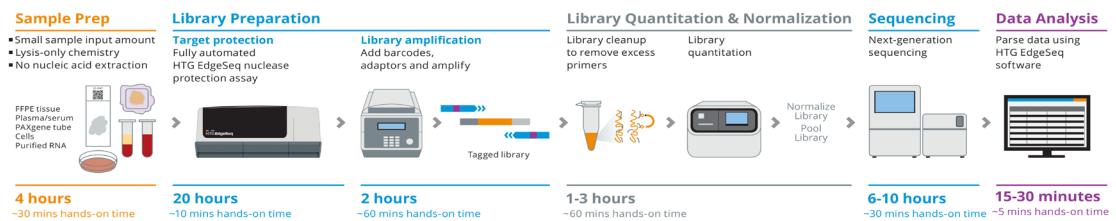


# HTG EdgeSeq miRNA Whole Transcriptome Assay

The HTG EdgeSeq miRNA Whole Transcriptome Assay (WTA) is a next generation sequencing (NGS) application that measures the expression of 2,083 human microRNAs (miRNAs) described in the miRBase v20 database. The assay is powered by HTG's quantitative nuclease protection assay and leverages the high sensitivity and dynamic range of NGS. The HTG EdgeSeq instrument automates the nuclease protection step in the library preparation process, significantly reducing the number of hands-on steps for fast and easy use of NGS platforms for miRNA analysis. The extraction-free, lysis-only chemistry significantly reduces sample input requirements compared to other methods and allows miRNA expression profiling from limited, precious FFPE tissues, cell lines, plasma/serum, PAXgene, and purified RNA.

## Automated on the HTG EdgeSeq system



## HTG EdgeSeq miRNA WTA features:

- Low sample input:** Use a single 5 µm FFPE tissue section, 1,250 cells, 12.5 µL of plasma/serum, 32 µL of PAXgene whole blood or 6.25 ng of purified RNA to obtain comprehensive molecular profile
- Extraction-free:** Avoid the hands-on time, complexity, cost and loss of sample fidelity normally associated with RNA extraction
- NGS-based:** Leverage the exquisite quantitation capability of NGS platforms to profile 2,083 human miRNAs
- Fewer steps:** HTG EdgeSeq chemistry is fully optimized and requires
  - No RNA Extraction
  - No rRNA Depletion
  - No cDNA Synthesis
  - No End Repair
  - No Size Selection
  - No Adapter Ligation
- Rapid results:** From sample to data in less than two days with about 3 hours of hands-on-time
- Simplified data analysis:** From FASTQ to tabular data in 15-30 minutes

### Achieve highly reproducible results from plasma samples

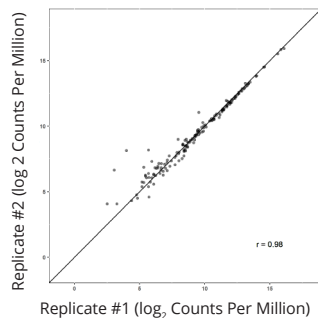


Figure 1. Pearson correlations of >0.95 are routinely obtained between replicates. Eight technical replicates of 12.5 µl plasma lysates were tested with HTG EdgeSeq miRNA WTA and sequenced on Illumina MiSeq.

### Generate robust data from precious FFPE samples

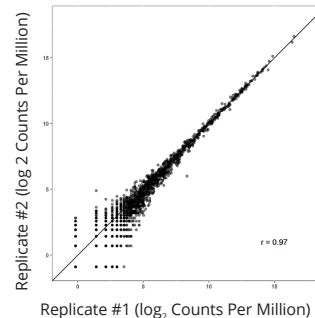


Figure 2. Equivalent expression profiles are demonstrated with a Pearson correlation,  $r$  of 0.97 for a single Colon Adenocarcinoma FFPE tissue slide sequenced on Illumina MiSeq.

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## Sample Requirements

Sample Type	Sample Input
FFPE Tissue	1.56-12.5 mm <sup>2</sup> of a 5 µm section
Plasma	12.5 µL
Serum	12.5 µL
PAXgene	32 µL
Cell Lines	1,250-5,000 cells
Purified RNA	6.25-25 ng

## Product Specifications

Design Source	miRbase v20
Targets	2,083

## Process Controls

Positive	1 positive probe
Negative	5 ANT probes

## Endogenous Controls

Common	ACTB, B2M, GAPDH, YWHAZ, PPIA
sRNA (Pol3)	RNU47, RNU75, RNY3, SNORA66
rRNA	RPL19, RPS20, RPL27, RSP12

## Ordering Information

Catalog #	Product Name	Description
Illumina (ILM) Next-Generation Sequencing Systems		
916-001-208	HTG EdgeSeq miRNA WTA ILM (2x8)	2 plates, 8 samples/plate
916-001-008	HTG EdgeSeq miRNA WTA ILM (4x8)	4 plates, 8 samples/plate
916-001-224	HTG EdgeSeq miRNA WTA ILM (1x24)	1 plate, 24 samples/plate
916-001-024	HTG EdgeSeq miRNA WTA ILM (4x24)	4 plates, 24 samples/plate
916-001-096	HTG EdgeSeq miRNA WTA ILM (1x96)	1 plate, 96 samples/plate
Ion Torrent (IT) Next-Generation Sequencing Systems		
916-001-308	HTG EdgeSeq miRNA WTA IT (2x8)	2 plates, 8 samples/plate
916-001-108	HTG EdgeSeq miRNA WTA IT (4x8)	4 plates, 8 samples/plate
916-001-324	HTG EdgeSeq miRNA WTA IT (1x24)	1 plate, 24 samples/plate
916-001-124	HTG EdgeSeq miRNA WTA IT (4x24)	4 plates, 24 samples/plate

## Ordering information

Email: [orders@htgmolecular.com](mailto:orders@htgmolecular.com) or contact your local sales representative.



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

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