Supplementary Table 1. Statistics for the contig genome assembly with MEGAHIT 1.1.1 of *Oreamnos americanus.*

|  |  |
| --- | --- |
|  | **Short-read assembly**  |
| **Total length** | 2,595 Mbp |
| **N50 / L50** | 8,423 bp / 87,093 contigs |
| **N90 / L90** | 1,442 bp / 345,296 contigs |
| **Total number of scaffolds** | 942,462 |
| **N count** | 0 |

Supplementary Table 2. Statistics for the contig genome assembly with Meraculous 2.0.4 of *Oreamnos americanus.*

|  |  |
| --- | --- |
|  | **Short-read assembly**  |
| **Total length** | 2,489 Mbp |
| **N50 / L50** | 24,510 bp / 28,926 contigs |
| **N90 / L90** | 5,851 bp / 107,981 contigs |
| **Total number of scaffolds** | 196,298 |
| **N count** | 0 |

Supplementary Table 3. A comparison of the North American mountain goat genome assembly to a subset of wild and domestic *Bovidae* whole genome assemblies. \*denotes that *Ovis canadensis* chromosome assignment is based off *Ovis aries*.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Species name** | **Common name** | **Assembly length (Mbp)** | **Scaffold N50 (bp)** | **Assigned to chromosomes?** | **Accession number** |
| ***Wild*** |  |  |  |  |  |
| *Oreamnos americanus* | North American mountain goat | 2,506 | 66,617,000 | No | TBD |
| *Bos mutus* | wild yak | 2,645 | 1,407,960 | No | BosGru\_v2.0 (GCA\_000298355.1) |
| *Bison bison bison* | american bison | 2,954 | 6,873,254 | No | Bison\_UMD1.0 (GCA\_000754665.1) |
| *Cervus elaphus hippelaphus*  | red deer | 3,439 | 107,358,006 | No | CerEla1.0 (GCA\_002197005.1) |
| *Odocoileus virginianus texanus* | white-tailed deer | 2,381 | 850,721 | No | Ovir.te\_1.0 (GCA\_002102435.1) |
| *Ovis canadensis canadensis* | bighorn sheep | 2,591 | 100,190,483 | Yes\* | ASM103953v1 (GCA\_001039535.1) |
|  |  |  |  |  |  |
| ***Domestic*** |  |  |  |  |  |
| *Bos taurus* | cow | 2,716 | 103,308,737 | Yes | ARS-UCD1.2 (GCA\_002263795.2) |
| *Ovis aries* | sheep | 2,619 | 100,079,507 | Yes | Oar\_v3.1 (GCA\_000298735.1) |
| *Capra hircus* | goat | 2,923 | 87,277,232 | Yes | ARS1 (GCA\_001704415.1) |
| *Bubalus bubalis* | water buffalo | 2,656 | 117,219,835 | Yes  | UOA\_WB\_1 (GCA\_003121395.1) |

Supplementary Table 4. Mapping statistics for the alignment of raw short-insert library reads to the scaffolded *Oreamnos americanus* genomeassembly with bowtie2.

|  |  |  |
| --- | --- | --- |
| **Number of reads / mates** | **% of total reads** | **Alignment** |
| 632,003,301 | 100.00% | total paired reads; of these: |
|  86,626,312 | 13.71% | aligned concordantly >1 times |
|  507,304,993 | 80.27% | aligned concordantly exactly 1 time |
|  38,071,996 |  | aligned concordantly 0 times; of these: |
|  8,071,100 | 1.28% | aligned discordantly 1 time |
|  30,000,896 (60,001,792 mates) |  | aligned 0 times concordantly or discordantly; of these: |
|  10,261,338 mates | 0.81% | aligned >1 times |
|  15,681,805 mates | 1.24% | aligned exactly 1 time |
|  34,058,649 mates | 2.69% | aligned 0 times |

Supplementary Table 5. Hypergeometric test results of GO enrichment of gene families unique to *Oreamnos americanus* in comparison to *Capra hircus, Equus cabalus, Bos taurus, Sus scrofa* and *Ovis aries*. Only families with p-values < 0.05 are shown.

|  |  |  |  |
| --- | --- | --- | --- |
| **GO** | **Function** | **Type** | **p-value** |
| GO:0060968 | regulation of gene silencing | biological process | 0.024 |
| GO:0031659 | positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell cycle | biological process | 0.034 |
| GO:0032784 | regulation of DNA-templated transcription, elongation | biological process | 0.039 |
| GO:0032044 | DSIF complex | cellular component | 0.015 |
| GO:0000228 | nuclear chromosome | cellular component | 0.048 |
| GO:0003964 | RNA-directed DNA polymerase activity | molecular function | 0.015 |
| GO:0043024 | ribosomal small subunit binding | molecular function | 0.019 |
| GO:0000155 | phosphorelay sensor kinase activity | molecular function | 0.024 |
| GO:0004322 | ferroxidase activity | molecular function | 0.043 |

Supplementary Table 6. Assembly quality metrics for the scaffolded + Chicago assembly based on FRC analysis with FRC\_align with parameters set as ‘--CEstats-PE-min -50 --CEstats-PE-max 50’.

|  |  |  |
| --- | --- | --- |
| **Feature** | **Description** | **Value** |
| COMPR\_PE | low CE-statistics computed on PE-reads | 681 |
| HIGH\_COV\_PE | high read coverage areas (all aligned reads) | 8,988 |
| HIGH\_NORM\_COV\_PE | high paired-read coverage areas (only properly aligned pairs) | 5,351 |
| HIGH\_OUTIE\_PE | high number of mis-oriented or too distant PE reads | 15 |
| HIGH\_SINGLE\_PE | high number of PE reads with unmapped pair | 25 |
| HIGH\_SPAN\_PE | high number of PE reads with pair mapped in a different contig/scaffold | 2,384 |
| LOW\_NORM\_COV\_PE | low paired-read coverage areas (only properly aligned pairs) | 2,437 |
| STRECH\_PE | high CE-statistics computed on PE-reads | 1,792 |

Supplementary Figure 1. KAT k-mer (k=27) frequency plot for the short-read assembly completed with Meraculous software.



Supplementary Figure 2. KAT k-mer (k=27) frequency plot for the scaffolded + Chicago assembly.



Supplementary Figure 3. The maximum likelihood phylogenetic tree for compete mitochondrial genomes of *Oreamnos americanus* (this study), *Capra hircus* (Genbank accession MK341077.1), *Ovis aries* (Genbank accession NC 001941.1), *Bos taurus* (Genbank accession GU947021.1), *Sus scrofa* (Genbank accession AY337045.1), *Equus cabalus* (Genbank accession AY584828.1) and *Homo sapiens* (Genbank accession GU170819.1). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. All positions containing gaps and missing data were eliminated resulting in a total of 8116 positions in the final dataset. Evolutionary analyses were conducted in MEGA7.

