



HTG EdgeSeq
System

Sample to Answer
in 36 Hours

HTG EdgeSeq System Workflow and Chemistry Overview

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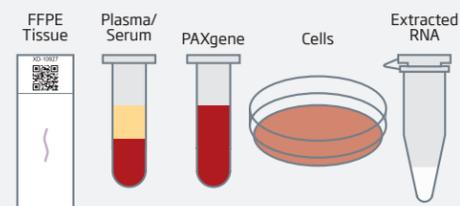


The HTG EdgeSeq system is a powerful molecular profiling tool for biopharmaceutical companies, academic research centers and translational medicine laboratories. The HTG EdgeSeq system provides an automated workflow solution based on HTG's extraction-free chemistry. The HTG EdgeSeq system is used with next-generation sequencing (NGS) instrumentation to produce gene expression profiles in about 36 hours.

Sample Preparation

4 hours

~30 minutes hands-on time



Library Preparation

20 hours Target Protection

~10 minutes hands-on time



2 hours Library Amplification

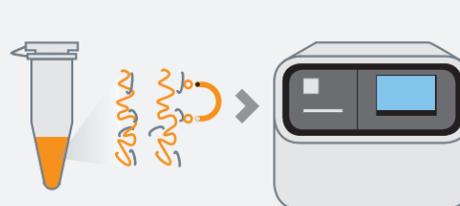
~60 minutes hands-on time



Quantitation and Normalization

1-3 hours

~60 minutes hands-on time



Next-Generation Sequencing

6-10 hours

~30 minutes hands-on time



Data Parsing

15-30 minutes

~5 minutes hands-on time



Sample Preparation

The HTG EdgeSeq system leverages our lysis-only chemistry allowing the use of small sample input amounts without the need for nucleic acid extraction. Samples*, such as 15 μ L of plasma or a single formalin-fixed, paraffin-embedded (FFPE) tissue section, are prepared with HTG's proprietary lysis buffer, incubated and pipetted into the wells of the HTG EdgeSeq sample plate. The simple, sample preparation eliminates several time-consuming, inefficient and error-prone pre-analytical steps.

HTG EdgeSeq assay kits include everything necessary to prepare samples, including lysis buffers, proteinase K and denaturation oil.



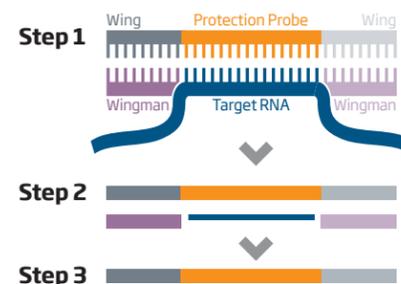
Library Preparation

Samples are loaded in the sample plate and placed in the HTG EdgeSeq processor where the (nuclease protection) chemistry is performed.

Step 1 HTG nuclease protection probes are added to the lysed sample. Wings on the side of the probe are used to add sequencing adapters and molecular barcodes, eliminating the need for ligation. Wingmen protect the wings.

Step 2 The probe, transcript and two wingman molecules produce a heteroduplex. S1 nuclease is added to degrade the nonhybridized probes and non-targeted RNA.

Step 3 After the S1 inactivation step and elimination of the RNA with heat and high pH, the protection probe is ready for tagging.



Step 4 Once the nuclease protection reaction has finished, samples are prepared for sequencing. PCR primers carrying the sequencing adapters and sample barcodes are used to individually tag each sample using a simple PCR reaction.



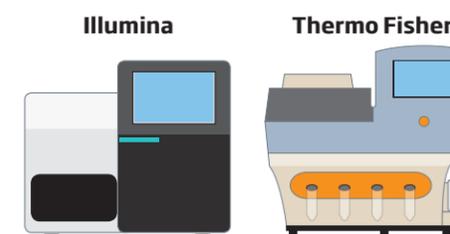
Quantitation and Normalization

Following amplification, the resulting PCR products undergo library cleanup to remove excess primers, and then are quantitated and pooled to generate the sequencing library.

Next-Generation Sequencing

The HTG EdgeSeq system comes pre-installed with HTG Edge host software. Expression data is generated using the FASTQ files from the sequencer and the sample sheet from the HTG Edge host computer. The set-up process takes less than 30 minutes for a typical Illumina MiSeq sequencer run and can be performed using a standard laptop or desktop computer.

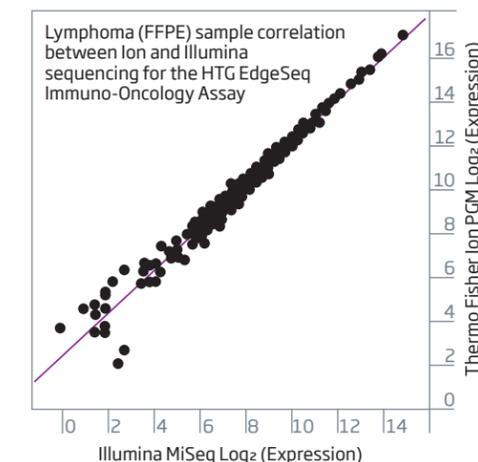
HTG EdgeSeq assays are compatible with common NGS instruments.



Data Parsing

HTG Edge host software parses and displays data with its simple, intuitive graphical user interface.

HTG EdgeSeq data demonstrate excellent reproducibility across leading NGS platforms with a Pearson correlation > 0.98 . Results from the same FFPE sample, using the HTG EdgeSeq Immuno-Oncology Assay, were highly correlated between the Thermo Fisher Ion PGM and the Illumina MiSeq sequencers.



* Please consult HTG for specific information on the procedure for preparing each sample type and the amount of material required.

For Research Use Only.
Not for use in diagnostic procedures.

For more information contact HTG Molecular Diagnostics
at 1-877-289-2615, info@htgmolecular.com or
contact your local HTG Molecular Diagnostics representative.
Visit www.htgmolecular.com



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HTG EdgeSeq processor is CE-marked and CSA-certified.

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