Supplementary Information for "Genotyping Short Tandem Repeats Across Copy Number Alterations, Aneuploidies, and Polyploid Organisms"

by

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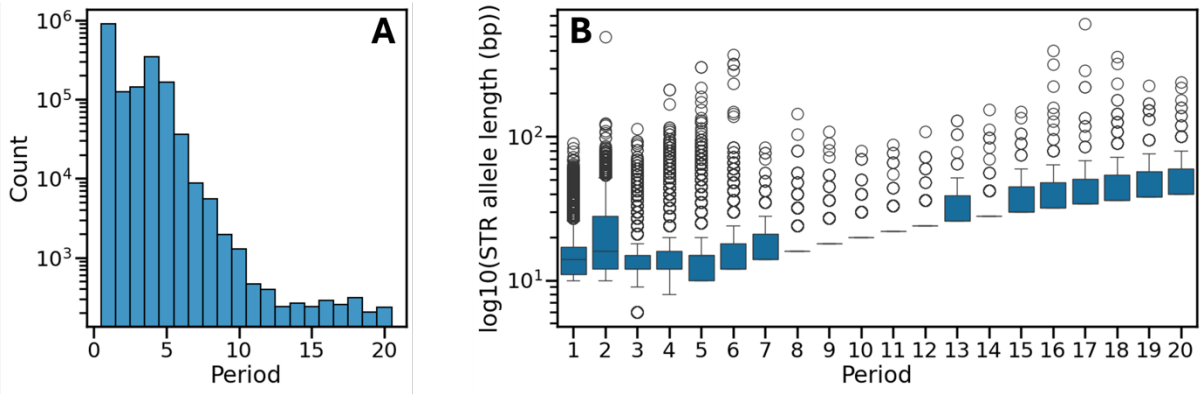
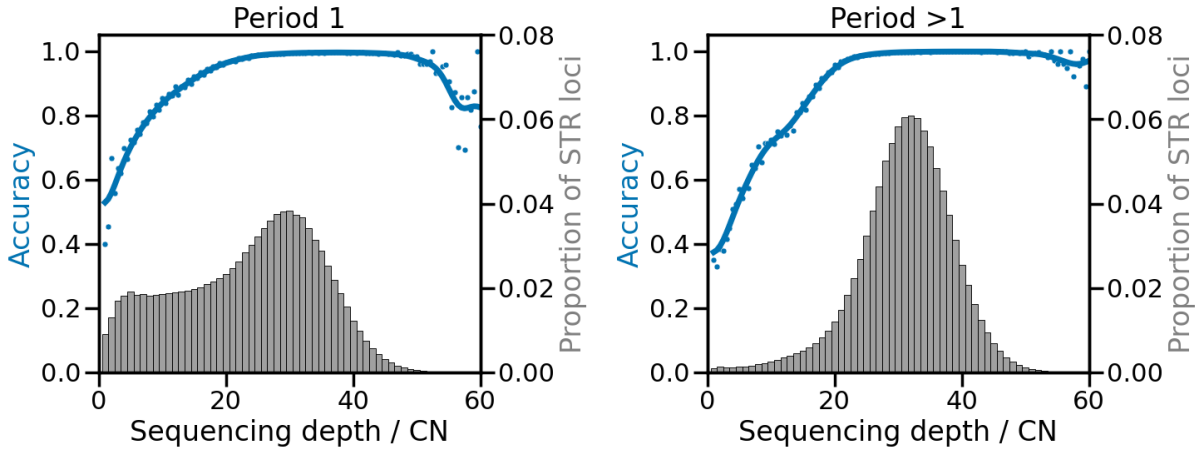
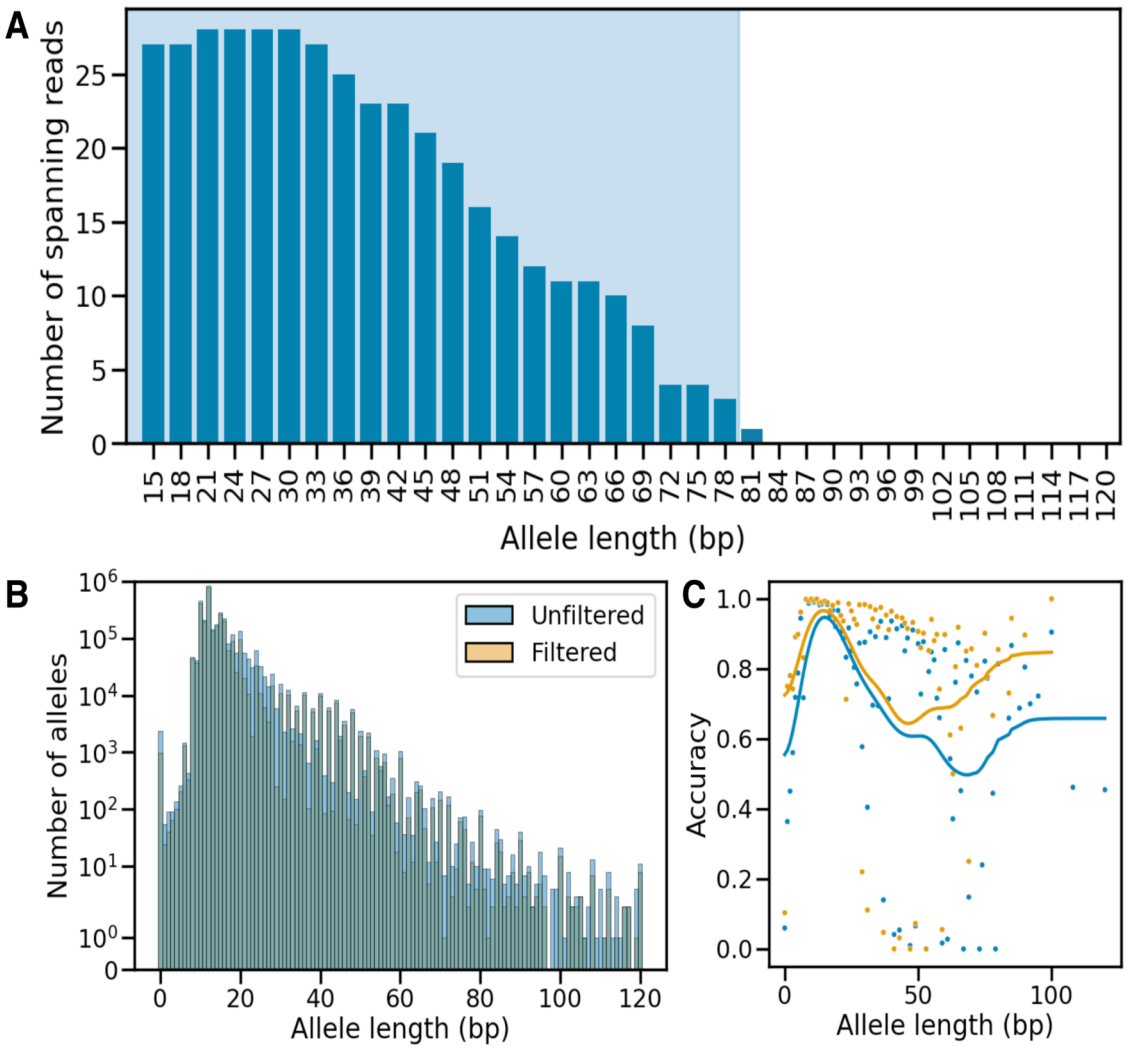


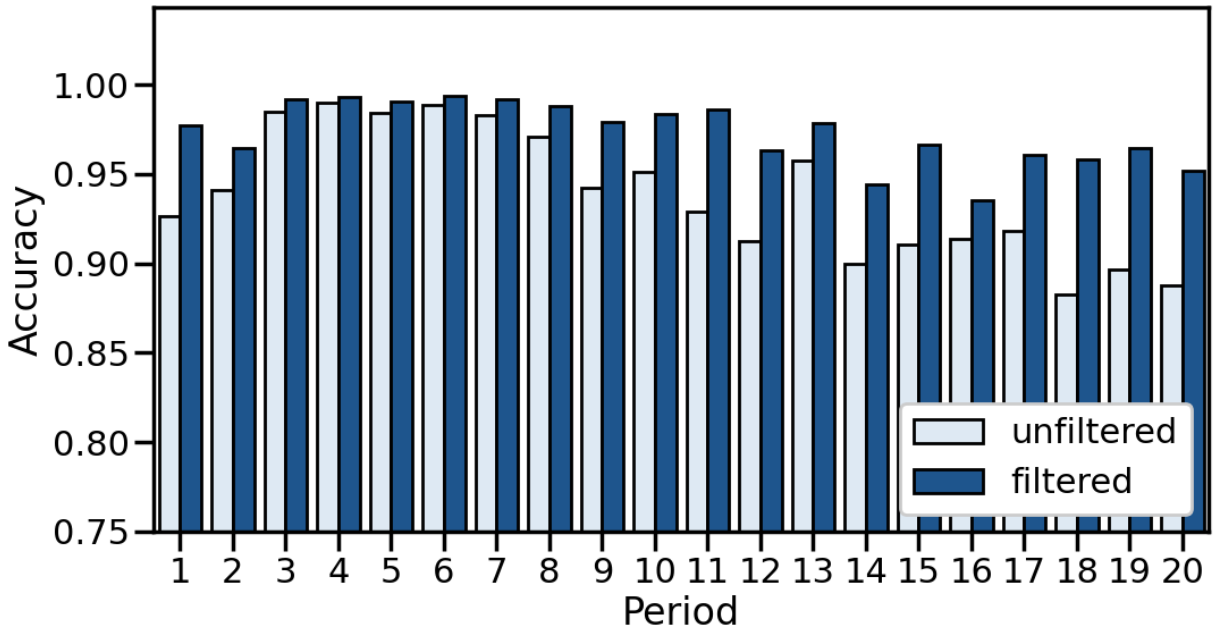
Supplementary Figure 1. Overview of repeat loci in the human STR panel used in this manuscript. **A)** Frequencies of different periods observed across the human STR panel. **B)** Boxplots showing the distribution of STR region lengths (in basepairs) for each STR period. Centre lines represent medians, shaded areas correspond to second and third quartiles, and whiskers extend to points that lie within 1.5 interquartile ranges of the lower and upper quartiles.



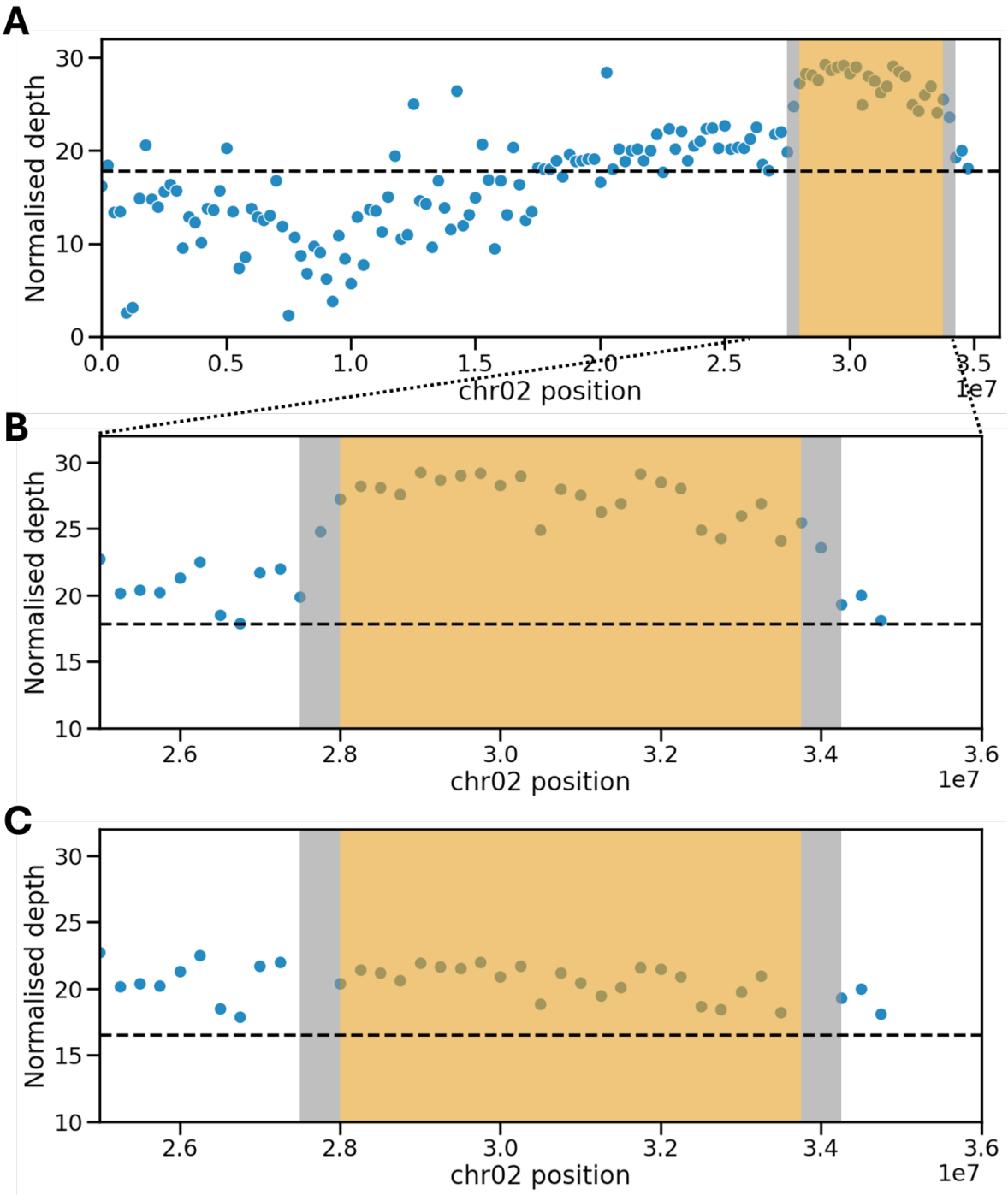
Supplementary Figure 2. Distribution of normalised sequencing depth observed by ConSTRain across repeat loci in HG002 WGS data. The left panel shows data for STRs with period 1. The right panel shows data for repeats with all other periods. X-axes show the sequencing depth normalised by the copy number of repeat loci. The left y-axes show the accuracy of allele length calls (blue line and dots). The right y-axes show the proportion of loci (grey histogram). Note: only normalised depth values between 0 and 60 are shown for visual clarity.



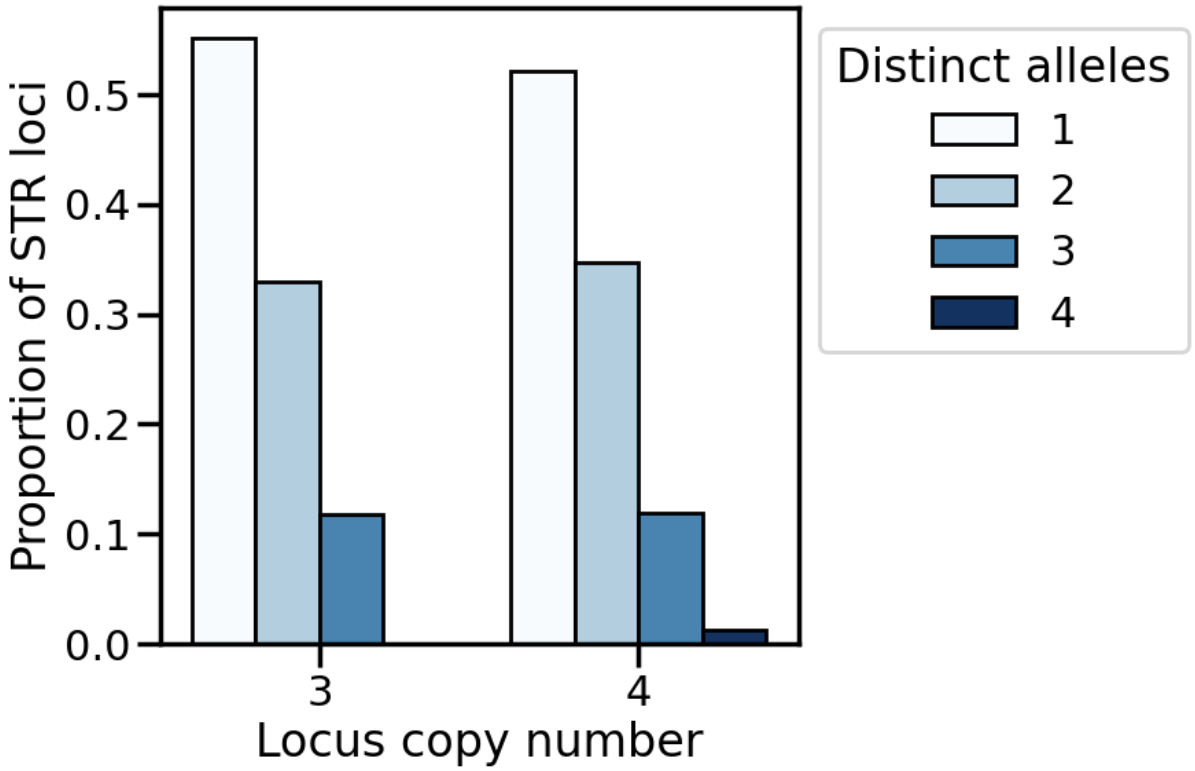
Supplementary Figure 3. The effect of STR allele length on genotyping with ConSTRain. **A)** A range of allele lengths between 15 and 120 basepairs (X-axis) was computationally generated for a trinucleotide locus in the human genome. The Y-axis shows how many spanning reads ConSTRain recovered from the alignments of simulated sequencing reads for each allele (150bp, paired-end, 30X coverage). The area of the graph where the background is shaded in blue indicates the range of alleles for which ConSTRain was able to infer the STR allele length. **B)** ConSTRain genotyping accuracy as a function of STR allele length across repeat loci in HG002 WGS data without any filtering. The X-axis shows the STR allele length in basepairs. The left Y-axis shows the accuracy of allele length calls (blue dots). The right Y-axis shows the proportion of loci with a given allele length (grey histogram). Note: only allele lengths for which at least 100 loci were observed are included. **C)** Same as B, but after filtering based on read depth (--min-norm-depth 12.0, --max-norm-depth 40.5).



Supplementary Figure 4. Accuracy of ConSTRain allele length calls across repeat periods. Accuracy values were obtained by comparing genotypes reported by ConSTRain to the ground truth Q100 haplotypes generated by the T2T consortium. Accuracy values before and after filtering (removing loci in segmental duplications, removing loci with low depth of coverage) are shown. Please note: y-axis starts at 0.75.



Supplementary Figure 5. Depth profile of chr02 in WGS of the SAMEA5752290 *Musa acuminata* sample. **A)** STRs on chr02 were assigned to bins of $2.5x10^5$ base pairs based on their coordinates. The y-axis shows the normalised depth of coverage reported by ConSTRain for STR loci, averaged per bin. The horizontal dashed line indicates the average normalised depth of coverage for STR loci across the whole chromosome. Based on the depth profile, the previously reported duplication was visually identified (shaded in orange). **B)** Close-up of the amplified area. **C)** Same as B, but this time the y-axis shows normalised depth values reported by ConSTRain when coordinates of the duplicated region were provided. Since no accurate breakpoints for the amplification were available, STRs located within 500kb of the orange region were discarded (shaded in grey).



Supplementary Figure 6. The number of distinct alleles observed at STR loci in a *Musa acuminata* WGS sample. The x-axis shows the copy number for STR loci located in a duplication on chr02 (4) and the rest of the genome (3). Y-axis shows the proportion of loci for which a certain number of distinct alleles was reported by ConSTRain.