Eukaryotic mRNA Sequencing

Eukaryotic mRNA sequencing (mRNA-seq) uses next-generation sequencing for analysis of the messenger RNA profile (transcriptome) of samples. Sequencing data allows for the identification of transcript isoforms and their abundance. Novogene's Eukaryotic mRNA-seq service delivers high quality data, publication-ready results, and personalised analysis pipelines to meet different research objectives.

Why Novogene?

Extensive experience with over 3000 projects

Industry-leading data quality guarantee

In house pipeline to meet different analysis requirement

Find out more: novogene.com

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Sample requirements

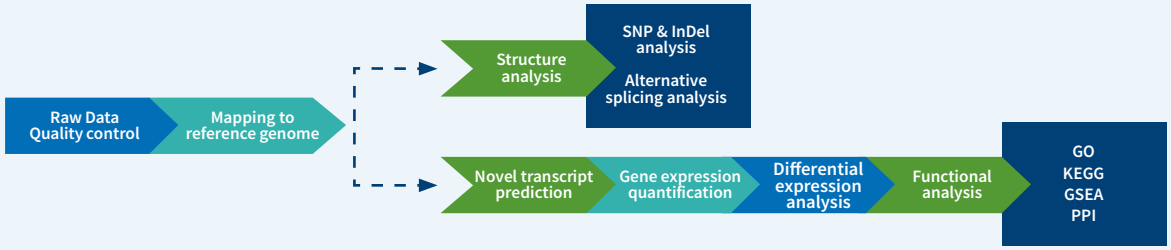
Sample Type	Amount	Volume	Concentration	RNA Integrity Number	Purity
Total RNA	≥0.4 μg (non-directional) ≥0.8 μg (directional)	≥ 20 μL	≥ 20 ng/μL	≥ 6.8 (Animal) ≥ 6.3 (Plant and Fungus) Smooth base line	OD260/280≥ 2.0 OD260/230 ≥ 2.0 No degradation No contamination

Sequencing parameters

Sample Type	Library type	Platform	Sequencing strategy	Recommended sequencing depth	Data quality
Total RNA	polyA enrichment & directional/non-directional RNA library.	Illumina NovaSeq 6000	Pair-end 150	Recommended: 15Gb for animals and plants, 3Gb for fungi. Minimum: 6Gb for animals and plants, 2Gb for fungi.	Q30 ≥ 85%
	rRNA removal & directional/ non-directional RNA library (required for FFPE samples).				Q30 ≥ 85%

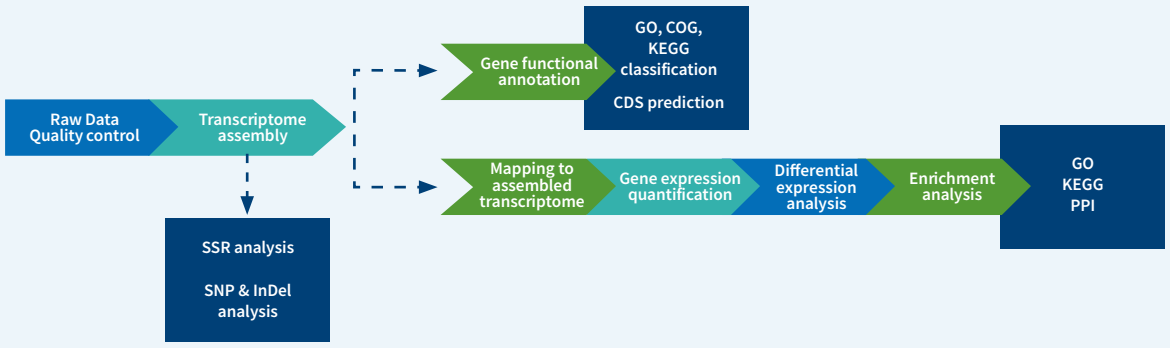
Analysis pipeline

Species with reference genome*



*Fusion gene analysis and DO/Reactome/DisGeNet enrichment analysis are available for human/mouse samples

Analysis pipeline



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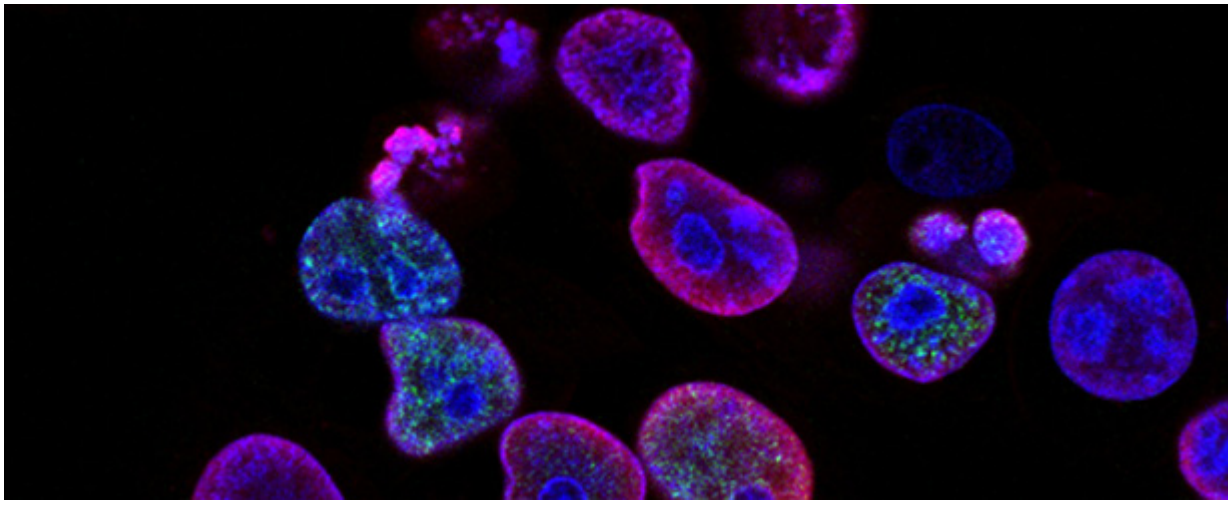
Case study

The Protozoan Inhibitor Atovaquone Affects Mitochondrial Respiration and Shows In Vitro Efficacy Against Glucocorticoid-Resistant Cells in Childhood B-Cell Acute Lymphoblastic Leukaemia.

Sbirkov et al., 2021. Frontiers in Oncology. DOI:10.3389/fonc.2021.632181.



Research objective:

To investigate the effectiveness of Atovaquone (Ato), a drug used in the treatment of malaria, against childhood acute lymphoblastomic leukaemia (cALL).

Sample collection:

REH cALL cell line provided by the University Hospital of Jena, Sup-B15 cell line purchased from DSMZ, Patient bone marrow samples from the Oncohaematology Unit at the University Clinic of Paediatrics.

Sequencing strategy:

Illumina NovaSeq 6000.

Data amount:

>20M clean reads per sample.

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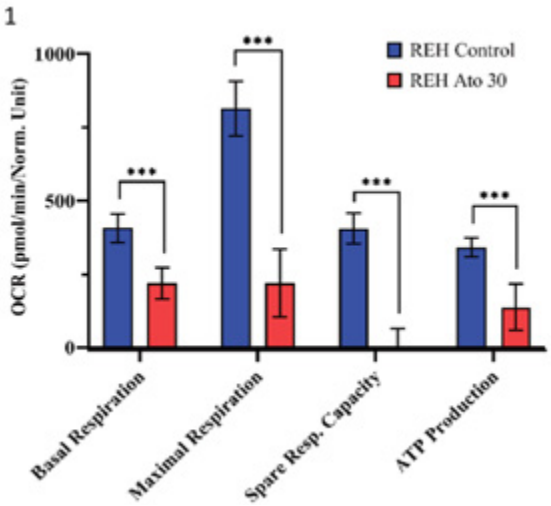
Results (partial results shown)

The phenotypic changes observed in Ato treated cells included reduced levels of basal and maximum respiration, decreased respiratory capacity of the cells and decreased ATP production (fig. 1).

Enrichment analysis of the genes with altered expression in the Ato treated cells explained some of the observed phenotypes. The genes were involved in cell metabolism, induction of apoptosis and cell cycle arrest (fig. 2), mechanisms crucial to tumour suppression.

1

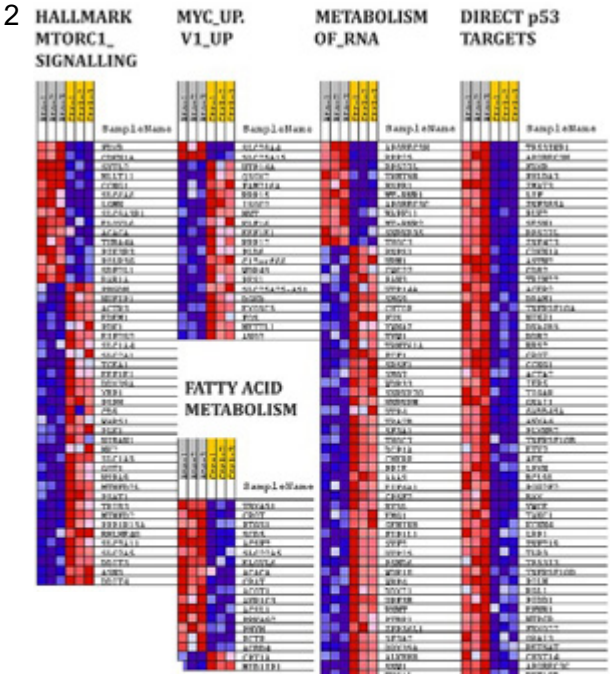


Conclusions

With the assistance of Novogene's RNA sequencing service, this study was able to highlight the anti-leukaemic affects of Atovaquone. Analysis of the genes with altered transcription levels showed downregulation of genes linked with cell proliferation and cancer progression, and upregulation of genes crucial for tumor suppression.

These findings present a promising new therapeutic approach to the treatment of cALL.

2



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