# RNA-Seq for Clinical Trials:

Quickly identify molecular markers to correlate with disease state or establish readout standard for assessment of drug treatment efficacy

Our GCLP compliant and high fidelity RNA-seq data complies with rigorous QA standards needed for clinical trials in the US.

RNA across different samples exhibit a high correlation value between the concentration of the External RNA Controls Consortium (ERCC) RNA control and the normalized sequencing reads, demonstrating high fidelity and repeatability of the procedures performed by Otogenetics.
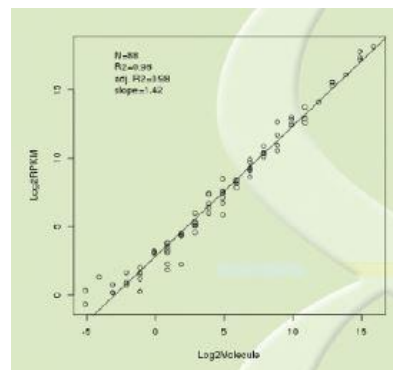
Learn more, faster with RNA-Seq Analysis:
Get your results faster and analyze the transcriptome with ease using our comprehensive bioinformatic analysis reports.
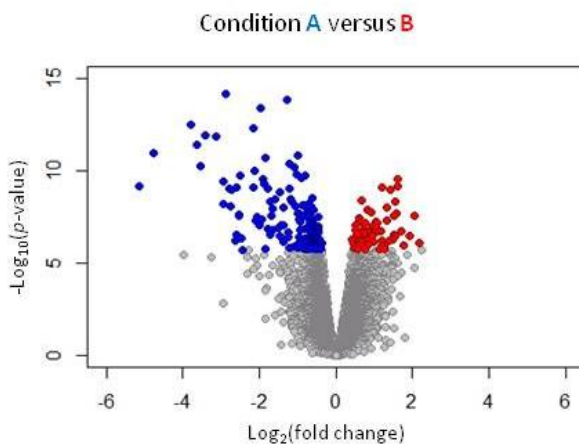

Fig 1. Differential expression
Volcano plots show statistical significance (Y-axis) vs. magnitude of differential expression (X-axis) for 2 conditions. Significant genes (negative log p-value >5) are highlighted.
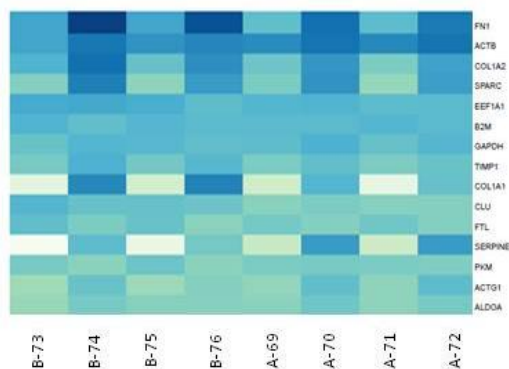

Figure 2. Heatmap.
Figure showing the expression data of the 15 most highly expressed genes in 8 samples. Blue indicates upregulated genes, in green are downregulated genes and in white are genes that do not change between conditions.

Assess drug treatment efficacy and identify gene targets by RNA-Seq analysis

Differential expression analysis can assist in your research to assess drug treatment efficacy as well as identify gene targets by comparing gene expression patterns in response to treatments.

RNA-Seq identifies potential gene targets and reveals efficacy during drug treatment of a rare form of cancer.
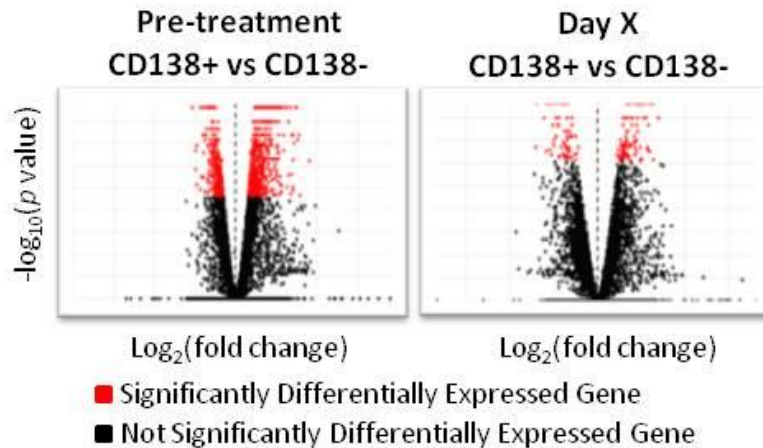
CD138 is a well known and attractive target for anticancer treatment of leukemia. Shown here, CD138+ and CD138- populations demonstrate a more similar expression profile X days post a test drug treatment.

Genes differentially expressed at pre-treatment versus at day X indicate potential targets of the treatment and can help you identify expression patterns predictive of therapeutic response. The reduction of differentially expressed genes in the two populations during treatment likely correlates with efficacy during drug treatment.

Why Otogenetics for your RNA-Sequencing needs?

- Our GCLP compliant and high fidelity RNA-seq data complies with rigorous QA standards needed for clinical trials in the US.
- RNA Extraction from varies sources
- Various workflows optimized for your needs, including low-input and small RNA
- Flexible RNA Sample Inputs, including FFPE
- Custom Workflows and Analysis