



Precision ID mtDNA Whole Genome Panel and Precision ID mtDNA Control Region Panel



Identify missing persons or analyze remains

The Applied Biosystems™ Precision ID NGS System for human identification can help you solve tough cases by getting more information from your challenging samples. By combining the Ion Chef™ System and the Ion S5™ or Ion S5™ XL System with Precision ID panels that target the mitochondrial genome, adopting next-generation sequencing (NGS) in your laboratory is now simpler than ever. Precision ID technology applies the simplicity of PCR to targeted sequencing, enabling from tens to thousands of genomic regions to be amplified simultaneously in a single PCR tube. With as little as 1 ng of DNA input, you can quickly and easily analyze your challenging samples with as few as 5 pipetting steps and 45 minutes of hands-on time.

Table 1. Precision ID mitochondrial panel specifications

	Precision ID mtDNA Whole Genome Panel	Precision ID mtDNA Control Region Panel
Target	16.569 kb mtGenome	1.2 kb (control region 16024-574)
Amplicon length	Average length of 163 bp with amplicon overlap of 11 bp	Average length of 153 bp with amplicon overlap of 18 bp
Primer pool size	<ul style="list-style-type: none"> • 2 primer pools of 81 primer pairs each • Primer pool 1 has 119 additional degenerate primers* • Primer pool 2 has 164 additional degenerate primers* 	<ul style="list-style-type: none"> • 2 primer pools of 7 primer pairs each • Primer pool 1 has 45 additional degenerate primers* • Primer pool 2 has 68 additional degenerate primers*
Input DNA recommended	1 ng	1 ng

* Degenerate primers were designed for primers that contained a SNP base with a global or specific population frequency of 10% or greater from the 1,000 genome data set, or had a Mitomap-observed count of 700 or greater.

Table 2. Sample throughput for Precision ID mitochondrial analysis panels by Ion Chip (assumes automated library preparation using the Ion Chef System).

Panel	Ion S5 chips		Ion PGM chips		
	Ion 520™ Chip	Ion 530™ Chip	Ion 314™ Chip	Ion 316™ Chip	Ion 318™ Chip
Precision ID mtDNA Whole Genome Panel (a)	16	64	2	8	16
Precision ID mtDNA Control Region Panel (b)	96	384	8	64	96

(a) 1,750X coverage of the genome. (b) 1,750X coverage of the control region.

Simplicity

- Small amplicons enable optimal coverage of degraded samples (Table 1)
- As little as 1 ng of input
- Automated library and template prep using the Ion Chef System

Scalability

- Multiple chip formats to meet your throughput needs
- Multiplex up to 64 samples with whole-genome analysis or up to 384 for control region analysis (Table 2)

Speed

- Less than 45 minutes of hands-on time for a DNA-to-data targeted sequencing workflow
- Sample to data in less than 2 days

The Applied Biosystems™ Precision ID mtDNA Whole Genome Panel is an innovative approach to mitochondrial DNA sequencing specifically developed for forensic applications. This mtDNA tiling approach, using amplicons that are only 163 bp average length, assists with obtaining optimal mtGenome coverage from highly compromised, degraded samples such as hair shafts, teeth, and bones (Figure 1).

The Applied Biosystems™ Precision ID mtDNA Control Region Panel is based on the same tiling approach used in the Precision ID mtDNA Whole Genome Panel. This targeted control region panel spans the entire 1.2 kb control region, which encompasses HV-I, HV-II, and HV- III, with the same optimal coverage for degraded forensic samples.

Mitochondrial DNA analysis is used by forensic scientists when samples such as teeth, bones, and hairs without a follicle (root) are collected from crime scenes, missing-person remains, or disaster areas. In these instances, even amplicon coverage and minimal strand bias are key factors that contribute to high-quality genetic results for successful identification of human remains. Automation of library preparation and template preparation using the Ion Chef System and sequencing on the Ion S5 System helps reduce variation that may be seen with manual workflows (Figure 2).

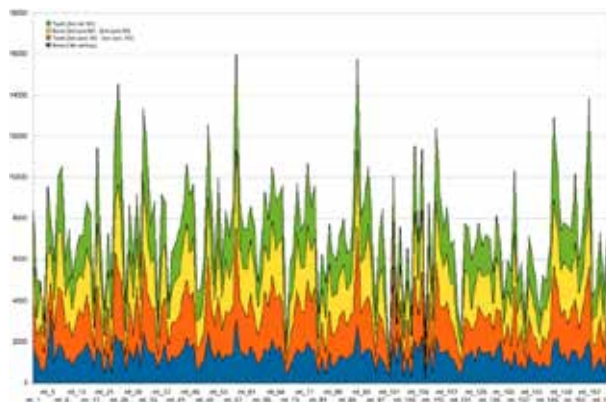


Figure 1. Whole-genome coverage of 4 samples of ancient tooth and bone samples was generated using 1 ng of input DNA, automated library preparation using the Ion Chef™ System, and sequencing on the Ion S5 System. The small amplicon design and the inclusion of degenerate primers in the Precision ID mtDNA Whole Genome Panel increase success with degraded and low starting-template DNA.

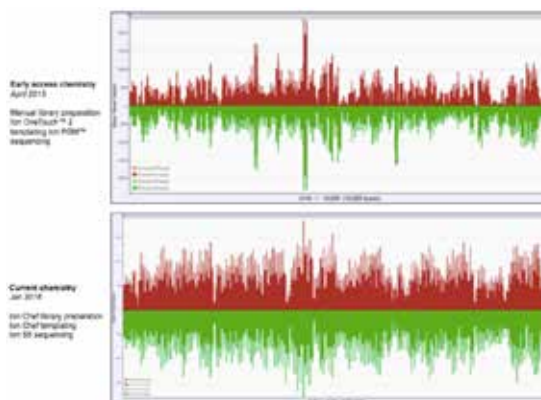


Figure 2. Comparison between manual and automated workflows using the Precision ID mtDNA Whole Genome Panel.

Ordering information

	Quantity	Cat. No.
Precision ID panels for human identification		
Precision ID mtDNA Whole Genome Panel	96 reactions	A30938
Precision ID mtDNA Control Region Panel	96 reactions	A31443
Precision ID Library Kit	96 reactions	A26435
Ion AmpliSeq Kit for Chef DL8	32 reactions	A29024

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