MiSeq FGx™ Forensic Genomics System

Solve more cases and generate more leads with the power and accuracy of Illumina next-generation sequencing.

Highlights

- **Fully Validated, Sample-to-Answer Solution**
  All-inclusive system ties library preparation, sequencing, data analysis, and reporting into a single integrated workflow
- **Simple, Streamlined Workflow**
  Interrogate 200 genetic markers in a single, streamlined workflow eliminating the need for multiple STR kits
- **Access a Wider Range of Informative SNPs**
  Biogeographical ancestry and phenotypic-informative SNPs provide valuable information not widely available with current technology
- **Superior Analysis of Challenging Samples**
  Advanced capacity to handle challenging samples such as complex mixtures or degraded DNA

Figure 1: MiSeq FGx Forensic Genomics Instrument—The MiSeq FGx instrument is a compact, fully validated next-generation sequencing platform for forensic genomics applications.

Introduction

The MiSeq FGx™ Forensic Genomics System is the first fully validated[1] sequencing system specifically designed for use in forensic genomics applications (Figure 1). With the high resolution and unmatched accuracy of next-generation sequencing (NGS), the MiSeq FGx System can transform the most fragile, degraded, or mixed samples into powerful results.

A Complete Sample-to-Answer Solution

The MiSeq FGx Forensic Genomics System delivers a complete DNA-to-Data workflow for the analysis of forensic DNA samples. The solution begins with the ForenSeq™ DNA Signature Prep Kit, which includes all reagents required to prepare up to 384 DNA libraries for sequencing (Figure 2). The MiSeq FGx Reagent Kit provides sequencing reagents, an RFID labeled reagent cartridge, and wash solution, which are then loaded onto the MiSeq FGx instrument along with the sequencing-ready DNA libraries. The intuitive touch screen interface provides simple, step-by-step guidance through each stage of the sequencing run including library and reagent loading, run configuration, and run monitoring. ForenSeq Universal Analysis Software delivers a powerful suite of forensic analysis capabilities including automatic detection of mixed DNA samples, generation of population statistics, and sample comparison. The software also enables estimation of visible traits and biogeographical ancestry markers that can provide crucial investigative leads in “no suspect” cases.

Simple, Streamlined Workflow

With current forensic capillary electrophoresis (CE) methods, limited DNA quantities may require forensic analysts to choose between available fragment length-based short tandem repeat (STR) tests. These trade-offs can result in lengthy, complex decision trees as technical limitations are weighed against potentially informative genetic data.

Figure 2: ForenSeq DNA Signature Prep Kit—The ForenSeq DNA Signature Prep Kit includes all reagents required to prepare 384 DNA libraries for sequencing, including PCR reagents, index adapters, and purification and normalization beads.

The MiSeq FGx System eliminates the need to choose between relevant STR tests by providing all currently available STR typing tests in a single workflow (Figure 3). One run with the MiSeq FGx System simultaneously interrogates ~200 genetic markers, including a combination of autosomal, X-, and Y-STRs. Furthermore, the low DNA input requirement of 1 ng enables testing of a broad range of samples where DNA quantity is limited.

For Research, Forensic, or Paternity Use Only - Not For Clinical, Diagnostic, or Therapeutic Use in Humans or Animals

AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
TCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTT
CGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACC
AACGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAA
AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
GATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGAGC
CGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAGTA

Access a Wider Range of Informative SNPs

Another casework challenge occurs when a complete autosomal STR profile is established, but no suspect is available for direct comparison, or no hits are found in national or local criminal databases. In addition to providing all autosomal STR markers currently utilized around the world for casework and criminal DNA databasing, the ForenSeq DNA Signature Prep Kit also contains marker sets not routinely available with traditional CE methods. These include a dense set of identity informative single nucleotide polymorphisms (iiSNPs),[2–3] which are informative for source attribution, biogeographical ancestry-informative SNPs (aiSNPs),[4] and phenotypic-informative SNPs (piSNPs),[5] which provide estimates of eye color (blue, intermediate, brown) and hair color (brown, red, black, blond). AiSNPs and piSNPs can be critical in generating tactical investigative leads from "no suspect" cases that may otherwise have reached dead ends.

Superior Analysis of Challenging Samples

The challenges presented by degraded DNA, low quantity DNA, or complex DNA mixtures can potentially complicate or derail an investigation. The MiSeq FGx System offers an enhanced capacity to analyze these types of challenging samples.

When analyzing partially or highly degraded DNA, the SNPs in the ForenSeq DNA Signature Prep Kit are targeted by amplicon sizes ≤ 125 bp, making them extremely well-suited for analysis of degraded DNA.[6] With complex DNA mixtures, the large number of markers included in the kit—many of which are highly polymorphic—enable an improved ability to detect low-level minor components that may go undetected by traditional methods.[6]

These capabilities, coupled with the inherent sensitivity of Illumina sequencing by synthesis (SBS) chemistry and the low DNA input requirement, provide superior resolution of a broad range of cases compared to conventional STR and CE analysis.

Easy, Optimized Software Solution

The MiSeq FGx System solution includes ForenSeq Universal Analysis Software: a fully optimized, software solution designed for forensic genomics applications (Figure 4). The software features a comprehensive suite of library management and analytical tools. These include data visualization at library and locus levels, STR and SNP allele genotype calling, visualization of intra-STR sequence variation, statistical estimates of combined genotype frequency, statistical estimates of biogeographical ancestry and phenotype, quality flagging, and automated report generation. ForenSeq Universal Analysis Software is delivered preinstalled on a dedicated, stand-alone server. The server is sold separately to maximize flexibility for each laboratory.

Exceptional Data Quality

The MiSeq FGx System leverages Illumina SBS chemistry—the most widely adopted next-generation sequencing technology in the industry.[7] Exceptional data quality is achieved by a proprietary, reversible terminator-based method that detects single bases as they are incorporated into massively parallel DNA strands. Fluorescent terminator dyes are imaged as each dNTP is added and then cleaved to allow incorporation of the next base. With all 4 reversible, terminator-bound dNTPs present during each sequencing cycle,

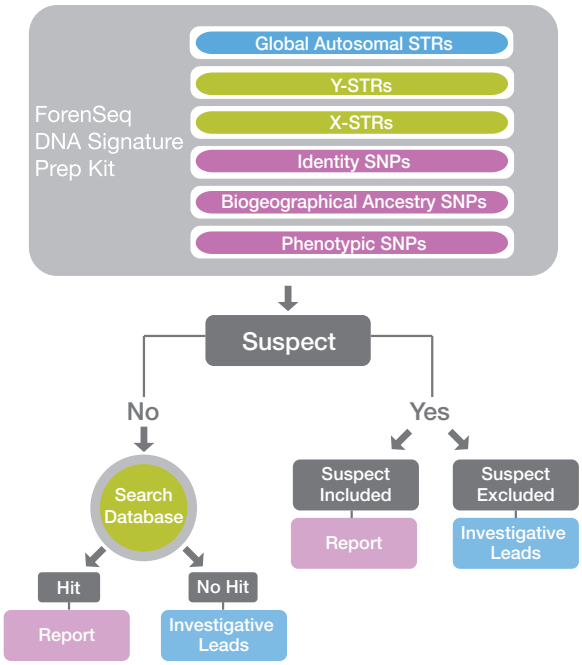

Figure 3: MiSeq FGx System Investigative Workflow—From a dedicated library preparation kit to automated data reports, the MiSeq FGx System offers the most complete, integrated workflow in the industry.

natural competition among bases minimizes incorporation bias.[8] Base calls are made directly from signal intensity measurements during each incorporation cycle, reducing raw error rates compared to other technologies.[9–12] The result is highly accurate base-by-base sequencing that virtually eliminates sequence context-specific errors, even within repetitive sequence regions or homopolymers.

Summary

The MiSeq FGx Forensic Genomics System is a fully validated sequencing system specifically designed for use in forensic genomics applications. The complete sample-to-answer system includes the ForenSeq DNA Signature Prep Kit, the MiSeq FGx Instrument, and the ForenSeq Universal Analysis Software package. With the speed and accuracy of Illumina next-generation sequencing, criminal justice has a powerful new ally.

Learn More

To learn more about the MiSeq FGx instrument, visit:
www.illumina.com/systems/miseq-fgx.ilmn

To learn about the ForenSeq DNA Signature Prep Kit, visit:
www.illumina.com/products/forenseq-dna-signature-kit.ilmn

For more on the ForenSeq Universal Analysis Software, visit:
www.illumina.com/informatics/sequencing-microarray-data-analysis/forenseq-universal-analysis-software.ilmn

To learn about mitochondrial DNA analysis with the MiSeq FGx System, visit:
www.illumina.com/applications/forensics/missing_persons_and_unidentified_human_remains.ilmn

For Research, Forensic, or Paternity Use Only - Not For Clinical, Diagnostic, or Therapeutic Use in Humans or Animals

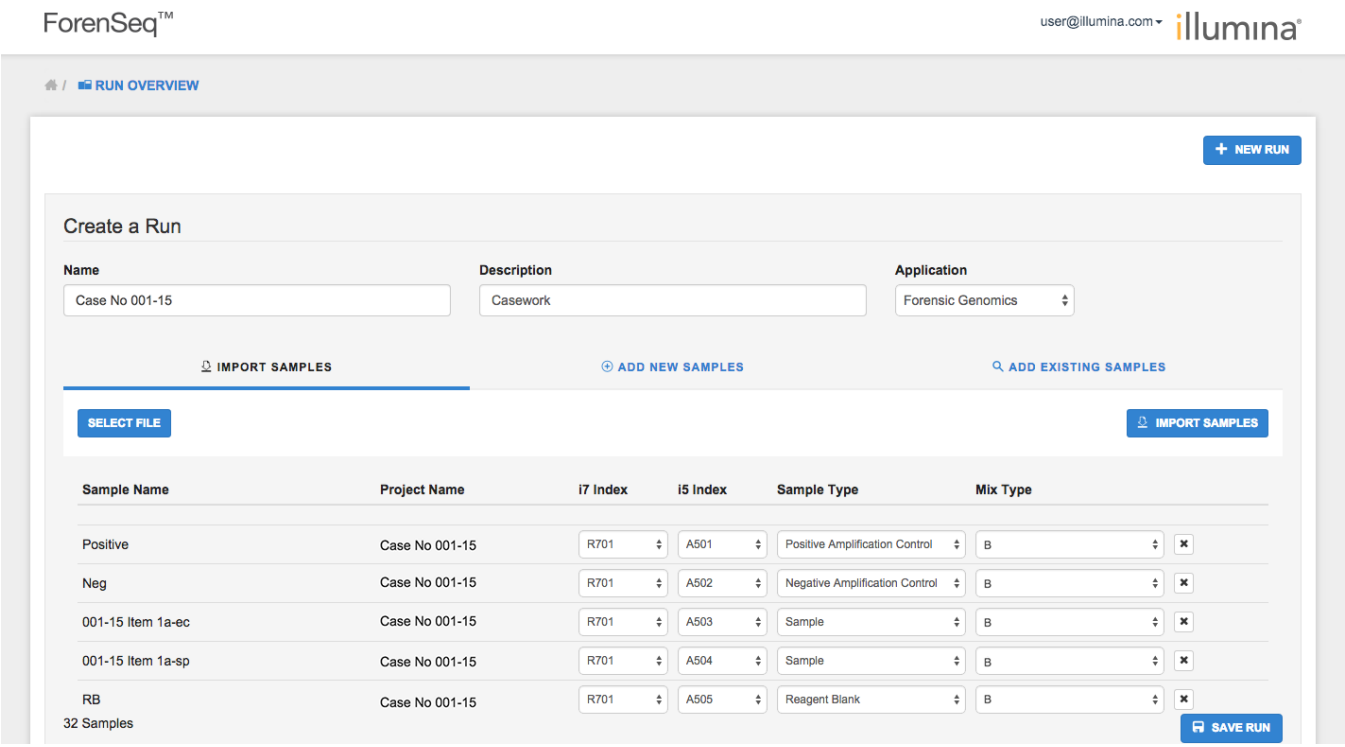

Figure 4: ForenSeq Universal Analysis Run Overview Screen—ForenSeq Universal Analysis Software features DNA library management tools, data analysis and visualization, and automated reporting. The Run Overview screen features easy data entry fields for Run Name and Run Description. Sample information, index combinations, and application options can also be imported with a tab delimited .txt file. Sample types include Known Sample, Forensic Sample, Reagent Blank, Negative Amplification Control, Positive Amplification Control, and Human Sequencing Control.

References

1. The full MiSeq FGx System workflow is validated per the Scientific Working Group on DNA Analysis Methods (SWGDAM) guidelines (www.swgdam.org).
2. Kidd KK, Pakstis AJ, Speed WC, et al. Developing a SNP panel for forensic identification of individuals. *Forensic Sci Int*. 2006;164(1): 20–32.
3. Sanchez JJ, Phillips C, Børsting C, et al. A multiplex assay with 52 single nucleotide polymorphisms for human identification. *Electrophoresis*. 2006;27(9): 1713–1724.
4. Kidd KK, Speed WC, Pakstis AJ, et al. Progress toward an efficient panel of SNPs for ancestry inference. *Forensic Sci Int Genet*. 2013;10: 23–32.
5. Walsh S, Liu F, Wollstein A, et al. The HIrisPlex system for simultaneous prediction of hair and eye colour from DNA. *Forensic Sci Int Genet.* 2013;7(1): 98–115.
6. Illumina (2014) ForenSeq DNA Signature Prep Kit Data Sheet (www.illumina.com/products/forenseq-dna-signature-kit.ilmn). Accesssed 15 April 2016.
7. Nakazato T, Ohta T, and Bono H. Experimental design-based functional mining and characterization of high-throughput sequencing data in the sequence read archive. *PLoS One.* 2013;22;8(10): e77910.
8. Bentley DR, Balasubramanian S, Swerdlow HP, et al. Accurate whole human genome sequencing using reversible terminator chemistry. *Nature.* 2008;456(7218): 53–9.
9. Ross MG, Russ C, Costello M, et al. Characterizing and measuring bias in sequence data. *Gen Biol.* 2013;14: R51.
10. Liu L, Li Y, Li S, Hu N, He Y, et al. Comparison of next-generation sequencing systems. *J Biomed Biotechnol.* 2012: 251364.
11. Sebastian J, Fritz JS, Karola P, et al. Updating benchtop sequencing performance comparison. *Nat Biotechnol.* 2013;31: 294-296.
12. Quail MA, Smith M, Coupland P, et al. A tale of three next generation sequencing platforms: comparison of Ion Torrent, Pacific Biosciences and Illumina MiSeq sequencers. *BMC Genomics.* 2012;13: 341.

Table 1: MiSeq FGx System Performance Parameters

Feature	Performance
Low Input DNA	robust performance ≥ 100 pg, optimal input 1 ng
Locus Multiplexing Capability	~200 loci
Accurate Low-level Mixture Detection	detects minor contributors at < 5% of major
Sample Multiplexing Capability[a]	8–96 samples
Deep Coverage	14 million reads per run
Short Amplicon Detection	≥ 65 bp

a. Multiplexing capability up to 384 samples currently in development.

For Research, Forensic, or Paternity Use Only - Not For Clinical, Diagnostic, or Therapeutic Use in Humans or Animals

AAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAA
AATCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACC
AACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTA
TTAACGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGAT
AAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAA
AAGATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGA
AACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAG

Table 2: MiSeq FGx Instrument Specifications

Instrument Configuration
RFID tracking for consumables
MiSeq FGx Control Software
Instrument Control Computer (Internal)[a]
Base Unit: Intel Core i7-2710QE 2.10 GHz CPU
Memory: 16 GB RAM
Hard Drive: 750 GB
Operating System: Windows 7 embedded standard
Operating Environment
Temperature: 22°C ± 3°C (66–77°F)
Humidity: Noncondensing 20%–80%
Altitude: Less than 2,000 m (6,500 ft)
Air Quality: Pollution degree rating of II
Ventilation: Maximum of 1,364 BTU/h
For Indoor Use Only
Light Emitting Diode (LED)
530 nm, 660 nm
Dimensions
W×D×H: 68.6 cm × 56.5 cm × 52.3 cm (27.0 in × 22.2 in × 20.6 in)
Weight: 54.5 kg (120 lbs)
Crated Weight: 90.9 kg (200 lbs)
Power Requirements
100–240V AC @ 50/60Hz, 10A, 400 W
Radio Frequency Identifier (RFID)
Frequency: 13.56 MHz
Power: 100 mW
Product Safety and Compliance
NRTL certified IEC 61010-1
CE marked
FCC/IC approved

b. Computer specifications are subject to change.

Maximize Performance and Productivity with Illumina Services, Training, and Consulting

Illumina service and support teams provide a full suite of expedient, customized solutions from initial trainings, to instrument support, and ongoing NGS education. Our support offerings include:

Professional Care Services

Illumina Consulting

- Illumina Forensic Genomics Validation Services
- Illumina Proof-of-Concept Services for instrument and library preparation testing
- Illumina Concierge Services for design assistance and product optimization
- Illumina Genomics IT Consulting Services
- Illumina Bioinformatics Professional Services

Product Care Services

- Tiered Instrument Service Plans + Add-On Services
- Instrument Compliance Services
- Instrument On-Demand Services

Illumina University Training

- Instructor-Led Training at Your Chosen Facility
- Instructor-Led Training at an Illumina Training Center
- Online Courses and Webinars

For more on Illumina support offerings, visit: www.illumina.com/services/instrument-services-training.html

Ordering Information

Product	Catalog No.
MiSeq FGx Instrument	SY–411–1001
MiSeq FGx Reagent Kit	TG–143–1001
ForenSeq DNA Signature Prep Kit (384 reactions)	TG–450–1001
ForenSeq Index Adapter Fixture	FC–451–1001
ForenSeq Universal Analysis Software	SE–550–1001

Illumina • 1.800.809.4566 toll-free (US) • +1.858.202.4566 tel • techsupport@illumina.com • www.illumina.com

For Research, Forensic, or Paternity Use Only - Not For Clinical, Diagnostic, or Therapeutic Use in Humans or Animals

© 2016 Illumina, Inc. All rights reserved. Illumina, ForenSeq, MiSeq FGx, and the pumpkin orange color are trademarks of Illumina, Inc. and/or its affiliate(s) in the U.S. and/or other countries. Pub. No. 1470-2014-004 Current as of 18 April 2016

illumina®

AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
TCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTT
CGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACC
AACGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAA
AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
GATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGAGC
CGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAGTA