

Our team can perform differential gene expression analyses using RNA-seq NGS data generated from Illumina and Ion Torrent platforms as well as data generated with the major commercial microarray providers such as Affymetrix, Illumina and Agilent.

Our differential expression data analysis services are cost efficient and provide rapid turnaround and high throughput.

We offer a number of pipelined solutions to remove analysis bottlenecks and get the most from your data:



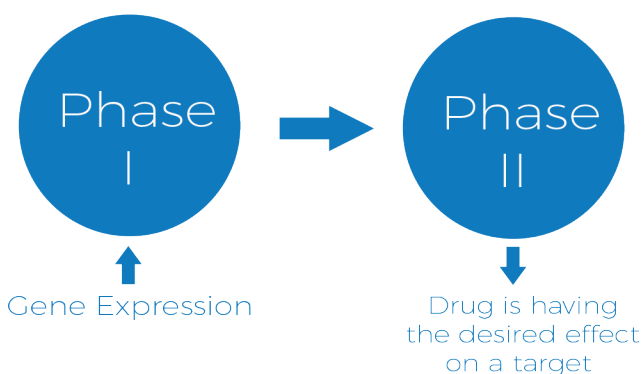
- Robust QC and summary statistics including automated outlier detection
- Identification of differentially expressed genes
- Functional enrichment analysis
- Network and pathway-based analysis
- Bespoke clustering and machine learning methods
- Meta-analyses of multiple datasets

**DIFFERENTIAL
EXPRESSION ANALYSIS**



With approximately 50% of drugs still failing due to lack of efficacy in Phase II, it is more important than ever that drug developers can make informed go- and no-go decisions as early as possible in the development process.

By using **gene expression** in Phase I trials you can identify off-target effects and address them early on. In addition, you can ensure there are no off-target effects of your compounds in healthy volunteers avoiding any surprises in your disease-compromised Phase II patients.



In Phase II, 'omics technologies can be utilised to monitor the response of your patient population to your compound with the information used to optimise dose levels, formulations and dosing regimes for further clinical development.

Following completion of Phase II trials, data can be analysed to investigate the genomic differences between responders and non-responders allowing **patient stratification** in later investigations and further development of companion diagnostics.

Fios Genomics offers a comprehensive analysis approach for augmenting clinical trial outcomes, ensuring you get the most information for your investment.