

Single Cell Genomics at Genotypic Technology




Single cell RNA sequencing has unparalleled potential to reveal gene expression at single cell resolution, thereby facilitating teasing of cellular heterogeneities, which get averaged out in bulk RNA sequencing. This approach has the potential of revolutionizing research where complex biological systems are involved operating through multiple cell types, behavior, and functions. From detecting rare cell types to delineating the transcriptome specific to such populations and understanding regulation of transcription at single-cell level are some of the breakthroughs that can advance our understanding of complex biological systems in health and disease.

We at Genotypic offer end-to-end single cell genomics services through our collaboration with 10X, right from facilitating study design and project consultation, selecting the appropriate kit and method, tissue lysis, cell collection, fixation & storage and transport to single cell isolation, library preparation, sequencing (with options of short or long reads appropriate to the research question) & bioinformatic analysis. Our expertise caters to your customised needs and requirements of your research, providing extensive and extended support throughout the project to analyse data that can answer your specific research questions.

👍 Genotypic Advantages

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★ Sample Requirements (for methods to prepare and store single cells, contact Sales)

 <p>✔ Cryopreserved</p> <ul style="list-style-type: none"> • Cultured cells • Single cell suspensions derived from dissociated tissues • Flow-sorted cells 	 <p>✔ Fresh</p> <ul style="list-style-type: none"> • Cultured cells • Single cell suspensions derived from dissociated tissues • Flow-sorted cells 	 <p>✔ Fixed</p> <p><small>(using 10X Fixed RNA Profiling reagents only, will be shipped by Genotypic)</small></p> <ul style="list-style-type: none"> • Cultured cells • Single cell suspensions derived from dissociated tissues • Flow-sorted cells
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📦 Genotypic Advantages

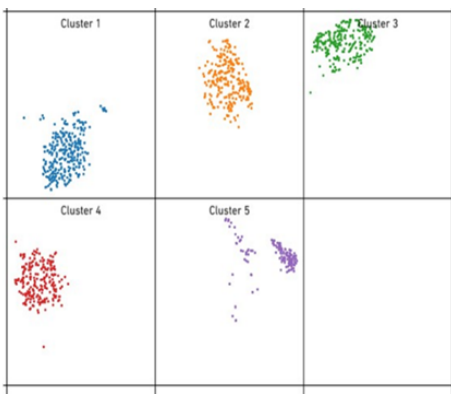
PLATFORM	READ LENGTH
Illumina short read	150bp paired-end on Illumina Short Read
ONT PromethION	Full length cDNA on PromethION

★ Recommended Sequencing Depth:

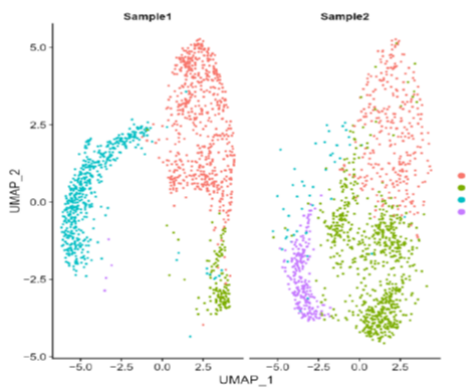
- Depends on
- Sample type
 - Research question to address

Data Analysis (deliverables will include):

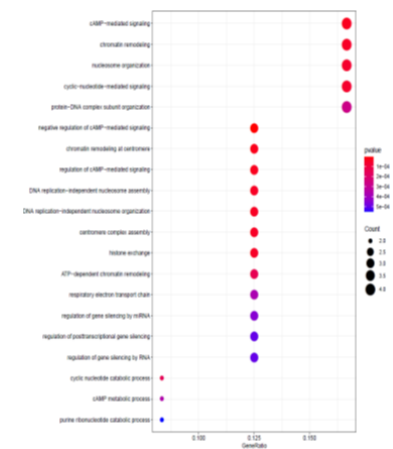
- Raw data preprocessing and quality check
- 10X barcode demultiplexing etc. using Cell Ranger
- Differential gene expression
- Identification of cell sub-population
- Gene expression analysis specific to sub-populations of interest
- Transcript enrichment, functional and pathway analyses and annotations
- In addition to above, long read data deliverables will include identification and quantification of transcript isoforms, transcript variants, splice junctions, fusion transcripts etc.



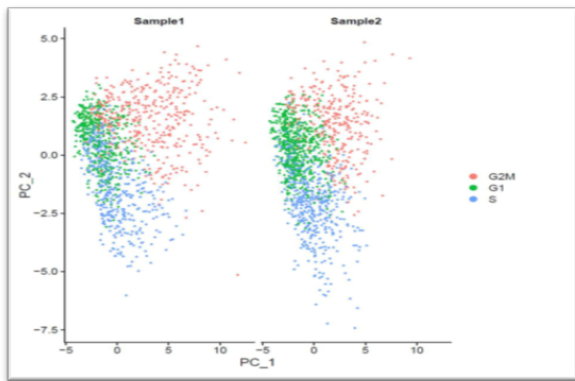
tSNE plots showing cell clusters/subpopulations



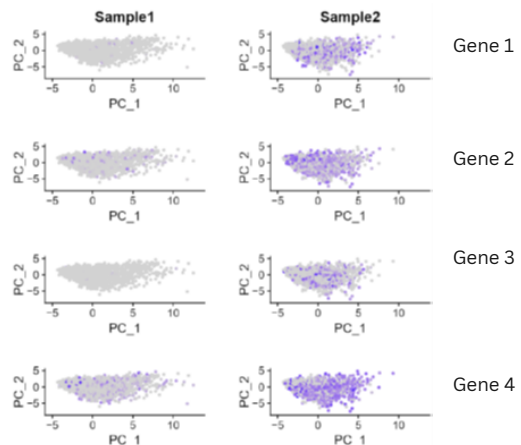
UMAP plot showing cell clusters/subpopulations



GO enrichment of top differentially regulated expressed genes



Integration of differential expression with cell cycle phase



Visualization using PCA plots of top differentially regulated expressed genes



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