

# Full Transcriptomes from Single Cell RNA-seq

**A novel sequencing method reducing scarcity from single cell experiments and enabling full characterisation of the transcriptome of the cell.**

## Unmet clinical need

Single-Cell RNA Sequencing (scRNA-Seq) technologies suffer from what is known as the 'scarcity' problem where lower expressed genes are underrepresented or not detected at all when compared to higher expressed genes. Scarcity means that the full transcriptome is never measured in single cells, which fundamentally limits the current applicability of scRNA-Seq to cell population identification.

## Solution

A kit based on an improved experimental protocol for scRNAseq that increases observed mean counts and removes spurious zeros (scarcity) while preserving statistical characteristics of the data. The method adapts the experiment to give low-expression genes more weight.

## Unique value

Through weighting the transcriptomes, this simple 2-step method can cost-effectively tackle the issue of scarcity. The method can be integrated with any commercially available single cell sequencing technology, as an "add-on" kit.

## Stage of development

The method has been experimentally proven, showing that you can down-weight high expressing genes and up-weight low expressing genes while preserving data quality. The team plans to work on scaling up the number of genes and validating the method across different cell types. The final product will be an experimental kit similar to probe panels frequently used in applications such as exome-sequencing.

## Research impact

This method can enable high resolution and high throughput characterisation of single cell data, unlocking the full potential of single cell experiments.

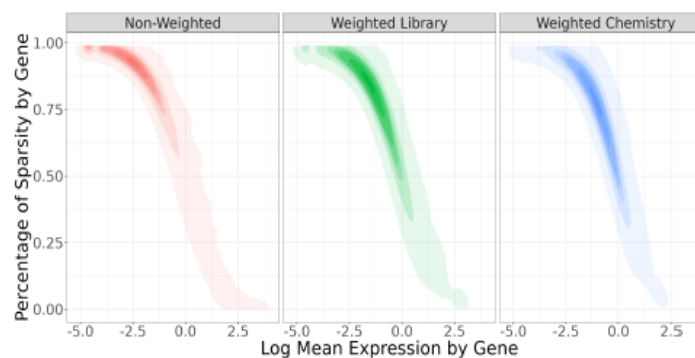
## Intellectual Property status

- Patent covering the method removing scarcity from single cell experiments.
- Priority filing Aug 2023 (GB 2312683.2). PCT filed April 2023 (WO2023209401A1).

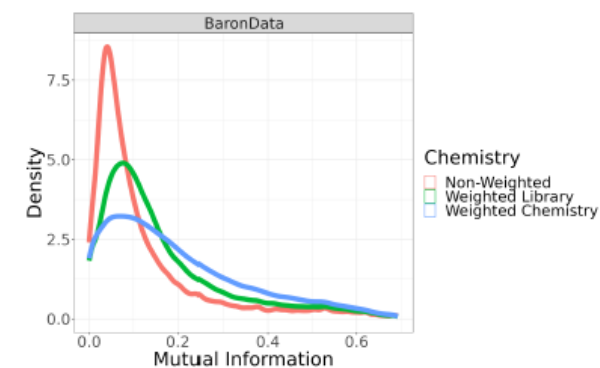
## Commercial Strategy

We are looking for industry partners with single cell sequencing platforms for co-development or licensing of the technology.

Reduces Overall Sparsity and Increases Mean



Overall Increase in the amount of Information



Weighted sequencing achieves fuller representation of transcriptome

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