**Baylor College of Medicine**

**Genomic & RNA Profiling Core Facility**

**Services Price List**

*Effective December 2024*

***PLEASE NOTE:***

*All prices listed are for internal Baylor College of Medicine researchers with the following exceptions:*

* *Dan L. Duncan Comprehensive Cancer Center and TMC Digestive Disease members (DLDCCC/DDC price list below BCM price list)*
* *External institutions and commercial companies, please contact* [*GARPcore@bcm.edu*](mailto:GARPcore@bcm.edu) *to inquire about prices.*
* ***Regular Baylor Pricing***

|  |  |  |  |
| --- | --- | --- | --- |
| **Service** | **Read Configuration** | **Reads  per sample** | **Cost  per sample** |
| 3’ Quant RNA-Seq (< 25 samples per batch) | SR 75 | +10M | $250 |
| 3’ Quant RNA-Seq (>= 25 samples per batch) | SR 75 | +10M | $220 |
|  |  |  |  |
| Total RNA-Seq with ribodepletion (< 25 samples per batch) | PE 100 | +50M | $450 |
| Total RNA-Seq with ribodepletion (>= 25 samples per batch) | PE 100 | +50M | $350 |
|  |  |  |  |
| PolyA-selected RNA-Seq | PE 100 | +20M | $250 |
|  |  |  |  |
| micro RNA-Seq (< 48 samples per batch) | SR 75 | +10M | $350 |
| micro RNA-Seq (>= 48 samples per batch) | SR 75 | +10M | $250 |
|  |  |  |  |
| Multiplexed RNA modification sequencing (<24 samples/batch) | PE100 | 25M + 25M | $750 |
| Multiplexed RNA modification sequencing (>=24 samples/batch) | PE100 | 25M + 25M | $715 |
|  |  |  |  |
| ChIP-Seq (< 25 samples per batch) | SR 75 | +50M | $270 |
| ChIP-Seq (>= 25 samples per batch) | SR 75 | +50M | $250 |
|  |  |  |  |
| CUT&RUN (<20 samples per batch) | SR 75 | +10M | $400 |
| CUT&RUN (>= 20 samples per batch) | SR 75 | +10M | $360 |
|  |  |  |  |
| Whole Genome Bisulfite Sequencing | PE 150 | 30X | $1,550 |
|  |  |  |  |
| 10X Visium GEX, 6.5mm, 50 µm (< 16 samples per batch) | As required | 100M | $2,170 |
| 10X Visium GEX, 6.5mm, 50 µm (>= 16 samples per batch) | As required | 100M | $1,990 |
|  |  |  |  |
| 10X Visium GEX, 11mm, 50 µm (< 8 samples per batch) | As required | 300M | $4490 |
| 10X Visium GEX, 11mm, 50 µm (>= 8 samples per batch) | As required | 300M | $3900 |
|  |  |  |  |
| 10X Visium HD 6.5mm (< 16 samples per batch) | As required | 300M | $3,850 |
| 10X Visium HD 6.5mm (>= 16 samples per batch) | As required | 300M | $3,550 |
|  |  |  |  |
| 10X Single Cell Prepared Libraries | As required | 50M | $280 |
| 10X Single Cell Prepared Libraries | As required | 100M | $540 |
| 10X Single Cell Prepared Libraries | As required | 200M | $900 |
| 10X Single Cell Prepared Libraries | As required | 300M | $1,250 |
|  |  |  |  |
| NovaSeq 6000, S4 flow cell (2.5B reads), 300 cycles, 1 lane | As desired | N/A | $4,800 |
|  |  |  |  |
| Nanopore Library Prep (cDNA-Seq, WGS) | As desired | N/A | $200 |
| Oxford Nanopore PromethION (1 flow cell) | N/A | N/A | $1,300 |

* ***Dan L. Duncan Comprehensive Cancer Center Member Pricing***

***PLEASE NOTE:***

* *Additional factors may necessitate deeper sequencing for any of the applications listed.*
* *To receive pricing information for other applications please contact* [*GARPcore@bcm.edu*](mailto:GARPcore@bcm.edu)*.*

|  |  |  |  |
| --- | --- | --- | --- |
| **Service** | **Read Configuration** | **Reads  per sample** | **Cost  per sample** |
|  |  |  |  |
| 3’ Quant RNA-seq (< 48 samples per batch) | SR 75 | +10M | $230 |
| 3’ Quant RNA-seq (>= 48 samples per batch) | SR 75 | +10M | $200 |
|  |  |  |  |
| Total RNA-Seq with ribodepletion (< 25 samples per batch) | PE 100 | +50M | $430 |
| Total RNA-Seq with ribodepletion (>= 25 samples per batch) | PE 100 | +50M | $330 |
|  |  |  |  |
| PolyA-selected RNA-Seq | PE 100 | +20M | $210 |
|  |  |  |  |
| micro RNA-Seq (< 48 samples per batch) | SR 75 | +10M | $310 |
| micro RNA-Seq (>= 48 samples per batch) | SR 75 | +10M | $230 |
|  |  |  |  |
| Multiplexed RNA modification sequencing (<24 samples/batch) | PE100 | 25M + 25M | $700 |
| Multiplexed RNA modification sequencing (>=24 samples/batch) | PE100 | 25M + 25M | $670 |
|  |  |  |  |
| ChIP-Seq (< 25 samples per batch) | SR 75 | +50M | $250 |
| ChIP-Seq (>= 25 samples per batch) | SR 75 | +50M | $230 |
|  |  |  |  |
| CUT&RUN (<20 samples per batch) | SR 75 | +10M | $350 |
| CUT&RUN (>= 20 samples per batch) | SR 75 | +10M | $320 |
|  |  |  |  |
| Whole Genome Bisulfite Sequencing | PE 150 | 30X | $1,500 |
|  |  |  |  |
| 10X Visium GEX, 6.5mm, 50 µm (< 16 samples per batch) | As required | 100M | $2,120 |
| 10X Visium GEX, 6.5mm, 50 µm (>= 16 samples per batch) | As required | 100M | $1,950 |
|  |  |  |  |
| 10X Visium GEX, 11mm, 50 µm (< 8 samples per batch) | As required | 300M | $3900 |
| 10X Visium GEX, 11mm, 50 µm (>= 8 samples per batch) | As required | 300M | $3860 |
|  |  |  |  |
| 10X Visium HD 6.5mm (< 16 samples per batch) | As required | 300M | $3,550 |
| 10X Visium HD 6.5mm (>= 16 samples per batch) | As required | 300M | $3,500 |
|  |  |  |  |
| 10X Single Cell Prepared Libraries | As required | 50M | $250 |
| 10X Single Cell Prepared Libraries | As required | 100M | $490 |
| 10X Single Cell Prepared Libraries | As required | 200M | $850 |
| 10X Single Cell Prepared Libraries | As required | 300M | $1,190 |
|  |  |  |  |
| NovaSeq 6000, S4 flow cell (2.5B reads), 300 cycles, 1 lane | As desired | N/A | $4,750 |
|  |  |  |  |
| Nanopore Library Prep (cDNA-Seq, WGS) | As desired | N/A | $175 |
| Oxford Nanopore PromethION (1 flow cell) | N/A | N/A | $1,250 |
|  |  |  |  |

***PLEASE NOTE:***

* *Additional factors may necessitate deeper sequencing for any of the applications listed.*
* *To receive pricing information for other applications please contact* [*GARPcore@bcm.edu*](mailto:GARPcore@bcm.edu)*.*

|  |  |  |
| --- | --- | --- |
| **Nanostring Processing** |  | **Cost per sample** |
| Nanostring for GEX | Regular | $34 |
| DLDCCC\* | $24 |

+Prices do not include NanoString reagents and master kits. Contact [GARPcore@bcm.edu](mailto:GARPcore@bcm.edu) for a quote.

\* Dan L. Duncan Comprehensive Cancer Center Member Pricing

|  |  |
| --- | --- |
| **DNA Shearing** | |
| **Instrument** | **Cost per hourly use** |
| Covaris LE220 | $50 |