



Figure 1

Phylogenetic tree used to define the relative age groups for the human and mouse genes. The labeled age classes were defined as the major evolutionary branching points with respect to the 27 genomes analyzed and the species of interest (human or mouse). Thus, genes are grouped according to their estimated time of appearance in evolution. For example, human genes in Age group 5 are presumed to have appeared after the split between birds and mammals, since they do not have homologues in the non-mammal species studied. On the other hand, they already existed in the least common ancestor (LCA) of all mammals, as evidenced by their respective homologues in *O. anatinus*. The species included in the analysis are: *C. elegans* (worm), *D. melanogaster* (fruitfly), *T. rubripes* (fugu), *X. tropicalis* (xenopus), *G. gallus* (chicken), *O. anatinus* (platypus), *M. domestica* (Gray Short-tailed opossum), *B. Taurus* (cow), *C. familiaris* (dog), *D. novemcinctus* (nine-banded armadillo), *E. telfairi* (lesser hedgehog tenrec), *E. europaeus* (west european hedgehog), *F. catus* (cat), *L. Africana* (elephant), *M. lucifugus* (bat), *S. araneus* (common shrew), *C. porcellus* (guinea pig), *M. musculus* (mouse), *O. princeps* (pika), *O. cuniculus* (rabbit), *R. norvegicus* (rat), *S. tridecemlineatu* (squirrel), *P. troglodytes* (chimpanzee), *M. mulatta* (macaque), *M. murinus* (gray mouse lemur), *O. garnettii* (bushbaby), and *H. sapiens* (human). For the analysis of the human genome, Age 1 includes only primate-specific genes, while for the analysis of the mouse genome, Age 1 includes only rabbit and rodent-specific genes. Note that the evolutionary time scale (in millions of years ago, MYA) is approximate.