**QP Code: PV25C003**

**Reg. No : .....**

**Name : .....**

# ST MARY'S COLLEGE (AUTONOMOUS), THRISSUR-20

## III SEMESTER (CBCSS - VPG) DEGREE EXAMINATIONS, OCTOBER 2025

## M.Voc. Applied Biotechnology

## GEC3AB10 : GENOMICS AND TRANSCRIPTOMICS

## 2024 Admission Onwards

**Time:3 Hours** **Maximum Weightage:30**

### Part A

*Short answer type questions. Answer **any four**.Weightage **2** for each.*
***(4x2 = 8 Weightage)***

1. Define physical, enzymatic, and chemical fragmentation.
2. Define library preparation in NGS.
3. Explain the purpose of blunt-end and adapter ligation in library preparation.
4. Define differential gene expression in RNA-seq analysis.
5. Use BWA and SAM tools to align sequencing reads to a reference genome.
6. Compare bead-based PCR and emulsion PCR in terms of efficiency, throughput, and cost.
7. Evaluate the impact of intergenic sequences on gene regulation.

### Part B

*Short essay-type questions. Answer **any four** .Weightage **3** for each.*
***(4x3 = 12 Weightage)***

8. Discuss the major achievements in the history of genome sequencing up to the early 2000s.
9. Describe the key differences between PacBio and Oxford Nanopore platforms.
10. Suggest a workflow to study microbial diversity in soil using metagenomics.
11. Apply bridge amplification to prepare clusters for high-throughput sequencing on an NGS platform.
12. Analyze the role of transposons in horizontal gene transfer in prokaryotes.
13. Compare haplotypes and SNPs in terms of structure, inheritance, and applications in disease studies.
14. Use phylogenetic software to analyze evolutionary relationships.

**Turn Over**

## Part C

*Essay-type questions. Answer **any two**. Weightage **5** for each.*
***(2x5 = 10 Weightage)***

15. Define the function of StringTie.
16. Explain how epigenetic changes such as DNA methylation and histone modifications regulate gene expression and contribute to cancer progression.
17. A new plant species has been discovered with potential medicinal properties. Apply de novo sequencing approaches to outline the workflow for generating its reference genome and identifying novel metabolic pathway genes.
18. Compare and contrast contig maps, restriction maps, and DNA sequence maps.

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