**Selection of primate species for study**

From a final dataset of high-quality neoplasm measurements (with >10 observations) in 52 primate species, we obtained gene-alignment data for a total of 9 UCSC-available primate genomes (*Gorilla gorilla, Pan paniscus, Nomascus leucogenys, Pan troglodytes, Pongo abelii, Propithecus coquereli, Microcebus murinus, Eulemur flavifrons, Callithrix jacchus*). When a species for which neoplasm measurement was not publicly available in the alignment, but there was a close species from the same genus, we used the latter, since -from a phylogenetic perspective- the same internal branches are studied, even if the leaves in the phylogeny change (for instance *Colobus guereza, Cebus apella, Saimiri sciureus*). Then, for species in which we had more than two measurements for the same genus, we did prioritized the one with the largest number of measurements and the closest phylogenetic distance in the tree (*Papio hamadryas, Eulemur mongoz, Macaca fuscata, Macaca silenus*). Finally, as we only had one species as representative of the Galagidae family both in our trees and in the trait dataset, we merged this information for the available species (*Galago moholi*).