UNIGENOME
Leading Genomics Innovations

Small RNA Sequencing & Analysis

A Lifesciences Division of
Unipath
SPECIALTY LABORATORY Ltd.

www.unigenome.in

Small RNA Sequencing and Analysis

Small noncoding RNAs act in gene silencing and post-transcriptional regulation of gene expression. Small RNA sequencing (sRNA-Seq) is a technique to isolate and sequence small RNA species, such as microRNAs (miRNAs). Small RNA-Seq can query thousands of small RNA and miRNA sequences with unprecedented sensitivity and dynamic range. With small RNA-Seq you can discover novel miRNAs and other small noncoding RNAs, and examine the differential expression of all small RNAs in any sample. You can characterize variations such as isomiRs with single-base resolution, as well as analyze any small RNA or miRNA without prior sequence or secondary structure information.

Due to their stability, clinical relevance, and functional role in disease pathogenesis, small RNAs have the potential to be important reporters of dysregulated cellular processes across a range of diseases. Evolving interest in comprehensively profiling the full range of small RNAs present in small tissue biopsies and in circulating biofluids, and how the profile differs with disease, has launched small RNA sequencing (RNASeq) into more frequent use.

Advantages of Small RNA Sequencing

Generate miRNA sequencing libraries directly from total RNA to understand the role of noncoding RNA.

- Understand how post-transcriptional regulation contributes to phenotype
- Identify novel biomarkers
- Capture the complete range of small RNA and miRNA species

Sample requirement for SMALL RNA profiling

- We accept total RNA, plant tissues, animal tissues etc.
- Isolated total RNA: 10-20µg of total RNA should be provided with RNA Integrity Number (RIN) > 6.
- RNA must not be degraded & should be free from DNA contamination.
- Quality control of RNA Samples: Samples will be subjected to both qualification, quantification and those having RIN > 6 will be QC passed. However, inclusion of low RIN value of the samples will be processed upon customer's confirmation.
- Unigenome will isolate total RNA from various parts of plant & animal tissues. Standardization is required for certain samples to obtain good quality & quantity suitable for small RNA experiment, and will be charged separately.

Plant TISSUES: (seedling, leaves, stem, flower, fruit, grain etc)

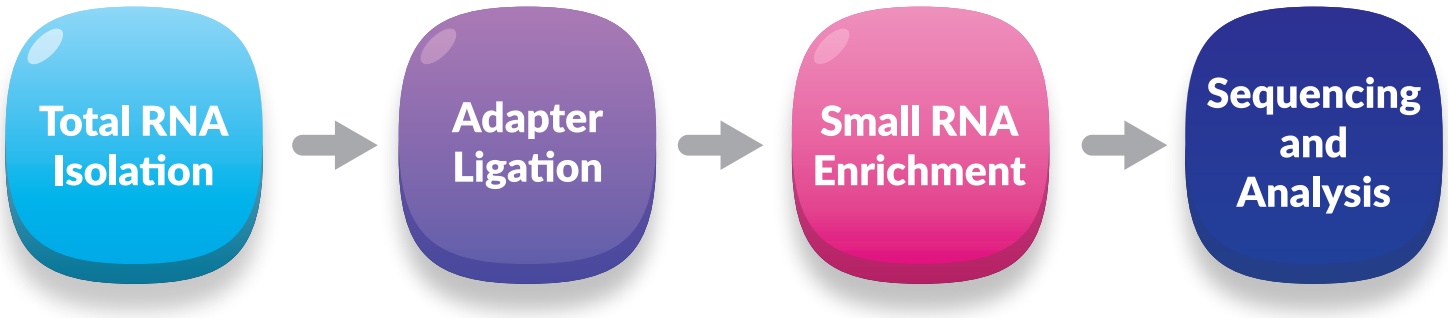
- Minimum 2-5 gm of tissue immersed in RNAlater should be provided.
- The volume of RNAlater should be at least ten times the volume of tissue.

Animal TISSUES: (Blood, epidermal etc)

- Minimum 2-5 gm of tissue sample should be provided in RNAlater.
- The volume of RNAlater should be at least ten times the volume of tissue.
- Blood Sample: 5-10ml of blood should be collected in Paxgene tube not in K2-EDTA tubes.

Note: All types of samples should be transported in dry ice (-20°C) containing cool packs to Unigenome Ahmedabad, Gujarat, India.

Workflow of Small RNA Sequencing



Small RNA Sequencing and Analysis on Illumina Platform

- Clean reads after filtration of adapter and low quality bases
- Mapping on non-coding RNA database to remove tRNAs, rRNAs etc.
- Mapping on known miRNA database to identify known miRNAs
- Expression profiling of known miRNAs
- Known miRNAs family classification
- Differential expression analysis of known miRNA (if more than 1 sample is provided)
- Novel miRNA identification and its structure prediction
- Target prediction for known and novel miRNAs
- Functional annotation of target identified
- Comprehensive compiled report and data deliverables

Note: Customized analysis as per client's need is provided for sRNA sequencing with additional charges

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