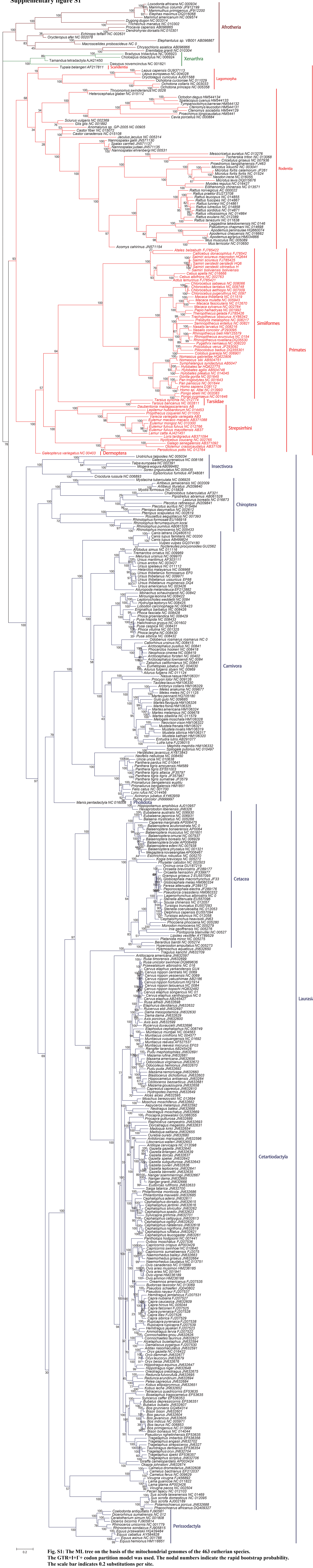


**Supplementary figure S1**





Supplementary Figure S2

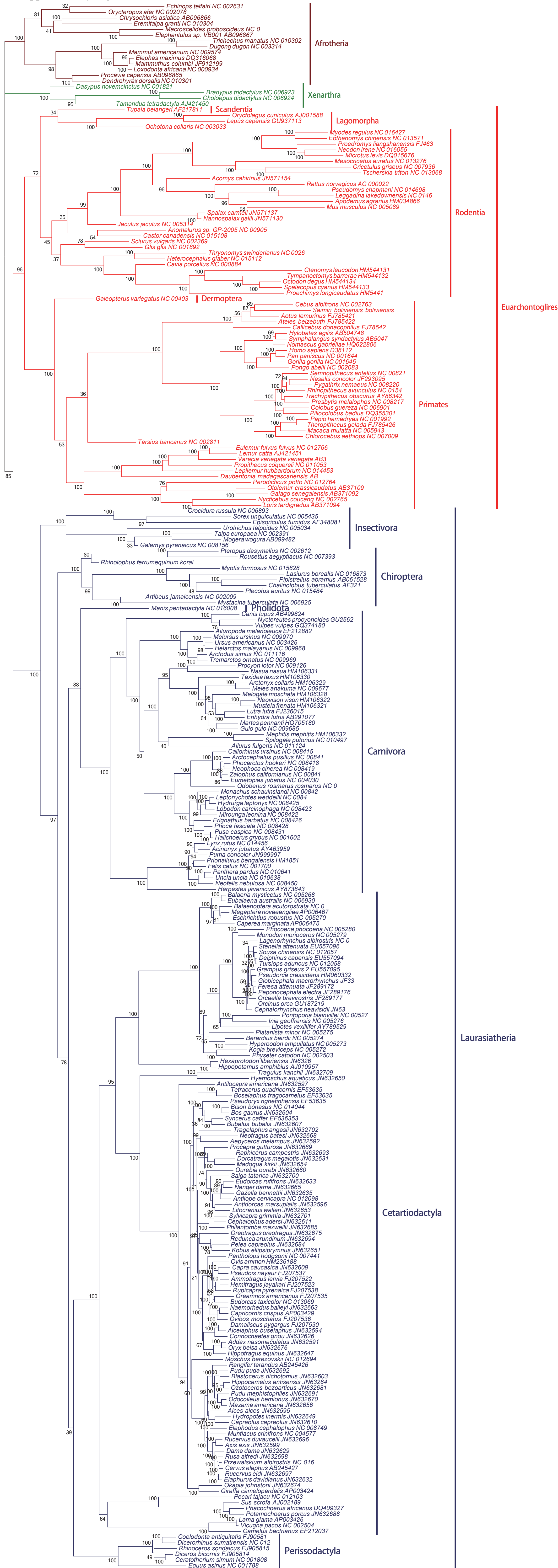


Fig. S2: The ML tree on the basis of the mitochondrial genomes of the 273 eutherian species. The GTR+I+Γ + codon partition model was used. The nodal numbers indicate the rapid bootstrap probability. The scale bar indicates 0.2 substitutions per site.



Supplementary Figure S3

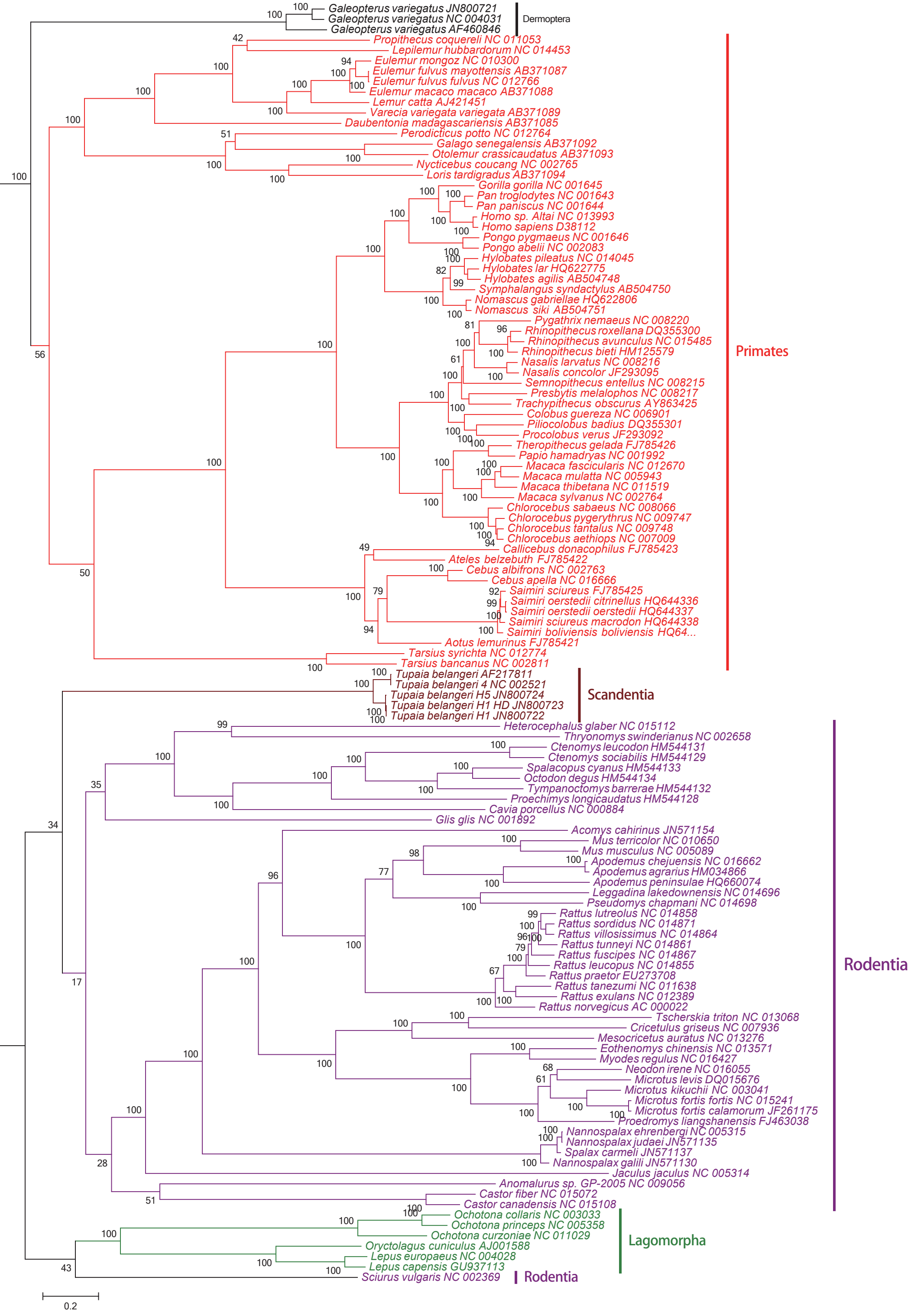


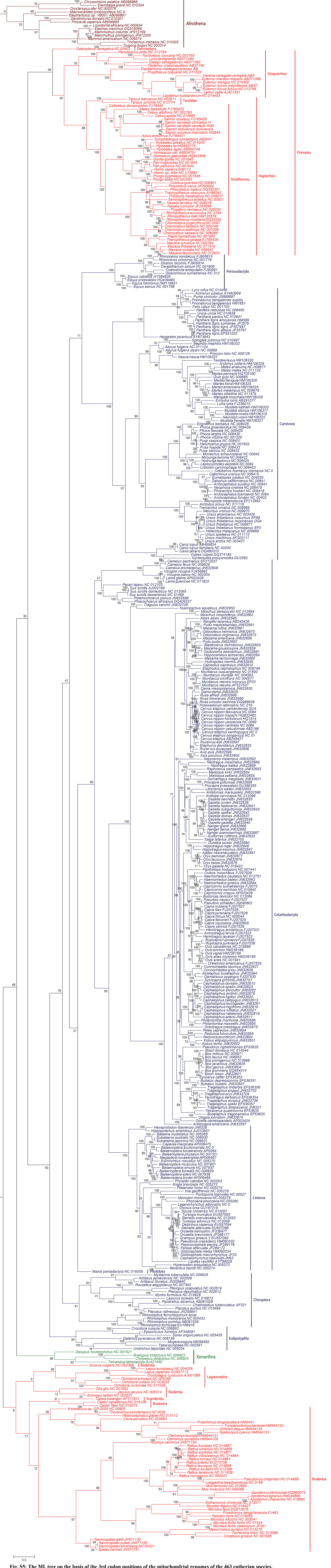
Fig. S3: The ML tree on the basis of the mitochondrial genomes of the 123 Euarchontoglires species. The GTR+I+ $\Gamma$  + codon partition model was used. The nodal numbers indicate the rapid bootstrap probability. The scale bar indicates 0.2 substitutions per site.





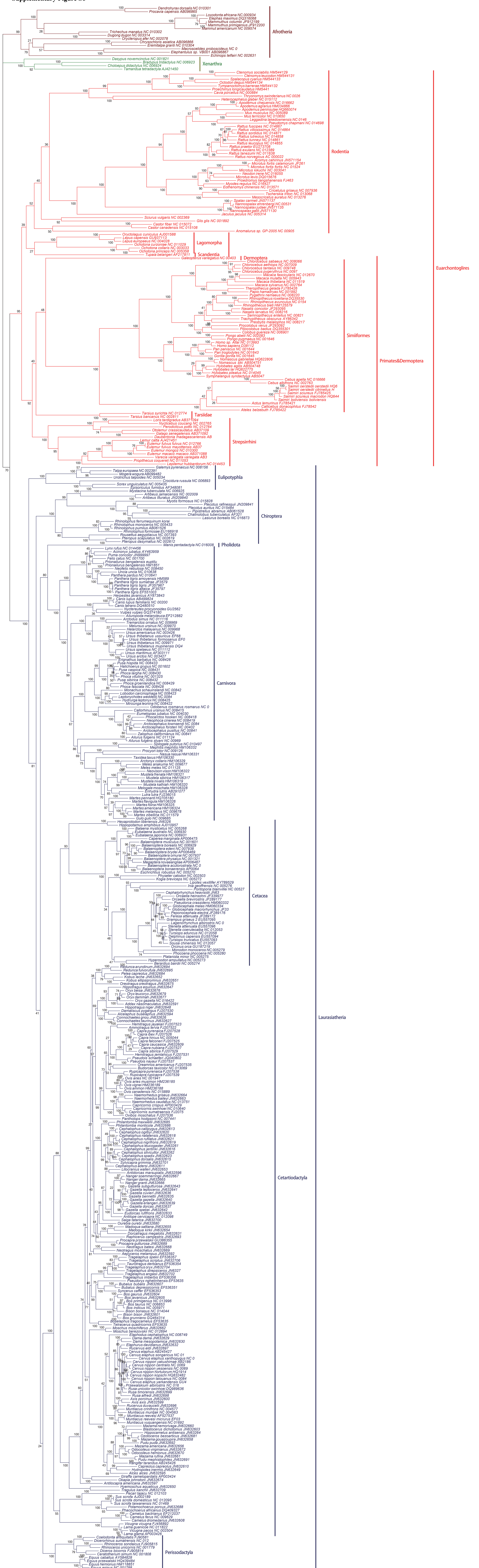


Supplementary Figure S5





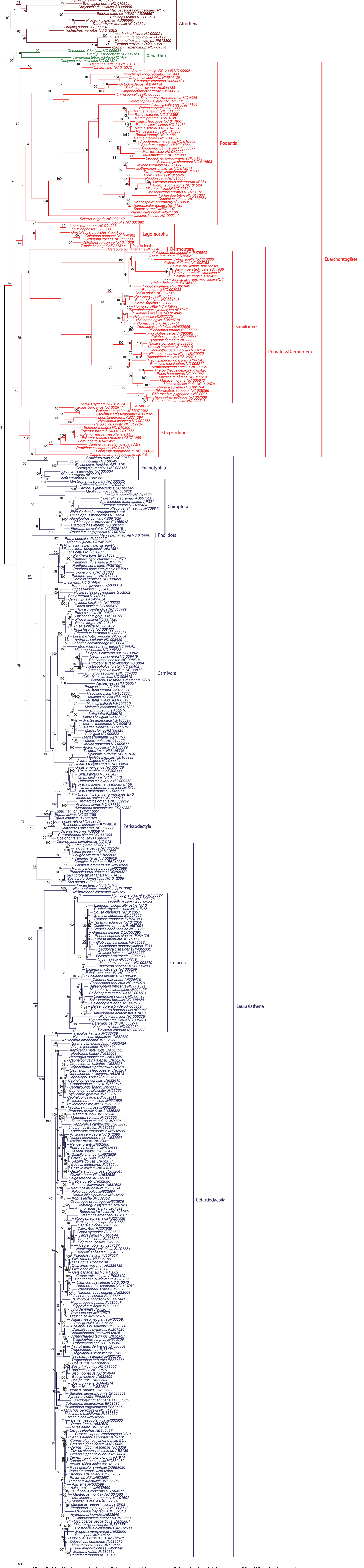
## Supplementary Figure S6



**Fig. S6:** The ML tree on the basis of the 1st and 2nd codon positions of the mitochondrial genomes of the 463 eutherian species. The GTR+I+G model was used. The node numbers indicate the a priori bootstrap probability. The scale bar indicates 0.05 substitutions per site.



Supplementary Figure S7





Supplementary Figure S8



Fig. S8: The MP tree on the basis of the mitochondrial genomes of the 463 eutherian species. The nodal numbers indicate the standard bootstrap probability.

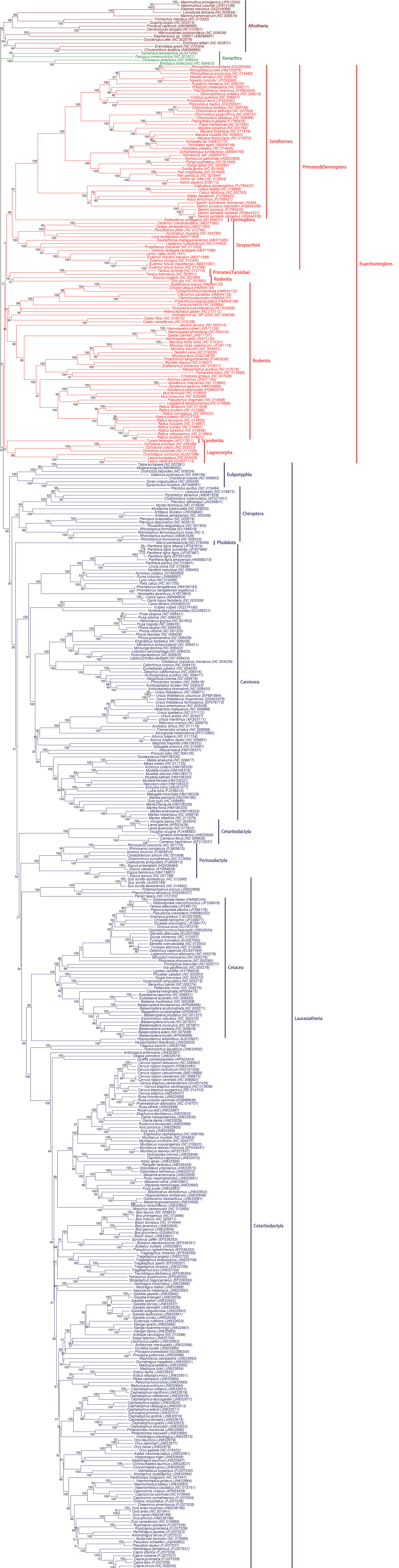




The scale bar indicates 0.05 substitutions per site, genetic distance. The nodal numbers indicate the standard bootstrap probability



Supplementary Figure S10





## Supplementary Figure S11



**Fig. S11: The ML tree on the basis of the mitochondrial genomes of the 67 Euarchontoglires species. The GTR+I+Γ+ codon partition model was used. The nodal numbers indicate the rapid bootstrap probability. 64 Euarchonta species (in-group) and 5 Glires species (out-group) were used. The scale bar indicates 0.2 substitutions per site.**



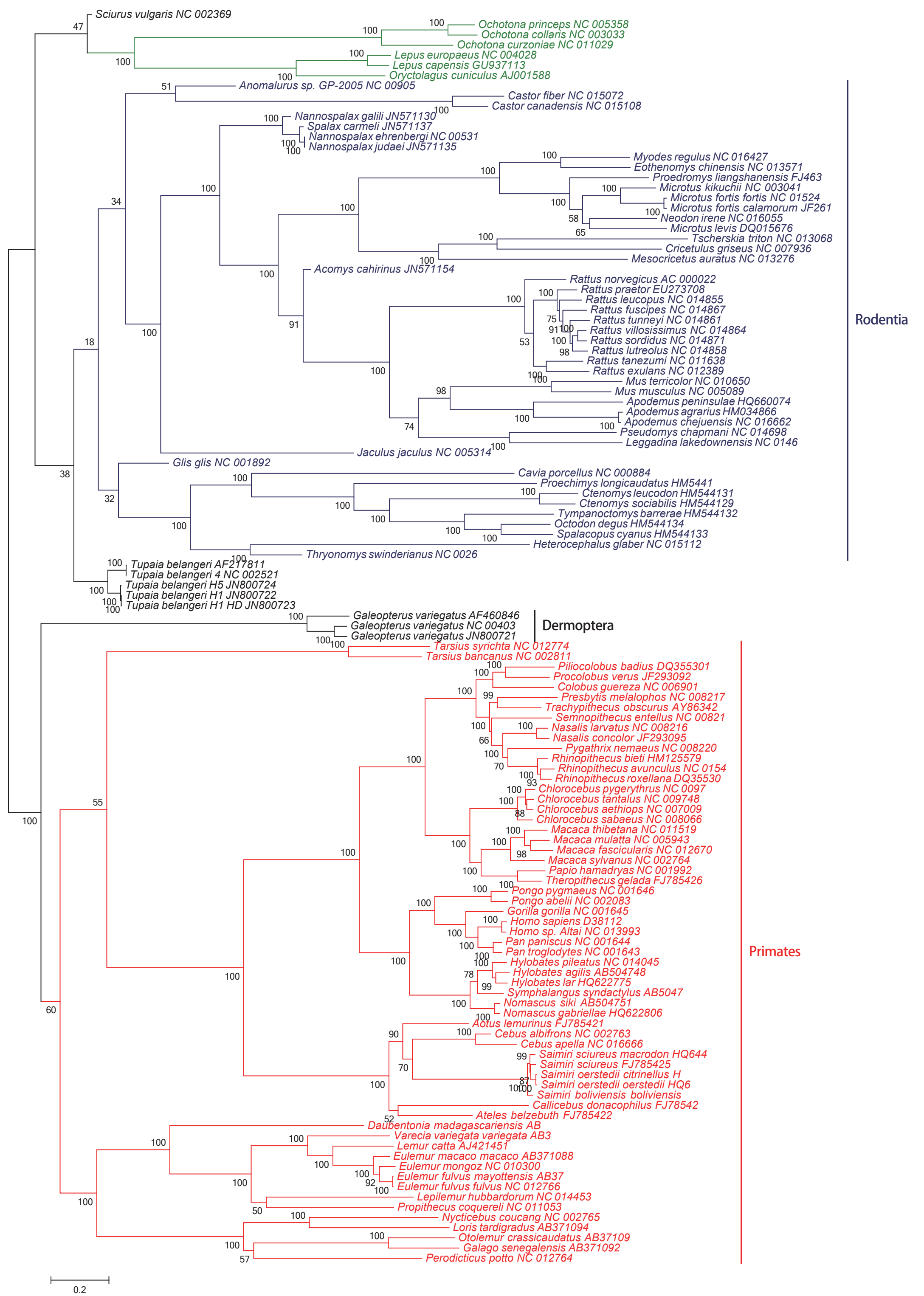
## Supplementary Figure S12



**Fig. S12: The ML tree on the basis of the mitochondrial genomes of the 69 Euarchontoglires species. The GTR+I+Γ+ codon partition model was used. The nodal numbers indicate the rapid bootstrap probability. 64 Euarchonta species (in-group) and 5 Glires species (out-group) were used. The scale bar indicates 0.2 substitutions per site.**



Supplementary Figure S13



**Fig. S13: The ML tree on the basis of the mitochondrial genomes of the 123 Euarchontoglires species.**  
**The GTR+I+Γ+codon partition model was used. The nodal numbers indicate the standard bootstrap probability.**  
**The scale bar indicates 0.2 substitutions per site.**



Fig. S14: The ML tree on the basis of the mitochondrial genomes of the 501 mammalian species. The GTR+I+Γ+codon partition model was used. The nodal numbers indicate the standard bootstrap probability. The scale bar indicates 0.2 substitutions per site.

