



Fig. EZ_ortholog_protein_comparison

Protein orthology comparison among seven mammalian genomes of cow, dog, human, mouse and rat (*Bos taurus*, *Canis familiaris*, *Homo sapiens*, *Mus musculus*, *Rattus norvegicus*) representing placental mammals, opossum (*Monodelphis domestica*) representing marsupials, and platypus (*Ornithorhynchus anatinus*) representing monotremes.

A) The vast majority of the mammalian genes are orthologous, with over half of them preserved as single-copy (dark blue); yet few thousands have independently duplicated in several species (blue); and another few thousands have been lost in some lineages (orange). Some genes are homologs but their orthology assignment was obscure (probably mostly due to methodology limitations and gene prediction errors), and some genes appear as unique, e.g. fast evolving genes that diverged beyond recognition.

B) The Venn diagram details the number of shared orthologous groups (note that duplicated gene counted as one) between laurasiatherians (cow and dog), human, rodents (mouse and rat), and non-placental mammals (opossum and platypus); showing that there are over a thousand of placental-specific orthologs, and that there are about a thousand of mammalian orthologs that have no human counterpart.

C) Distribution of protein identity between human and the other species orthologs for a subset of strictly conserved single-copy orthologs. Although more distantly related carnivores show a distinctively higher protein identity to human genes than rodents that are known to evolve faster.

D) Maximum likelihood phylogeny tree reconstructed using protein sequences of single-copy orthologs. The estimated branch length is proportional to molecular evolutionary rates, and the published estimates of speciation geological time are annotated.