

The Primate Genome Project also generated high-quality reference genomes for another 16 primate species that were used in the accompanying papers to reveal hybrid speciation during the rapid radiation of the macaques (29), the homoploid hybrid speciation in the snub-nosed monkey *Rhinopithecus* genus (30), social evolution in the Asian colobines driven by cold adaptation (31), and the evolutionary adaptations of slow lorises (32). All genomic

data have been published openly and can be freely accessed in the National Center for Biotechnology Information (NCBI) Assembly Database under the accession information described in this study.

A genomic phylogeny of living primates

We next performed phylogenomic analyses comprising the 27 newly generated genomes, another 22 published primate genomes, one

long-read genome from *Nycticebus pygmaeus* reported in an accompanying paper (32), and two close relatives of primates, the Sunda flying lemur (*Galeopterus variegatus*) and the Chinese tree shrew (*Tupaia belangeri chinensis*) (33), as outgroups (table S8). We constructed whole-genome-wide phylogenetic trees using ExaML under a GTR+GAMMA model (34). Altogether, ~433.5 Mbp of gap-free data for syntenic orthologous sequences were retrieved

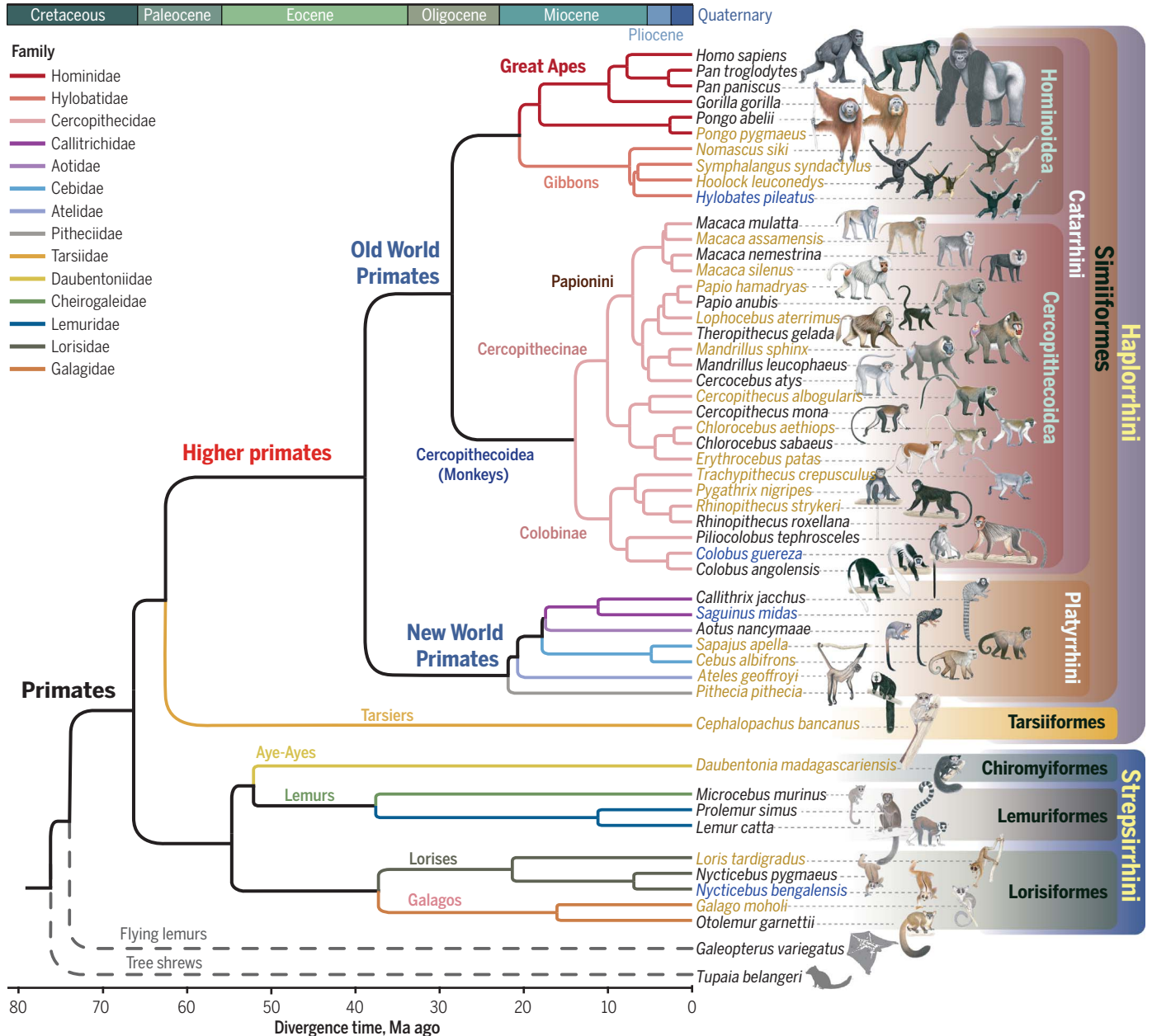


Fig. 1. Genomic phylogeny of primates. The maximum likelihood method was used to infer the primate species tree from whole-genome sequences across 52 species, including 50 primate species and two outgroup species (the Sunda flying lemur and the Chinese tree shrew) with 100 bootstraps under a GTR+GAMMA model. The divergence time was estimated using fossil calibrations (fig. S11) and the MCMCtree algorithm. The yellow and blue species names represent

those genomes newly produced in this study. The genomes of the species marked in blue were assembled at the chromosome level. The genomes of the species marked in black were downloaded from the NCBI and Ensembl databases (table S8). Monkey pictures are copyrighted by Stephen D. Nash/IUCN/SSC Primate Specialist Group and are used in this study with their permission.