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Title: Potential highly polymorphic short tandem repeat markers for enhanced forensic identity testing

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Highlights

- Scanned thousands of polymorphic short tandem repeats in the human genome for potential use in forensic applications
- Identified 793 potential candidate short tandem repeats with estimated high heterozygosity (>80%), reduced allele spread (≤ 10) and repeat motifs of at least four nucleotides (tetranucleotides and greater)
- Sequenced and characterized 248 short tandem repeat candidate markers using the Illumina TruSeq Custom Amplicon v1.5 kit, STRait Razor v3, PANDAseq and in-house Microsoft Excel workbooks
- Identification of 53 short tandem repeat markers meeting the desired criteria of high heterozygosity, reduced allele spread, and nucleotide motif size that may be suitable for enhanced DNA mixture de-convolution efforts

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