Performance Evaluation of the ForenSeq mtDNA Control Region Solution

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Introduction

Massively parallel sequencing (MPS) of human mitochondrial DNA (mtDNA) is faster, cheaper, and more reproducible than traditional Sanger sequencing, permitting routine quality control, and quality assurance.

The purpose of this study was to compare ForenSeq mtDNA Control Region Kit and sequenced results. MPS is a powerful tool for the detection of low level variants. A lower detection threshold is required for accurate detection in samples with low template concentration.

Materials and Methods

Sensitivity studies were conducted to obtain the ideal input range and limit of detection for the ForenSeq mtDNA Control Region Kit under optimal conditions. MPS libraries were sequenced by MPS. MPS libraries were sequenced by MPS. MPS libraries were sequenced by MPS.

Results & Discussion

Various samples were analyzed using 8 different MPS concentrations (1, 4, 10, 20, 40, 100, 200, 400 ng). MPS libraries were sequenced by MPS. MPS libraries were sequenced by MPS. MPS libraries were sequenced by MPS. MPS libraries were sequenced by MPS. MPS libraries were sequenced by MPS. MPS libraries were sequenced by MPS. MPS libraries were sequenced by MPS.

Conclusions

The ForenSeq mtDNA Control Region solution is a rapid, high-throughput solution for the analysis of the control region of the human mtDNA genome.

Table 6. Variants Observed for Tooth and Bone DNA Extract Samples

Table 7. Detection of Minor Contributor Variants in Mixture Samples

Table 8. Coverage Relative to Sample Multiplicity: 12 x 48 Libraries per MiSeq FGx Micro Flow Cell

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