

Better ape genome assemblies could help us understand what ‘make us uniquely human’

New, higher-quality assemblies of great ape genomes have now been generated without the guidance of the human reference genome. The effort to reduce “humanizing” discovery bias in great ape genomes provides a clearer view of the genetic differences that arose as humans diverged from other primates.

In the June 8 issue of *Science*, researchers report on improved orangutan and chimpanzee genomes that were built from scratch using long-read PacBio sequencing and long-range mapping technology.

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The newest investigation provides the most comprehensive catalog of genetic variants that were gained or lost on different ape lineages. Some of these variants affect how genes are differentially expressed among humans and apes.

The researchers examined the possible influence of some of the genetic variants and gene function regulators on such areas as human and ape dietary differences, anatomy, and brain formation.

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The researchers on this study predict that more advanced, long-range sequencing and mapping technologies, and even longer-read sequencing, will assist in increasing knowledge on the evolutionary journey taken by the great apes and our human ancestors.

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“Our goal,” said [researcher Evan] Eichler, “is to generate multiple ape genomes with as high quality as the human genome. Only then will we be able to truly understand the genetic differences that make us uniquely human.”

Read full, original post: [Improved ape genome assemblies provide new insights into human evolution](#)