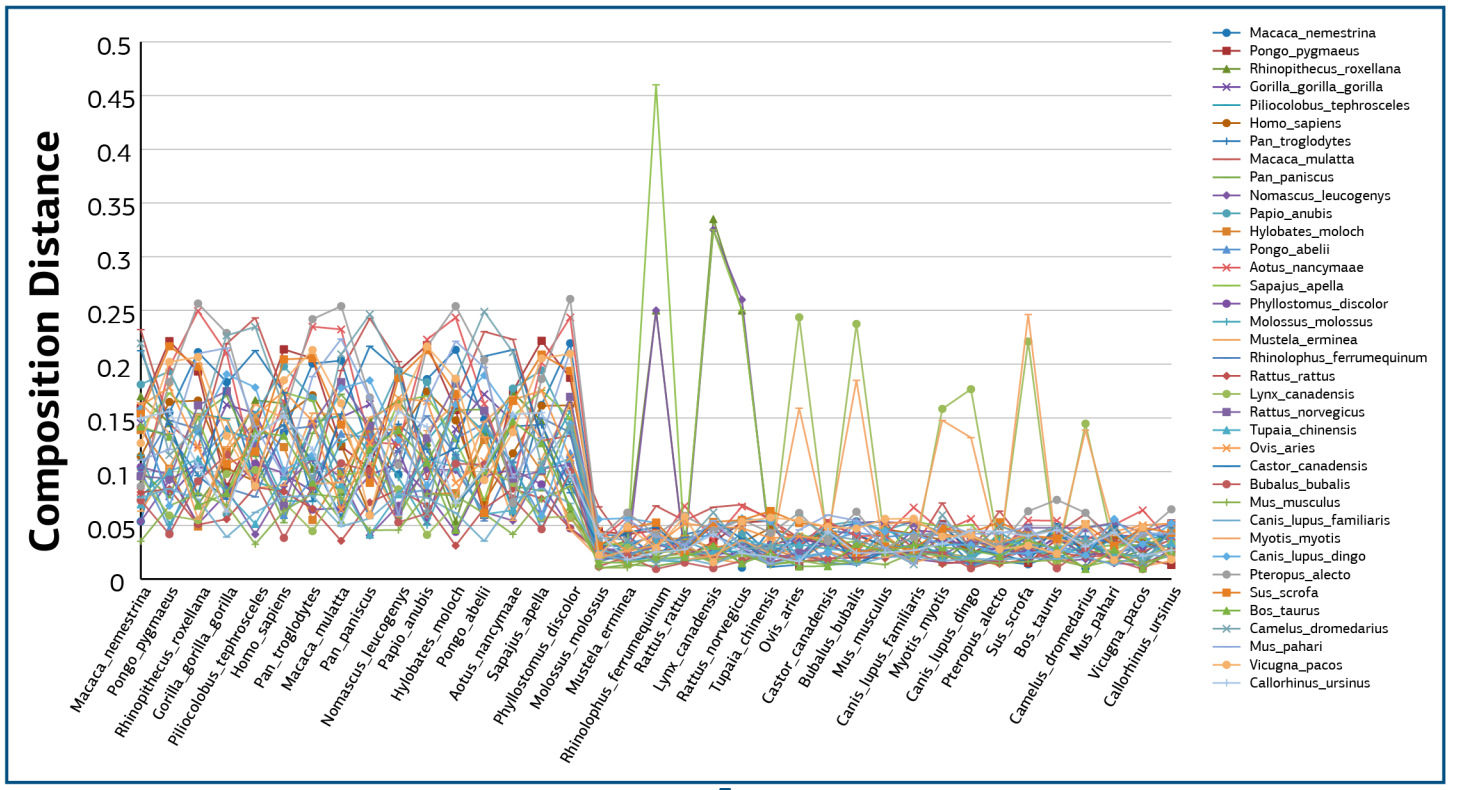
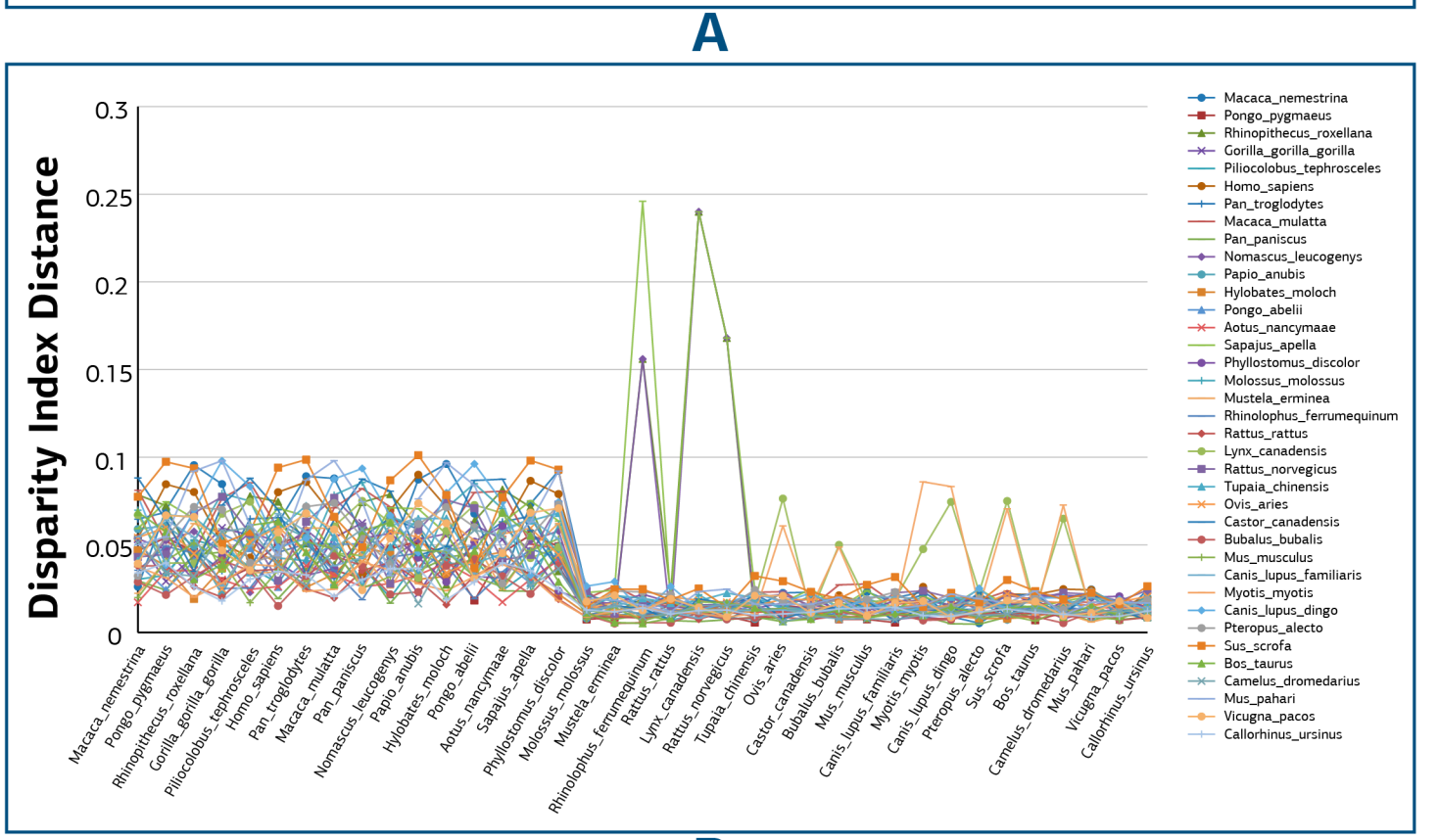
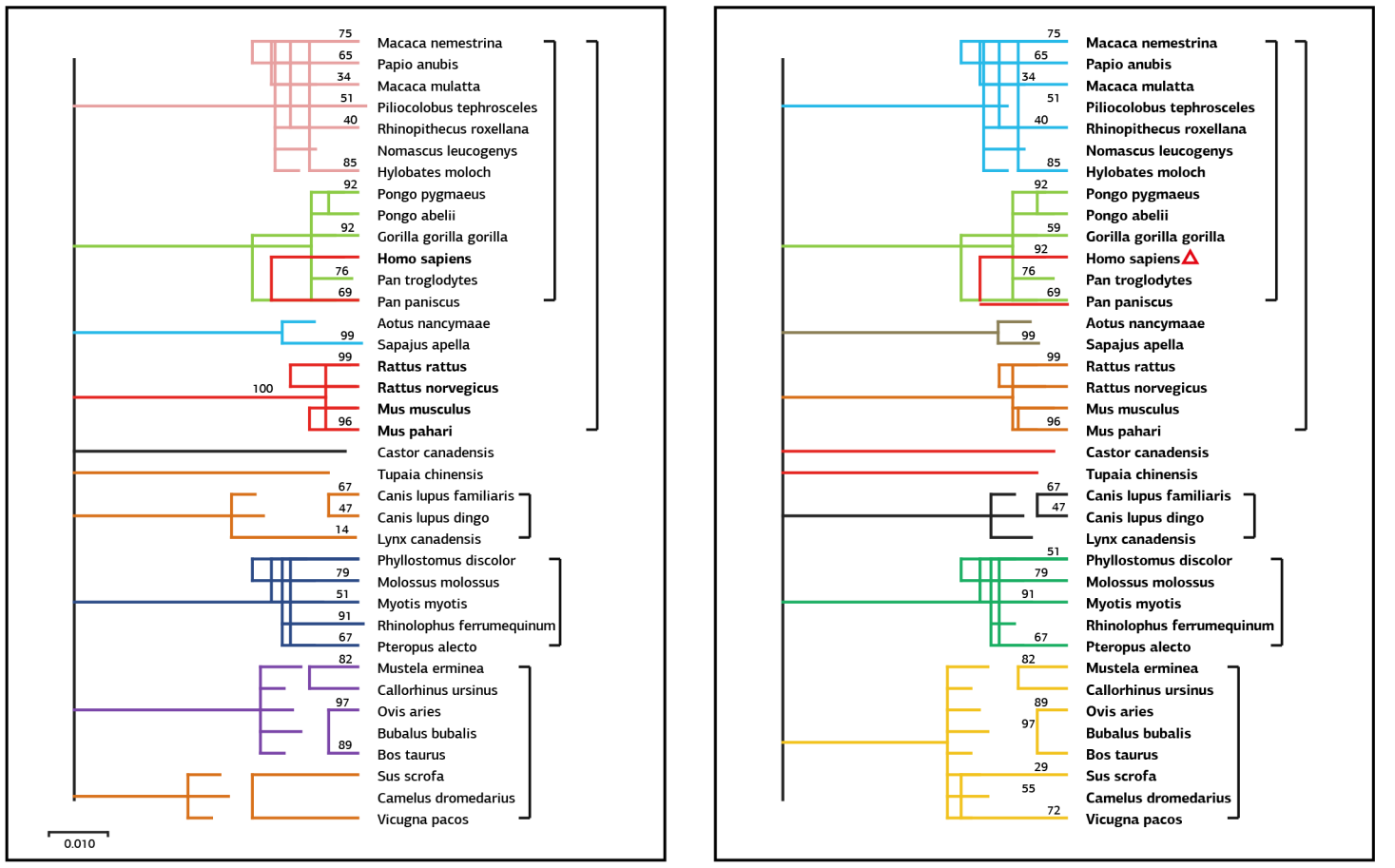


A



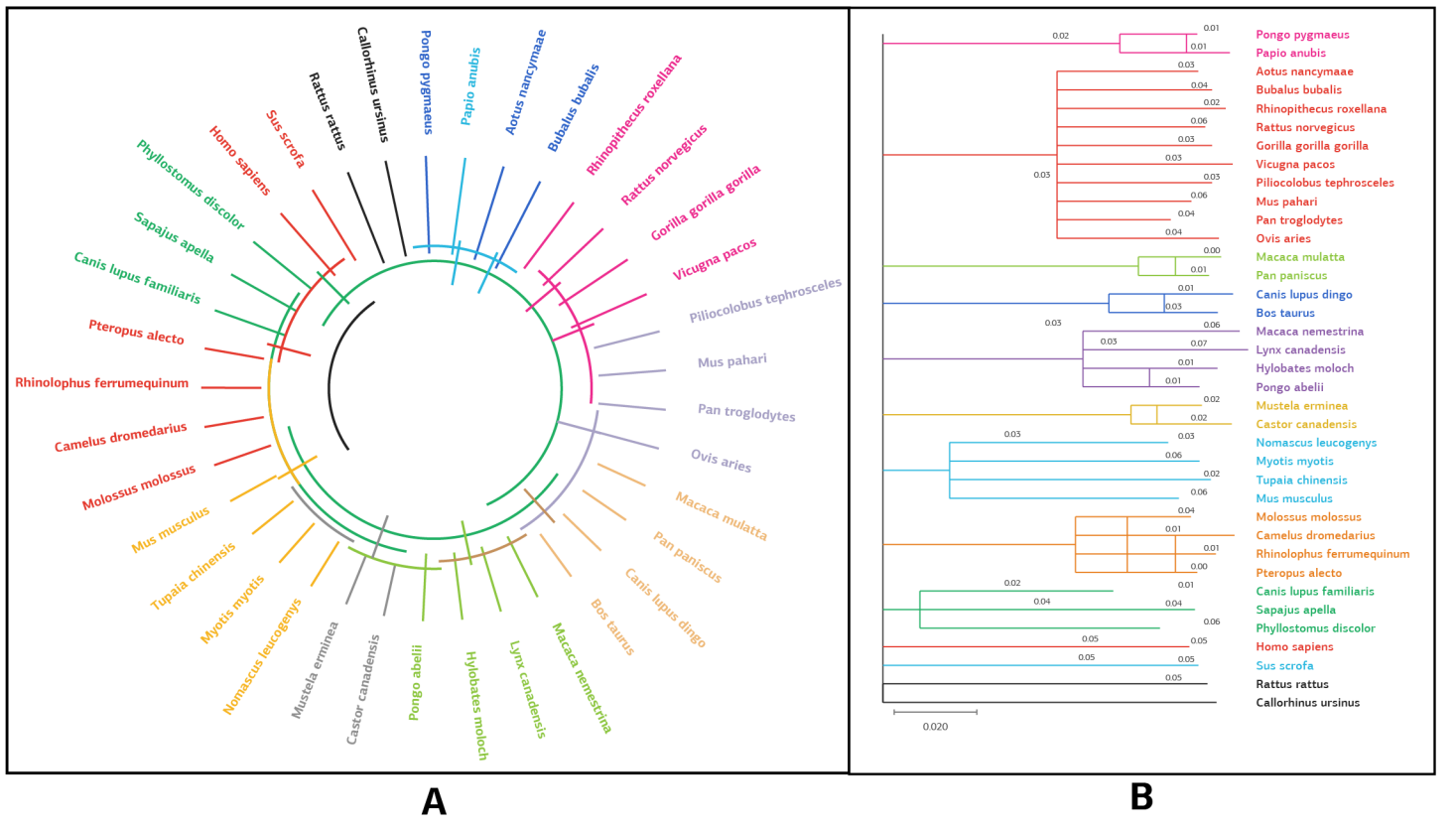
B

Supplementary Figure 1. (A) Composite distances of MYC oncoproteins across taxonomic groups, indicating that differences in composition are most pronounced among closely related organisms.



Supplementary Figure 2. Bootstrap Consensus Tree>Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method. The bootstrap consensus tree inferred from 500 replicates is taken to represent the evolutionary history of the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) is shown next to the branches. Homo sapiens taxon is colored in red color in light green cluster.



Supplementary Figure 3. Time tree analysis using the RelTime method

A time tree inferred by applying the RelTime method to the user-supplied phylogenetic tree whose branch lengths were calculated using the Maximum Likelihood (ML) method and the JTT matrix-based substitution model. Homo sapiens taxon is colored in red color in light green cluster. The time tree was computed using 1 calibration constraint. The Tao et al. method was used to set minimum and maximum time boundaries on nodes for which calibration densities were provided. The estimated log likelihood value of the tree is -5557.47. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.1679)).