



# ORG.one: Rapid Sequencing of Any Endangered Species, Anywhere, by Anyone



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## Expanding genomic resources for endangered species

### Supporting open access data

Data are accessible by anyone, anywhere, fostering rapid and collaborative conservation efforts

### Faster, equitable and more localised sequencing

Empower teams to rapidly study species close to the sample's origin using the latest sequencing approaches

### Promoting an active and distributed community

Local communities, conservationists, scientists and bioinformaticians working together to enhance collective knowledge



Partnership support providing extraction and sequencing reagents to ORG.one participants

### Brown-headed Spider Monkey

*Ateles fusciceps fusciceps*  
CRITICALLY ENDANGERED



Ecuadorian endemic sequenced using low-cost, small footprint MinION, achieving 21x coverage, and assembled to generate first draft genome (Nanopore-only).

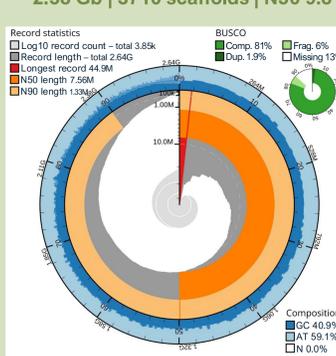
**2.58 Gb | 3710 scaffolds | N50 9.8 Mb | BUSCO 84.3%**

|                                  |             |             |
|----------------------------------|-------------|-------------|
| Record statistics                | BUSCO       | Composition |
| Log10 record count - total 3.85k | Comp. 81%   | GC 40.9%    |
| Record length - total 2.64G      | Dup. 1.9%   | AT 59.1%    |
| Longest record 44.9M             | Frag. 6%    | N 0.0%      |
| N50 length 7.56M                 | Missing 13% |             |
| N90 length 1.23M                 |             |             |

Full process from DNA extraction to assembly performed locally in Ecuador.

Genomic tools in development to assess inbreeding and gene flow in the wild.

Pozo et al 2024. G3: Genes | Genomes | Genetics. p.jkae014




### Butternut (White walnut)

*Juglans cinerea*  
ENDANGERED

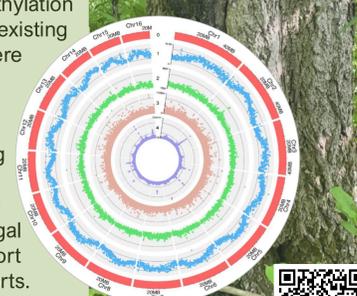
**539 Mb | 16 chromosomes | N50 35 Mb | BUSCO 99.0%**

Chromosomal-scale genome assembled from 100x coverage (Nanopore-only) by university students in new programme training the next generation at the University of Connecticut.

Nanopore sequencing co-produced methylation data (5mC), and existing RNA-seq data were incorporated into assembly.

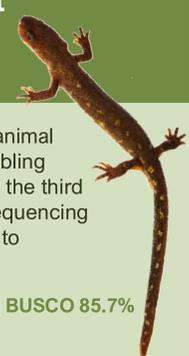
Genome enabling research into hybridisation and resistance to fungal infection to support conservation efforts.

Guzman-Torres et al. 2024. G3: Genes | Genomes | Genetics. 14(2). jkad189


### Montseny brook newt

*Calotriton arnoldi*  
CRITICALLY ENDANGERED



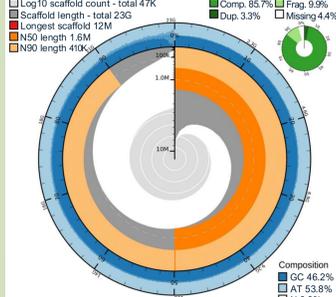
Salamanders have some of the largest animal genomes. Thus, sequencing and assembling reference genomes is challenging. Only the third Caudata *de novo* genome, Nanopore sequencing was combined with other genomic data to assemble this >22 Gb genome.

**22.89 Gb | 47,257 scaffolds | N50 1.6 Mb | BUSCO 85.7%**

|                                  |              |             |
|----------------------------------|--------------|-------------|
| Scaffold statistics              | BUSCO        | Composition |
| Log10 scaffold count - total 47K | Comp. 85.7%  | GC 46.2%    |
| Scaffold length - total 23G      | Dup. 3.3%    | AT 53.8%    |
| Longest scaffold 12M             | Frag. 9.9%   | N 0.0%      |
| N50 length 1.6M                  | Missing 4.4% |             |
| N90 length 419k                  |              |             |

Population studies (WGS and ddRAD) revealed two isolated populations, with minimal gene flow. Bottlenecks led to both populations exhibiting low genomic diversity (long ROH) but not inbreeding.

Talavera et al. 2024. iScience. 27(1). 108665






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