

PowerSeq™ SYSTEMS: MASSIVELY PARALLEL SEQUENCING SYSTEMS FOR FORENSIC DNA ANALYSIS

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The prototype PowerSeq™ Systems include primers and amplification master mix for sequencing autosomal short tandem repeats (STRs), Y-chromosome STRs, the mitochondrial DNA control region, or any combination of the three in a single assay on an Illumina MiSeq® System. The selected STR loci are the same as used in the commercial PowerPlex® Fusion and PowerPlex® Y23 Systems that are routinely used for capillary electrophoresis-based forensic DNA analysis. The combination of these STR loci and Amelogenin makes this multiplex an effective tool for human identification using next generation sequencing and maintains compatibility with existing databases worldwide. Massively parallel sequencing allows laboratories access to mtDNA analysis using a simpler, yet potentially high-throughput workflow. Increased mixture deconvolution and heteroplasmy resolution are achieved by deep sequencing coverage and digital read counts, compared to traditional sequencing methods. Additionally, the use of small amplicons to sequence the mitochondrial control region improves sequencing results from degraded samples. Data will be presented demonstrating performance of the PowerSeq™ Systems, outlining the strengths and limitations of current massively parallel sequencing technologies for routine forensic analysis. To ensure optimum results, quantification of the library is important. Using qPCR technology, the PowerSeq™ Quant MS System allows for determination of the concentration of next-generation sequencing libraries generated with the PowerSeq™ Systems. The PowerSeq™ Quant MS has been optimized so that the results are compatible with Illumina MiSeq® platforms.

Data will be presented demonstrating that the performance of the PowerSeq™ Systems is suitable for forensic analysis. In addition, we will outline the strengths as well as the limitations of current massively parallel sequencing technologies for routine forensic analysis.