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Characterization of Genetic Sequence Variation of 58 STR Loci in Four Major Population Groups

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Highlights

- First comprehensive population study of sequence variation in 58 STR markers
- Sequence-based genotyping captures both repeat region and flanking region variation
- Hundreds of additional alleles were identified by MPS compared with length-based genotyping
- Results obtained by MPS and CE are highly concordant
- An up-to-date compendium of all known alleles for each marker has been generated

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