Ultra-low input mRNA sequencing (Ultra-low input mRNA-seq)

This sequencing service is able to generate high-quality libraries directly from live cells (100-1,000 cells) or 1-10 ng of total RNA. It provides the excellent sensitivity needed to obtain full-length transcript information from high-quality total RNA (RIN >8) or intact cells by using oligo(dT) priming. Through even gene-body coverage and accurate representation of GC-rich transcripts, this chemistry enables reliable analysis of transcript isoforms, gene fusions, point mutations, and more.

**Highlights**

* provide a solution for the samples with limit material
* an alternative method to supplement single-cell RNA sequencing with lower price



**Sample submission requirements**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Service | Sample Type | Recommend Amount | Minimum Amount | Minimum concentration | Quality |
| Ultra-low input mRNA-seq | Total RNA | 10 ng | 7 ng | 1 ng/ul | Recommend: RIN>8Required: RIN>7  |
| Live cells | 1000-100 cells | 100 cells |  | Cell viability: >85% |

* RIN stands for RNA integrity number, which is evaluated by measuring the ratio of 28S:18S
* Concentration must be measured by Qubit
* We recommend to sort live cells at UTH flow cytometry core (<https://www.uth.edu/imm/service-centers/flow-cytometry/> )
* The core has the rights to determine if the samples are qualified for the experiment
* Please check the core (cgc@uth.tmc.edu or 713-500-7933) for more information.

**Service workflow**



**Useful documents**

* SMART-Seq v4 Ultra Low Input RNA KIt
* SMART-Seq v4 PLUS Kit