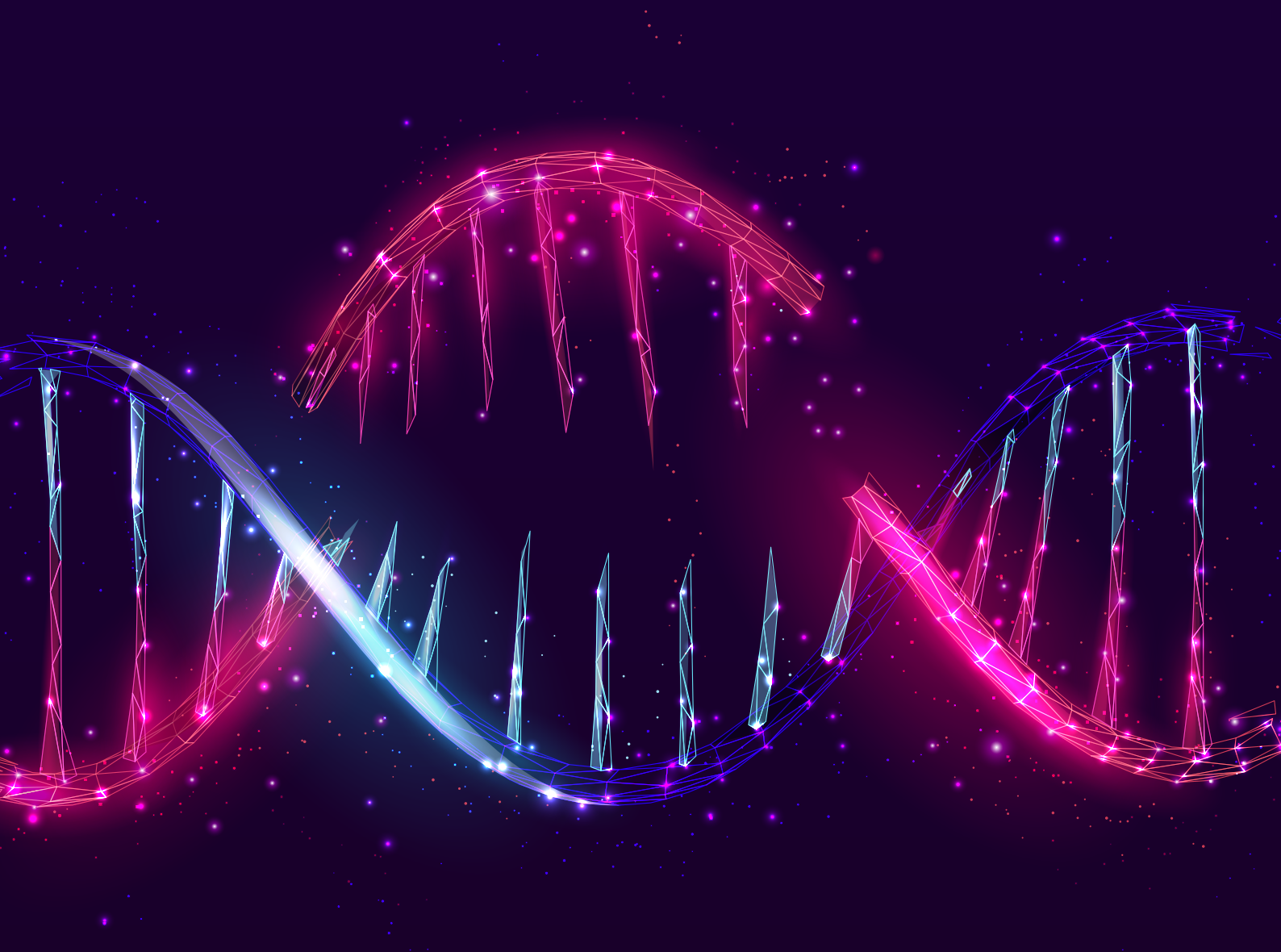


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CASE STUDY

# RNA-seq analysis of PDX samples



## Client's Challenge

To conduct extensive analysis of RNA-Seq data to derive useful biological insights from the PDX cancer models

## Input

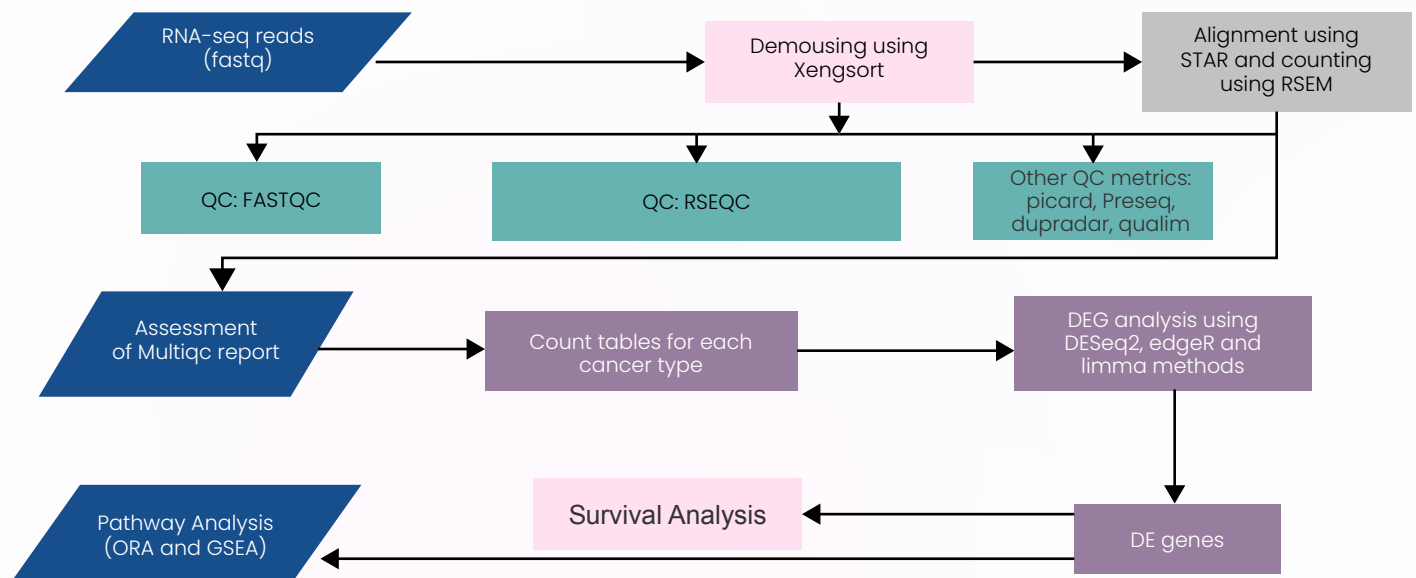
Illumina reads

## Background

- FASTQ reads were obtained from PDX models. The reads need to be demoused first to extract human tumor-specific reads.
- RNA-Seq data can provide useful insights into cancer biology, a thorough analysis of the expressed genes can identify useful biomarkers and targets for therapy.
- Perturbation of genes related to critical pathways cause disease, the identification of which can help us solve disease.
- Integration of gene expression data along with time-to-event data can help us prioritize gene candidates.

## Process Workflow/Methodology

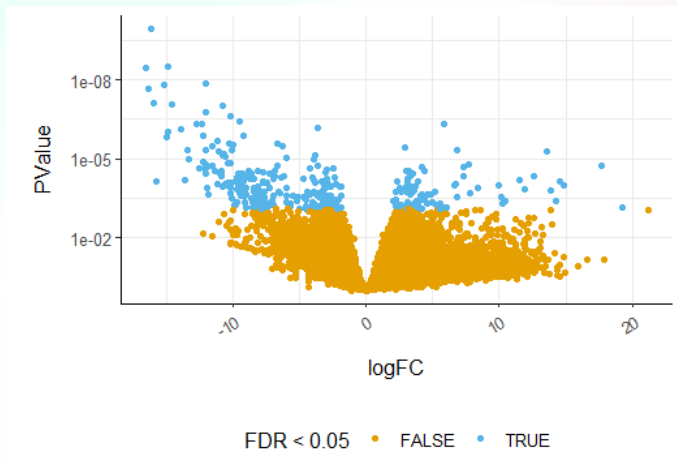
RNA-Seq data were processed using the workflow shown below and samples were assessed through a number of QC methods



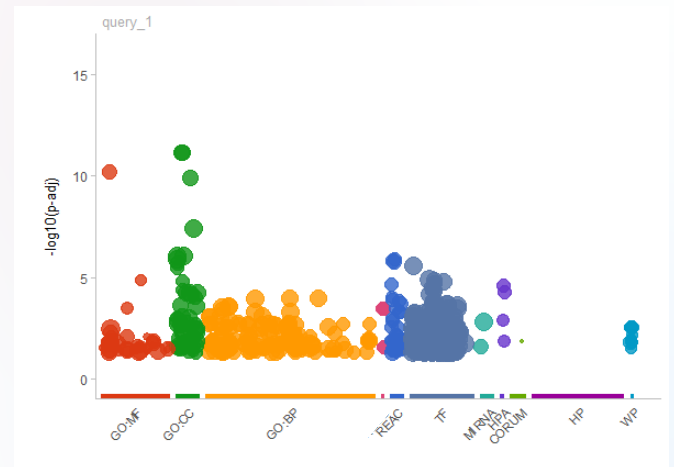
## Results & Conclusion

RNA-seq data were processed using the workflow shown below and samples were assessed through a number of QC methods

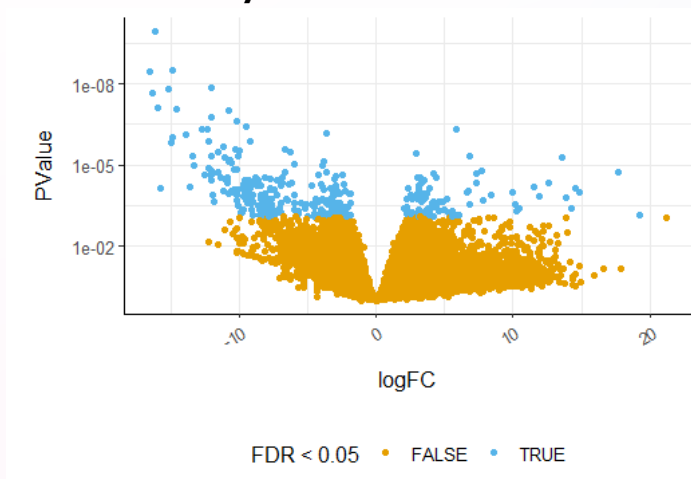
### Volcano plot of DE genes



### Pathways Enrichment Analysis



### Survival Analysis



We have successfully performed RNA-sequencing analysis of the PDX samples obtained from multiple cancer samples and have identified set of genes that are linked to treatment response, association with critical pathways and being connected with tumour survival



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