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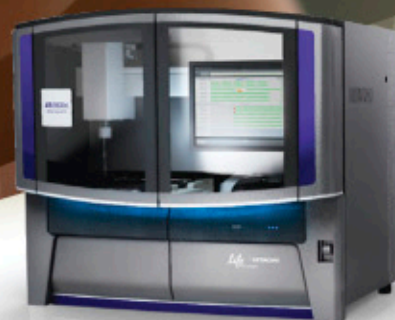
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Make Directional RNA-Seq Libraries in Less Than 3 Hours

EPICENTRE's new ScriptSeq™ mRNA-Seq Library Preparation Kit (Illumina-compatible) uses a unique terminal-tagging technology that simplifies the preparation of mRNA-Seq libraries from any animal, plant, or bacterial species.

ScriptSeq Illumina-compatible libraries:

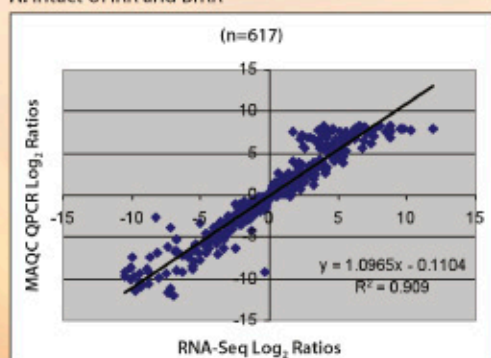
- Enable directional sequencing.
- Are made in 3 hours without the need for adaptor ligation.
- Are barcode-capable. Easily incorporate Illumina-compatible barcodes (available separately) or user-defined barcodes.
- Demonstrate high concordance with MAQC qPCR results.

*Covered by issued and/or pending patents.

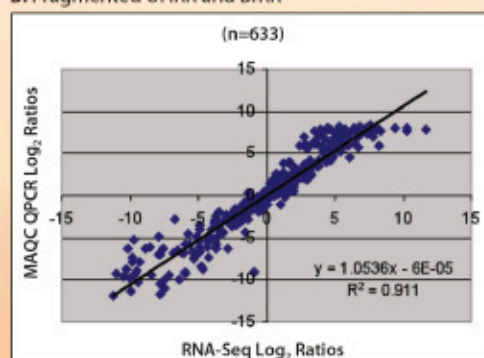
ScriptSeq™ mRNA-Seq Library Preparation Kit (Illumina-compatible) generates libraries for directional sequencing in less than 3 hours. Times for each step are shown in hours:minutes.

Conventional mRNA-Seq Method		ScriptSeq™ Method
Fragment RNA	(1:00)	Fragment RNA and synthesize di-tagged cDNA (1:40)*
Synthesize cDNA	(4:30)	
Ligate adaptors	(2:00)	Clean up cDNA (0:10)
Size-select from gel	(1:30)	—
Enrich library by PCR	(1:00)	Enrich library by PCR (1:00)
Total Time:	10:00	Total Time: ~3:00 <i>*single-tube reaction</i>

A. Intact UHRR and BrRR



B. Fragmented UHRR and BrRR



Correlation of gene expression between EPICENTRE ScriptSeq™ libraries and corresponding MAQC data.

A) Libraries prepared from rRNA-depleted, intact UHRR and BrRR. B) Libraries prepared from partially fragmented, rRNA-depleted UHRR and BrRR. UHRR, Universal Human Reference RNA; BrRR, Brain Reference RNA.

ScriptSeq™ mRNA-Seq Library Preparation Kit (Roche Titanium-compatible) and ScriptMiner™ Small RNA-Seq Library Preparation Kit (Illumina-compatible) are also available. For more information, visit: www.EpiBio.com/rnaseq



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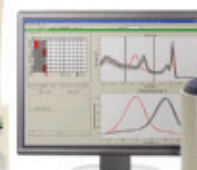
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Plant Biology: The CSHL Plant Biology program focuses primarily on development, stem cells, morphogenesis, plant genomics and epigenetics.

Genomics and Bioinformatics: The CSHL Genomics program uses state-of-the-art technologies including high-throughput sequencing, copy number variation analysis and transcriptome analysis. Efforts are ongoing to understand genomic variation associated with several human diseases as well as elucidating and characterizing new functional outputs of the genome.

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Barley	Ornamentals
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Brassicacae	Plant Interactions/Pests
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Forest Tree	Soybean Genomics
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