

## GENOME SEQUENCING

# The Complete Genome Sequences of five Neotropical Carnivores

Paola Pulido-Santacruz<sup>1</sup>, Alejandra Bonilla-Sanchez<sup>2,3</sup>, Alejandra Niño-Reyes<sup>4</sup>, Eduardo Eizirik<sup>5</sup>, Stacy Pirro<sup>6</sup>

<sup>1</sup> School of Sciences and Engineering, Universidad del Rosario, Bogotá, Colombia, <sup>2</sup> Corporación Mamíferos de Alta Montaña, Itagüí, Antioquia, Colombia,

<sup>3</sup> Grupo Mastozoología y Colección Teriológica, Universidad de Antioquia, Medellín, Antioquia, Colombia, <sup>4</sup> Laboratorio de Biología Molecular e Genómica, Escola da Saude e da Vida, Pontifícia Universidade Católica de Rio grande do Sul – PUCRS, Porto Alegre, RS, Brazil, <sup>5</sup> Laboratorio de Biología Molecular e Genómica, Escola da Saude e da Vida, Pontifícia Universidade Católica de Rio grande do Sul – PUCRS, Porto Alegre, RS, Brazil, <sup>6</sup> Iridian Genomes, USA

<https://doi.org/10.56179/001c.159377>

---

## Biodiversity Genomes

---

Genomic resources remain scarce for many ecologically important tropical species, and collaboration among governmental and research institutions is key to addressing this gap. Here we report genome sequences for five species of Neotropical carnivores, providing valuable data for future studies on the evolution, ecology, and conservation of Neotropical mammals.

## Methods

Blood samples of *Eira barbara*, *Cerdocyon thous*, *Puma concolor*, *Galictis vittata*, and *Bassaricyon neblina* were obtained through donations from regional environmental authorities in Colombia, from rescued or confiscated animals. These samples were incorporated into the Neotropical Carnivore Sample Bank at Universidad del Rosario, an initiative designed to consolidate a curated repository of biological samples from Neotropical carnivores. Genome sequencing was conducted as part of ongoing efforts to expand genomic resources for Neotropical carnivores.

## Data Availability

taxname	accession
Bassaricyon neblina	PRJNA1313331
Cerdocyon thous	PRJNA1433537
Eira barbara	PRJNA1433536
Galictis vittata	PRJNA1313326
Puma concolor	PRJNA1433538

---

## Funding

Funding was provided by Iridian Genomes, grant# IRGEN\_RG\_2021-1345 Genomic Studies of Eukaryotic Taxa.

## Acknowledgments

Blood samples were collected under the scientific research permit 001431 (12 July 2024) issued by the National Environmental Licensing Authority of Colombia. Samples of *Galictis vittata* and *Bassaricyon neblina* were exported for sequencing under export permit No. 00403 granted by the National Environmental Licensing Authority (ANLA) of Colombia. Samples of *Eira*

*barbara*, *Cerdocyon thous*, and *Puma concolor* were exported for sequencing under export permit No. 48160 issued by the Ministry of Environment and Sustainable Development of Colombia.

Submitted: March 22, 2026 EDT. Accepted: March 24, 2026 EDT. Published: March 24, 2026 EDT.

## REFERENCES

- Bankevich, Anton, Sergey Nurk, Dmitry Antipov, et al. 2012. "SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing." *Journal of Computational Biology*, ahead of print. <https://doi.org/10.1089/cmb.2012.0021>.
- Bolger, Anthony M., Marc Lohse, and Bjoern Usadel. 2014. "Trimmomatic: A Flexible Trimmer for Illumina Sequence Data." *Bioinformatics* 30 (15): 2114–20. <https://doi.org/10.1093/bioinformatics/btu170>.
- Kieras, M., K. O'Neill, and S. Pirro. 2021. "Zanfona, a Genome Assembly Finishing Tool for Paired-End Illumina Reads." <https://github.com/zanfona734/zanfona>.