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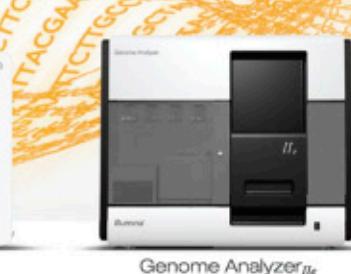
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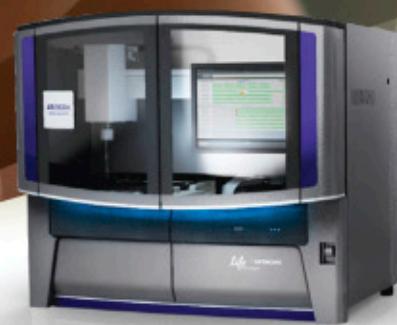
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# Make Directional RNA-Seq Libraries in Less Than 3 Hours

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:

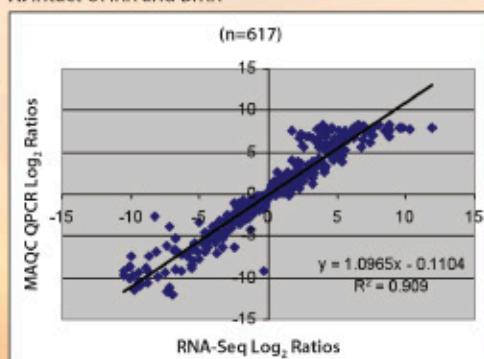
- Enable directional sequencing.
- Are made in 3 hours without the need for adaptor ligation.
- Are barcode-capable. Easily incorporate Illumina-compatible barcodes (available separately) or user-defined barcodes.
- Demonstrate high concordance with MAQC qPCR results.

**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.

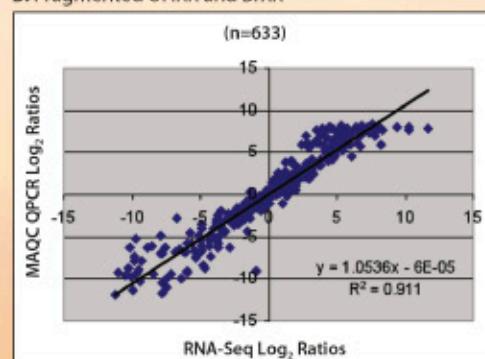
Conventional mRNA-Seq Method	ScriptSeq™ Method
Fragment RNA	(1:00)
Synthesize cDNA	(4:30)
Ligate adaptors	(2:00)
Size-select from gel	(1:30)
Enrich library by PCR	(1:00)
Total Time:	10:00
	Total Time: *single-tube reaction
	~3:00

\*Covered by issued and/or pending patents.

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](http://www.EpiBio.com/rnaseq)



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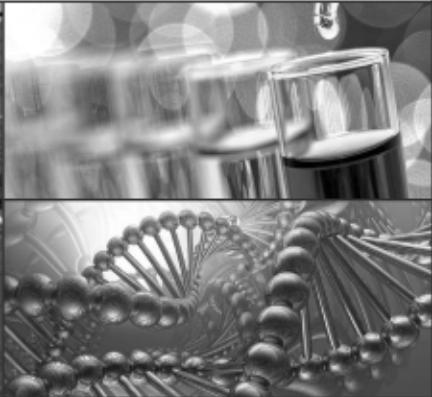
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Roger Beachy, USDA/Washington  
Joe Ecker, Salk Institute  
Ed Green, UC Santa Cruz  
Dave Lipman, NCBI, NLM, NIH  
Sharon Long, Stanford University  
Michael Lynch, Indiana University  
Pam Ronald, UC Davis

## Workshops

- Abiotic Stress
- Allele Mining
- Animal Epigenetics
- Apomixis
- Aquaculture
- Arthropod Genomics
- Banana Genomics
- Barley
- Bioinformatics
- Brachypodium Genomics
- Brassicas
- Cacao Genome Sequencing
- Cassava Genomics
- Cattle/Sheep/Swine
- Citrus Genome
- Coffee
- Comparative Genomics
- Cool Season Legumes
- Cotton Genome Initiative
- Cucurbit
- Ecological Genomics
- Equine
- Evolution of Genome Size
- Forage & Turf Plants
- Forest Tree
- Fruit/Nuts
- Functional Genomics
- Fungal Genomics
- Gene Expression Analysis
- Genomics Assisted Breeding
- Genomics for Disease Resistance
- Grape Genome Initiative
- Grass Genome Initiative
- Host-Microbe Interactions
- Large Insert DNA Library
- Lolium Genome Initiative
- Maize
- Molecular Markers
- Mutation Screening
- Oats
- Ornamentals
- Phylogenomics
- Plant Cytogenetics
- Plant Interactions/Pests
- Plant Introgression
- Plant Reproductive Genomics
- Polypliody
- Population & Conservation
- Poultry
- Proteomics
- QTL Cloning
- Rice Blast
- Rice Functional Genomics
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- Sex Chromosomes
- Solanaceae
- Somatic Genome
- Soybean Genomics
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