

## UNCOVERING HUMAN EVOLUTION THROUGH T2T SEQUENCING OF OUR CLOSEST RELATIVES

A Nature study<sup>1</sup> presents fully resolved, gapless genomes (T2T) of our closest relatives: chimpanzee, bonobo, gorilla, Bornean orangutan, Sumatran orangutan and siamang (a gibbon). These high-quality genomes allow, for the first time, direct comparison without relying on the human reference genome and eliminating previous biases.

Thanks to long-read sequencing and advanced assembly techniques, the researchers resolved highly repetitive and previously inaccessible regions, like centromeres, segmental duplications, immunoglobulin loci, and the MHC region, that are critical for understanding adaptive evolution, immune function, and genomic rearrangements.

This resource is revolutionary because it (i) reveals lineage-specific structural variants and gene duplications tied to traits unique to each species; (ii) identifies ancestral regions under selection that shaped the human genome; (iii) improves annotation of thousands of genes relevant to brain development, immunity, and reproduction.

Ultimately, these T2T ape genomes provide a comprehensive, unbiased reference for tracing the evolutionary paths that led to modern humans.

1. <https://www.nature.com/articles/s41586-025-08816-3>