-----	0.88	2.29	-----
39TaxonSet_day	Atlantogenata (2GTR+4C+4Γ)	Afrotheria	Xenarthra	
2ln(BF)	-----	16.08	6.54	-----

Supplementary Table S5

(A) 39TaxonSet Genome Details			
Species Name	Common Name	Genome Version	Genome Coverage
<i>Ailuropoda melanoleuca</i>	Giant Panda	ailMel1	73X
<i>Bos taurus</i>	Cow	Btau_4.0	7X
<i>Callithrix jacchus</i>	Marmoset	calJac3	6X
<i>Canis familiaris</i>	Dog	CanFam_2.0	7X
<i>Cavia porcellus</i>	Guinea pig	cavPor3	6.79X
<i>Choloepus hoffmanni</i>	Sloth	choHof1	2.05X
<i>Dasypus novemcinctus</i>	Armadillo	dasNov2	2X
<i>Dipodomys ordii</i>	Kangaroo Rat	dipOrd1	1.85
<i>Echinops telfairi</i>	Tenrec	TENREC	2X
<i>Equus caballus</i>	Horse	EquCab2	6.79X
<i>Erinaceus europaeus</i>	Hedgehog	eriEur1	1.86X
<i>Felis catus</i>	Cat	CAT	1.87X
<i>Gallus gallus</i>	Chicken	WASHUC2	7.1X
<i>Gorilla gorilla</i>	Gorilla	gorGor3	35X
<i>Homo sapiens</i>	Human	GRCh37.p2	Deep
<i>Loxodonta africana</i>	Elephant	loxAfr3	7X
<i>Macaca mulatta</i>	Macaque	MMUL_1.0	6.1x
<i>Macropus eugenii</i>	Wallaby	Meug_1.0	2X
<i>Microcebus murinus</i>	Mouse Lemur	micMur1	1.93X
<i>Monodelphis domestica</i>	Opossum	monDom5	7.33 X
<i>Mus musculus</i>	Mouse	NCBIM37	7X
<i>Myotis lucifugus</i>	Microbat	myoLuc1	1.7X
<i>Ochotona princeps</i>	Pika	OchPri2.0	1.93X
<i>Ornithorhynchus anatinus</i>	Platypus	OANA5	6X
<i>Oryctolagus cuniculus</i>	Rabbit	oryCun2.0	7X
<i>Otolemur garnettii</i>	Bushbaby	otoGar1	1.5X
<i>Pan troglodytes</i>	Chimpanzee	CHIMP2.1	8X
<i>Pongo pygmaeus</i>	Orangutan	PPYG2	6X
<i>Procavia capensis</i>	Hyrax	proCap1	2.19X
<i>Pteropus vampyrus</i>	Megabat	pteVam1	2.63X
<i>Rattus norvegicus</i>	Rat	RGSC3.4	7x
<i>Sorex araneus</i>	Shrew	sorAra1	1.9X
<i>Spermophilus tridecemlineatus</i>	Squirrel	speTri1	1.9X
<i>Sus scrofa</i>	Pig	Sscrofa9	4X
<i>Tarsius syrichta</i>	Tarsier	tarSyr1	1.82X
<i>Tupaia belangeri</i>	Treeshrew	tupBel1	2X
<i>Tursiops truncatus</i>	Dolphin	turTru1	2.59X
<i>Ursus maritimus</i>	Polar Bear	version 1	85X
<i>Vicugna pacos</i>	Alpaca	vicPac1	2.51X

(B) 39TaxonSet Ensembl Gene ID's

Gene Names	VPS41 (2583 bp)	AQR (4788 bp)
Ailuropoda melanoleuca	ENSAMEG00000008248	ENSAMEG00000005194
Bos taurus	ENSBTAG00000007305	ENSBTAG00000012712
Callithrix jacchus	ENSCJAG00000012686	ENSCJAG00000021021
Canis familiaris	ENSCAFG00000003582	ENSCAFG00000008304
Cavia porcellus	ENSCPOG00000006142	ENSCPOG00000000810
Choloepus hoffmanni	ENSCHOG00000003431	ENSCHOG00000013653
Dasypus novemcinctus	ENSDNOG00000006684	ENSDNOG00000013414
Dipodomys ordii	ENSDORG00000015881	ENSDORG00000015152
Echinops telfairi	ENSETEG00000012877	ENSETEG00000003032
Equus caballus	ENSECAG00000006943	ENSECAG00000016399
Erinaceus europaeus	ENSEEUG00000003925	ENSEEUG00000003975
Felis catus	ENSFCAG00000019210	ENSFCAG00000014069
Gallus gallus	ENSGALG00000012301	ENSGALG00000009838
Gorilla gorilla	ENSGGOG00000006665	ENSGGOG00000014073
Homo sapiens	ENSG00000006715	ENSG00000021776
Loxodonta africana	ENSLAFG00000015987	ENSLAFG00000017667
Macaca mulatta	ENSMMUG00000010042	ENSMMUG00000002337
Macropus eugenii	ENSMEUG00000013286	ENSMEUG00000011715
Microcebus murinus	ENSMICG00000005036	ENSMICG00000016979
Monodelphis domestica	ENSMODG00000012622	ENSMODG00000001369
Mus musculus	ENSMUSG00000041236	ENSMUSG00000040383
Myotis lucifugus	ENSMLUG00000008811	ENSMLUG00000006223
Ochotona princeps	ENSOPRG00000015527	ENSOPRG00000016495
Ornithorhynchus anatinus	ENSOANG00000005418	ENSOANG00000002565
Oryctolagus cuniculus	ENSOCUG00000000676	ENSOCUG00000003488
Otolemur garnettii	ENSOGAG00000000684	ENSOGAG00000016007
Pan troglodytes	ENSPTRG00000019104	ENSPTRG00000006891
Pongo pygmaeus	ENSPPYG00000017621	ENSPPYG00000006319
Procavia capensis	ENSPCAG00000000409	ENSPCAG00000009005
Pteropus vampyrus	ENSPVAG00000012959	ENSPVAG00000010329
Rattus norvegicus	ENSRNOG00000012940	ENSRNOG00000008912
Sorex araneus	ENSSARG00000007573	ENSSARG00000009090
Spermophilus tridecemlineatus	ENSSTOG00000007343	ENSSTOG00000000395
Sus scrofa	ENSSSCG00000016772	ENSSSCG00000004802
Tarsius syrichta	ENSTSYG00000001895	ENSTSYG00000004244
Tupaia belangeri	ENSTBEG00000006161	ENSTBEG00000013900
Tursiops truncatus	ENSTTRG00000004214	ENSTTRG00000014800
Ursus maritimus	Uma_R003863	Uma_R013970
Vicugna pacos	ENSVPAG00000002802	ENSVPAG00000010622

Gene Names	ZCCHC8 (2397 bp)	OTC (1077 bp)
Ailuropoda melanoleuca	ENSAMEG00000014731	ENSAMEG00000007121
Bos taurus	ENSBTAG00000006114	ENSBTAG00000001488
Callithrix jacchus	ENSCJAG00000020409	ENSCJAG00000020777
Canis familiaris	ENSCAFG00000007859	ENSCAFG00000014023
Cavia porcellus	ENSCPOG00000014385	ENSCPOG00000012895
Choloepus hoffmanni	ENSCHOG00000007155	ENSCHOG00000011955
Dasyopus novemcinctus	ENSDNOG00000008881	ENSDNOG00000009387
Dipodomys ordii	ENSDORG00000008756	ENSDORG00000014052
Echinops telfairi	ENSETEG00000004735	ENSETEG00000010341
Equus caballus	ENSECAG00000006984	ENSECAG00000022838
Erinaceus europaeus	ENSEEUG00000015198	ENSEEUG00000007831
Felis catus	ENSFCAG00000010608	ENSFCAG00000010876
Gallus gallus	ENSGALG00000004486	ENSGALG00000016254
Gorilla gorilla	ENSGGOG00000027926	ENSGGOG00000011703
Homo sapiens	ENSG00000033030	ENSG00000036473
Loxodonta africana	ENSLAFG00000016477	ENSLAFG00000009919
Macaca mulatta	ENSMMUG00000013643	ENSMMUG00000013493
Macropus eugenii	ENSMEUG00000003497	ENSMEUG00000007728
Microcebus murinus	ENSMICG00000013486	ENSMICG00000011724
Monodelphis domestica	ENSMODG00000012264	ENSMODG00000021104
Mus musculus	ENSMUSG00000029427	ENSMUSG00000031173
Myotis lucifugus	ENSMLUG00000005334	ENSMLUG00000009014
Ochotona princeps	ENSOPRG00000013758	ENSOPRG00000011374
Ornithorhynchus anatinus	ENSOANG00000006199	ENSOANG00000007118
Oryctolagus cuniculus	ENSOCUG00000013759	ENSOCUG00000010532
Otolemur garnettii	ENSOGAG00000015900	ENSOGAG00000008763
Pan troglodytes	ENSPTRG00000005579	ENSPTRG00000021799
Pongo pygmaeus	ENSPPYG00000005068	ENSPPYG00000020246
Procavia capensis	ENSPCAG00000016551	ENSPCAG00000006225
Pteropus vampyrus	ENSPVAG00000001276	ENSPVAG00000014696
Rattus norvegicus	ENSRNOG00000001243	ENSRNOG00000003370
Sorex araneus	ENSSARG00000003982	ENSSARG00000008781
Spermophilus tridecemlineatus	ENSSTOG00000001683	ENSSTOG00000004056
Sus scrofa	ENSSSCG00000009792	ENSSSCG00000012236
Tarsius syrichta	ENSTSYG00000011362	ENSTSYG00000000488
Tupaia belangeri	ENSTBEG00000006192	ENSTBEG00000009278
Tursiops truncatus	ENSTTRG00000015809	ENSTTRG00000004947
Ursus maritimus	Uma_R006093	Uma_R006015
Vicugna pacos	ENSVPAG00000011459	ENSVPAG00000000726

Gene Names	NSUN2 (2640 bp)	SART3 (3024 bp)
Ailuropoda melanoleuca	ENSAMEG00000002744	ENSAMEG00000016374
Bos taurus	ENSBTAG00000015466	ENSBTAG00000031846
Callithrix jacchus	ENSCJAG00000008689	ENSCJAG00000015330
Canis familiaris	ENSCAFG00000010334	ENSCAFG00000011352
Cavia porcellus	ENSCPOG00000008196	ENSCPOG00000010969
Choloepus hoffmanni	ENSCHOG00000003644	ENSCHOG00000011750
Dasyopus novemcinctus	ENSDNOG00000013848	ENSDNOG00000019498
Dipodomys ordii	ENSDORG00000010247	ENSDORG00000014360
Echinops telfairi	ENSETEG00000000983	ENSETEG00000011292
Equus caballus	ENSECAG00000016357	ENSECAG00000000314
Erinaceus europaeus	ENSEEUG00000001691	ENSEEUG00000002954
Felis catus	ENSFCAG00000015602	ENSFCAG00000014041
Gallus gallus	ENSGALG00000013064	ENSGALG00000004887
Gorilla gorilla	ENSGGOG00000016583	ENSGGOG00000011562
Homo sapiens	ENSG00000037474	ENSG00000075856
Loxodonta africana	ENSLAFG00000009411	ENSLAFG00000007167
Macaca mulatta	ENSMMUG00000002561	ENSMMUG00000017124
Macropus eugenii	ENSMEUG00000007117	ENSMEUG00000006799
Microcebus murinus	ENSMICG00000016549	ENSMICG00000013052
Monodelphis domestica	ENSMODG00000002039	ENSMODG00000002859
Mus musculus	ENSMUSG00000021595	ENSMUSG00000018974
Myotis lucifugus	ENSMLUG00000009609	ENSMLUG00000007906
Ochotona princeps	ENSOPRG00000011324	ENSOPRG00000015817
Ornithorhynchus anatinus	ENSOANG00000009243	ENSOANG00000008794
Oryctolagus cuniculus	ENSOCUG00000007918	ENSOCUG00000016285
Otolemur garnettii	ENSOGAG00000015015	ENSOGAG00000000932
Pan troglodytes	ENSPTRG00000016715	ENSPTRG00000005404
Pongo pygmaeus	ENSPPYG00000015332	ENSPPYG00000004919
Procavia capensis	ENSPCAG00000010931	ENSPCAG00000007505
Pteropus vampyrus	ENSPVAG00000010643	ENSPVAG00000007442
Rattus norvegicus	ENSRNOG00000017254	ENSRNOG00000000702
Sorex araneus	ENSSARG00000006235	ENSSARG00000005401
Spermophilus tridecemlineatus	ENSSTOG00000004090	ENSSTOG00000002376
Sus scrofa	ENSSSCG00000017104	ENSSSCG00000009946
Tarsius syrichta	ENSTSYG00000005709	ENSTSYG00000013923
Tupaia belangeri	ENSTBEG00000014695	ENSTBEG00000008888
Tursiops truncatus	ENSTTRG00000012662	ENSTTRG00000003993
Ursus maritimus	Uma_R014187	Uma_R014972
Vicugna pacos	ENSVPAG00000005110	ENSVPAG00000009997

Gene Names	KIFAP3 (2496 bp)	DNAJC10 (2430 bp)
Ailuropoda melanoleuca	ENSAMEG00000011131	ENSAMEG00000009718
Bos taurus	ENSBTAG00000017727	ENSBTAG00000008390
Callithrix jacchus	ENSCJAG00000009954	ENSCJAG00000011295
Canis familiaris	ENSCAFG00000015067	ENSCAFG00000014289
Cavia porcellus	ENSCPOG00000010161	ENSCPOG00000012956
Choloepus hoffmanni	ENSCHOG00000005760	ENSCHOG00000000617
Dasypus novemcinctus	ENSDNOG00000016340	ENSDNOG00000013020
Dipodomys ordii	ENSDORG00000001434	ENSDORG00000004387
Echinops telfairi	ENSETEG00000016187	ENSETEG00000018686
Equus caballus	ENSECAG00000002798	ENSECAG00000010084
Erinaceus europaeus	ENSEEUG00000006338	ENSEEUG00000009196
Felis catus	ENSFCAG00000000812	ENSFCAG00000009493
Gallus gallus	ENSGALG00000021047	ENSGALG00000008862
Gorilla gorilla	ENSGGOG00000025510	ENSGGOG00000012233
Homo sapiens	ENSG00000075945	ENSG00000077232
Loxodonta africana	ENSLAFG00000018434	ENSLAFG00000007093
Macaca mulatta	ENSMMUG00000010081	ENSMMUG00000014394
Macropus eugenii	ENSMEUG00000012868	ENSMEUG00000004546
Microcebus murinus	ENSMICG00000012379	ENSMICG00000006441
Monodelphis domestica	ENSMODG00000003544	ENSMODG00000010507
Mus musculus	ENSMUSG00000026585	ENSMUSG00000027006
Myotis lucifugus	ENSMLUG00000006635	ENSMLUG00000000680
Ochotona princeps	ENSOPRG00000000747	ENSOPRG00000016914
Ornithorhynchus anatinus	ENSOANG00000000884	ENSOANG00000003626
Oryctolagus cuniculus	ENSOCUG00000013824	ENSOCUG00000001784
Otolemur garnettii	ENSOGAG00000010111	ENSOGAG00000006969
Pan troglodytes	ENSPTRG00000001666	ENSPTRG00000012707
Pongo pygmaeus	ENSPPYG00000000524	ENSPPYG00000012994
Procavia capensis	ENSPCAG00000000492	ENSPCAG00000011713
Pteropus vampyrus	ENSPVAG00000015994	ENSPVAG00000001575
Rattus norvegicus	ENSRNOG00000002544	ENSRNOG00000006803
Sorex araneus	ENSSARG00000008695	ENSSARG00000014338
Spermophilus tridecemlineatus	ENSSTOG00000003065	ENSSTOG00000003870
Sus scrofa	ENSSSCG00000006282	ENSSSCG00000016017
Tarsius syrichta	ENSTSYG00000003475	ENSTSYG00000003191
Tupaia belangeri	ENSTBEG00000005864	ENSTBEG00000017350
Tursiops truncatus	ENSTTRG00000004084	ENSTTRG00000002627
Ursus maritimus	Uma_R001380	Uma_R002066
Vicugna pacos	ENSVPAG00000005139	ENSVPAG00000003968

Gene Names	MTIF2 (2232 bp)	ADNP (3375 bp)
Ailuropoda melanoleuca	ENSAMEG00000003983	ENSAMEG00000013360
Bos taurus	ENSBTAG00000015481	ENSBTAG00000000340
Callithrix jacchus	ENSCJAG00000010030	ENSCJAG00000000563
Canis familiaris	ENSCAFG00000002829	ENSCAFG00000011576
Cavia porcellus	ENSCPOG00000005823	ENSCPOG00000001591
Choloepus hoffmanni	ENSCHOG00000012644	ENSCHOG00000011573
Dasyopus novemcinctus	ENSDNOG00000004817	ENSDNOG00000001749
Dipodomys ordii	ENSDORG00000006292	ENSDORG00000014663
Echinops telfairi	ENSETEG00000001075	ENSETEG00000011996
Equus caballus	ENSECAG00000009169	ENSECAG00000009307
Erinaceus europaeus	ENSEEUG00000002375	ENSEEUG00000007786
Felis catus	ENSFCAG00000013626	ENSFCAG00000009790
Gallus gallus	ENSGALG00000008117	ENSGALG00000007989
Gorilla gorilla	ENSGGOG00000007681	ENSGGOG00000003120
Homo sapiens	ENSG00000085760	ENSG00000101126
Loxodonta africana	ENSLAFG00000007341	ENSLAFG00000004139
Macaca mulatta	ENSMMUG00000030833	ENSMMUG00000002761
Macropus eugenii	ENSMEUG00000008935	ENSMEUG00000007857
Microcebus murinus	ENSMICG00000017441	ENSMICG00000015956
Monodelphis domestica	ENSMODG00000001833	ENSMODG00000016350
Mus musculus	ENSMUSG00000020459	ENSMUSG00000051149
Myotis lucifugus	ENSMLUG00000017067	ENSMLUG00000000002
Ochotona princeps	ENSOPRG00000010479	ENSOPRG00000002985
Ornithorhynchus anatinus	ENSOANG00000011187	ENSOANG00000008675
Oryctolagus cuniculus	ENSOCUG00000003617	ENSOCUG00000014704
Otolemur garnettii	ENSOGAG00000004306	ENSOGAG00000005381
Pan troglodytes	ENSPTRG00000011929	ENSPTRG00000013623
Pongo pygmaeus	ENSPPYG00000012403	ENSPPYG00000011130
Procavia capensis	ENSPCAG00000007183	ENSPCAG00000006836
Pteropus vampyrus	ENSPVAG00000016474	ENSPVAG00000016481
Rattus norvegicus	ENSRNOG00000004161	ENSRNOG00000010975
Sorex araneus	ENSSARG00000004548	ENSSARG00000008308
Spermophilus tridecemlineatus	ENSSTOG00000008159	ENSSTOG00000014656
Sus scrofa	ENSSSCG00000008404	ENSSSCG00000007473
Tarsius syrichta	ENSTSYG00000000850	ENSTSYG00000012059
Tupaia belangeri	ENSTBEG00000004711	ENSTBEG00000002890
Tursiops truncatus	ENSTTRG00000013952	ENSTTRG00000009011
Ursus maritimus	Uma_R004647	Uma_R006267
Vicugna pacos	ENSVPAG00000007092	ENSVPAG00000004917

Gene Names	EEF2K (2193 bp)	GARS (2340 bp)
Ailuropoda melanoleuca	ENSAMEG00000003619	ENSAMEG00000006652
Bos taurus	ENSBTAG00000017662	ENSBTAG00000018972
Callithrix jacchus	ENSCJAG00000009038	ENSCJAG00000008595
Canis familiaris	ENSCAFG00000017716	ENSCAFG00000003086
Cavia porcellus	ENSCPOG00000012053	ENSCPOG00000007547
Choloepus hoffmanni	ENSCHOG00000001768	ENSCHOG00000003253
Dasyopus novemcinctus	ENSDNOG00000014417	ENSDNOG00000014486
Dipodomys ordii	ENSDORG00000014075	ENSDORG00000002672
Echinops telfairi	ENSETEG00000009801	ENSETEG00000012196
Equus caballus	ENSECAG00000022924	ENSECAG00000019373
Erinaceus europaeus	ENSEEUG00000010309	ENSEEUG00000010646
Felis catus	ENSFCAG00000006271	ENSFCAG00000011415
Gallus gallus	ENSGALG00000006982	ENSGALG00000005694
Gorilla gorilla	ENSGGOG00000015267	ENSGGOG00000004916
Homo sapiens	ENSG00000103319	ENSG00000106105
Loxodonta africana	ENSLAFG00000022827	ENSLAFG00000002496
Macaca mulatta	ENSMMUG00000017725	ENSMMUG00000004719
Macropus eugenii	ENSMEUG00000009920	ENSMEUG00000001741
Microcebus murinus	ENSMICG00000015211	ENSMICG00000012159
Monodelphis domestica	ENSMODG00000007732	ENSMODG000000021163
Mus musculus	ENSMUSG00000035064	ENSMUSG00000029777
Myotis lucifugus	ENSMLUG00000003713	ENSMLUG00000002043
Ochotona princeps	ENSOPRG00000014635	ENSOPRG00000005342
Ornithorhynchus anatinus	ENSOANG00000003263	ENSOANG00000006262
Oryctolagus cuniculus	ENSOCUG00000008067	ENSOCUG00000005295
Otolemur garnettii	ENSOGAG00000007716	ENSOGAG00000013321
Pan troglodytes	ENSPTRG00000007877	ENSPTRG00000019042
Pongo pygmaeus	ENSPPYG00000007179	ENSPPYG00000017673
Procavia capensis	ENSPCAG00000008045	ENSPCAG00000007199
Pteropus vampyrus	ENSPVAG00000002146	ENSPVAG00000013565
Rattus norvegicus	ENSRNOG00000016448	ENSRNOG00000011052
Sorex araneus	ENSSARG00000005316	ENSSARG00000008410
Spermophilus tridecemlineatus	ENSSTOG00000011767	ENSSTOG00000015493
Sus scrofa	ENSSSCG00000007839	ENSSSCG00000016677
Tarsius syrichta	ENSTSYG00000014564	ENSTSYG00000008538
Tupaia belangeri	ENSTBEG00000008051	ENSTBEG00000008972
Tursiops truncatus	ENSTTRG00000010505	ENSTTRG00000000334
Ursus maritimus	Uma_R012648	Uma_R005962
Vicugna pacos	ENSVPAG00000006489	ENSVPAG00000009438

Gene Names	ANKMY2 (1419 bp)	AATF (1854 bp)
Ailuropoda melanoleuca	ENSAMEG00000010451	ENSAMEG00000013539
Bos taurus	ENSBTAG00000010980	ENSBTAG00000021927
Callithrix jacchus	ENSCJAG00000000950	ENSCJAG00000015449
Canis familiaris	ENSCAFG00000002428	ENSCAFG00000017869
Cavia porcellus	ENSCPOG00000011512	ENSCPOG00000006037
Choloepus hoffmanni	ENSCHOG00000004511	ENSCHOG00000007578
Dasyopus novemcinctus	ENSDNOG00000001659	ENSDNOG00000011100
Dipodomys ordii	ENSDORG00000010876	ENSDORG00000006957
Echinops telfairi	ENSETEG00000004567	ENSETEG00000003518
Equus caballus	ENSECAG00000014046	ENSECAG00000008531
Erinaceus europaeus	ENSEEUG00000001282	ENSEEUG00000002847
Felis catus	ENSFCAG00000009108	ENSFCAG00000010567
Gallus gallus	ENSGALG00000010804	ENSGALG00000005420
Gorilla gorilla	ENSGGOG00000007522	ENSGGOG00000002706
Homo sapiens	ENSG00000106524	ENSG00000108270
Loxodonta africana	ENSLAFG00000003941	ENSLAFG00000006402
Macaca mulatta	ENSMMUG00000017041	ENSMMUG00000021669
Macropus eugenii	ENSMEUG00000002318	ENSMEUG00000007299
Microcebus murinus	ENSMICG00000009932	ENSMICG00000004226
Monodelphis domestica	ENSMODG00000001600	ENSMODG00000003279
Mus musculus	ENSMUSG000000036188	ENSMUSG00000018697
Myotis lucifugus	ENSMLUG00000014935	ENSMLUG00000014754
Ochotona princeps	ENSOPRG00000010614	ENSOPRG00000009390
Ornithorhynchus anatinus	ENSOANG00000012340	ENSOANG00000011510
Oryctolagus cuniculus	ENSOCUG00000016409	ENSOCUG00000014434
Otolemur garnettii	ENSOGAG00000007596	ENSOGAG00000013792
Pan troglodytes	ENSPTRG00000018950	ENSPTRG00000009051
Pongo pygmaeus	ENSPPYG00000017764	ENSPPYG00000008215
Procavia capensis	ENSPCAG00000001061	ENSPCAG00000006324
Pteropus vampyrus	ENSPVAG00000003173	ENSPVAG00000015638
Rattus norvegicus	ENSRNOG00000005623	ENSRNOG00000002778
Sorex araneus	ENSSARG00000002908	ENSSARG00000010626
Spermophilus tridecemlineatus	ENSSTOG00000002497	ENSSTOG00000002458
Sus scrofa	ENSSSCG00000015360	ENSSSCG00000017693
Tarsius syrichta	ENSTSYG00000000150	ENSTSYG00000000789
Tupaia belangeri	ENSTBEG00000009896	ENSTBEG00000008058
Tursiops truncatus	ENSTTRG00000009861	ENSTTRG00000008903
Ursus maritimus	Uma_R014144	Uma_R001159
Vicugna pacos	ENSVPAG00000008437	ENSVPAG00000004492

Gene Names	BLMH (1620 bp)	MED23 (4254 bp)
Ailuropoda melanoleuca	ENSAMEG00000003935	ENSAMEG00000010269
Bos taurus	ENSBTAG00000021370	ENSBTAG00000012418
Callithrix jacchus	ENSCJAG00000013781	ENSCJAG00000003056
Canis familiaris	ENSCAFG00000019005	ENSCAFG00000000380
Cavia porcellus	ENSCPOG00000005048	ENSCPOG00000004032
Choloepus hoffmanni	ENSCHOG00000006832	ENSCHOG00000007125
Dasyopus novemcinctus	ENSDNOG00000001075	ENSDNOG00000007197
Dipodomys ordii	ENSDORG00000008206	ENSDORG00000008716
Echinops telfairi	ENSETEG00000003849	ENSETEG00000018836
Equus caballus	ENSECAG00000019323	ENSECAG00000024638
Erinaceus europaeus	ENSEEUG00000014030	ENSEEUG00000005722
Felis catus	ENSFCAG00000004048	ENSFCAG00000008778
Gallus gallus	ENSGALG00000004259	ENSGALG00000002787
Gorilla gorilla	ENSGGOG00000005500	ENSGGOG00000000978
Homo sapiens	ENSG00000108578	ENSG00000112282
Loxodonta africana	ENSLAFG00000003205	ENSLAFG00000003872
Macaca mulatta	ENSMMUG00000001026	ENSMMUG00000017544
Macropus eugenii	ENSMEUG00000008938	ENSMEUG00000010004
Microcebus murinus	ENSMICG00000000348	ENSMICG00000002926
Monodelphis domestica	ENSMODG00000009909	ENSMODG00000017578
Mus musculus	ENSMUSG00000020840	ENSMUSG00000019984
Myotis lucifugus	ENSMLUG00000002547	ENSMLUG00000016810
Ochotona princeps	ENSOPRG00000007918	ENSOPRG00000002530
Ornithorhynchus anatinus	ENSOANG00000012661	ENSOANG00000010194
Oryctolagus cuniculus	ENSOCUG00000003644	ENSOCUG00000001817
Otolemur garnettii	ENSOGAG00000000825	ENSOGAG00000014102
Pan troglodytes	ENSPTRG00000008959	ENSPTRG00000018601
Pongo pygmaeus	ENSPPYG00000008132	ENSPPYG00000017008
Procavia capensis	ENSPCAG00000013742	ENSPCAG00000006923
Pteropus vampyrus	ENSPVAG00000009283	ENSPVAG00000013512
Rattus norvegicus	ENSRNOG00000003563	ENSRNOG00000013422
Sorex araneus	ENSSARG00000007533	ENSSARG00000001435
Spermophilus tridecemlineatus	ENSSTOG00000004203	ENSSTOG00000014273
Sus scrofa	ENSSSCG00000017796	ENSSSCG00000004196
Tarsius syrichta	ENSTSYG00000011723	ENSTSYG00000010323
Tupaia belangeri	ENSTBEG00000005398	ENSTBEG00000008570
Tursiops truncatus	ENSTTRG00000016341	ENSTTRG00000011360
Ursus maritimus	Uma_R010737	Uma_R003992
Vicugna pacos	ENSVPAG00000003571	ENSVPAG00000005655

Gene Names	ACTR8 (1884 bp)	ARMC8 (2034 bp)
Ailuropoda melanoleuca	ENSAMEG00000002430	ENSAMEG00000006293
Bos taurus	ENSBTAG00000011180	ENSBTAG00000019952
Callithrix jacchus	ENSCJAG00000007566	ENSCJAG00000002405
Canis familiaris	ENSCAFG00000008248	ENSCAFG00000007523
Cavia porcellus	ENSCPOG00000007166	ENSCPOG00000008104
Choloepus hoffmanni	ENSCHOG00000008989	ENSCHOG00000011317
Dasyopus novemcinctus	ENSDNOG00000019728	ENSDNOG00000012301
Dipodomys ordii	ENSDORG00000007783	ENSDORG00000004357
Echinops telfairi	ENSETEG00000015720	ENSETEG00000014732
Equus caballus	ENSECAG00000013264	ENSECAG00000014265
Erinaceus europaeus	ENSEEUG00000013533	ENSEEUG00000010280
Felis catus	ENSFCAG00000013028	ENSFCAG0000001954
Gallus gallus	ENSGALG00000005385	ENSGALG0000001179
Gorilla gorilla	ENSGGOG00000000679	ENSGGOG00000023535
Homo sapiens	ENSG00000113812	ENSG00000114098
Loxodonta africana	ENSLAFG00000001366	ENSLAFG00000010681
Macaca mulatta	ENSMMUG00000019269	ENSMMUG00000021285
Macropus eugenii	ENSMEUG00000008205	ENSMEUG00000014908
Microcebus murinus	ENSMICG00000013353	ENSMICG00000016079
Monodelphis domestica	ENSMODG00000012508	ENSMODG00000018559
Mus musculus	ENSMUSG00000015971	ENSMUSG00000032468
Myotis lucifugus	ENSMLUG00000009558	ENSMLUG00000001644
Ochotona princeps	ENSOPRG00000002241	ENSOPRG00000015648
Ornithorhynchus anatinus	ENSOANG00000007741	ENSOANG00000015678
Oryctolagus cuniculus	ENSOCUG00000009085	ENSOCUG00000015134
Otolemur garnettii	ENSOGAG00000016944	ENSOGAG00000004029
Pan troglodytes	ENSPTRG00000015029	ENSPTRG00000015442
Pongo pygmaeus	ENSPPYG00000013784	ENSPPYG00000014140
Procavia capensis	ENSPCAG00000012206	ENSPCAG00000002788
Pteropus vampyrus	ENSPVAG00000016289	ENSPVAG00000004759
Rattus norvegicus	ENSRNOG00000015280	ENSRNOG00000014521
Sorex araneus	ENSSARG00000000461	ENSSARG00000000988
Spermophilus tridecemlineatus	ENSSTOG00000000501	ENSSTOG00000000788
Sus scrofa	ENSSSCG00000011458	ENSSSCG00000011658
Tarsius syrichta	ENSTSYG00000001438	ENSTSYG00000002216
Tupaia belangeri	ENSTBEG00000007123	ENSTBEG00000000517
Tursiops truncatus	ENSTTRG00000017288	ENSTTRG00000004031
Ursus maritimus	Uma_R001469	Uma_R004120
Vicugna pacos	ENSVPAG00000012550	ENSVPAG00000011713

Gene Names	NOL10 (2079 bp)	RAB3GAP1 (3069 bp)
Ailuropoda melanoleuca	ENSAMEG00000011438	ENSAMEG00000016369
Bos taurus	ENSBTAG00000002716	ENSBTAG00000013449
Callithrix jacchus	ENSCJAG00000006602	ENSCJAG00000011643
Canis familiaris	ENSCAFG00000003435	ENSCAFG00000005042
Cavia porcellus	ENSCPOG00000007706	ENSCPOG00000008653
Choloepus hoffmanni	ENSCHOG00000002784	ENSCHOG00000005085
Dasyopus novemcinctus	ENSDNOG00000003577	ENSDNOG00000010284
Dipodomys ordii	ENSDORG00000001331	ENSDORG00000007961
Echinops telfairi	ENSETEG00000009068	ENSETEG00000011950
Equus caballus	ENSECAG00000015177	ENSECAG00000012270
Erinaceus europaeus	ENSEEUG00000006076	ENSEEUG00000007610
Felis catus	ENSFCAG00000009255	ENSFCAG00000003640
Gallus gallus	ENSGALG00000016445	ENSGALG00000012214
Gorilla gorilla	ENSGGOG00000034826	ENSGGOG00000015070
Homo sapiens	ENSG00000115761	ENSG00000115839
Loxodonta africana	ENSLAFG00000010489	ENSLAFG00000012024
Macaca mulatta	ENSMMUG00000010671	ENSMMUG00000014630
Macropus eugenii	ENSMEUG00000005659	ENSMEUG00000009674
Microcebus murinus	ENSMICG00000004805	ENSMICG00000013854
Monodelphis domestica	ENSMODG00000014784	ENSMODG00000000835
Mus musculus	ENSMUSG00000061458	ENSMUSG00000036104
Myotis lucifugus	ENSMLUG00000012309	ENSMLUG00000016499
Ochotona princeps	ENSOPRG00000013092	ENSOPRG00000001388
Ornithorhynchus anatinus	ENSOANG00000014497	ENSOANG00000007985
Oryctolagus cuniculus	ENSOCUG00000016892	ENSOCUG00000002022
Otolemur garnettii	ENSOGAG00000010494	ENSOGAG00000013299
Pan troglodytes	ENSPTRG00000011651	ENSPTRG00000012491
Pongo pygmaeus	ENSPPYG00000012653	ENSPPYG00000012813
Procavia capensis	ENSPCAG00000002635	ENSPCAG00000007910
Pteropus vampyrus	ENSPVAG00000006339	ENSPVAG00000004437
Rattus norvegicus	ENSRNOG00000005344	ENSRNOG00000003953
Sorex araneus	ENSSARG00000005947	ENSSARG00000004796
Spermophilus tridecemlineatus	ENSSTOG00000005485	ENSSTOG00000010563
Sus scrofa	ENSSSCG00000008635	ENSSSCG00000015695
Tarsius syrichta	ENSTSYG00000010119	ENSTSYG00000013533
Tupaia belangeri	ENSTBEG00000000452	ENSTBEG00000010992
Tursiops truncatus	ENSTTRG00000013158	ENSTTRG00000009802
Ursus maritimus	Uma_R006504	Uma_R012479
Vicugna pacos	ENSVPAG00000005394	ENSVPAG00000001483

Gene Names	PHF3 (6462 bp)	KDSR (1020 bp)
Ailuropoda melanoleuca	ENSAMEG00000002413	ENSAMEG00000006361
Bos taurus	ENSBTAG00000019139	ENSBTAG00000007723
Callithrix jacchus	ENSCJAG00000001708	ENSCJAG00000006662
Canis familiaris	ENSCAFG00000002493	ENSCAFG00000000067
Cavia porcellus	ENSCPOG00000007146	ENSCPOG00000014417
Choloepus hoffmanni	ENSCHOG00000003555	ENSCHOG00000010363
Dasyopus novemcinctus	ENSDNOG00000016118	ENSDNOG00000015783
Dipodomys ordii	ENSDORG00000000873	ENSDORG00000002042
Echinops telfairi	ENSETEG00000003120	ENSETEG00000011800
Equus caballus	ENSECAG00000023016	ENSECAG00000020472
Erinaceus europaeus	ENSEEUG00000009324	ENSEEUG00000014218
Felis catus	ENSFCAG00000002244	ENSFCAG00000008377
Gallus gallus	ENSGALG00000016267	ENSGALG00000012882
Gorilla gorilla	ENSGGOG00000007906	ENSGGOG00000013317
Homo sapiens	ENSG00000118482	ENSG00000119537
Loxodonta africana	ENSLAFG00000013686	ENSLAFG00000000575
Macaca mulatta	ENSMMUG00000017160	ENSMMUG00000006578
Macropus eugenii	ENSMEUG00000010891	ENSMEUG00000013375
Microcebus murinus	ENSMICG00000010727	ENSMICG00000001582
Monodelphis domestica	ENSMODG00000018699	ENSMODG00000005258
Mus musculus	ENSMUSG00000048874	ENSMUSG00000009905
Myotis lucifugus	ENSMLUG00000011843	ENSMLUG00000000120
Ochotona princeps	ENSOPRG00000010869	ENSOPRG00000013624
Ornithorhynchus anatinus	ENSOANG00000002194	ENSOANG00000006349
Oryctolagus cuniculus	ENSOCUG00000015520	ENSOCUG00000014159
Otolemur garnettii	ENSOGAG00000006167	ENSOGAG00000002334
Pan troglodytes	ENSPTRG00000018315	ENSPTRG00000010080
Pongo pygmaeus	ENSPPYG00000016744	ENSPPYG00000009213
Procavia capensis	ENSPCAG00000002297	ENSPCAG00000004130
Pteropus vampyrus	ENSPVAG00000007922	ENSPVAG00000000126
Rattus norvegicus	ENSRNOG00000011756	ENSRNOG00000002781
Sorex araneus	ENSSARG00000002147	ENSSARG00000012765
Spermophilus tridecemlineatus	ENSSTOG00000012986	ENSSTOG00000007407
Sus scrofa	ENSSSCG00000004267	ENSSSCG00000004892
Tarsius syrichta	ENSTSYG00000003081	ENSTSYG00000009477
Tupaia belangeri	ENSTBEG00000000688	ENSTBEG00000012339
Tursiops truncatus	ENSTTRG00000011558	ENSTTRG00000005087
Ursus maritimus	Uma_R013974	Uma_R004384
Vicugna pacos	ENSVPAG00000005928	ENSVPAG00000008324

Gene Names	YLPM1 (6975 bp)	UTP20 (8544 bp)
Ailuropoda melanoleuca	ENSAMEG00000018299	ENSAMEG00000016416
Bos taurus	ENSBTAG00000008287	ENSBTAG00000003239
Callithrix jacchus	ENSCJAG00000020522	ENSCJAG00000001913
Canis familiaris	ENSCAFG00000016981	ENSCAFG00000006964
Cavia porcellus	ENSCPOG00000027568	ENSCPOG00000003129
Choloepus hoffmanni	ENSCHOG00000013132	ENSCHOG00000003532
Dasypus novemcinctus	ENSDNOG00000005057	ENSDNOG00000016845
Dipodomys ordii	ENSDORG00000016716	ENSDORG00000014762
Echinops telfairi	ENSETEG00000009066	ENSETEG00000019983
Equus caballus	ENSECAG00000016305	ENSECAG00000006876
Erinaceus europaeus	ENSEEUG00000014265	ENSEEUG00000003774
Felis catus	ENSFCAG00000006370	ENSFCAG00000006150
Gallus gallus	ENSGALG00000010277	ENSGALG00000011643
Gorilla gorilla	ENSGGOG00000014195	ENSGGOG00000004904
Homo sapiens	ENSG00000119596	ENSG00000120800
Loxodonta africana	ENSLAFG00000012536	ENSLAFG00000012983
Macaca mulatta	ENSMMUG00000004255	ENSMMUG00000012891
Macropus eugenii	ENSMEUG00000002409	ENSMEUG00000015457
Microcebus murinus	ENSMICG00000006067	ENSMICG00000015736
Monodelphis domestica	ENSMODG00000006168	ENSMODG00000003141
Mus musculus	ENSMUSG00000021244	ENSMUSG00000004356
Myotis lucifugus	ENSMLUG00000004983	ENSMLUG00000002313
Ochotona princeps	ENSOPRG00000011778	ENSOPRG00000010546
Ornithorhynchus anatinus	ENSOANG00000009814	ENSOANG00000005578
Oryctolagus cuniculus	ENSOCUG00000008083	ENSOCUG00000010475
Otolemur garnettii	ENSOGAG00000001323	ENSOGAG00000015130
Pan troglodytes	ENSPTRG00000006541	ENSPTRG00000005349
Pongo pygmaeus	ENSPPYG00000006231	ENSPPYG00000004871
Procavia capensis	ENSPCAG00000006232	ENSPCAG00000012791
Pteropus vampyrus	ENSPVAG00000006658	ENSPVAG00000008113
Rattus norvegicus	ENSRNOG00000027317	ENSRNOG00000005823
Sorex araneus	ENSSARG00000003296	ENSSARG00000002796
Spermophilus tridecemlineatus	ENSSTOG00000014581	ENSSTOG00000015995
Sus scrofa	ENSSSCG00000002372	ENSSSCG00000000869
Tarsius syrichta	ENSTSYG00000009612	ENSTSYG00000003040
Tupaia belangeri	ENSTBEG00000013683	ENSTBEG00000011917
Tursiops truncatus	ENSTTRG00000001907	ENSTTRG00000017195
Ursus maritimus	Uma_R002267	Uma_R002376
Vicugna pacos	ENSVPAG00000003067	ENSVPAG00000011620

Gene Names	RECK (2943 bp)	ECD (2091 bp)
Ailuropoda melanoleuca	ENSAMEG00000009966	ENSAMEG00000016960
Bos taurus	ENSBTAG0000000076	ENSBTAG00000000315
Callithrix jacchus	ENSCJAG00000010143	ENSCJAG00000007511
Canis familiaris	ENSCAFG00000002281	ENSCAFG00000014617
Cavia porcellus	ENSCPOG00000006953	ENSCPOG00000004428
Choloepus hoffmanni	ENSCHOG00000002985	ENSCHOG00000002175
Dasyopus novemcinctus	ENSDNOG00000008915	ENSDNOG00000009333
Dipodomys ordii	ENSDORG00000012827	ENSDORG00000007680
Echinops telfairi	ENSETEG00000016237	ENSETEG00000014869
Equus caballus	ENSECAG00000010426	ENSECAG00000022704
Erinaceus europaeus	ENSEEUG00000010339	ENSEEUG00000000796
Felis catus	ENSFCAG00000012761	ENSFCAG00000008497
Gallus gallus	ENSGALG00000012626	ENSGALG00000002686
Gorilla gorilla	ENSGGOG00000003313	ENSGGOG00000016428
Homo sapiens	ENSG00000122707	ENSG00000122882
Loxodonta africana	ENSLAFG00000008926	ENSLAFG00000004754
Macaca mulatta	ENSMMUG00000022613	ENSMMUG00000011280
Macropus eugenii	ENSMEUG00000005729	ENSMEUG00000006994
Microcebus murinus	ENSMICG00000017672	ENSMICG00000013871
Monodelphis domestica	ENSMODG00000002595	ENSMODG00000000149
Mus musculus	ENSMUSG00000028476	ENSMUSG00000021810
Myotis lucifugus	ENSMLUG00000006798	ENSMLUG00000004522
Ochotona princeps	ENSOPRG00000014513	ENSOPRG00000001027
Ornithorhynchus anatinus	ENSOANG00000014877	ENSOANG00000001121
Oryctolagus cuniculus	ENSOCUG00000015652	ENSOCUG00000017621
Otolemur garnettii	ENSOGAG00000007846	ENSOGAG00000003488
Pan troglodytes	ENSPTRG00000020928	ENSPTRG00000002622
Pongo pygmaeus	ENSPPYG00000019072	ENSPPYG00000002345
Procavia capensis	ENSPCAG00000009601	ENSPCAG00000001558
Pteropus vampyrus	ENSPVAG00000017912	ENSPVAG00000012992
Rattus norvegicus	ENSRNOG00000014863	ENSRNOG00000042253
Sorex araneus	ENSSARG00000000257	ENSSARG00000013642
Spermophilus tridecemlineatus	ENSSTOG00000004971	ENSSTOG00000002128
Sus scrofa	ENSSSCG00000005338	ENSSSCG00000010295
Tarsius syrichta	ENSTSYG00000002242	ENSTSYG00000011497
Tupaia belangeri	ENSTBEG00000008707	ENSTBEG00000006690
Tursiops truncatus	ENSTTRG00000016280	ENSTTRG00000000816
Ursus maritimus	Uma_R009607	Uma_R012585
Vicugna pacos	ENSVPAG00000006648	ENSVPAG00000007257

Gene Names	NUP85 (2061 bp)
Ailuropoda melanoleuca	ENSAMEG00000009192
Bos taurus	ENSBTAG00000016126
Callithrix jacchus	ENSCJAG00000014508
Canis familiaris	ENSCAFG00000004729
Cavia porcellus	ENSCPOG00000001185
Choloepus hoffmanni	ENSCHOG00000001340
Dasyopus novemcinctus	ENSDNOG00000018516
Dipodomys ordii	ENSDORG00000005137
Echinops telfairi	ENSETEG00000019962
Equus caballus	ENSECAG00000019159
Erinaceus europaeus	ENSEEUG00000015676
Felis catus	ENSFCAG00000014513
Gallus gallus	ENSGALG00000007974
Gorilla gorilla	ENSGGOG00000006439
Homo sapiens	ENSG00000125450
Loxodonta africana	ENSLAFG00000002866
Macaca mulatta	ENSMMUG00000018018
Macropus eugenii	ENSMEUG00000016629
Microcebus murinus	ENSMICG00000007562
Monodelphis domestica	ENSMODG00000007246
Mus musculus	ENSMUSG00000020739
Myotis lucifugus	ENSMLUG00000015211
Ochotona princeps	ENSOPRG00000010899
Ornithorhynchus anatinus	ENSOANG00000008323
Oryctolagus cuniculus	ENSOCUG00000006648
Otolemur garnettii	ENSOGAG00000001612
Pan troglodytes	ENSPTRG00000009637
Pongo pygmaeus	ENSPPYG00000008621
Procavia capensis	ENSPCAG00000015658
Pteropus vampyrus	ENSPVAG00000008429
Rattus norvegicus	ENSRNOG00000003673
Sorex araneus	ENSSARG00000008043
Spermophilus tridecemlineatus	ENSSTOG00000015175
Sus scrofa	ENSSSCG00000017207
Tarsius syrichta	ENSTSYG00000010481
Tupaia belangeri	ENSTBEG00000002209
Tursiops truncatus	ENSTTRG00000014395
Ursus maritimus	Uma_R000880
Vicugna pacos	ENSVPAG00000011848

(C) 39TaxonSet (unedited alignment) %GC Content

Gene Names	VPS41 (2583 bp)	AQR (4788 bp)	ZCCHC8 (2397 bp)
Ailuropoda_melanoleuca	45.26	39.91	44.22
Bos_taurus	43.94	40.08	43.6
Callithrix_jacchus	41.97	39.08	32.46
Canis_familiaris	43.67	39.66	43.97
Cavia_porcellus	46.03	20.89	38.72
Choloepus_hoffmanni	35.11	29.87	20.61
Dasypus_novemcinctus	34.26	29.05	30.41
Dipodomys_ordii	40.15	33.73	30.96
Echinops_telfairi	13.05	36.05	36.88
Equus_caballus	44.33	39.93	43.01
Erinaceus_europaeus	29.62	34.75	32.62
Felis_catus	21.76	24.16	42.85
Gallus_gallus	41.31	37.43	36.63
Gorilla_gorilla	37.44	38.99	42.39
Homo_sapiens	41.58	38.97	41.64
Loxodonta_africana	42.93	40.69	42.72
Macaca_mulatta	40.65	40.6	42.39
Macropus_eugenii	36.31	26.48	37.17
Microcebus_murinus	35.58	29.64	38.63
Monodelphis_domestica	54.24	37.45	43.8
Mus_musculus	43.75	44.42	46.14
Myotis_lucifugus	38.79	36.55	23.45
Ochotona_princeps	39.37	29.49	48.98
Ornithorhynchus_anatinus	46.19	58.46	43.6
Oryctolagus_cuniculus	44.06	40.08	45.72
Otolemur_garnettii	36.97	34.19	29.45
Pan_troglodytes	41.66	39.08	41.09
Pongo_abelii	41.58	38.7	41.76
Procavia_capensis	37.71	35.67	41.97
Pteropus_vampyrus	42.2	34.92	43.97
Rattus_norvegicus	43.55	43.61	43.85
Sorex_araneus	36.74	34.84	39.05
Spermophilus_tridecemlineatus	32.87	27.86	34.92
Sus_scrofa	50.56	36.13	41.59
Tarsius_syrichta	31.24	35.9	23.11
Tupaia_belangeri	41.73	31.85	36.17
Tursiops_truncatus	44.41	39.75	41.8
Ursus_maritimus	44.25	37.68	43.97
Vicugna_pacos	27.84	40.66	30.16

Gene Names	OTC (1077 bp)	NSUN2 (2640 bp)	SART3 (3024 bp)
Ailuropoda_melanoleuca	44.75	44.55	52.94
Bos_taurus	45.78	51.59	39.38
Callithrix_jacchus	43.83	43.94	51.59
Canis_familiaris	43.64	44.24	52.65
Cavia_porcellus	42.06	49.96	53.44
Choloepus_hoffmanni	26.93	26.29	29.07
Dasyopus_novemcinctus	39.18	36.7	39.29
Dipodomys_ordii	26.56	36.48	53.37
Echinops_telfairi	39.28	45.19	37.33
Equus_caballus	44.75	43.3	55.49
Erinaceus_europaeus	37.6	34.36	52.94
Felis_catus	40.48	37.95	45.3
Gallus_gallus	42.8	41.52	40.28
Gorilla_gorilla	43.73	31.02	50.3
Homo_sapiens	43.64	42.46	50.23
Loxodonta_africana	44.57	44.02	52.78
Macaca_mulatta	44.2	42.5	50.56
Macropus_eugenii	25.81	20.91	42.13
Microcebus_murinus	39.46	35.95	51.62
Monodelphis_domestica	43.83	34.81	43.82
Mus_musculus	44.38	43.48	55.49
Myotis_lucifugus	37.51	36.48	43.52
Ochotona_princeps	20.8	37.35	52.88
Ornithorhynchus_anatinus	48.65	42.73	51.22
Oryctolagus_cuniculus	42.99	41.59	56.98
Otolemur_garnettii	36.4	33.79	45.93
Pan_troglodytes	34.73	42.99	50.2
Pongo_abelii	43.64	42.73	51.42
Procavia_capensis	27.76	35.15	46.43
Pteropus_vampyrus	40.3	45.49	47.85
Rattus_norvegicus	45.13	45.04	53.7
Sorex_araneus	22.28	17.58	49.14
Spermophilus_tridecemlineatus	38.44	37.35	52.74
Sus_scrofa	43.36	52.95	37.24
Tarsius_syrichtha	44.38	38.71	42.29
Tupaia_belangeri	34.91	39.47	48.28
Tursiops_truncatus	44.75	43.98	54.66
Ursus_maritimus	39.28	41.52	52.88
Vicugna_pacos	37.98	27.05	30.19

Gene Names	KIFAP3 (2496 bp)	DNAJC10 (2430 bp)
Ailuropoda_melanoleuca	37.5	38.68
Bos_taurus	38.42	37.78
Callithrix_jacchus	37.38	38.19
Canis_familiaris	37.14	38.6
Cavia_porcellus	37.62	40.91
Choloepus_hoffmanni	35.58	27.61
Dasyopus_novemcinctus	34.46	30.62
Dipodomys_ordii	34.74	31.6
Echinops_telfairi	32.69	35.51
Equus_caballus	37.14	38.31
Erinaceus_europaeus	33.81	33.33
Felis_catus	24.16	35.84
Gallus_gallus	41.43	40.82
Gorilla_gorilla	37.26	37.86
Homo_sapiens	37.54	38.07
Loxodonta_africana	38.98	37.94
Macaca_mulatta	37.06	37.41
Macropus_eugenii	21.88	22.72
Microcebus_murinus	26.16	34.07
Monodelphis_domestica	34.74	36.95
Mus_musculus	41.87	42.22
Myotis_lucifugus	34.09	26.38
Ochotona_princeps	31.17	35.84
Ornithorhynchus_anatinus	42.63	42.67
Oryctolagus_cuniculus	37.86	37.45
Otolemur_garnettii	26.52	28.64
Pan_troglodytes	37.62	37.82
Pongo_abelii	36.46	38.02
Procavia_capensis	31.45	37.74
Pteropus_vampyrus	37.34	35.47
Rattus_norvegicus	41.43	42.14
Sorex_araneus	26.76	34.07
Spermophilus_tridecemlineatus	23.72	30.58
Sus_scrofa	37.98	31.77
Tarsius_syrichta	32.45	34.98
Tupaia_belangeri	32.25	22.35
Tursiops_truncatus	35.06	29.59
Ursus_maritimus	37.38	37.08
Vicugna_pacos	35.82	35.93

Gene Names	MTIF2 (2232 bp)	ADNP (3375 bp)	EEF2K (2193 bp)
Ailuropoda_melanoleuca	40.77	44.53	57
Bos_taurus	41.13	45.48	58.05
Callithrix_jacchus	39.65	43.2	56.04
Canis_familiaris	40.41	44.18	55.31
Cavia_porcellus	40.23	43.97	55.36
Choloepus_hoffmanni	29.12	31.79	39.03
Dasyopus_novemcinctus	30.78	31.7	39.35
Dipodomys_ordii	34.36	44.89	36.53
Echinops_telfairi	42.79	48.06	48.97
Equus_caballus	40.86	43.88	57.14
Erinaceus_europaeus	34.05	42.4	46.28
Felis_catus	25.9	31.05	49.57
Gallus_gallus	41.49	31.59	46.65
Gorilla_gorilla	39.83	42.93	49.43
Homo_sapiens	39.92	42.93	56.86
Loxodonta_africana	41.22	45.72	55.22
Macaca_mulatta	38.98	43.02	56.63
Macropus_eugenii	32.03	37.13	39.67
Microcebus_murinus	37.32	42.81	44.92
Monodelphis_domestica	38.44	39.82	47.88
Mus_musculus	41.17	44.95	55.45
Myotis_lucifugus	28.67	42.1	56.45
Ochotona_princeps	40.41	27.94	58.78
Ornithorhynchus_anatinus	43.46	59.79	46.06
Oryctolagus_cuniculus	34.9	53.51	57.77
Otolemur_garnettii	28.05	42.34	39.12
Pan_troglodytes	39.56	42.79	56.54
Pongo_abelii	39.78	42.9	56.86
Procavia_capensis	42.07	35.2	42.82
Pteropus_vampyrus	39.25	38.34	58.05
Rattus_norvegicus	41.85	44.74	55.63
Sorex_araneus	39.25	51.97	27.09
Spermophilus_tridecemlineatus	30.56	37.69	47.24
Sus_scrofa	39.87	44.74	47.42
Tarsius_syrichta	35.48	44.33	38.26
Tupaia_belangeri	37.59	42.04	41.09
Tursiops_truncatus	36.6	44.21	56.13
Ursus_maritimus	40.95	44.44	56.95
Vicugna_pacos	39.7	43.94	44.69

Gene Names	GARS (2340 bp)	ANKMY2 (1419 bp)	AATF (1854 bp)
Ailuropoda_melanoleuca	46.32	40.87	46.28
Bos_taurus	45.98	39.96	48.49
Callithrix_jacchus	45	40.52	47.57
Canis_familiaris	45.68	39.25	45.95
Cavia_porcellus	38.5	43.27	41.48
Choloepus_hoffmanni	39.44	33.54	34.3
Dasyopus_novemcinctus	31.62	26.57	39.05
Dipodomys_ordii	47.56	26.15	29.77
Echinops_telfairi	41.2	39.25	49.35
Equus_caballus	43.29	40.45	47.03
Erinaceus_europaeus	27.86	19.03	40.35
Felis_catus	37.82	34.6	36.35
Gallus_gallus	48.21	43.9	47.52
Gorilla_gorilla	45.3	39.96	42.45
Homo_sapiens	45.04	40.03	45.58
Loxodonta_africana	45.43	40.24	41.96
Macaca_mulatta	34.06	40.38	45.69
Macropus_eugenii	41.88	31.85	41.1
Microcebus_murinus	41.97	32.91	29.67
Monodelphis_domestica	28.08	50.81	43.74
Mus_musculus	47.18	44.82	42.34
Myotis_lucifugus	41.28	37.14	41.96
Ochotona_princeps	44.36	40.45	36.41
Ornithorhynchus_anatinus	57.14	42.85	45.25
Oryctolagus_cuniculus	48.59	47.57	47.14
Otolemur_garnettii	40.64	38.55	36.79
Pan_troglodytes	45.17	40.1	45.63
Pongo_abelii	45.6	39.82	45.52
Procavia_capensis	45.43	29.53	42.93
Pteropus_vampyrus	48.63	33.69	44.61
Rattus_norvegicus	47.22	45.45	41.69
Sorex_araneus	30.04	39.32	40.61
Spermophilus_tridecemlineatus	34.23	26.07	36.89
Sus_scrofa	47.91	23.54	46.66
Tarsius_syrichta	43.46	38.41	30.96
Tupaia_belangeri	42.05	29.95	35.98
Tursiops_truncatus	39.32	40.03	45.74
Ursus_maritimus	39.36	37	40.51
Vicugna_pacos	42.26	40.73	37.59

Gene Names	BLMH (1620 bp)	MED23 (4254 bp)	ACTR8 (1884 bp)
Ailuropoda_melanoleuca	39.32	42.5	47.93
Bos_taurus	39.38	42.88	48.46
Callithrix_jacchus	39.94	41.65	46.44
Canis_familiaris	39.32	42.62	45.91
Cavia_porcellus	39.88	48.24	47.45
Choloepus_hoffmanni	34.88	31.48	29.3
Dasyopus_novemcinctus	41.6	31.9	43.37
Dipodomys_ordii	29.26	33.69	45.44
Echinops_telfairi	33.95	40.53	46.39
Equus_caballus	31.67	43.51	42.89
Erinaceus_europaeus	25.93	33.4	42.36
Felis_catus	32.28	32.23	36.62
Gallus_gallus	41.98	43.46	46.97
Gorilla_gorilla	39.38	41.82	46.87
Homo_sapiens	39.44	41.7	46.97
Loxodonta_africana	38.64	42.38	47.19
Macaca_mulatta	39.38	41.49	46.71
Macropus_eugenii	51.6	34.67	40.92
Microcebus_murinus	32.41	29.38	27.18
Monodelphis_domestica	39.75	40.79	54.3
Mus_musculus	39.2	47.44	50.48
Myotis_lucifugus	40.19	36.2	39.49
Ochotona_princeps	46.48	29.95	47.56
Ornithorhynchus_anatinus	41.85	43.44	37.9
Oryctolagus_cuniculus	40.25	42.24	55.15
Otolemur_garnettii	35.49	33.31	47.4
Pan_troglodytes	50.25	41.26	46.97
Pongo_abelii	39.63	41.49	46.34
Procavia_capensis	47.47	37.02	37.63
Pteropus_vampyrus	45.49	41.21	46.5
Rattus_norvegicus	39.32	47.39	50.96
Sorex_araneus	28.33	30.35	49.73
Spermophilus_tridecemlineatus	33.27	32.6	25.37
Sus_scrofa	21.48	40.86	46.34
Tarsius_syrichtha	44.81	42.03	39.65
Tupaia_belangeri	31.79	38.81	33.92
Tursiops_truncatus	48.46	42.31	45.28
Ursus_maritimus	39.2	41.98	47.66
Vicugna_pacos	38.89	35.14	46.5

Gene Names	ARMC8 (2034 bp)	NOL10 (2079 bp)
Ailuropoda_melanoleuca	41.99	44.3
Bos_taurus	42.97	43.67
Callithrix_jacchus	41.4	41.51
Canis_familiaris	42.53	43.43
Cavia_porcellus	42.18	53.44
Choloepus_hoffmanni	27.38	34.78
Dasyopus_novemcinctus	28.86	33.14
Dipodomys_ordii	32.6	25.73
Echinops_telfairi	33.24	39.11
Equus_caballus	41.94	41.46
Erinaceus_europaeus	40.86	33.86
Felis_catus	22.27	41.65
Gallus_gallus	42.77	41.22
Gorilla_gorilla	41.79	26.17
Homo_sapiens	42.23	41.08
Loxodonta_africana	43.22	40.79
Macaca_mulatta	40.9	40.02
Macropus_eugenii	31.76	26.55
Microcebus_murinus	39.92	26.12
Monodelphis_domestica	39.48	38.14
Mus_musculus	44.99	44.4
Myotis_lucifugus	28.61	36.03
Ochotona_princeps	47.59	31.31
Ornithorhynchus_anatinus	35	33.29
Oryctolagus_cuniculus	43.61	47.67
Otolemur_garnettii	31.17	28.52
Pan_troglodytes	39.53	41.08
Pongo_abelii	36.63	40.69
Procavia_capensis	27.34	35.26
Pteropus_vampyrus	41.64	41.27
Rattus_norvegicus	44.35	44.3
Sorex_araneus	40.61	41.41
Spermophilus_tridecemlineatus	17.85	31.46
Sus_scrofa	18.24	45.74
Tarsius_syrichtha	29.74	37.23
Tupaia_belangeri	36.38	33.62
Tursiops_truncatus	36.73	38.43
Ursus_maritimus	37.41	38.24
Vicugna_pacos	42.18	35.4

Gene Names	RAB3GAP1 (3069 bp)	PHF3 (6462 bp)
Ailuropoda_melanoleuca	42.1	37.71
Bos_taurus	42.95	40.14
Callithrix_jacchus	41.22	37.73
Canis_familiaris	41.61	37.56
Cavia_porcellus	41.38	38.35
Choloepus_hoffmanni	36.66	23.49
Dasyopus_novemcinctus	30.34	23.77
Dipodomys_ordii	37.44	33.19
Echinops_telfairi	26.07	36.49
Equus_caballus	42.33	40.13
Erinaceus_europaeus	34.41	35.93
Felis_catus	26.75	21.08
Gallus_gallus	44.12	39.03
Gorilla_gorilla	42.59	37.82
Homo_sapiens	42.49	37.77
Loxodonta_africana	42.49	38.64
Macaca_mulatta	42.52	37.67
Macropus_eugenii	30.43	31.45
Microcebus_murinus	25.42	20.81
Monodelphis_domestica	40.8	35.22
Mus_musculus	46.56	42.73
Myotis_lucifugus	35.29	33.81
Ochotona_princeps	25.94	22.75
Ornithorhynchus_anatinus	51.42	24.14
Oryctolagus_cuniculus	42.07	37.94
Otolemur_garnettii	34.25	29.93
Pan_troglodytes	42.23	37.71
Pongo_abelii	41.87	37.08
Procavia_capensis	41.25	36.46
Pteropus_vampyrus	40.76	35.42
Rattus_norvegicus	41.87	42.6
Sorex_araneus	29.23	39.17
Spermophilus_tridecemlineatus	23.49	21.82
Sus_scrofa	32.62	38.84
Tarsius_syrichta	39.23	38.19
Tupaia_belangeri	32.68	34.99
Tursiops_truncatus	40.8	39.69
Ursus_maritimus	40.01	37.64
Vicugna_pacos	34.77	33.87

Gene Names	KDSR (1020 bp)	YLPM1 (6975 bp)	UTP20 (8544 bp)
Ailuropoda_melanoleuca	44.31	47.83	41.08
Bos_taurus	48.43	43.77	41.32
Callithrix_jacchus	46.96	46.74	40.46
Canis_familiaris	43.82	43.01	40.75
Cavia_porcellus	45.49	35.74	55.36
Choloepus_hoffmanni	44.51	22.14	31.71
Dasyopus_novemcinctus	20.39	36.95	28.8
Dipodomys_ordii	41.67	32.79	32.75
Echinops_telfairi	37.25	42.31	38.47
Equus_caballus	40.98	42.94	41.07
Erinaceus_europaeus	32.25	29.02	28.11
Felis_catus	35.88	21.82	31.12
Gallus_gallus	43.33	42.71	45.67
Gorilla_gorilla	47.45	46.47	40.73
Homo_sapiens	47.65	46.71	40.91
Loxodonta_africana	44.22	42.98	41.57
Macaca_mulatta	47.94	38.77	40.78
Macropus_eugenii	39.61	36.24	40.86
Microcebus_murinus	43.43	36.36	34.53
Monodelphis_domestica	43.73	40.06	45.46
Mus_musculus	49.71	42.02	45.59
Myotis_lucifugus	41.37	33.32	38.9
Ochotona_princeps	50.59	40.11	36.94
Ornithorhynchus_anatinus	37.45	42.64	40.15
Oryctolagus_cuniculus	50.69	29.56	41.43
Otolemur_garnettii	38.92	35.8	37.84
Pan_troglodytes	47.65	42.32	40.19
Pongo_abelii	47.55	15.76	35.42
Procavia_capensis	37.35	34.62	31.65
Pteropus_vampyrus	42.16	41.48	40.95
Rattus_norvegicus	50.69	44.03	35.67
Sorex_araneus	35.98	30.32	27.97
Spermophilus_tridecemlineatus	38.82	36.16	33.82
Sus_scrofa	48.92	47.25	42.59
Tarsius_syrichta	38.33	39.35	38.25
Tupaia_belangeri	23.33	32.54	34.49
Tursiops_truncatus	48.24	38.22	38.88
Ursus_maritimus	41.96	47.37	40.78
Vicugna_pacos	43.63	26.05	36.4

Gene Names	RECK (2943 bp)	ECD (2091 bp)	NUP85 (2061 bp)
Ailuropoda_melanoleuca	46.14	41.46	49.68
Bos_taurus	47.23	41.94	52.74
Callithrix_jacchus	45.36	43.14	49.73
Canis_familiaris	45.97	40.94	48.67
Cavia_porcellus	48.28	41.13	50.32
Choloepus_hoffmanni	33.3	29.41	34.11
Dasyopus_novemcinctus	37.82	28.6	32.9
Dipodomys_ordii	35.44	35.1	38.14
Echinops_telfairi	34.11	35.29	44.93
Equus_caballus	45.84	40.27	49.3
Erinaceus_europaeus	24.57	40.55	32.75
Felis_catus	29.7	29.08	38.04
Gallus_gallus	39.01	47.25	51.24
Gorilla_gorilla	43.8	41.08	49.93
Homo_sapiens	45.84	43.66	49.59
Loxodonta_africana	45.4	42.95	51.43
Macaca_mulatta	45.84	40.84	49.64
Macropus_eugenii	22.6	39.93	34.84
Microcebus_murinus	37.44	28.41	44.93
Monodelphis_domestica	35.47	41.18	45.41
Mus_musculus	50.93	46.68	49.54
Myotis_lucifugus	36.29	23.91	49.88
Ochotona_princeps	43.56	43.42	50.9
Ornithorhynchus_anatinus	52.29	45.86	53.37
Oryctolagus_cuniculus	50.87	41.85	55.9
Otolemur_garnettii	41.79	31.37	26.93
Pan_troglodytes	45.87	38.69	49.54
Pongo_abelii	45.57	41.03	49.78
Procavia_capensis	35.61	21.33	37.8
Pteropus_vampyrus	41.56	28.26	49.2
Rattus_norvegicus	52.02	25.39	49.64
Sorex_araneus	46.79	31.37	40.66
Spermophilus_tridecemlineatus	36.94	26.11	36.2
Sus_scrofa	44.55	41.08	50.8
Tarsius_syrichtha	45.16	41.27	24.84
Tupaia_belangeri	47.71	23.67	31.49
Tursiops_truncatus	43.63	41.08	50.07
Ursus_maritimus	43.43	41.94	45.95
Vicugna_pacos	38.23	37.06	27.95

(D) 39TaxonSet (unedited alignment) Model Fit Test P values

Gene Names	VPS41 (2583 bp)	AQR (4788 bp)	ZCCHC8 (2397 bp)
Ailuropoda_melanoleuca	0.00	0.00	1.00
Bos_taurus	0.00	0.00	1.00
Callithrix_jacchus	0.00	0.00	1.00
Canis_familiaris	0.00	0.00	1.00
Cavia_porcellus	0.00	1.00	1.00
Choloepus_hoffmanni	0.00	0.00	1.00
Dasypus_novemcinctus	0.00	0.00	0.00
Dipodomys_ordii	0.00	1.00	1.00
Echinops_telfairi	1.00	0.00	1.00
Equus_caballus	0.00	0.00	1.00
Erinaceus_europaeus	0.00	0.00	0.00
Felis_catus	0.01	0.00	1.00
Gallus_gallus	0.00	0.00	0.00
Gorilla_gorilla	0.00	0.00	0.00
Homo_sapiens	0.00	0.00	0.00
Loxodonta_africana	0.00	0.00	0.96
Macaca_mulatta	0.00	0.00	0.00
Macropus_eugenii	0.00	0.98	1.00
Microcebus_murinus	0.00	0.00	0.09
Monodelphis_domestica	0.01	0.00	0.00
Mus_musculus	0.00	0.06	1.00
Myotis_lucifugus	0.00	0.00	0.00
Ochotona_princeps	0.00	0.00	1.00
Ornithorhynchus_anatinus	0.00	0.00	0.00
Oryctolagus_cuniculus	0.00	0.00	1.00
Otolemur_garnettii	0.00	0.00	0.00
Pan_troglodytes	0.00	0.00	0.00
Pongo_abelii	0.00	0.00	0.00
Procyon_capensis	0.00	0.00	1.00
Pteropus_vampyrus	0.00	0.00	1.00
Rattus_norvegicus	0.00	0.00	1.00
Sorex_araneus	0.00	0.00	1.00
Spermophilus_tridecemlineatus	0.00	0.00	1.00
Sus_scrofa	0.00	0.00	0.00
Tarsius_syrichta	0.00	0.00	1.00
Tupaia_belangeri	0.00	0.00	1.00
Tursiops_truncatus	0.00	0.00	0.89
Ursus_maritimus	0.00	0.00	1.00
Vicugna_pacos	0.00	0.00	0.00
Overall Fit of the Simulation	0.00	0.00	1.00

Gene Names	OTC (1077 bp)	NSUN2 (2640 bp)	SART3 (3024 bp)
Ailuropoda_melanoleuca	0.06	0.00	0.00
Bos_taurus	0.05	1.00	1.00
Callithrix_jacchus	0.13	0.00	0.00
Canis_familiaris	0.03	0.00	0.00
Cavia_porcellus	0.05	1.00	0.00
Choloepus_hoffmanni	1.00	1.00	1.00
Dasypus_novemcinctus	0.04	0.99	0.00
Dipodomys_ordii	0.50	1.00	1.00
Echinops_telfairi	0.40	1.00	1.00
Equus_caballus	0.12	0.00	0.00
Erinaceus_europaeus	0.38	1.00	1.00
Felis_catus	0.02	1.00	0.00
Gallus_gallus	0.79	0.00	0.00
Gorilla_gorilla	0.11	1.00	0.00
Homo_sapiens	0.17	0.00	0.00
Loxodonta_africana	0.23	1.00	0.00
Macaca_mulatta	0.15	0.00	0.00
Macropus_eugenii	0.00	0.00	0.00
Microcebus_murinus	0.00	1.00	0.00
Monodelphis_domestica	0.11	0.00	0.00
Mus_musculus	0.18	0.00	0.03
Myotis_lucifugus	0.22	0.00	1.00
Ochotona_princeps	1.00	1.00	1.00
Ornithorhynchus_anatinus	0.00	0.00	1.00
Oryctolagus_cuniculus	0.18	1.00	1.00
Otolemur_garnettii	1.00	0.09	0.00
Pan_troglodytes	1.00	0.00	0.00
Pongo_abelii	0.20	0.00	0.00
Procavia_capensis	0.01	1.00	0.00
Pteropus_vampyrus	0.25	1.00	0.00
Rattus_norvegicus	0.22	0.00	0.00
Sorex_araneus	1.00	1.00	0.29
Spermophilus_tridecemlineatus	0.29	0.00	1.00
Sus_scrofa	1.00	1.00	1.00
Tarsius_syrichta	0.01	0.00	0.00
Tupaia_belangeri	1.00	1.00	0.00
Tursiops_truncatus	0.05	0.48	0.00
Ursus_maritimus	1.00	0.18	0.00
Vicugna_pacos	1.00	1.00	1.00
Overall Fit of the Simulation	1.00	1.00	0.55

Gene Names	KIFAP3 (2496 bp)	DNAJC10 (2430 bp)	MTIF2 (2232 bp)
Ailuropoda_melanoleuca	0.00	0.00	0.00
Bos_taurus	0.00	0.00	0.03
Callithrix_jacchus	0.00	0.00	0.00
Canis_familiaris	0.00	0.00	0.00
Cavia_porcellus	0.00	0.08	0.00
Choloepus_hoffmanni	0.00	0.00	1.00
Dasypus_novemcinctus	0.00	0.00	1.00
Dipodomys_ordii	1.00	1.00	0.00
Echinops_telfairi	0.00	0.59	0.00
Equus_caballus	0.00	0.00	0.00
Erinaceus_europaeus	0.00	1.00	0.19
Felis_catus	1.00	0.00	0.00
Gallus_gallus	1.00	0.00	0.01
Gorilla_gorilla	0.00	0.00	0.00
Homo_sapiens	0.00	0.00	0.00
Loxodonta_africana	0.01	0.00	1.00
Macaca_mulatta	0.00	0.00	0.00
Macropus_eugenii	0.10	0.00	1.00
Microcebus_murinus	0.00	0.00	0.00
Monodelphis_domestica	0.02	0.00	0.00
Mus_musculus	1.00	0.83	0.01
Myotis_lucifugus	0.00	1.00	1.00
Ochotona_princeps	0.00	0.00	0.01
Ornithorhynchus_anatinus	1.00	1.00	0.09
Oryctolagus_cuniculus	0.00	0.00	1.00
Otolemur_garnettii	0.00	0.00	1.00
Pan_troglodytes	0.00	0.00	0.00
Pongo_abelii	0.00	0.00	0.00
Procavia_capensis	0.00	0.00	0.00
Pteropus_vampyrus	1.00	0.00	0.00
Rattus_norvegicus	1.00	0.28	0.00
Sorex_araneus	1.00	0.00	0.00
Spermophilus_tridecemlineatus	0.00	0.00	1.00
Sus_scrofa	0.00	1.00	0.00
Tarsius_syrichta	0.91	0.00	1.00
Tupaia_belangeri	0.00	0.00	0.00
Tursiops_truncatus	0.00	1.00	0.00
Ursus_maritimus	0.00	0.01	0.00
Vicugna_pacos	0.00	0.00	0.00
Overall Fit of the Simulation	0.03	0.00	0.64

Gene Names	ADNP (3375 bp)	EEF2K (2193 bp)	GARS (2340 bp)
Ailuropoda_melanoleuca	0.00	0.01	0.00
Bos_taurus	0.00	0.00	0.00
Callithrix_jacchus	0.00	0.00	0.00
Canis_familiaris	0.00	0.04	0.00
Cavia_porcellus	0.00	0.05	0.00
Choloepus_hoffmanni	0.00	0.00	0.00
Dasypus_novemcinctus	0.00	0.00	0.00
Dipodomys_ordii	0.00	1.00	0.00
Echinops_telfairi	0.00	0.00	1.00
Equus_caballus	0.00	0.00	0.00
Erinaceus_europaeus	0.00	0.00	1.00
Felis_catus	0.00	0.01	0.00
Gallus_gallus	0.00	0.00	0.00
Gorilla_gorilla	0.00	1.00	0.00
Homo_sapiens	0.00	0.00	0.00
Loxodonta_africana	0.00	0.08	0.00
Macaca_mulatta	0.00	0.00	1.00
Macropus_eugenii	0.00	0.00	1.00
Microcebus_murinus	0.00	0.00	0.00
Monodelphis_domestica	0.00	0.00	1.00
Mus_musculus	0.00	0.06	0.00
Myotis_lucifugus	0.00	0.00	0.00
Ochotona_princeps	0.00	0.00	0.00
Ornithorhynchus_anatinus	0.00	1.00	0.00
Oryctolagus_cuniculus	0.00	0.00	0.00
Otolemur_garnettii	0.00	0.04	0.00
Pan_troglodytes	0.00	0.00	0.00
Pongo_abelii	0.00	0.00	0.00
Procavia_capensis	0.00	0.06	0.00
Pteropus_vampyrus	0.00	0.00	0.00
Rattus_norvegicus	0.00	0.02	0.00
Sorex_araneus	0.00	1.00	1.00
Spermophilus_tridecemlineatus	0.00	0.00	0.00
Sus_scrofa	0.00	1.00	0.00
Tarsius_syrichta	0.00	1.00	0.00
Tupaia_belangeri	0.00	1.00	0.00
Tursiops_truncatus	0.00	0.00	0.00
Ursus_maritimus	0.00	0.01	0.00
Vicugna_pacos	0.00	1.00	0.00
Overall Fit of the Simulation	0.00	0.47	0.00

Gene Names	ANKMY2 (1419 bp)	AATF (1854 bp)	BLMH (1620 bp)
Ailuropoda_melanoleuca	0.00	1.00	1.00
Bos_taurus	0.00	1.00	1.00
Callithrix_jacchus	0.00	1.00	1.00
Canis_familiaris	0.00	1.00	1.00
Cavia_porcellus	0.00	1.00	1.00
Choloepus_hoffmanni	0.00	1.00	1.00
Dasypus_novemcinctus	0.00	1.00	0.05
Dipodomys_ordii	0.99	0.00	1.00
Echinops_telfairi	0.00	1.00	1.00
Equus_caballus	0.00	1.00	1.00
Erinaceus_europaeus	0.00	1.00	1.00
Felis_catus	0.00	1.00	1.00
Gallus_gallus	0.00	1.00	1.00
Gorilla_gorilla	0.00	1.00	1.00
Homo_sapiens	0.00	1.00	1.00
Loxodonta_africana	0.00	1.00	1.00
Macaca_mulatta	0.00	1.00	1.00
Macropus_eugenii	1.00	1.00	0.24
Microcebus_murinus	0.00	1.00	1.00
Monodelphis_domestica	1.00	1.00	1.00
Mus_musculus	0.25	1.00	1.00
Myotis_lucifugus	1.00	1.00	1.00
Ochotona_princeps	1.00	1.00	0.08
Ornithorhynchus_anatinus	0.00	1.00	1.00
Oryctolagus_cuniculus	1.00	1.00	1.00
Otolemur_garnettii	0.00	1.00	1.00
Pan_troglodytes	0.00	1.00	0.54
Pongo_abelii	0.00	1.00	1.00
Procavia_capensis	1.00	1.00	0.00
Pteropus_vampyrus	1.00	1.00	0.02
Rattus_norvegicus	1.00	1.00	1.00
Sorex_araneus	0.00	1.00	1.00
Spermophilus_tridecemlineatus	1.00	1.00	1.00
Sus_scrofa	1.00	1.00	1.00
Tarsius_syrichta	0.00	1.00	0.01
Tupaia_belangeri	0.00	1.00	1.00
Tursiops_truncatus	0.00	1.00	0.08
Ursus_maritimus	1.00	1.00	1.00
Vicugna_pacos	0.00	1.00	1.00
Overall Fit of the Simulation	0.00	1.00	1.00

Gene Names	MED23 (4254 bp)	ACTR8 (1884 bp)	ARMC8 (2034 bp)
Ailuropoda_melanoleuca	0.00	0.00	0.00
Bos_taurus	0.00	0.00	0.00
Callithrix_jacchus	0.00	0.00	0.00
Canis_familiaris	0.00	0.00	0.00
Cavia_porcellus	1.00	0.00	0.00
Choloepus_hoffmanni	1.00	0.00	0.00
Dasypus_novemcinctus	1.00	0.00	0.00
Dipodomys_ordii	0.00	0.00	1.00
Echinops_telfairi	0.00	0.10	0.01
Equus_caballus	0.00	0.00	0.00
Erinaceus_europaeus	0.00	0.00	0.00
Felis_catus	0.00	1.00	0.00
Gallus_gallus	0.00	0.00	0.00
Gorilla_gorilla	0.00	0.00	0.00
Homo_sapiens	0.00	0.00	0.00
Loxodonta_africana	0.00	0.00	0.00
Macaca_mulatta	0.00	0.00	0.00
Macropus_eugenii	0.00	0.03	0.00
Microcebus_murinus	0.00	1.00	0.00
Monodelphis_domestica	0.00	0.14	0.00
Mus_musculus	1.00	0.00	0.00
Myotis_lucifugus	0.00	0.00	1.00
Ochotona_princeps	0.00	0.02	1.00
Ornithorhynchus_anatinus	1.00	0.01	1.00
Oryctolagus_cuniculus	0.00	0.06	0.00
Otolemur_garnettii	0.00	0.00	0.00
Pan_troglodytes	0.00	0.00	0.00
Pongo_abelii	0.00	0.00	1.00
Procavia_capensis	0.00	1.00	0.00
Pteropus_vampyrus	0.00	0.00	0.00
Rattus_norvegicus	1.00	0.00	0.01
Sorex_araneus	0.00	0.00	1.00
Spermophilus_tridecemlineatus	0.00	1.00	1.00
Sus_scrofa	0.00	0.00	1.00
Tarsius_syrichta	0.00	0.00	0.00
Tupaia_belangeri	0.00	0.00	0.23
Tursiops_truncatus	0.00	0.00	0.00
Ursus_maritimus	0.00	0.00	1.00
Vicugna_pacos	0.00	0.00	0.00
Overall Fit of the Simulation	0.00	0.00	1.00

Gene Names	NOL10 (2079 bp)	RAB3GAP1 (3069 bp)	PHF3 (6462 bp)
Ailuropoda_melanoleuca	0.00	0.00	0.00
Bos_taurus	0.00	0.00	1.00
Callithrix_jacchus	0.00	0.00	0.00
Canis_familiaris	0.00	0.00	0.00
Cavia_porcellus	0.00	0.00	1.00
Choloepus_hoffmanni	0.00	0.00	1.00
Dasypus_novemcinctus	0.00	0.00	1.00
Dipodomys_ordii	0.00	0.00	1.00
Echinops_telfairi	0.00	0.06	1.00
Equus_caballus	0.00	0.00	1.00
Erinaceus_europaeus	0.00	0.00	0.00
Felis_catus	0.00	0.00	1.00
Gallus_gallus	0.00	0.00	0.00
Gorilla_gorilla	1.00	0.00	0.00
Homo_sapiens	0.00	0.00	0.00
Loxodonta_africana	0.00	0.00	0.00
Macaca_mulatta	0.00	0.00	0.00
Macropus_eugenii	0.00	0.00	1.00
Microcebus_murinus	0.00	0.00	1.00
Monodelphis_domestica	0.00	0.00	0.00
Mus_musculus	0.00	0.97	1.00
Myotis_lucifugus	1.00	0.00	0.00
Ochotona_princeps	0.00	0.01	1.00
Ornithorhynchus_anatinus	1.00	0.00	1.00
Oryctolagus_cuniculus	0.00	0.00	0.00
Otolemur_garnettii	0.00	0.00	1.00
Pan_troglodytes	0.00	0.00	0.00
Pongo_abelii	0.00	0.00	0.00
Procavia_capensis	0.00	0.00	1.00
Pteropus_vampyrus	0.00	0.00	0.00
Rattus_norvegicus	0.00	1.00	1.00
Sorex_araneus	0.00	1.00	1.00
Spermophilus_tridecemlineatus	0.00	0.00	0.00
Sus_scrofa	0.00	1.00	1.00
Tarsius_syrichta	0.00	0.00	1.00
Tupaia_belangeri	1.00	0.00	0.00
Tursiops_truncatus	0.00	0.00	1.00
Ursus_maritimus	0.00	0.00	0.00
Vicugna_pacos	0.00	1.00	1.00
Overall Fit of the Simulation	0.00	0.00	1.00

Gene Names	KDSR (1020 bp)	YLPM1 (6975 bp)	UTP20 (8544 bp)
Ailuropoda_melanoleuca	1.00	1.00	0.00
Bos_taurus	0.05	1.00	0.00
Callithrix_jacchus	0.00	1.00	0.00
Canis_familiaris	0.00	1.00	0.00
Cavia_porcellus	0.00	1.00	0.00
Choloepus_hoffmanni	0.00	1.00	0.00
Dasypus_novemcinctus	0.00	1.00	0.00
Dipodomys_ordii	1.00	1.00	0.00
Echinops_telfairi	0.00	1.00	0.00
Equus_caballus	0.24	1.00	0.00
Erinaceus_europaeus	1.00	1.00	0.00
Felis_catus	1.00	1.00	0.00
Gallus_gallus	0.00	1.00	0.00
Gorilla_gorilla	0.00	1.00	0.00
Homo_sapiens	0.00	1.00	0.00
Loxodonta_africana	0.00	1.00	0.00
Macaca_mulatta	0.00	1.00	0.00
Macropus_eugenii	0.00	1.00	0.00
Microcebus_murinus	1.00	1.00	0.00
Monodelphis_domestica	0.00	1.00	0.00
Mus_musculus	0.15	1.00	0.00
Myotis_lucifugus	1.00	1.00	0.00
Ochotona_princeps	0.98	1.00	0.00
Ornithorhynchus_anatinus	1.00	1.00	0.00
Oryctolagus_cuniculus	0.67	1.00	0.00
Otolemur_garnettii	1.00	1.00	0.00
Pan_troglodytes	0.00	1.00	0.00
Pongo_abelii	0.00	1.00	0.00
Procavia_capensis	0.15	1.00	0.00
Pteropus_vampyrus	1.00	1.00	0.00
Rattus_norvegicus	0.37	1.00	1.00
Sorex_araneus	1.00	1.00	0.00
Spermophilus_tridecemlineatus	1.00	1.00	0.00
Sus_scrofa	0.07	1.00	0.00
Tarsius_syrichta	0.00	1.00	0.00
Tupaia_belangeri	1.00	1.00	0.00
Tursiops_truncatus	0.01	1.00	0.00
Ursus_maritimus	1.00	1.00	0.00
Vicugna_pacos	1.00	1.00	0.00
Overall Fit of the Simulation	1.00	1.00	0.00

Gene Names	RECK (2943 bp)	ECD (2091 bp)	NUP85 (2061 bp)
Ailuropoda_melanoleuca	0.00	0.40	0.00
Bos_taurus	0.00	1.00	0.00
Callithrix_jacchus	0.00	0.00	0.00
Canis_familiaris	0.00	0.54	0.00
Cavia_porcellus	0.00	1.00	0.00
Choloepus_hoffmanni	0.00	1.00	0.00
Dasypus_novemcinctus	0.00	1.00	0.00
Dipodomys_ordii	0.00	1.00	0.00
Echinops_telfairi	0.55	1.00	0.96
Equus_caballus	0.00	0.18	0.00
Erinaceus_europaeus	0.00	0.07	0.00
Felis_catus	1.00	1.00	0.00
Gallus_gallus	0.00	0.05	0.00
Gorilla_gorilla	0.00	0.62	0.00
Homo_sapiens	0.00	0.00	0.00
Loxodonta_africana	0.00	1.00	0.00
Macaca_mulatta	0.00	0.31	0.00
Macropus_eugenii	0.00	1.00	0.00
Microcebus_murinus	0.00	1.00	0.00
Monodelphis_domestica	1.00	1.00	0.00
Mus_musculus	0.85	1.00	0.00
Myotis_lucifugus	0.23	1.00	0.00
Ochotona_princeps	0.08	1.00	0.00
Ornithorhynchus_anatinus	0.00	1.00	1.00
Oryctolagus_cuniculus	0.57	1.00	1.00
Otolemur_garnettii	0.00	1.00	0.00
Pan_troglodytes	0.00	1.00	0.00
Pongo_abelii	0.00	0.62	0.00
Procavia_capensis	0.00	0.60	0.00
Pteropus_vampyrus	0.00	1.00	0.00
Rattus_norvegicus	0.98	1.00	0.00
Sorex_araneus	0.14	1.00	1.00
Spermophilus_tridecemlineatus	1.00	1.00	0.00
Sus_scrofa	0.00	1.00	0.00
Tarsius_syrichta	0.00	1.00	0.00
Tupaia_belangeri	0.00	1.00	1.00
Tursiops_truncatus	0.00	0.99	0.00
Ursus_maritimus	0.00	0.00	0.00
Vicugna_pacos	0.00	0.04	0.00
Overall Fit of the Simulation	0.00	1.00	0.00

Taxa	66TaxonSet_nuc			66TaxonSet_aa			66TaxonSet_day			
	GTR	CAT	CAT-GTR	GTR	JTT	CAT	CAT-GTR	GTR	CAT	CAT_GTR
Chinese_hamster	8.22	8.26	7.81	-0.27	-0.38	-0.28	-0.34	8.22	8.26	7.81
Siberian_mole	2.47	1.44	1.63	1.02	1.15	1.06	1.08	2.47	1.44	1.63
Black_headed_spirder_monkey	0.45	0.29	0.5	-0.98	-0.8	-0.76	-0.85	0.45	0.29	0.5
Jamaican_fruit_bat	11.25	9.91	10.59	0.3	0.46	0.44	0.6	11.25	9.91	10.59
Mountain_paca	-0.16	-0.18	-0.23	0.56	0.91	0.58	0.63	-0.16	-0.18	-0.23
North_american_beaver	0.82	0.72	0.48	-0.77	-0.78	-0.8	-0.77	0.82	0.72	0.48
Star_nosed_mole	0.51	0.42	0.6	-1.03	-0.9	-0.92	-0.98	0.51	0.42	0.6
Linnaeus_two_toed_sloth	-0.39	-0.57	-0.46	-0.73	-0.61	-0.7	-0.76	-0.39	-0.57	-0.46
Dog	-0.28	-0.36	-0.29	0.2	0.08	0.03	0.01	-0.28	-0.36	-0.29
Goeldis_marmoset	-0.42	-0.38	-0.36	-0.03	0.12	0.11	0.24	-0.42	-0.38	-0.36
Hoffmanns_Two_toed_Sloth	-1.43	-1.64	-1.82	-1.18	-1.09	-1.06	-1.32	-1.43	-1.64	-1.82
White_Rhinoceros	-1.05	-1	-1.25	-0.22	-0.28	-0.27	-0.08	-1.05	-1	-1.25
Montane_guinea_pig	1.56	1.39	2.26	-1.24	-1.09	-1.02	-1	1.56	1.39	2.26
Colugo	0.38	0.48	0.52	1.18	1.15	0.94	1.23	0.38	0.48	0.52
Big_hairy_armadillo	-0.4	-0.55	-0.6	1.48	1.51	1.59	1.43	-0.4	-0.55	-0.6
Pacarana	0.8	-0.02	0.1	0.73	0.77	0.93	0.55	0.8	-0.02	0.1
Kangaroo_Rat	6.43	5.65	4.93	0.7	0.48	0.49	0.58	6.43	5.65	4.93
Opossum	8.91	15.74	9.26	-0.02	0.08	0.32	0.15	8.91	15.74	9.26
Horse	1.34	1.35	1.4	-0.24	-0.25	-0.32	-0.08	1.34	1.35	1.4
Southern_white_breasted_hedgehog	4.37	3.47	3.62	-0.75	-0.96	-1.11	-0.84	4.37	3.47	3.62
North_american_porcupine	-1.31	-1.46	-1.46	-0.79	-0.85	-0.72	-0.85	-1.31	-1.46	-1.46
Rufous_elephant_shrew	-1.62	-1.8	-1.85	-1.61	-1.46	-1.51	-1.8	-1.62	-1.8	-1.85
Six_banded_armadillo	-0.61	-0.63	-0.68	1.12	1.3	1.49	1.28	-0.61	-0.63	-0.68
Lesser_Hedgehog_Tenrec	-1.09	-1.48	-1.45	0.76	0.89	0.96	0.69	-1.09	-1.48	-1.45
Cat	8.27	8.78	9.35	-0.57	-0.56	-0.64	-0.5	8.27	8.78	9.35
Hippo	13.38	13.27	14.58	0.4	0.44	0.28	0.66	13.38	13.27	14.58
Malayan_Porcupine	7.76	5.69	5.47	0.52	0.61	0.59	0.48	7.76	5.69	5.47
Black_gibbon	2.04	1.78	1.93	1.31	1	0.97	1.51	2.04	1.78	1.93
Naked_mole_rat	2.82	2.97	2.46	-1.02	-1.24	-1.01	-0.97	2.82	2.97	2.46
Capybara	-0.34	-0.35	-0.35	1.15	0.73	1.29	1.22	-0.34	-0.35	-0.35
Human	-0.08	-0.03	0.05	1.22	1.06	1.15	1.57	-0.08	-0.03	0.05
Elephant	2.48	2.25	2.59	-0.41	-0.5	-0.46	-0.31	2.48	2.25	2.59
Ring_tailed_lemur	10.77	12.26	10.67	1.31	1.36	0.77	1.41	10.77	12.26	10.67
Llama	12.75	15.01	15.37	-0.51	-0.4	-0.63	-0.49	12.75	15.01	15.37
Ocelot	6.5	6.86	6.75	-0.79	-0.72	-0.79	-0.66	6.5	6.86	6.75
Hazel_Dormouse	7.55	7.37	7.76	1.02	0.83	0.52	0.55	7.55	7.37	7.76
Coypu	6.33	4.79	5.66	0.7	0.83	0.85	0.72	6.33	4.79	5.66
Tammar_wallaby	5.37	5.14	3.65	-1	-0.98	-0.92	-0.87	5.37	5.14	3.65
Macaque	0.68	0.69	0.85	0.57	0.59	0.57	1.12	0.68	0.69	0.85
Mouse	-0.48	-0.71	-0.82	-0.95	-0.98	-1	-0.98	-0.48	-0.71	-0.82
Humpback_Whale	11.62	11.55	12.72	-0.03	0.16	-0.1	0	11.62	11.55	12.72
Chinese_Pangolin	2.25	2.77	2.09	0.76	0.53	0.55	0.63	2.25	2.77	2.09
Short_eared_elephant_shrew	-0.35	-0.67	-0.89	0.43	0.31	0.33	0.36	-0.35	-0.67	-0.89
Giant_slit eater	-0.84	-1.13	-0.99	1.02	1.38	1.29	1.28	-0.84	-1.13	-0.99
Egyptian_slit_nosed_bat	-1.04	-0.93	-1.15	0.95	0.82	0.93	1.07	-1.04	-0.93	-1.15
Aardvark	50.16	54.95	15.48	-0.42	-0.27	-0.43	-0.4	50.16	54.95	15.48
Northern_pika	1.86	1.01	1.11	-0.15	-0.21	-0.21	-0.18	1.86	1.01	1.11
Forest_giraffe	10.88	14.04	11.12	-1.08	-1.04	-1.17	-1.14	10.88	14.04	11.12
Rock	-1.09	-1.15	-1.12	-0.08	-0.04	0.09	0.01	-1.09	-1.15	-1.12
Springhare	3.41	2.94	2.4	0.53	0.48	0.72	0.47	3.41	2.94	2.4
Indian_flying_fox	2.75	2.56	2.53	-1	-1.17	-1.15	-0.77	2.75	2.56	2.53
Jaguar	4.44	4.63	4.45	-0.18	-0.32	-0.34	-0.16	4.44	4.63	4.45
Long_haired_rousette	-0.76	-0.95	-0.81	-0.72	-0.81	-0.87	-0.67	-0.76	-0.95	-0.81
Rat	-0.93	-1.35	-1.44	1.11	0.94	0.87	0.82	-0.93	-1.35	-1.44
Common_shrew	0.51	0.58	0.69	1.44	1.6	1.73	1.8	0.51	0.58	0.69
Cotton_tailed_rabbit	-0.99	-0.96	-0.85	0.2	0.29	0.26	0.34	-0.99	-0.96	-0.85
Pig	-0.79	-0.79	-0.76	0.53	0.69	0.33	0.41	-0.79	-0.79	-0.76
Antelope	-0.48	-0.23	-0.26	0.32	0.17	0.41	0.42	-0.48	-0.23	-0.26
Malayan_Tapir	0.08	0.24	0.08	0.62	0.32	0.22	0.38	0.08	0.24	0.08
Pygmy_treeshrew	-0.66	-0.67	-0.62	0.43	0.35	0.42	0.56	-0.66	-0.67	-0.62
Manatee	6.95	11.96	9.95	1.53	1.7	1.47	1.93	6.95	11.96	9.95
Tarsier	-2.35	-3.26	-3.69	-0.47	-0.41	-0.34	-0.17	-2.35	-3.26	-3.69
Chipmunk	5.1	4.37	4.56	-0.39	-0.4	-0.51	-0.45	5.1	4.37	4.56
Dolphin	0.59	0.32	0.28	0.58	0.34	0.43	0.56	0.59	0.32	0.28
Anteater	-0.96	-0.96	-0.97	1.17	1.34	1.51	1.33	-0.96	-0.96	-0.97
Brown_bear	-1.01	-1.71	-1.67	-0.12	-0.17	-0.15	-0.12	-1.01	-1.71	-1.67
Global Test	5.11	4.13	3.47	-0.38	-0.4	-0.23	-0.34	5.11	4.13	3.47
39TaxonSet_nuc				39TaxonSet_aa				39TaxonSet_day		
Taxa	GTR	CAT	CAT_GTR	GTR	CAT	CAT-GTR	JTT	GTR	CAT	CAT-GTR
Alpaca	-0.855	-0.92	-0.931	-0.25	-0.34	-0.41	-0.51	-0.57	-0.75	-0.64
Armadillo	5.151	6.894	6.243	4.46	4.44	4.59	4.42	7.22	6.25	6.98
Bushbaby	3.126	3.22	2.809	-0.41	-0.52	-0.4	-0.47	0.2	0.16	0.3
Cat	-0.464	-0.484	-0.577	-0.5	-1.39	-1.32	-1.34	-0.75	-0.75	-0.51
Chicken	-0.791	-0.861	-0.725	1.8	2.65	2.98	0.31	0.74	1.33	1.6
Chimp	2.864	2.905	2.901	0.76	0.89	0.99	0.53	2	1.98	3.22
Common shrew	120.13	114.856	90.821	0.38	0.47	0.5	0.4	0.35	0.55	0.21
Cow	1.134	1.343	1.181	-0.04	-0.11	-0.02	-0.1	0.14	0.03	0.04
Dog	3.874	3.899	3.755	0.62	0.53	0.64	0.31	2.72	4.16	4.52
Dolphin	-0.492	-0.501	-0.521	-0.19	-0.17	0.01	-0.09	-0.36	-0.26	-0.16
Elephant	-0.056	0.004	0.084	-0.86	-1	-0.9	-0.73	-0.69	-0.56	-0.69
Giant_panda	0.217	0.216	0.299	1.04	0.96	1.17	0.7	0.97	1	0.99
Gorilla	2.651	2.72	2.757	1.19	1.51	1.52	0.81	1.17	1.68	3.04
Guineapig	63.624	65.276	68.763	15.56	16.86	18.22	14.89	9.13	11.43	15.57
Hedgehog	0.638	0.64	0.862	1.28	1.26	1.25	1.04	-0.91	-0.85	-0.97
Horse	-0.112	-0.147	-0.101	-0.87	-1.02	-0.83	-0.87	-0.61	-0.63	-0.69
Human	2.664	2.736	2.751	0.65	0.72	0.84	0.41	1.69	1.67	2.84
Kangaroo_rat	0.198	0.431	0.398	-1.6	-1.61	-1.61	-1.56	0.4	0.74	0.58
Macaque	-0.131	-0.123	-0.109	0	-0.03	0.09	-0.16	1.39	1.69	1.57
Marmoset	4.123	3.582	3.597	0.92	0.85	0.98	0.57	1.03	1.69	2.48
Megabat	4.509	4.248	4.759	0.11	-0.02	0.09	-0.17	0.46	0.45	0.36
Microbat	1.899	1.953	1.621	-1.06	-1.19	-1.18	-1.04	1.42	1.34	1.16
Mouse	1.342	1.485	1.179	10.28	10.38	11.57	8.27	7.26	9.02	8.1
Mouse_lemur	36.014	36.069	35.335	0.5	0.53	0.58	0.58	0.24	0.38	0.39
Opossum	4.073	4.278	4.968	0.96	1.2	1.38	0.48	0	0.19	0.17
Orangutan	0.973	0.723	0.801	2.42	2.22	2.48	2.01	1.78	1.84	2.14
Pig	3.205	3.22	3.255	0.44	0.27	0.48	0.27	0.28	0.08	0.15
Pika	1.043	1.159	1.448	3.87	3.45	3.57	3.3	1.66	2.15	1.74
Platypus	37.821	35.952	36.041	1.57	1.95	2.15	0.37	0.84	1.31	1.38
Polar_bear	21.04	18.384	19.182	1.02	1.08	1.12	0.57	0.02	-0.23	-0.12
Rabbit	0.114	0.137	0.225	0.58	0.77	0.71	0.43	-0.72	-0.76	-0.78
Rat	44.138	49.289	51.649	7.16	6.63	7.28	5.92	9.57	8.7	8.05
Rock_Hyrax	29.815	29.022	29.214	0.94	0.77	0.81	0.91	1.51	1.07	0.98
Sloth	5.468	6.555	6.269	1.76	1.81	1.82	1.66	3.44	4.78	3.92
Squirrel	6.327	4.759	3.713	0.78	0.68	0.77	0.77	0.48	0.53	0.38
Tarsier	1.881	1.609	1.732	-0.15	-0.25	-0.21	-0.27	1.7	1.57	1.7
Tenrec	58.605	56.11	53.433	3.95	3.83	3.93	3.57	3.98	3.67	3.87
Treeshrew	-0.183	-0.195	-0.192	-0.98	-1	-0.88	-0.94	1.13	0.73	1.29
Wallaby	-1.119	-1.233	-1.116	-1.17	-1.26	-1.19	-1.8	-1.13	-1.1	-1.12
Global Test	15.0575	14.1466	14.0589	1.84	2.56	3	0.21	0.91	1.68	2.29

Supplementary Table S7

	GTR+1C+4Γ	CAT	CAT-GTR	JTT+4Γ
66TaxonSet_nuc				
GTR+1C+4Γ	-----	-100.29 +/- 526.107	-34.44 +/- 490.493	-----
CAT	100.29 +/- 526.107	-----	65.85 +/- 420.09	-----
CAT-GTR	34.44 +/- 490.493	-65.85 +/- 420.09	-----	-----
66TaxonSet_aa				
GTR+1C+4Γ	-----	4.027 +/- 282.575	3.278 +/- 231.908	-96.413 +/- 428.08
CAT	-4.027 +/- 282.575	-----	-0.749 +/- 270.183	-100.44 +/- 301.984
CAT-GTR	-3.278 +/- 231.908	0.749 +/- 270.183	-----	-99.691 +/- 400.85
JTT+4Γ	100.44 +/- 301.984	96.413 +/- 428.08	99.691 +/- 400.85	-----
66TaxonSet_day				
GTR+1C+4Γ	-----	-242.631 +/- 333.541	-101.255 +/- 386.988	-----
CAT	242.631 +/- 333.541	-----	141.376 +/- 288.149	-----
CAT-GTR	101.255 +/- 386.988	-141.376 +/- 288.149	-----	-----
39TaxonSet_nuc				
GTR+1C+4Γ	-----	2243.06 +/- 608.593	2123.03 +/- 743.054	-----
CAT	-2243.06 +/- 608.593	-----	-120.03 +/- 713.875	-----
CAT-GTR	-2123.03 +/- 743.054	120.03 +/- 713.875	6	-----
39TaxonSet_aa				
GTR+1C+4Γ	-----	160.76 ±719.299	354.51 ±840.00	-454.41 ±620.417
CAT	-160.76 ±719.299	-----	193.75 ±347.529	-615.17 ±389.729
CAT-GTR	-354.51 ±840.609	-193.75 ±347.529	-----	-808.92 ±408.97
JTT+4Γ	454.41 ±620.417	615.17 ±389.729	808.92 ±408.97	-----
39TaxonSet_day				
GTR+1C+4Γ	-----	213.38 +/- 612.319	710.49 +/- 658.564	-----
CAT	-213.38 +/- 612.319	-----	497.11 +/- 512.718	-----