Difference Between Exome and RNA Sequencing

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Key Difference – Exome vs RNA Sequencing

Nucleic acid sequencing is the technique which determines the order of nucleotides in a particular fragment of DNA or RNA of an organism. Sequencing is important in identifying the DNA and RNA makeup of the cell and distinguishing certain genes which code for functional proteins; thus, sequencing can be used to understand the mutations of these genes and gene expressions. Sanger Sequencing method or the more advanced Next generation sequencing methods are the sequencing methods that are commonly utilized. **Exome sequencing is the sequencing of the complete set of exons or coding DNA regions present in an organism whereas RNA sequencing is the sequencing procedure of Ribonucleic acids (RNA).** This is the key difference between exome and RNA sequencing.

What is Exome Sequencing?

Exome is a subset of the genome which consists of the coding genes of a particular organism. Coding genes are named as exons and are transcribed into mRNA and then translated into amino acid sequences. During post transcriptional modifications, RNA splicing mechanism in eukaryotes remove the introns (non coding regions), and the exons remain. There are two main techniques in which exome sequencing is done: solution based and array based.

In solution-based exome sequencing, DNA samples are fragmented using either restriction enzymes or mechanical method and denatured by heat. In this technique, biotinylated oligonucleotide probes (baits) are used to selectively hybridize with target regions in the genome. Magnetic streptavidin beads are used for the binding step. Binding is followed by a washing step where the unbound and non-targeted sequences are washed away. The bound targets are then amplified using Polymerase Chain reaction (PCR) and then are sequenced using Sanger sequencing or Next Generation Sequencing techniques.

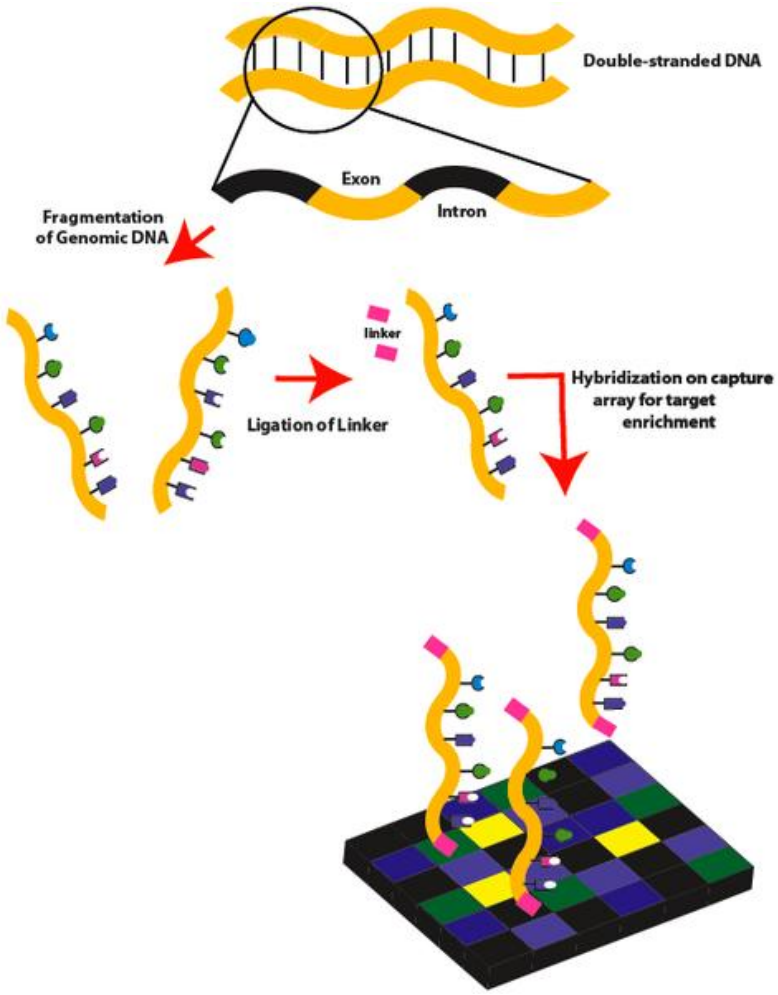

Figure 01: Exome Sequencing

Array based method is also similar to the solution based method, except that DNA fragments are captured into a micro array, and then the binding and the washing steps follow before being sequenced.

Exome sequencing is used in many applications such as genetic diagnosis of diseases, in gene therapy, in identifying novel genetic markers, in agriculture to identify various beneficial agronomic traits and in plant breeding procedures.

What is RNA Sequencing?

RNA sequencing is based on the transcriptome, which is the complete transcripts of the cell. The key goals of RNA sequencing are to catalogue all species of the transcript, including mRNA, non-coding RNA, and small RNA, to determine the transcriptional structure of genes and to quantify the expression levels of each

transcript during development. During RNA sequencing, hybridization technologies (which were complementary DNA derived from mature mRNA sequences) were initially used for sequencing. At present, a more accurate and an advanced through-put technique is used for RNA sequencing.

In RNA sequencing, a sample of RNA which can be total RNA or fractionated RNA is converted to its complementary DNA (cDNA) using reverse transcription, and a cDNA library is prepared. Each cDNA fragment is attached to adaptors on both sides (pair end sequencing) or on one side (single end sequencing). These tagged sequences are sequenced using Sanger sequencing or next generation, like exome sequencing.

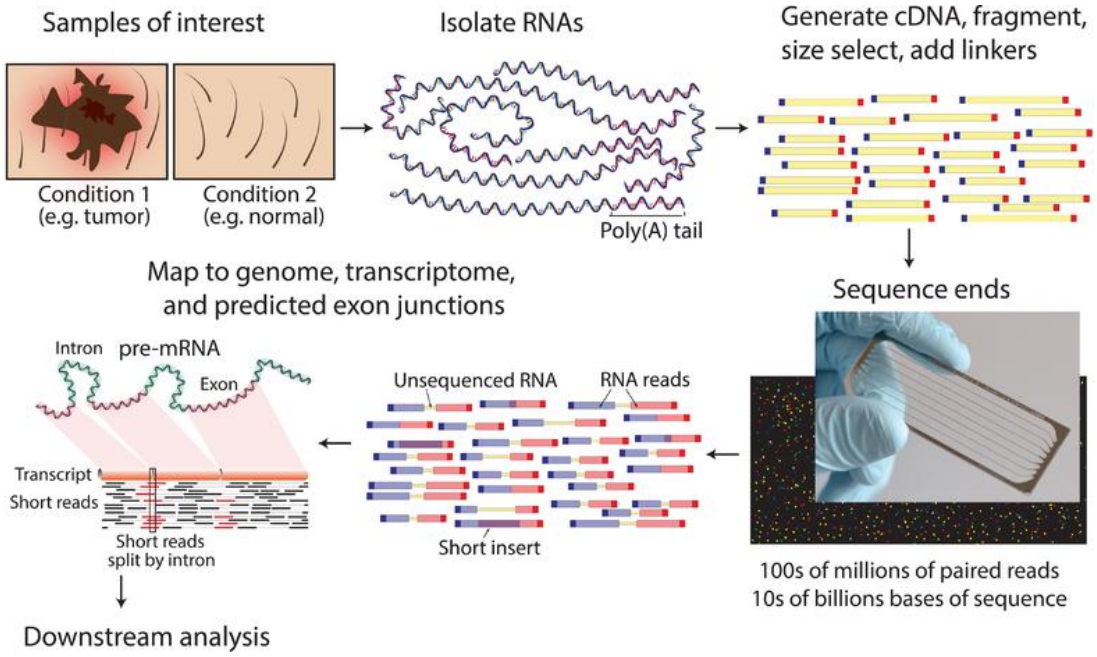

Figure 02: RNA Sequencing

What are the similarities between Exome and RNA Sequencing?

- Short selected fragments or the entire set of DNA / RNA can be used for Exome or RNA sequencing.
- Sequenced fragments are preserved in libraries.
- Sanger sequencing or Next Generation sequencing can be used.
- Both are in vitro sequencing methods.
- Sequenced fragments can be determined by fluorescent tags.

What is the difference between Exome and RNA Sequencing?

Exome vs RNA Sequencing	
Exome sequencing is the sequencing of the complete set of exons or coding DNA regions present in an organism.	RNA sequencing refers to the sequencing procedure of Ribonucleic acids (RNA); the transcriptome.
Starting Sample	
Genomic DNA is the starting sample of exome sequencing.	RNA is the starting sample of RNA sequencing.
Composition	
This contains only coding regions of the total DNA known as Exons	This contains RNA-mRNA / transcriptome.
Sequencing	
There are two main methods of exome sequencing; solution based and array based technologies.	RNA sequencing is done via the preparation of a cDNA library by extracting the total RNA or fragmented RNA.

Summary – Exome vs RNA Sequencing

Exome is the complete set of coding regions of an organism and the techniques involved in the determination of exact nucleotide order of Exome is known as exome sequencing. RNA sequencing is the technique involved in the determination of the nucleotide order of the RNA of an organism. This is the difference between exome and RNA sequencing.

References:

1.Wang, Zhong, et al. "RNA-Seq: a revolutionary tool for transcriptomics." Nature reviews. Genetics, U.S. National Library of Medicine, Jan. 2009, Available here. Accessed 3 Sept. 2017.
2.Warr, Amanda, et al. "Exome Sequencing: Current and Future Perspectives." G3: Genes|Genomes|Genetics, Genetics Society of America, Aug. 2015, Available here. Accessed 3 Sept. 2017.

Image Courtesy:

1. "Exome Sequencing Workflow 1a" By Malachi Griffith, Jason R. Walker, Nicholas C. Spies, Benjamin J. Ainscough, Obi L. Griffith – (CC BY 2.5) via Commons Wikimedia
2. "Journal.pcbi.1004393.g002" By SarahKusala – Own work (CC BY 3.0) via Commons Wikimedia

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