Additional File 1 - Tables

Manuscript “High-quality nanopore assemblies of three endangered Neotropical primates”

Table S1. Overall SSR Counts across Genomes

# Genomes	Mean	SD
14	70755	22094

Table S2: SSR Counts by Species and Sequencing Technology

Species	Technology	Total SSRs	% Under 75 bp	Perfect SSRs	% Perfect
Ateles belzebuth	Short-Read	59850	98.2	58135	97.1
Ateles chamek	Short-Read	58404	98.3	56743	97.2
Ateles geoffroyi	Short-Read	65336	97.9	63209	96.7
Ateles marginatus	Short-Read	61496	98.2	59740	97.1
Ateles paniscus	Short-Read	61229	98.0	59354	96.9
Cebus imitator	Short-Read	78990	94.9	74323	94.1
Cebus olivaceous	Short-Read	98722	92.3	91075	92.3
Cebus unicolor	Short-Read	91869	93.4	84984	92.5
Ateles belzebuth	Nanopore	63471	96.7	60766	95.7
Ateles fusciceps	Nanopore	71172	97.9	69076	97.1
Ateles hybridus	Nanopore	75736	96.7	72642	95.9
Cebus aequatorialis	Nanopore	112240	92.3	102705	91.5
Cebus albifrons	Nanopore	18179	91.3	16681	91.8
Ateles geoffroyi	SMRT	73877	92.5	69944	94.7

Table S3a. Summary of SSRs in GCA_963573605.1_PGDP_AteBel_genomic.fna and results of BLASTs against USFQ_Abelze_01.fasta

Statistic	N
Total G1 SSRs	59850
Perfect G1 SSRs	58135
Perfect G1 SSRs with full length L and R flanks	55866
..... where either flank BLASTs to G2	55723
..... where both flanks BLAST to G2	54778
..... where both flanks BLAST to G2 and delta_length <= 50	54008
..... where either or both flanks miss G2	945

Table S3b. Summary of SSRs in USFQ_Abelze_01.fasta and results of BLASTs against GCA_963573605.1_PGDP_AteBel_genomic.fna

Statistic	N
Total G2 SSRs	63471
Perfect G2 SSRs	60766
Perfect G2 SSRs with full length L and R flanks	60740
..... where either flank BLASTs to G1	60174
..... where both flanks BLAST to G1	58463
..... where both flanks BLAST to G1 and delta_length <= 50	56540
..... where either or both flanks miss G1	1711