

A better reference genome for the rhesus macaque

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A large team of researchers from the U.S., Italy and Germany has developed a new and improved reference genomic assembly for the rhesus macaque. In their paper published in the journal *Science*, the group describes using advanced sequencing techniques to create the reference and why they believe the new reference genome will be so

important to medical scientists.

As the researchers note, the rhesus macaque is the [animal model](#) most often studied in [medical science](#) due to biological characteristics that overlap with those of humans. For example, research with [rhesus macaques](#) has led to a better understanding of the HIV virus and how to treat people who have contracted it. The species also played a large role in work related to the Ebola vaccine and in creating therapies for treating neurological disorders. And as the researchers also note, such research has been reliant on [genome](#) data for the rhesus macaque that has been around since 2007. They further note that technology used to sequence genomes has improved dramatically over the past decade and thus the time appeared ripe for updating the reference genome for the rhesus macaque.

The work involved using the newest tools in the field to improve contiguity—in this case by 120-fold. The group also annotated the genome using 6.5 million full-length transcripts. Additionally, they conducted whole-genome sequencing on [tissue samples](#) from 853 test animals and identified approximately 10.5 million indel variants—and almost 86 million single-nucleotide variants. The researchers suggest such variants (especially those resulting from damage) could be used by medical specialists looking to better understand the nature of autism and other neurologically based development diseases in humans. The researchers also closed approximately 99.7% of the gaps that were present in the prior sequence.

The result was the creation of a new reference genomic assembly for the rhesus macaque that is far superior to any others that exist. The researchers expect the new reference to play a significant role in medical research in the future.

More information: Sequence diversity analyses of an improved rhesus

macaque genome enhance its biomedical utility, *Science* (2020).
[science.sciencemag.org/cgi/doi ... 1126/science.abc6617](https://science.sciencemag.org/cgi/doi/10.1126/science.abc6617)

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