PRODUCT DATA SHEET

Whole Transcriptome Sequencing

Experienced provider as the sequencing center for the Genotype Tissue Expression (GTEx) project

Performance at scale: Over 24,000 whole transcriptomes have been sequenced at Broad to date

PRODUCT OVERVIEW

Whole Transcriptome Sequencing has become an invaluable tool for performing fundamental research surrounding transcript discovery and expression analyses including isoform detection, fusion transcript discovery, differential expression profiling, allele specific mutation validation, and transcriptome assembly. Working closely with scientists witih and outside the Broad Institute, Broad Genomic Services has performed a thorough evaluation of available technologies and optimized processing conditions including read depth, fragment insert-size, and sample cleanup to provide the highest quality whole transcriptome sequencing products possible.

Leveraging core competencies in process design, molecular biology, laboratory automation and integrated LIMS and analysis tools, we have developed products capable of producing hundreds of high-quality whole transcriptome libraries per week.

ROBUST WORKFLOW

RNA samples are prepared using a standard strand-specific mRNA sample preparation kit, modified for improved performance, multiplexing and integration into out automated platform. ERCC RNA controls are added prior to poly(A) selection providing additional control for variability including quality of the starting material, level of cellularity, RNA yield, and batch to batch variation. RNA library quality and insert-size is assessed by RQS value (equivalent to RIN) and RNA library quantity is verified by both pico QC and qPCR prior to sequencing.

WHAT'S INCLUDED:

- Sample Receipt & Plating
- ERCC RNA Control Addition
- Poly(A) selection
- Stranded cDNA Synthesis
- Sample Fidelity QC (96 SNP fingerprinting) Available with Sample Qualification of matching DNA

PRODUCT REQUIREMENTS:

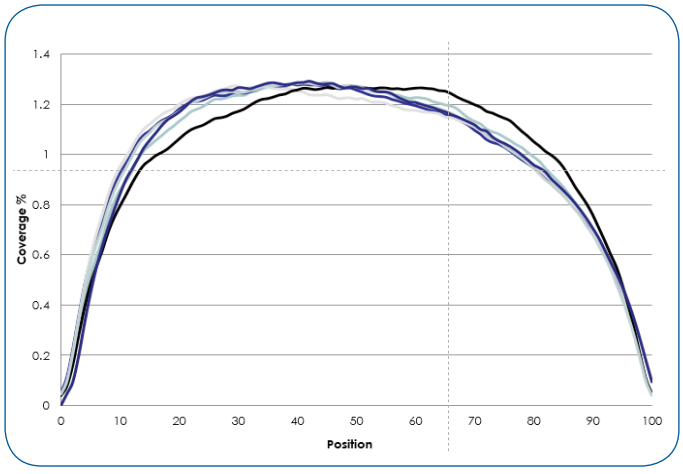
- 150ng of purified total RNA
- Fresh/frozen tissue, blood, or cell pellets that preferably yield >250ng of RNA (seperate charge will be applied for extractions)
- Minimum Sample data including Collaborator Participant ID, Collaborator Sample ID, Gender

DATA DELIVERABLE:

- 50 Million & 100 Million reads aligned pairs
- STAR aligned to human genome assembly (hg19)
- De-Multiplexed, aggregated Picard BAM file with insert size and alignment summary
- Data accessed via secure online digital transfer

SPECIFICATIONS

% Stranded	% mRNA Bases	% PF Bases Aligned	Insert Size	Deliverable
99.5	73.0	93.8 ± 0.4	500bp	50M & 100M paired reads



BROAD INSTITUTE

GENOMIC SERVICES

FOR MORE INFORMATION

Web: genomics.broadinstitute.org

Email: genomics@broadinstitute.org