Symbiont
Life Sciences

Your Complete Solution for Genomics Services

CORPORATE BROCHURE

support@symbiontcs.com | www.symbiontcs.com

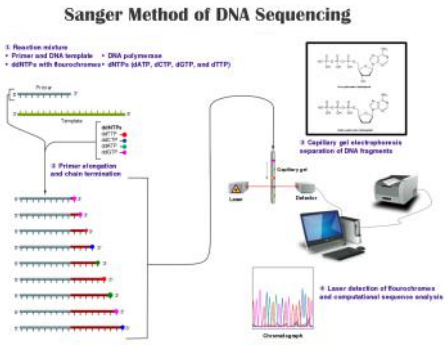
About Symbiont Life Sciences

Symbiont is a life sciences company catering to the needs of the researchers of various domain specific to Human, Plant, Microbes Veterinary, Marine related industry and academia, research and diagnostics. we have self reliance of domain expertise and strong presence in genomics services (Sequencing Services through NGS & Sanger). We also have excellent track records in handling sequencing of all types of samples through Ilumina(Novoseq), Pacbio(Sequel) Platforms.

Genomics Services

Sanger Sequencing

A DNA primer complementing the template DNA (the DNA to be sequenced) is used in Sanger sequencing to be a starting point for DNA synthesis. In the presence of the four deoxynucleotide triphosphates (dNTPs: A, G, C, and T), the polymerase expands the primordial by adding the additional dNTP to the DNA strand of the template. Four dideoxynucleotide triphosphates (ddNTPs: ddATP, ddGTP, ddCTP, and ddTTP) labeled with a distinct fluorescent dye are used to terminate the synthesis process to establish which nucleotide is incorporated in the nucleotide chain.

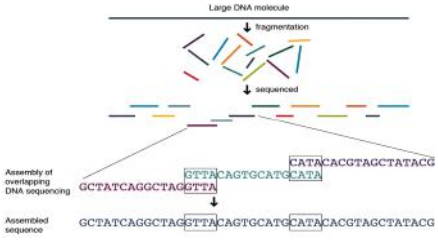


Compared to dNTPs, ddNTPs has a removed oxygen atom from the ribonucleotide, so it can not form a connection to the next nucleotide. Upon synthesis, the reaction products are loaded into four lanes of a single gel, depending on the different chain-terminating nucleotide and are subjected to gel electrophoresis. Thus the DNA sequence is determined according to their sizes.

Next Generation Sequencing

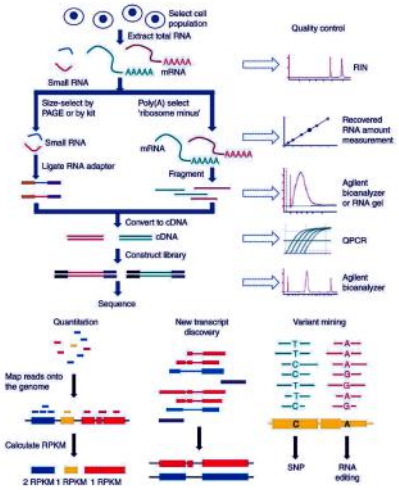
Whole Genome Sequencing

Whole genome sequencing is the determination of the full DNA sequence of the genome of an organism at a single time , which includes both chromosomal DNA and the DNA found in mitochondria and chloroplasts. Whole genome sequencing gives both de novo sequencing and re-sequencing a powerful method. De novo sequencing refers to sequencing of a novel genome with no available reference sequence. De novo assembly coverage quality is dependent on the size and continuity of the contigs. De novo sequencing generates a species' first genome map, thus providing a valuable sequence of reference for re-sequencing.



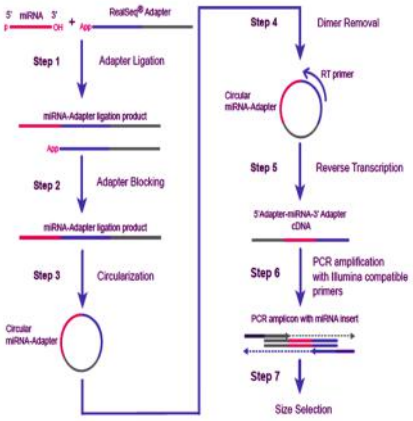
Transcriptome Sequencing

RNA-Seq is the leading mapping and quantification tool for transcriptomes using Next Generation Sequencing (NGS) technology. The transcriptome refers to the complete collection of transcripts in a cell which provides transcript level information for a specific stage of development or physiological condition. It is important to understand the transcriptome to interpret the functional elements of the genome, and to understand the development and disease. The main purpose of transcriptomics involves cataloging all transcript species; determining the transcriptional gene structure; and quantifying each transcript's expression levels under different conditions.



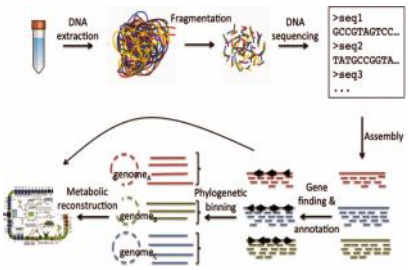
Small rna Sequencing

Small RNA species generally include the most common and well-studied microRNA (miRNA), small interfering RNA (siRNA), and piwi-interacting RNA (piRNA), as well as other types of small RNA, such as small nucleolar RNA (snoRNA) and small nuclear RNA (snRNA). Small RNA is a type of low-abundant, short-length (< 200nt), non-protein-coding, polyadenylated RNAs. Small populations of RNA can vary significantly between various types and species of tissues. Small RNAs are generally formed by fragmentation of longer RNA sequences, using dedicated sets of enzymes and other proteins.



Metagenomics Sequencing

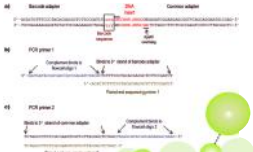
There are huge differences exist between microorganisms and higher eukaryotes. In addition to its smaller genome, most bacteria have a single circular chromosome (sometimes more than one chromosome, linear chromosomes or linear and circular chromosome combinations). The genes in the microbial genomes are typically a single continuous stretch of DNA, while bacterial genome occasionally includes many forms of introns.



A further significant distinction is the presence of plasmids in the bacterial genome. Plasmids, the extra-chromosomal circular DNA, can be transferred via horizontal DNA transfer, which mediates the rapid evolution of microorganisms. Virus is an infectious non-cellular organism consisting of a core of DNA or RNA surrounded by a protein coat.

Genotyping Sequencing

Single nucleotide polymorphisms (SNPs) are bi-allelic (usually) nucleotide variants occurring at a frequency of around one in 1,000 bp across the genome. They can be present in genome coding, non-coding, and intronic regions, and can influence gene and transcript level transcription factor binding, gene splicing, protein folding, and many other components.



Symbiont
Life Sciences

Registered Address
Symbiont Life Sciences
1 Mosque Street,
Mylapore, Chennai - 600 004
Tamil Nadu, India.
Ph: +91- 6374347907

support@symbiontcs.com | www.symbiontcs.com