

Development of forensic genomics research toolkits by the use of Massively Parallel Sequencing

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Stellingen behorend bij het proefschrift

Development of forensic genomics research toolkits by the use of Massively Parallel Sequencing

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- 1. The quality of Sanger sequencing as golden standard is overrated.
- 2. The lack of MPS analysis standards delays the implementation of MPS in forensic casework.
- 3. Well discussed STR sequencing nomenclature is essential for worldwide exchange of sequencing data.
- 4. Fragment length is the only relevant detail for comparing CE and sequence data. (this thesis)
- 5. It would be beneficial for the scientific community if respected journals demand wet lab validation for selection of new loci. (this thesis)
- 6. It is surprising that PCR hybrids are hardly mentioned in forensic literature.
- PCR hybrids are likely to be the next limiting factor for mixture analysis. (this thesis)
- 8. The level of implementation of MPS as routine forensic tool will depend mostly on the cost of commercially available assays. (this thesis)
- 9. Bioinformatic support is a prerequisite for pioneers in Massively Parallel Sequencing.
- 10. For routine implementation of MPS, software should be available that can be operated by technicians without extensive bioinformatic experience.
- 11. Microhaplotypes have limited potential when the fragment size exceeds 150 base pairs.
- 12. Making music while doing a PhD can help to keep a well-balanced stress level.