MOCK MISSING PERSON STUDY WITH SINGLE HAIR ROOTS AND BONE SAMPLES USING CAPILLARY ELECTROPHORESIS & NEXT GENERATION SEQUENCING WORKFLOWS

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Hair roots and compromised bones are notorious of providing limited amounts of genomic DNA from casework samples. Analysts will more often than not, skip post-extraction quantification knowing that there are insufficient quantities to report a full Short Tandem Repeat (STR) profile from current Capillary Electrophoresis (CE) technologies. The QuantiFiler® Trio DNA Quantification Kit is able to successfully detect and quantify picogram levels of genomic DNA (gDNA) extracted from bones and <5mm hair roots. Analysts are now enabled to accurately calculate input quantities for downstream processing. Despite having accurate gDNA quants, an incomplete STR profile will be generated for compromised samples. A modified PrepFiler Express BTA™ protocol has been developed that not only captures nuclear DNA, but also mitochondrial DNA. Though it is possible to create mitochondrial profiles through Sanger sequencing, it is very time consuming, labor intensive, and solely targets the hypervariable regions (HV1 & HVII). Therefore, a short amplicon (≤175 base pairs) whole mitochondrial tiling path was developed for the Next Generation Sequencing (NGS) Ion Personal Genome Machine (PGM™) System to facilitate sequencing of the entire mitochondrial genome of highly degraded samples. This short amplicon design increases discrimination of compromised samples outside of the HV1 & HVII regions. The HID-Ion AmpilSeq™ Ancestry and Identity Panels were both used in tandem with the mitochondrial panel to target the gDNA and serve as a complement to incomplete CE STR profiles. Hair roots and buccal samples were processed through the PGM™ system, and the results compared to current CE STR results.