# Special promotion for new service: Free library preparation for Flex scRNAseq!!

## Flex scRNAseq (single-cell RNAseq using fixed cells)

Flex scRNAseq uses paraformaldehyde (PFA) fixation to enable the collection, shipment, and analysis of samples to a central location without compromising integrity or data quality. This opens up new possibilities for throughput, batched analysis and sample accessibility to more samples, such as the formalin-fixed, paraffin-embedded (FFPE) tissue. With a scalable workflow, it is now possible to profile up to a million fixed single cells simultaneously, allowing flexibility in scheduling while meeting the specific needs of translational and clinical labs.

### Highlights
- Preserve biological states and fragile cells by fixing fresh samples at the collection point.
- Unlock new possibilities in single-cell analysis by accessing archived samples (FFPE).
- The sequencing cost is about half as regular 3' scRNAseq if there are more than 4 samples.
- The detection of gene expressions uses probe sets
- Only human and mouse tissues are available for the service.

### The Flex vs Regular 3' scRNAseq Promotion details:
1. Available for **1 project with 4 mouse samples for UTHealth faculties**. (First come first serve)
2. The samples will prepare the Flex scRNAseq libraries and the regular 3' scRNAseq libraries side by side
3. **25% off** for the library preparation of regular scRNAseq and **Free** for the library preparation of Flex scRNAseq
4. Present the data comparison in a webinar with CGC and 10x Genomics when the project is completed

The estimation of the cost of the promotion project (**total $12,222 after $7023 off**)

### The promotion for **4 samples** with 10,000 cells/sample

|  | Flex scRNAseq | regular scRNAseq |  |
|---|---|---|---|
| Library preparation | ~~$4899~~  $0 | ~~$8496~~  $6372 |  |
| Sequencing (estimated) | $1650 (600M reads) | $4200 (1900 M reads) |  |
| **Total (estimated)** | ~~$6549~~  $1650 | ~~$12696~~  $10,572 | ➡ $12,222 |

Flex scRNAseq vs regular 3' scRNAseq

|  | Flex scRNAseq | regular scRNAseq |
|---|---|---|
| Sample type | Cells or nuclei<br>Can be cells from FFPE | Cells or nuclei |
| Sample status | Fixed | Freshly prepared |
| Species compatibility | Human and mouse | Multiple species |
| Cell throughput | Up to 10,000 cells | Up to 10,000 cells |
| Transcriptome capture | Transcriptome probes | PloyT  enrichment |
| Minimum Sequencing depth | 10K reads/cell | 20K reads/cell |