

EUKARYOTIC Whole Genome Sequencing

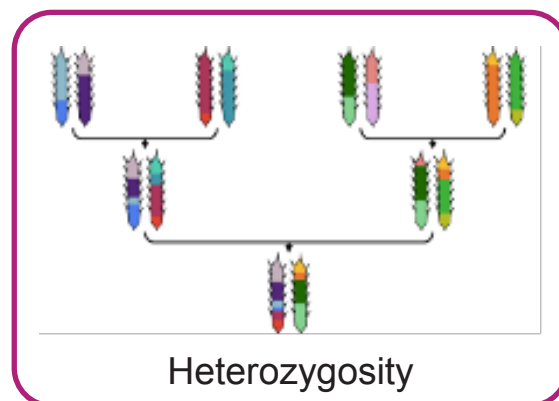
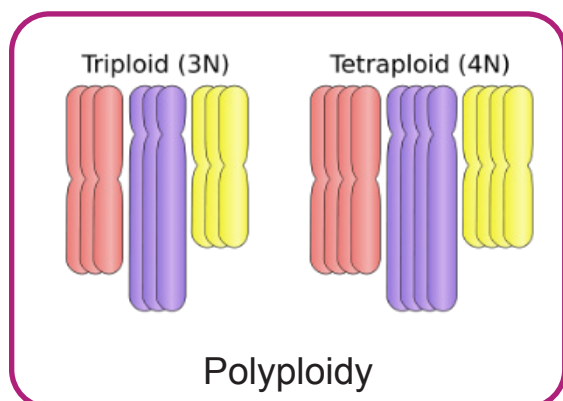
Tailored Genomics for the Most Complex Organisms

Animals, insects, plants, fungi, protists are all some of the well-known **eukaryotes**. The eukaryotes are any single-celled or multicellular organism with a **clear defined nucleus** containing its **chromosomal DNA**. Their chromosomes are numerous, **linear in structure**, and most likely to be a set of two copies especially in complex organisms. Moreover, in plants, it is well-recorded that some plants can have multiple copies of chromosomes which is known as **polyploid organisms**.

Another aspect of their chromosome is that homologous genes in each set of chromosomes do not always have the exact same DNA sequence; a phenomenon known as **heterozygosity**. Lastly, eukaryotes not only have chromosomal DNA, they also possess organelles which have their own chromosome namely the **mitochondrial DNA** and the **chloroplast DNA** and together they form a unit known as the **genome**.

These defining features are some of the aspects of a eukaryotic cells which actually makes it especially challenging to sequence their genomes. Nevertheless, **Genetika Science Indonesia** are up to these challenges and we can **offer unique solutions tailored** to each and every **specific quirks** that eukaryotic samples may have.

Unique Features of The Eukaryote Genome



Genome assembly is one of the key processes of **whole genome sequencing**. It is a required step and yet not all genome assemblies are created equal. The quality of the resulting genome assembly totally depends on the **quality of the input data**.

The lowest possible quality of a genome assembly is called **draft genome** and as the name suggests, it is a rough estimation of the real genome. **Low accuracy or shorter length sequencing data** heavily impacts the quality and the completeness of assembled DNA sequence. On the other end of the spectrum, **reference-grade** genomes are the assembled genome that is the **closest representation of the real genome**.



PacBio Vega



HIGH ACCURACY

Sequencing free of systematics errors.



UNIFORM COVERAGE

No Bias for high GC regions.



LONG READS

Up to 25 kb in length.

SAMPLE REQUIREMENTS:

- **For raw samples:** good condition and good handling of sample. Contact us for more information
- **For gDNA samples:** high-quality DNA (DIN > 7) with minimum amount of 60 ng/μL.

BIOINFORMATICS ANALYSIS:

- Genome size prediction and genome heterozygosity analysis.
- Identification and annotation of all protein CDS and genes.
- Assembled genome of top 5 genus in fasta format.

KEY DELIVERABLES:

- **Raw sequencing outputs.**
- **Final assembly sequence of chromosomal DNA.**
- **Final assembly sequence of mitochondrial DNA.** (for animals) or chloroplast DNA (for plants).

- Genome completeness analysis (BUSCO analysis).
- DNA sequence visualization (using Circos).
- Taxonomy annotation.



PT. Genetika Science Indonesia

Green Lake City, Rukan Great Wall Blok C No. 19-21,
Kel. Petir, Kec. Cipondoh, Kota Tangerang,
Banten 15147, Indonesia.

SCAN HERE

