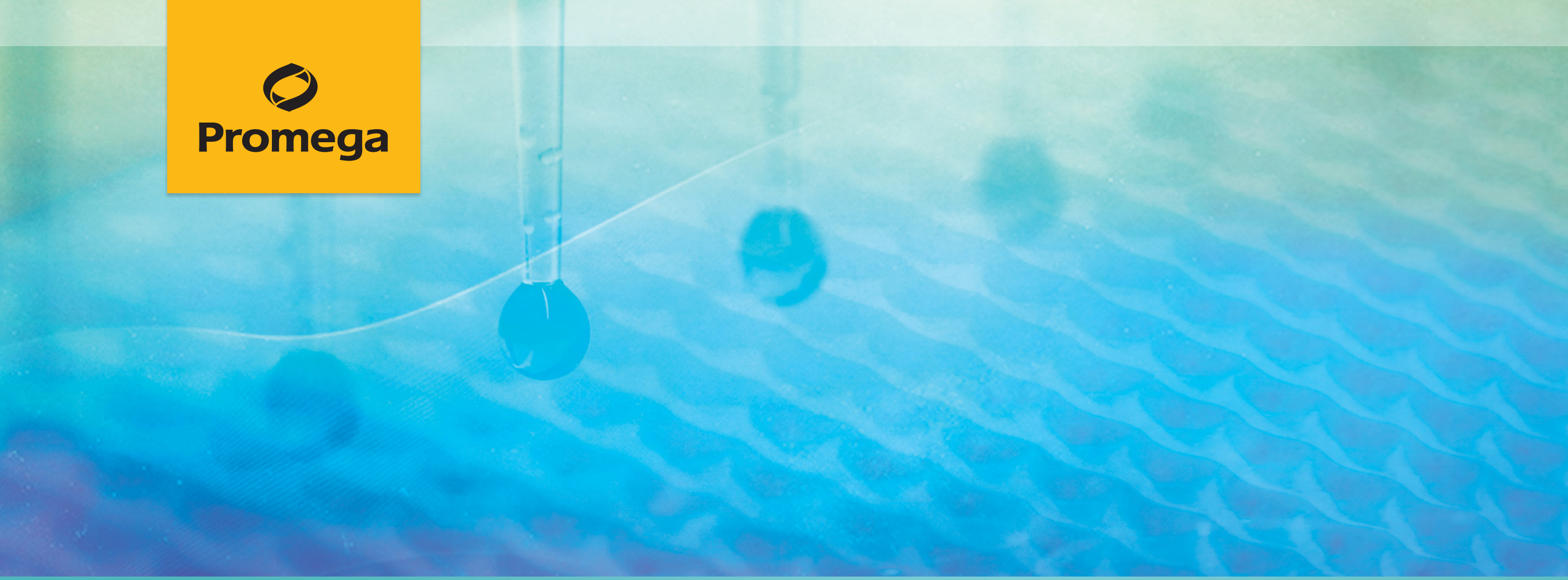
Promega



PowerSeq™ 46GY System

Eases the transition to MPS for forensic laboratories

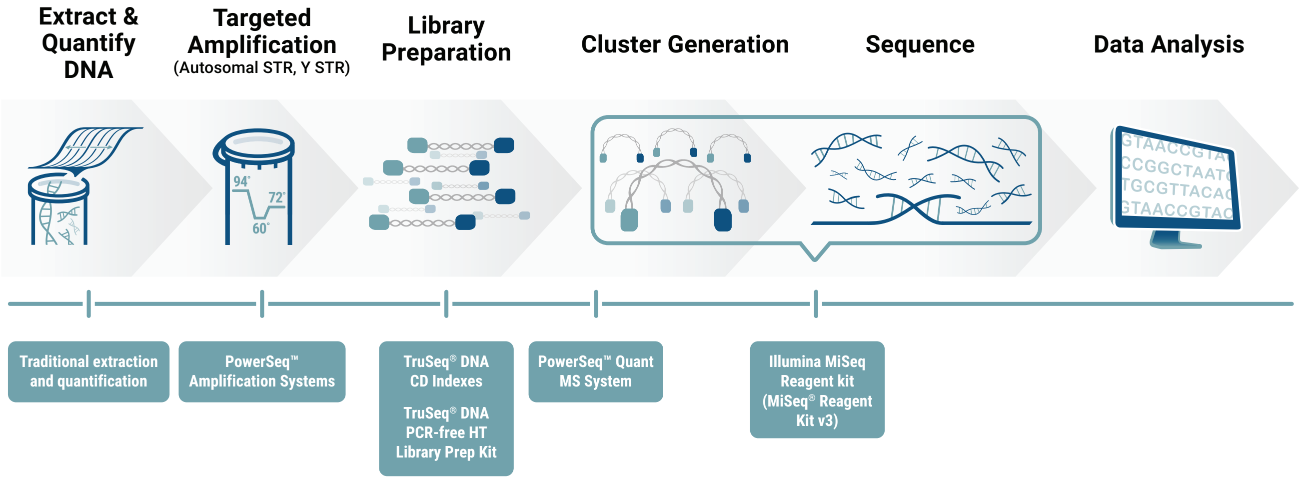
The Power to Solve... *from Sample to Analysis*

Coming Soon!

The Power to Solve... *from Sample to Analysis*

The Promega PowerSeq™ Systems enable forensic laboratories to take advantage of the increased discriminatory power that Massively Parallel Sequencing (MPS) technology offers. Using MPS enables both length-and sequence-based identification of relevant STR loci.

Additionally, MPS has several advantages over currently available CE technology, including the potential to improve mixture interpretation, identification of sequence polymorphisms, a high dynamic range, and greater multiplex capabilities.



Extract & Quantify DNA

Targeted Amplification (Autosomal STR, Y STR)

Library Preparation

Cluster Generation

Sequence

Data Analysis

Traditional extraction and quantification

PowerSeq™ Amplification Systems

TruSeq® DNA CD Indexes

TruSeq® DNA PCR-free HT Library Prep Kit

PowerSeq™ Quant MS System

Illumina MiSeq Reagent kit (MiSeq® Reagent Kit v3)

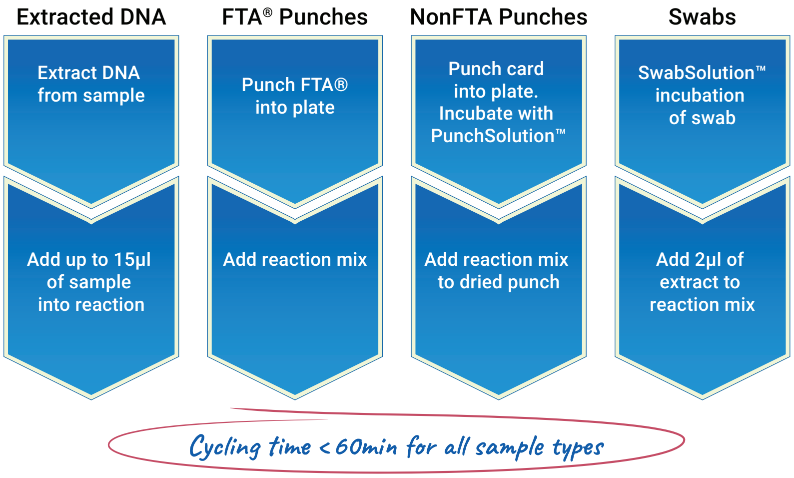
The PowerSeq™ 46GY System combines globally used autosomal STR loci with 23 loci from the PowerPlex® Y23 System in a single assay on an Illumina MiSeq® System. The combination of these STR loci and Amelogenin makes this multiplex an effective tool for human identification using MPS and maintains compatibility with existing databases worldwide. By using markers that analysts are already familiar with, the PowerSeq™ 46GY System offers a way for laboratories to transition smoothly to include MPS in their menu of techniques, while it also ensures users are not burdened with excess information that most laboratories are currently unable to use.

		PowerPlex® Fusion System	PowerPlex® Y23 System	PowerSeq™ 46GY System
		24 loci	23 loci	46 loci
ESS/CODIS Loci	D1S1656	●		●
	D2S441	●		●
	D2S1338	●		●
	D3S1358	●		●
	D8S1179	●		●
	D10S1248	●		●
	D12S391	●		●
	D16S539	●		●
	D18S51	●		●
	D19S433	●		●
	D21S11	●		●
	D22S1045	●		●
	FGA	●		●
	TH01	●		●
	vWA	●		●
CODIS Loci	D5S818	●		●
	D7S820	●		●
	D13S317	●		●
	CSF1PO	●		●
	TPOX	●		●
Other Loci	Amelogenin	●		●
	Penta D	●		●
	Penta E	●		●
	SE33			
	D6S1043			
Y-STR Loci	DYS19		●	●
	DYS385a/b		●	●
	DYS389I		●	●
	DYS389II		●	●
	DYS390		●	●
	DYS391	●	●	●
	DYS392		●	●
	DYS393		●	●
	DYS437		●	●
	DYS438		●	●
	DYS439		●	●
	DYS448		●	●
	DYS456		●	●
	DYS458		●	●
	DYS481		●	●
	DYS533		●	●
	DYS549		●	●
	DYS570		●	●
	DYS576		●	●
	DYS635		●	●
	DYS643		●	●
	Y-GATA-H4		●	●

Amplicons for each locus are designed to be in a range of 140–300bp, thereby enabling their use with degraded DNA samples.

Sample Types

The PowerSeq® 46GY System works with all sample types typically encountered by forensic casework and database laboratories.



Extracted DNA

Extract DNA from sample

Add up to 15µl of sample into reaction

FTA® Punches

Punch FTA® into plate

Add reaction mix

NonFTA Punches

Punch card into plate. Incubate with PunchSolution™

Add reaction mix to dried punch

Swabs

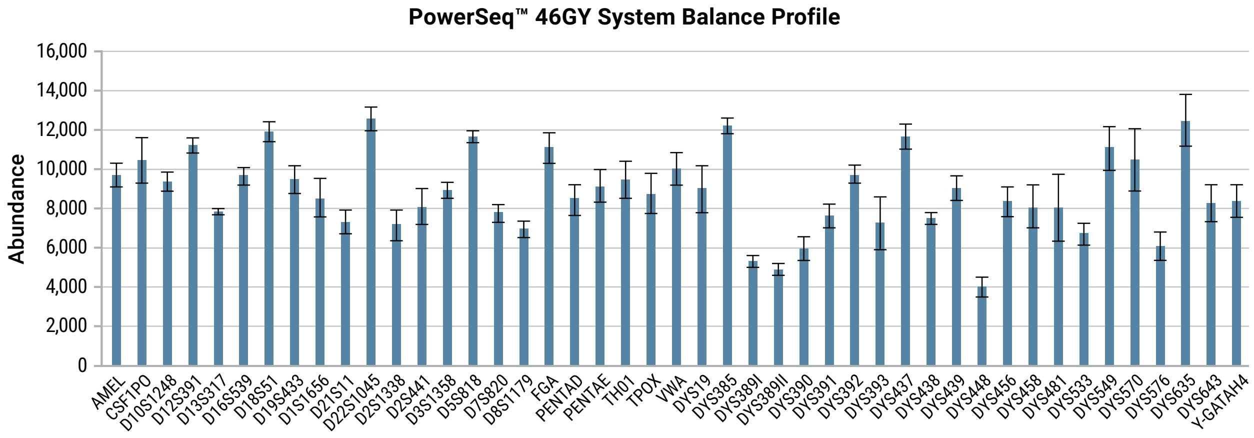
SwabSolution™ incubation of swab

Add 2µl of extract to reaction mix

Cycling time < 60min for all sample types

Balance Profile

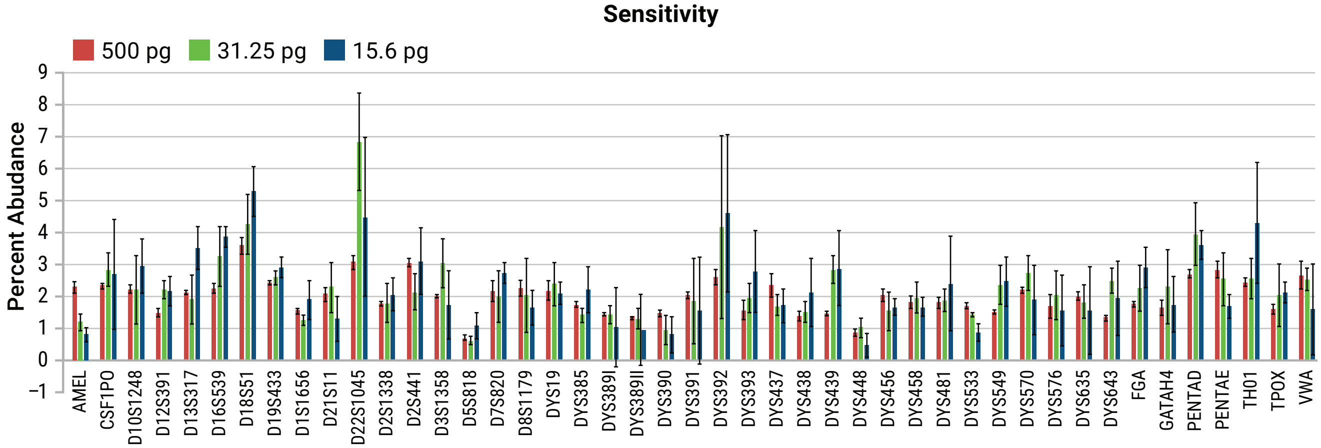
Inter-locus balance is an important feature of a forensic casework testing kit for use in identification of minor-contributor alleles in mixture samples. The data below demonstrate the balance achieved with the PowerSeq™ 46GY System.



Total abundance per locus using 500pg 2800M Control DNA (n = 3). To control for sample loading on the MiSeq® instrument, abundance per locus was normalized to average of total abundance for sample set. A pool of 96 samples was sequenced simultaneously using MiSeq® Reagent Kit v3, 2 × 300 cycles. Data were analyzed with ExactID® software (Battele Memorial Institute).

Sensitivity

The PowerSeq™ 46GY System offers the same sensitivity that laboratories have come to depend on when using our PowerPlex® Systems. Full profiles can be obtained with as little as 31.25pg of input DNA. As shown in the following figure, the balance at low template inputs is comparable to the balance seen at the recommended input amount of 500pg.

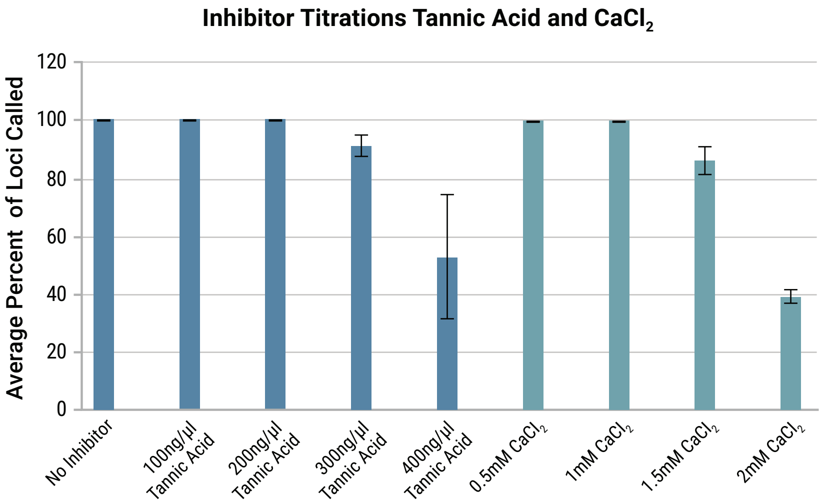


Percent of total allele calls per locus at different amounts of 2800M Control DNA (n = 3). A pool of 44 samples was sequenced simultaneously using MiSeq® Reagent Kit v3, 2 × 300 cycles. Data were analyzed with STRait Razor v2.0 (University of North Texas Health Science Center).

Full profiles can be obtained with as little as 31.25pg of input DNA.

Inhibitor Tolerance

The PowerSeq™ 46GY System performs well, even in the presence of large amounts of inhibitors, thereby increasing your success rate and minimizing the need to re-amplify samples.



Inhibitor Titrations Tannic Acid and $CaCl_2$

2800M Control DNA was amplified in triplicate in the presence of increasing amounts of common inhibitors. A pool of 32 samples amplified in the presence of tannic acid or $CaCl_2$ was sequenced simultaneously using MiSeq® Reagent Kit v3, 2 × 300 cycles.

Mixture Analysis

The evaluation and interpretation of complex forensic DNA mixtures continues to challenge forensic laboratories. MPS offers the ability to distinguish alleles with similar length for detecting minor DNA contributors in a complex mixture and the PowerSeq™ 46GY System further helps overcome this challenge by providing improved balance between loci.

Locus	Average Calculated Female:Male Ratio 1:1	Average Calculated Female:Male Ratio 2:1	Average Calculated Female:Male Ratio 5:1	Average Calculated Female:Male Ratio 9:1	Average Calculated Female:Male Ratio 19:1
D1S1656	1.3	2.4	5.5	12.4	27
D21S11	1.3	2.5	6.7	8.3	13
D8S1179	1.2	2.3	6.7	12.9	14,19,62
TPOX	1.5	2.7	7.3	13	22,23,52

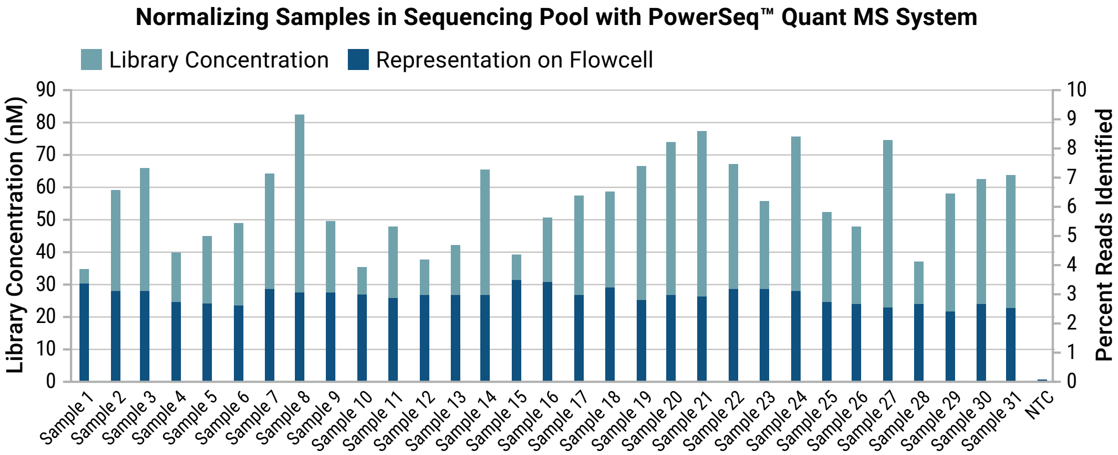
Average ratios calculated for loci with unique alleles for the two contributors. (N=3). Ratio for each replicate of the 19:1 mixture is shown for D8S1179 and TPOX.

Library Quantification

The PowerSeq™ Quant MS System is designed for library quantification, a critical step in the MPS workflow. Accurate quantification of a library determines the optimal amount of adapter-ligated fragments for cluster generation. Accurate quantification also helps ensure even representation of each library on the chip, resulting in more consistent and reproducible sequencing results.

The PowerSeq™ Quant MS System is a qPCR-based system that directly measures the number of DNA molecules present in your libraries. Unlike quantification of your sample prior to STR amplification where human-specific quantification is critical, library quantification does not need to be human-specific, because it targets adapter sequences for the Illumina MiSeq platform.

Use of the PowerSeq™ Quant MS System can help ensure that your libraries are evenly represented and precisely quantified on the MiSeq® flowcell.



Thirty-two libraries were quantified using the PowerSeq™ Quant MS System. The resulting values were used to normalize loading of samples into a final sequencing pool. The percent of reads identified for each sample from the total reads generated in the sequencing run demonstrates how evenly each sample was represented on the MiSeq® flowcell in relation to all libraries sequenced.

The PowerSeq™ Quant MS System is compatible with the following instruments:

- Applied Biosytems 7500
- Applied Biosystems 7500 Fast
- Roche LightCycler® 96/384
- BioRad CFX

Ordering Information

Product	Size	Cat.#
PowerSeq™ 46GY System	100 reactions	**PS4600**
PowerSeq™ Quant MS System	500 reactions	**PS5500**

Supporting Products

Product	Size	Cat.#
QuantiFluor® ONE dsDNA System	100 reactions	**E4871**
	500 reactions	**E4870**
QuantiFluor® dsDNA System	100µl	**E2671**
	1ml	**E2670**

To learn more, email: **genetic@promega.com**

The Power to Solve - *from Sample to Analysis*

DNA Isolation

Maxwell® FSC Instrument

A compact, plug-and-play instrument for automated DNA extraction

Maxwell® RSC 48 Instrument

Compact, automated nucleic acid purification platform that processes up to 48 samples simultaneously to yield high quality nucleic acids

Maxwell® FSC DNA IQ™ Casework Kit

Optimal extraction of DNA from forensic casework samples

Casework Extraction Kit

Preprocessing reagents to assist in DNA IQ™ chemistry extraction of DNA from challenging samples

DNA™ IQ System ID

Manual and large platform automatable purification of DNA free of PCR inhibitors

Differex™ System ID

Easy separation of sperm and epithelial cell fractions

Casework Direct Kit, Custom

Rapid screening of sexual assault evidence and processing of Touch DNA samples prior to quantification of human DNA using the PowerQuant® System and amplification using PowerPlex® Systems

Quantification

Plexor® HY System ID

Quantitative PCR for both total human and male DNA in a single reaction

PowerQuant® System ID

A 5-dye, 4-target hydrolysis probe-based quantitative PCR assay for assessing total human and male DNA concentrations, degradation levels and the presence of inhibitors

STR Amplification

STR Amplification

PowerPlex® Fusion System ID DA

A rapid 24-plex suitable for casework, paternity and database testing and designed to meet the new CODIS recommendations

PowerPlex® Fusion 6C System ID DA

A rapid 27-plex, including SE33, suitable for casework and databasing testing and designed to meet the new CODIS recommendations

PowerPlex® Y23 System ID DA

Male-specific STR genotyping kit with 23 Y-STR loci; includes protocols for both casework and databasing

PowerPlex® ESX and ESI Fast System ID DA

Rapid human identification STR assays that meet ENFSI recommendations for use in casework, paternity and database testing

PowerPlex® 35GY 8C System* ID DA

An 8-color multiplex containing autosomal and Y-STR loci designed for use on the Spectrum CE System

Analysis

Spectrum CE System*

8 or 24-capillary electrophoresis instrument that combines state-of-the-art STR analysis with increased run flexibility and 4-plate capacity

Spectrum Compact CE System*

Benchtop, 4-capillary electrophoresis instrument capable of Sanger sequencing and fragment analysis

Massively Parallel Sequencing

Massively Parallel Sequencing

PowerSeq™ 46GY System* DA

Massively parallel sequencing of autosomal and Y STR loci in a single assay on an Illumina MiSeq platform

PowerSeq™ CRM Nested System* DA

Massively parallel sequencing of control region of mitochondrial genome using a nested amplification protocol

MPS Library Quantification

PowerSeq™ Quant MS System*

Quantification of prepared MPS libraries for Illumina platforms, enabling efficient pooling and flow cell representation

ID **Identity Automation™:** Fully developed and tested high-throughput solutions with Promega installation, training and support

DA **Direct Amp Compatible**

For validation services, visit:
www.promega.com/validationservices

**Coming Soon*

PROMEGA CORPORATION • 2800 WOODS HOLLOW ROAD • MADISON, WI 53711-5399 USA • TELEPHONE 608-274-4330