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Hippocamelus bisulcus (Chilean guemal)

Accession: PRJNA1509444 ID: 1509444

Hippocamelus bisulcus Genome sequencing

This BioProject aims to generate genomic resources for *Hippocamelus bisulcus* (huemul), the endangered South Andean deer, using Oxford Nanopore Technologies long-read sequencing. [More...](#)

Accession	PRJNA1509444
Data Type	Genome sequencing
Scope	Monoisolate
Organism	Hippocamelus bisulcus [Taxonomy ID: 397614] Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Cervidae; Odocoileinae; Hippocamelus; Hippocamelus bisulcus
Submission	Registration date: 7-Aug-2026 Centro de Investigaciones en Toxicología Ambiental y Agrobiotecnología del Comahue (CITAAC)
Relevance	Evolution

Project Data:

Resource Name	Number of Links
SEQUENCE DATA	
Nucleotide (total)	38
WGS master	1
Genomic DNA	37
OTHER DATASETS	
Assembly	1

▼ Assembly details:

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Assembly	Level	WGS	Chrs	BioSample	Taxonomy
GCA_060697595.1	Chromosome	JCCBW1000000000	37	SAMN62312241	Hippocamelus bisulcus

▼ SRA Data Details

Parameter	Value
Data volume, Gbases	57
Data volume, Mbytes	42668



An official website of the United States government
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Documentation

Genome assembly Hbis_v1.0

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API

FTP

Submitted GenBank assembly

GCA_060697595.1



Taxon

[Hippocamelus bisulcus](#) (Chilean guemal)

Isolate

SCp

WGS project

[JCCBW101](#)

Assembly type

haploid

Submitter

Centro de Investigaciones en Toxicología Ambiental y Agrobiotecnología del Comahue (CITAAC)

Date

Sep 1, 2026



BLAST the reference genome

Assembly statistics

GenBank

Genome size

2.5 Gb

Feedback

	GenBank
Total ungapped length	2.5 Gb
Number of chromosomes	36
Number of organelles	1
Number of scaffolds	342
Scaffold N50	68.6 Mb
Scaffold L50	15
Number of contigs	1,581
Contig N50	8.7 Mb
Contig L50	89
GC percent	41.5
Genome coverage	22.4x
Assembly level	Chromosome
View sequences	view GenBank sequences

Sample details

BioSample ID
[SAMN62312241](#)

Description
Hippocamelus bisulcus combined reads for genome assembly

Comment
This BioSample represents sequencing reads from two independently sampled Hippocamelus bisulcus individuals that were combined computationally for genome assembly. Shehuen (SAMN62264853) contributed 10,162,317 reads (90.2% of total reads) and Coiron (SAMN62264854) contributed 1,102,669 reads (9.8%). No biological samples or DNA were physically pooled.

Submitter
Centro de Investigaciones en Toxicologia Ambiental y Agrobiotecnologia del Comahue (CITAAC)

Isolate
Shehuen_Coiron_pool

Development stage
juvenile-adult

Collection date
2024

[View more](#)



Assembly methods

Sequencing technology
Oxford Nanopore MinION

Additional genomes

[Browse all Hippocamelus bisulcus genomes \(1\)](#)

BioProject

[PRJNA1509444](#)
Hippocamelus bisulcus Genome sequencing

Chromosomes

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Chromosome	GenBank	RefSeq	Size (bp)	GC content (%)	Unlocalized cou...	Action
1	CM193357.1	n/a	111,056,174	40	0	⋮
2	CM193358.1	n/a	103,180,191	42.5	0	⋮
3	CM193359.1	n/a	101,960,126	41.5	0	⋮
4	CM193360.1	n/a	96,509,317	40.5	0	⋮
5	CM193361.1	n/a	102,562,774	41	0	⋮
6	CM193362.1	n/a	93,076,862	41	0	⋮
7	CM193363.1	n/a	87,637,288	42	0	⋮
8	CM193364.1	n/a	76,690,392	40	0	⋮
9	CM193365.1	n/a	80,238,454	43.5	0	⋮
10	CM193366.1	n/a	79,394,451	41.5	0	⋮
11	CM193367.1	n/a	76,806,560	42.5	0	⋮
12	CM193368.1	n/a	69,136,242	42	0	⋮
13	CM193369.1	n/a	70,450,182	39	0	⋮
14	CM193370.1	n/a	68,564,101	40.5	0	⋮

Feedback

Chromosome	GenBank	RefSeq	Size (bp)	GC content (%)	Unlocalized cou...	Action
15	CM193371.1	n/a	76,939,590	40.5	0	⋮
16	CM193372.1	n/a	65,603,999	42.5	0	⋮
17	CM193373.1	n/a	61,013,115	45.5	0	⋮
18	CM193374.1	n/a	59,179,022	40	0	⋮
19	CM193375.1	n/a	60,419,949	39	0	⋮
20	CM193376.1	n/a	61,526,008	45.5	0	⋮
21	CM193377.1	n/a	57,045,818	38.5	0	⋮
22	CM193378.1	n/a	59,125,616	41.5	0	⋮
23	CM193379.1	n/a	57,276,051	43.5	0	⋮
24	CM193380.1	n/a	54,161,968	40	0	⋮
25	CM193381.1	n/a	52,677,687	38.5	0	⋮
26	CM193382.1	n/a	52,515,818	42.5	0	⋮
27	CM193383.1	n/a	47,809,729	43	0	⋮
28	CM193384.1	n/a	48,189,417	44	0	⋮
29	CM193385.1	n/a	50,331,872	40	0	⋮
30	CM193386.1	n/a	55,025,897	42.5	0	⋮
31	CM193387.1	n/a	44,116,267	42.5	0	⋮
32	CM193388.1	n/a	42,586,171	41.5	0	⋮
33	CM193389.1	n/a	41,285,799	47	0	⋮
34	CM193390.1	n/a	38,138,899	41.5	0	⋮
X	CM193391.1	n/a	45,720,906	39	0	⋮
Y	CM193392.1	n/a	2,390,332	43.5	0	⋮

Note: This genome assembly includes 306 unplaced scaffolds. ⓘ

Revision history

This record has not been revised



GenBank	RefSeq	Name	Level	Date	Action
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