

## **COMPARISON OF STR PROFILING FROM LOW TEMPLATE DNA EXTRACTS WITH AND WITHOUT THE CONSENSUS PROFILING METHOD**

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The consensus profiling method was introduced to overcome the exaggerated stochastic effects associated with low copy number DNA typing. However little empirical evidence has been provided which shows that a consensus profile, derived from dividing a sample into separate aliquots and including only alleles seen at least twice, is more reliable than a profile obtained by amplifying the entire low template DNA (LTDNA) extract in one reaction. Therefore this study aimed to investigate the quality of consensus profiles compared to profiles obtained using the whole LTDNA extract for amplification.

The results of this study demonstrated that performing STR typing on non-split DNA extracts produced profiles with a higher percentage of correct loci compared to the consensus profiling technique. Consensus profiling did eliminate any spurious alleles from the final profile. However there was a notable increase in allele and locus drop out when a LTDNA sample was divided prior to amplification. This loss of information indicates that consensus profiling may not be producing the most informative STR profile for samples where the template amount is limited. ☞