**Genome collinearity analysis illuminates the evolution of donkey chromosome 1 and horse chromosome 5 in perissodactyls: A comparative study**

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**Supplementary Figure 1**

Dot-plot alignments of the 32 chromosomes of *E. caballus* (ECA, x-axis) to the 31chromosome-length scaffolds of *E. asinus asinus* (EAS, y-axis) using D-Genies (default parameters). The chromosome-length scaffolds of donkey were offered by DNA Zoo. The colors correspond to similarity values that were binned in four groups (<25%, 25%–50%, 50%–75%, and >75% similarity). This diagram depicts the direction of the genome sequence prior to adjustment.

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Supplementary Figure 2

Inverted breakpoint detailed analysis of EAS1 using Mauve v2.4.0. Each contiguously colored region is a locally collinear block (LCB), which is a region without rearrangement of the homologous backbone sequence. LCBs below a genome’s center line are in the reverse complement orientation relative to the reference genome. The lines between genomes trace each orthologous LCB through each of the genomes. The diagram shows detailed structural variations in the genome using Mauve V2.4.0; color boxes represent orthologous blocks.

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Supplementary Table 1: Genomic assembly data sources. Links to genome assemblies file website

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Species | Abbreviation | Common name | 2n | Database | Website link | |
| *Equus asinus asinus* | EAS | Donkey | 62 | DNA ZOO | https://www.dropbox.com/s/my36jgqte50j2sc/ASM303372v1\_HiC.fasta.gz?dl=0 |
| *Equus caballus* | ECA | Horse | 64 | NCBI | https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/002/863/925/GCF\_002863925.1\_EquCab3.0/GCF\_002863925.1\_EquCab3.0\_genomic.fna.gz |
| *Equus burchellii* | EBU | Plains zebra | 44 | DNA ZOO | https://www.dropbox.com/s/tormwrmtzhayrc5/Equus\_quagga\_HiC.fasta.gz?dl=0 |
| *Ceratotherium simum* | CSI | white rhinoceros | 82 | DNA ZOO | https://www.dropbox.com/s/oqm312vygoh3csn/CerSimSim1.0\_HiC.fasta.gz?dl=0 |
| *Tapirus indicus* | TIN | Malayan tapir | 52 | DNA ZOO | https://www.dropbox.com/s/vmq9iudk5cuyte0/Tapirus\_indicus\_HiC.fasta.gz?dl=0 |
| *Balaenoptera musculus* | BMU | Blue whale | 38 | NCBI | https://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/873/245/GCA\_009873245.2\_mBalMus1.v2/GCA\_009873245.2\_mBalMus1.v2\_genomic.fna.gz |
| *Homo sapiens* | HSA | Human | 46 | NCBI | https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/001/405/GCF\_000001405.39\_GRCh38.p13/GCF\_000001405.39\_GRCh38.p13\_genomic.fna.gz |

Supplementary Table 2: Genome annotation data sources. Links to genome annotation file website

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Species | Abbreviation | Common name | Database | Website link |
| *Equus asinus asinus* | EAS | Donkey | NCBI | ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/001/305/755/GCF\_001305755.1\_ASM130575v1/GCF\_001305755.1\_ASM130575v1\_genomic.gff.gz |
| *Equus caballus* | ECA | Horse | NCBI | https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/002/863/925/GCF\_002863925.1\_EquCab3.0/GCF\_002863925.1\_EquCab3.0\_genomic.gff.gz |
| *Bos taurus* | BTA | Cattle | NCBI | https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/002/263/795/GCF\_002263795.1\_ARS-UCD1.2/GCF\_002263795.1\_ARS-UCD1.2\_genomic.gff.gz |
| *Sus scrofa* | SSC | Pig | NCBI | ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/003/025/GCF\_000003025.6\_Sscrofa11.1/GCF\_000003025.6\_Sscrofa11.1\_genomic.gff.gz |
| *Mus musculus* | MMU | House mouse | NCBI | https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/001/635/GCF\_000001635.26\_GRCm38/GCF\_000001635.26\_GRCm38.p6\_genomic.gff |
| *Homo sapiens* | HSA | Human | NCBI | https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/001/405/GCF\_000001405.39\_GRCh38.p13/GCF\_000001405.39\_GRCh38.p13\_genomic.gff.gz |