

MASSIVELY PARALLEL SEQUENCING OF THE WHOLE MITOCHONDRIAL GENOME USING THE POWERSEQ™ WGM SYSTEM

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In certain cases where evidence was exposed to harsh conditions that can degrade DNA, mitochondrial DNA (mtDNA) sequencing may be essential for obtaining suitable DNA results. Massively parallel sequencing (MPS) has many advantages over traditional Sanger sequencing for mtDNA analysis, including increased resolution of mixtures and heteroplasmy, high-throughput sample processing, and the ability to sequence the whole mitochondrial genome in fewer reactions. Whole mitochondrial sequencing can give added power of discrimination over control region alone.

The PowerSeq™ WGM System is designed to enable analysis of the entire 16,569 bp human mitochondrial genome using MPS. It includes reagents to amplify 161 small amplicons (167 bp average) covering the entire mtDNA genome in a single multiplex reaction. Targeting small amplicons improves the chance for successful analysis of degraded samples where nuclear DNA may be of low quantity or quality. We show here that the PowerSeq™ WGM System gives accurate full mitochondrial DNA profiles compared to Sanger sequencing, with sensitivity for complete and accurate analysis with as little as 60 pg of total DNA input.