Additional Files 2 - Figures

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

Supplementary Figure Legends

Figure S1. Total Number of SSRs Recovered from 14 Platyrrhine Genomes by Sequencing Technology. Total number of simple sequence repeats (SSRs) identified across 14 *Ateles* and *Cebus* reference genomes grouped according to sequencing technology (Oxford Nanopore, short-read Illumina, and PacBio SMRT). Each point represents one genome assembly, and boxplots summarize the distribution of total SSR counts for each sequencing platform. No significant differences in total SSR abundance were observed among sequencing technologies.

Figure S2. SSR Counts by Species and Sequencing Technology. Distribution of SSR counts according to repeat motif length (2- to 6-bp motifs and compound SSRs) across *Ateles* and *Cebus* genome assemblies. Panels are grouped by sequencing technology (Oxford Nanopore, short-read Illumina, and PacBio SMRT). Red boxes indicate genomes generated in this study using Oxford Nanopore sequencing. SSR distributions across repeat motif lengths are highly consistent among species within each genus and comparable across sequencing technologies.

Figure S3. Top 12 Canonical SSR Motifs by Species and Sequencing Technology. Heat maps showing the proportion of all possible canonical SSR motifs detected for repeat motif lengths ranging from 2 to 6 bp across *Ateles* and *Cebus* genome assemblies generated using Oxford Nanopore, short-read Illumina, or PacBio SMRT sequencing. Percentages indicate the occupancy of the theoretical canonical motif space for each repeat length. Red boxes highlight the Oxford Nanopore genome assemblies generated in this study.

Figure S4. Occupancy of Canonical SSR Motif Space. Relative abundance of the 12 most common canonical SSR motifs identified in each *Ateles* and *Cebus* genome assembly. Assemblies are grouped according to sequencing technology (Oxford Nanopore, short-read Illumina, and PacBio SMRT). Motifs not included among the 12 most abundant categories are grouped as "All Others." Red boxes identify the Oxford Nanopore assemblies generated in this study.

Figure S5. Distribution of Differences in SSR Length between *Ateles belzebuth* Genome Assemblies. Distribution of absolute length differences for high-confidence reciprocal SSR loci identified between the Oxford Nanopore assembly generated in this study (USFQ_Abelze_01) and the published GenBank assembly (GCA_963573605.1). Histograms show the frequency of SSR length differences when SSRs identified in each genome are compared with their reciprocal loci in the alternative assembly. The distribution is strongly centered at zero, indicating that most reciprocal SSRs have identical repeat lengths in both assemblies.

Figure S1: Total Number of SSRs Recovered from 14 Platyrrhine Genomes by Sequencing Technology

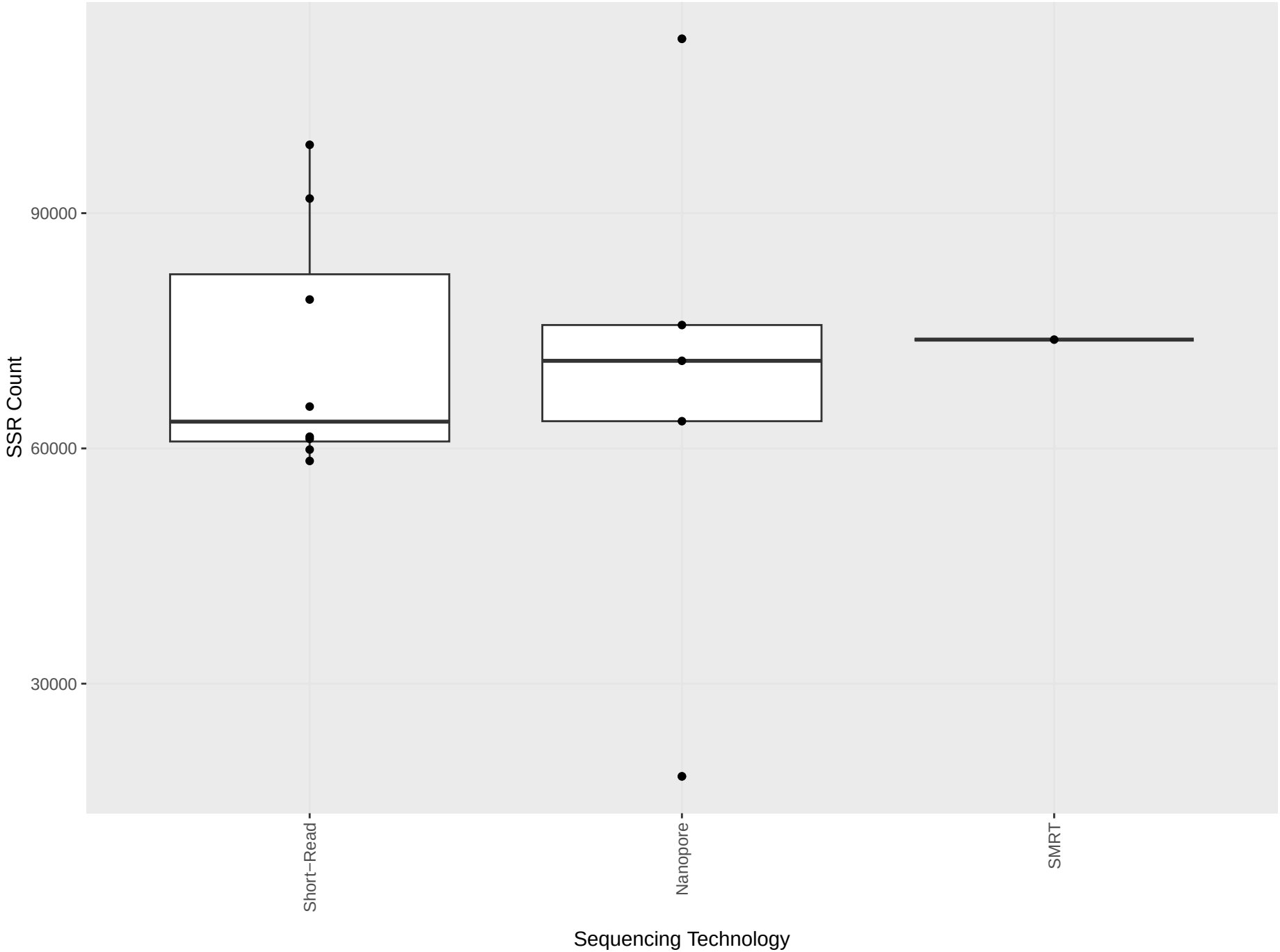
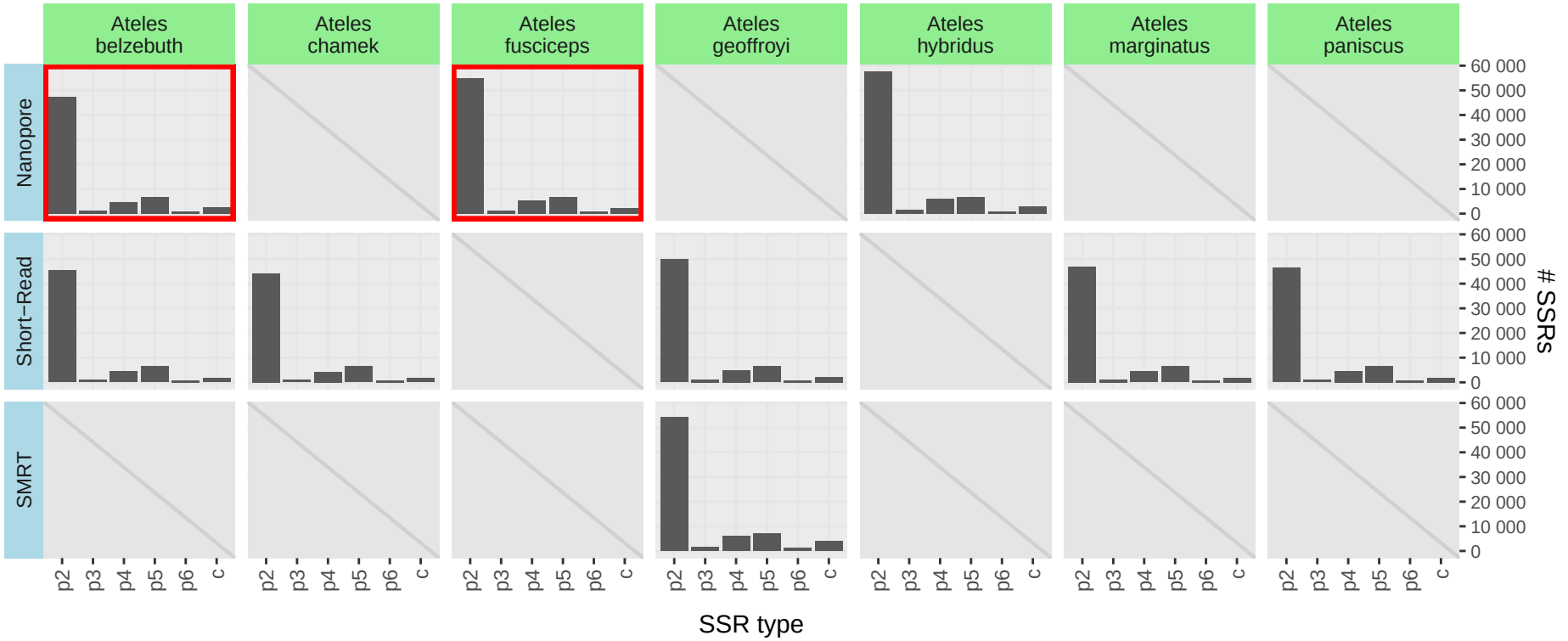


Figure S2: A) SSR Counts by Species and Sequencing Technology



B) SSR Counts by Species and Sequencing Technology

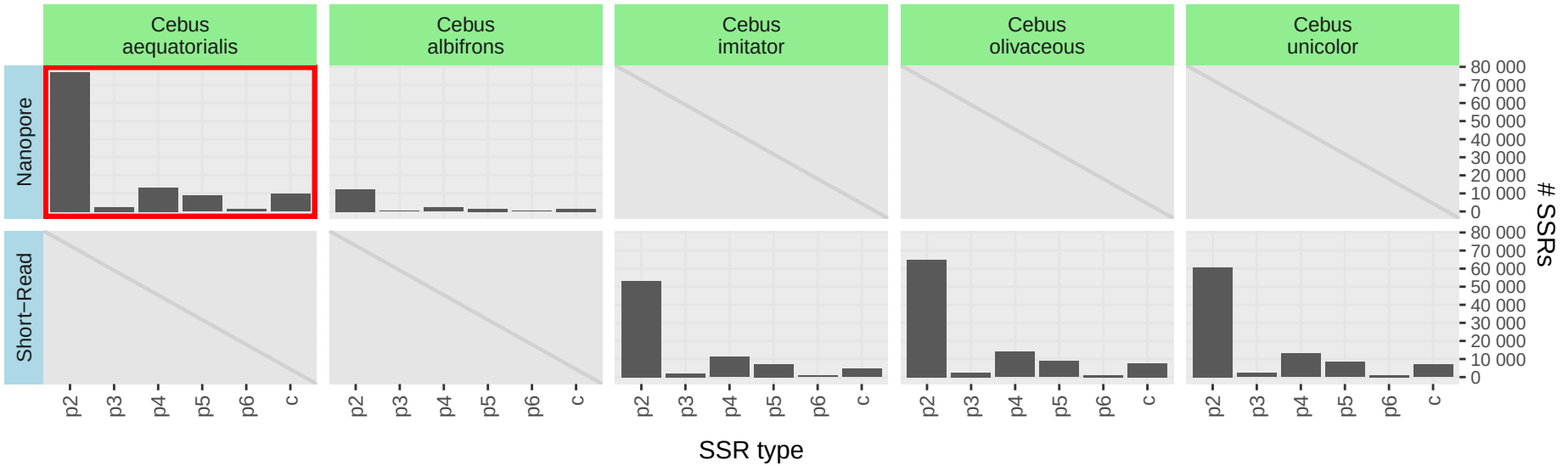
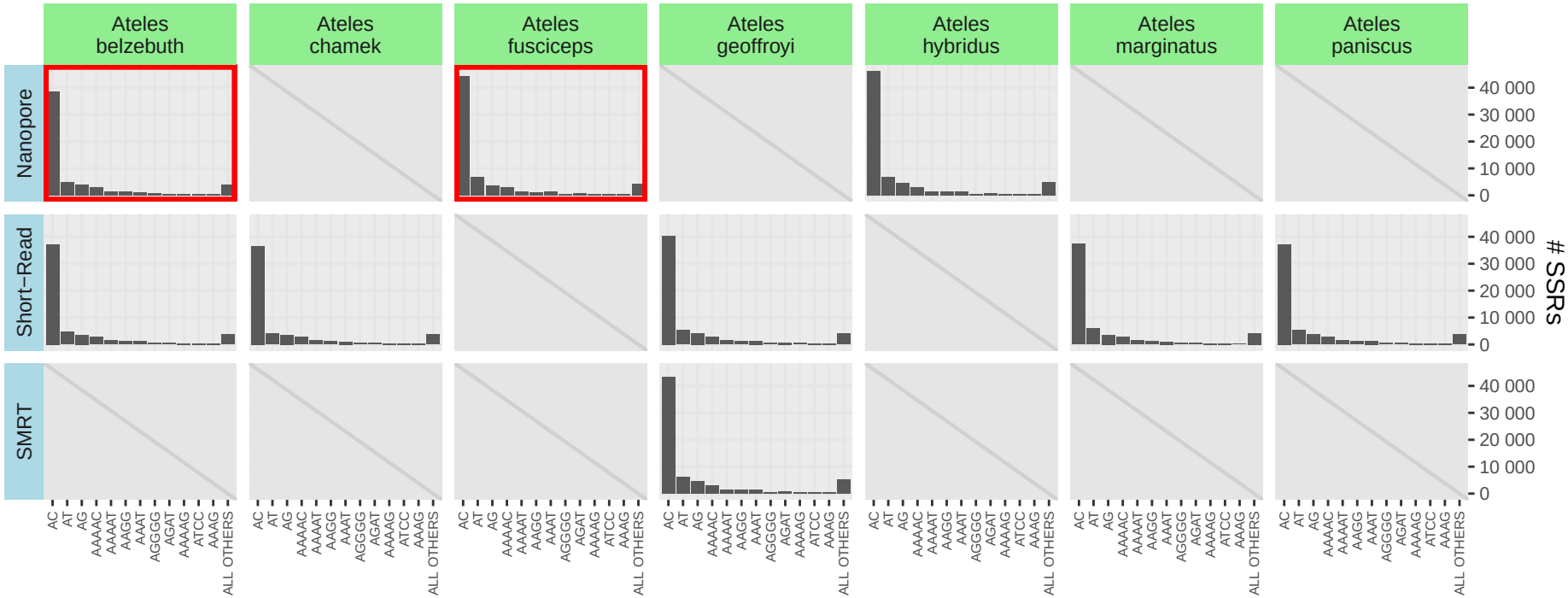


Figure S3: A)Top 12 Canonical SSR Motifs by Species and Sequencing Technology



B)Top 12 Canonical SSR Motifs by Species and Sequencing Technology

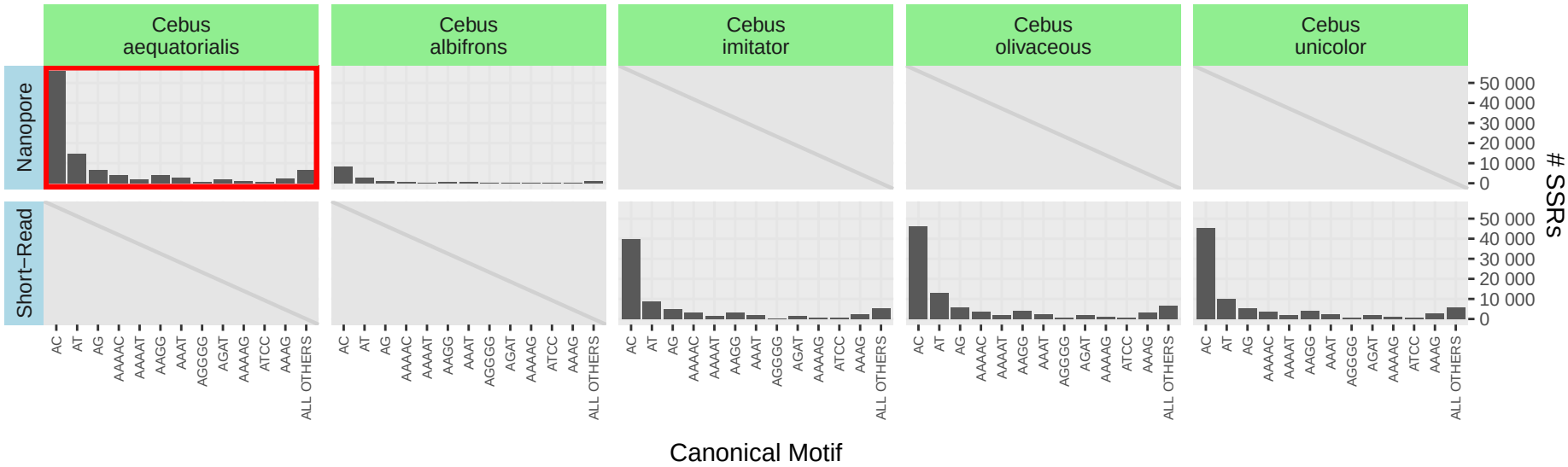
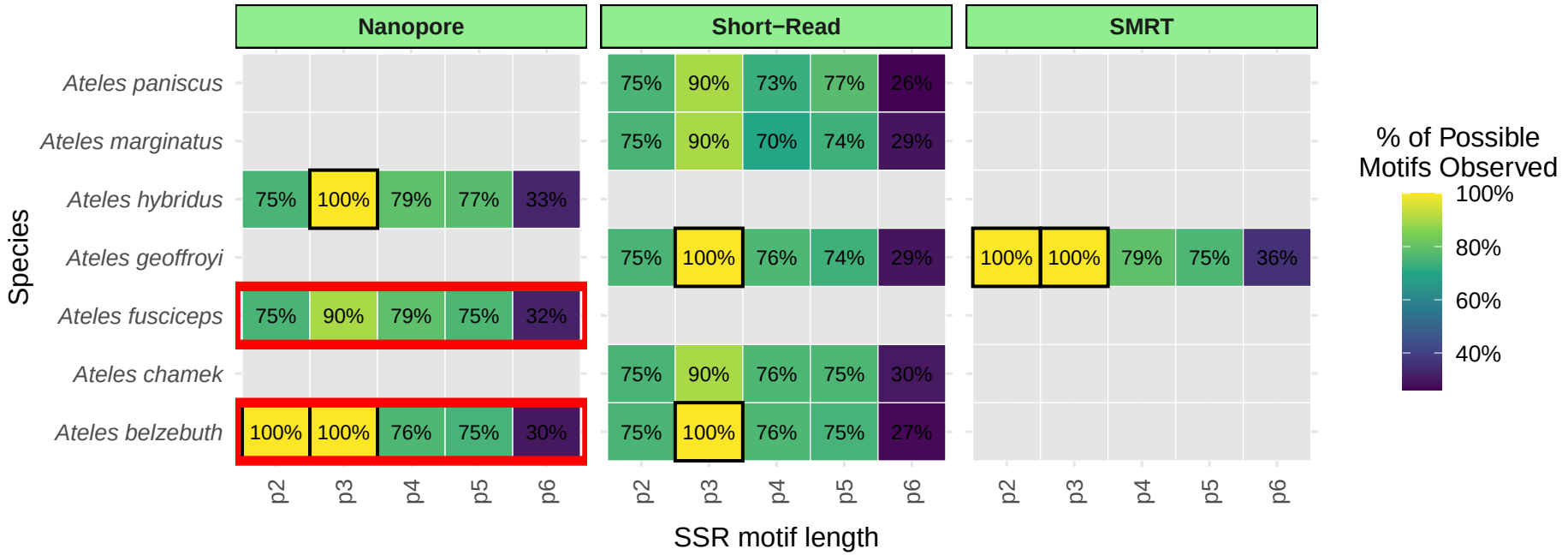


Figure S4: A) Occupancy of Canonical SSR Motif Space



B) Occupancy of Canonical SSR Motif Space

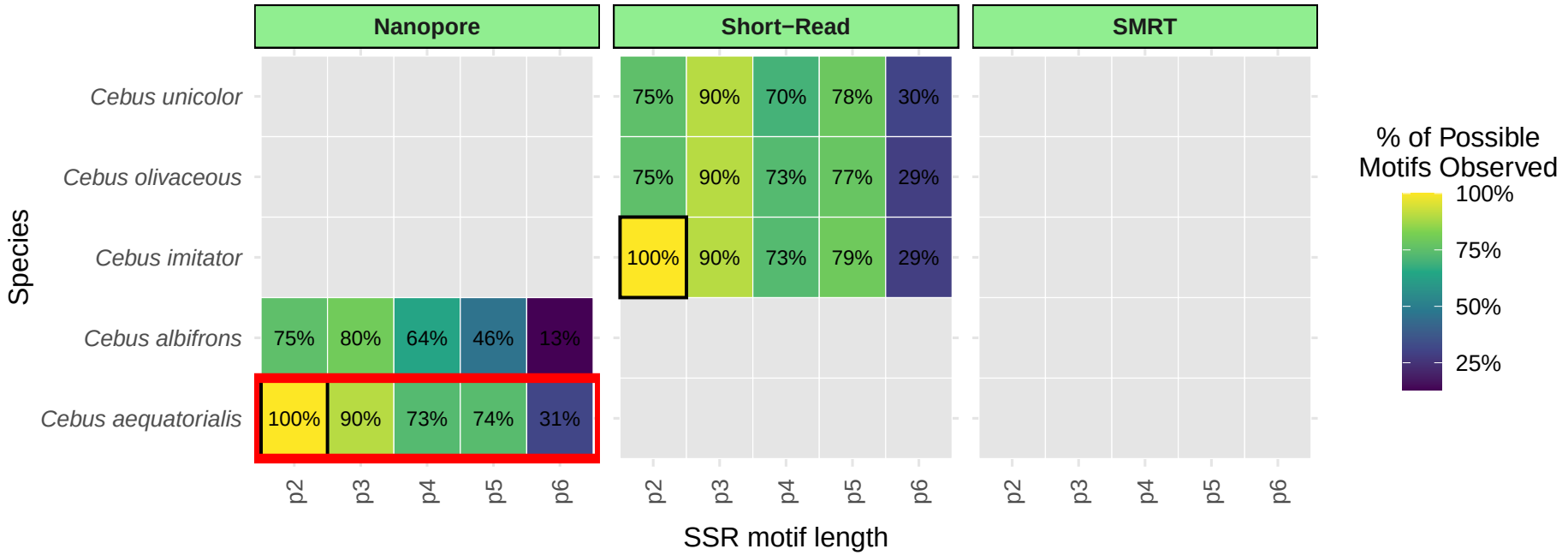
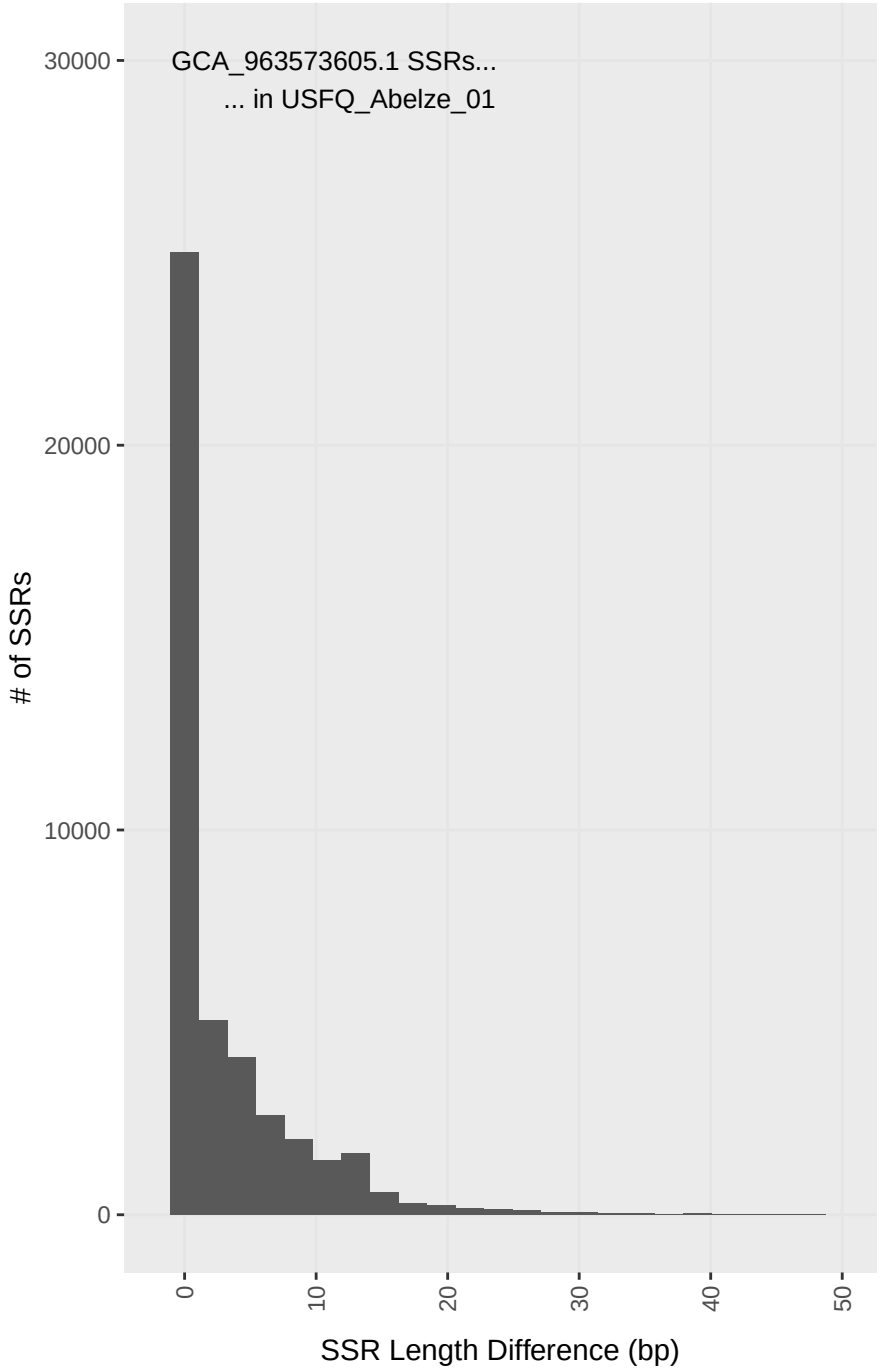


Figure S5: A)Distribution of Differences in SSR Length



B) Distribution of Differences in SSR Length

