

Supplementary Figure 1. The tree of 36 mammal species analyzed in this study.

## The trees with fossil calibrations for MCMCTree:

## Calibration Strategy 1:

(P001_Platypus,((P002_Opossum,P003_Wallaby),(((P004_Tenrec,(P005_Rock_hyrax,P006_Eleph ant)),(P007_Armadillo,P008_Sloth)),(((P009_Hedgehog,P010_Common_shrew),(c((P011_Dolphin ,P012_Cow),P013_Pig),P014_Alpaca),((P015_Horse,(P016_Dog,P017_Cat)),(P018_Megabat,P019_ Microbat)) )),(((P020_Rabbit,P021_Pika),(P022_Squirrel,(P023_Guinea_pig,(P024_Kangaroo_rat,( P025_Mouse,P026_Rat)) )) ),(P027_Tree_shrew,((P028_Bushbaby,P029_Mouse_lemur),(P030_Tar sier,(P031_Marmoset,(P032_Rhesus,(P033_Orangutan,(P034_Gorilla,(P035_Chimp,P036_Human) )J)J))'S2N(0.698,65,3.65,-3400,65.02,13.75,11409)')J))J)'B(162.9,191.1)';

## Calibration Strategy 2:

(P001_Platypus,((P002_Opossum,P003_Wallaby)'L(64.85,0.1,1.0,0.001)',(((P004_Tenrec,(P005_R ock_hyrax,P006_Elephant)'L(61.8,0.1,1.0,0.001)')'L(64.85,0.1,1.0,0.001)',(P007_Armadillo,P008_ Sloth)'L(58.3,0.1,1.0,0.001)'),(((P009_Hedgehog,P010_Common_shrew)'L(58.3,0.1,1.0,0.001)',(C( (P011_Dolphin,P012_Cow),P013_Pig),P014_Alpaca),((P015_Horse,(P016_Dog,P017_Cat)'L(43.3,0 .1,1.0,0.001)'),(P018_Megabat,P019_Microbat)'L(55.5,0.1,1.0,0.001)')))'L(64.85,0.1,1.0,0.001)',((c P020_Rabbit,P021_Pika)'L(53,0.1,1.0,0.001)',(P022_Squirrel,(P023_Guinea_pig,(P024_Kangaroo_ rat,(P025_Mouse,P026_Rat)) ))'L(56.8,0.1,1.0,0.001)')'L(63.4,0.1,1.0,0.001)',(P027_Tree_shrew,(( P028_Bushbaby,P029_Mouse_lemur),(P030_Tarsier,(P031_Marmoset,(P032_Rhesus,(P033_Oran gutan,(P034_Gorilla,(P035_Chimp,P036_Human)) )) )) )'S2N(0.698,65,3.65,3400,65.02,13.75,11409)')'L(64.85,0.1,1.0,0.001)')'L(64.85,0.1,1.0,0.001)')'L(64.85,0.1,1.0,0.001) ')'L(64.85,0.1,1.0,0.001)')'L(127.5,0.1,1.0,0.001)')'B(166.2,191.1)';

## Sequence alignment:

Sequences for 14,632 orthologous genes for the 36 mammal species were downloaded from the ENSEMBL database. The sequences were aligned and edited as explained in dos Reis et al. 2012. Proc. Roy. Soc. B. 279: 3491-3500. The large sequence alignment ( 21 Mbp ) used in this study is available from http://abacus.gene.ucl.ac.uk/zieng/data.html.

