EVALUATION OF THE ForenSeq™ SYSTEM FOR SEQUENCE=BASED STR TYPING

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The recent commercial availability of massively parallel sequencing components and systems designed specifically for forensic use has improved the feasibility of sequence-based typing of nuclear DNA markers commonly examined for forensic purposes. One such commercial assay, the ForenSeq™ DNA Signature Prep Kit (compatible with the MiSeq FGx™ instrument; Illumina, Inc., San Diego, CA), simultaneously targets 58 short tandem repeat (STR) loci, along with up to 172 single nucleotide polymorphisms depending on the primer set selected. The associated ForenSeq™ Universal Analysis Software (UAS) performs all secondary and tertiary data analyses, and presents the resulting STR genotypes in a repeat number format familiar to forensic scientists. We evaluated the potential utility of the ForenSeq™ assay and software system for STR typing via examination of more than 100 high quality DNA samples amplified at the target DNA input. The performance of the assay/software combination was considered with respect to marker recovery metrics, and genotype concordance was assessed both across sample or lineage replicates and with standard capillary electrophoresis based repeat number data. Additionally, the prevalence and characteristics of loci with different UAS quality control indicators were examined to assist in developing sample processing and data interpretation strategies for streamlined, high-volume genotype production from reference quality specimens.