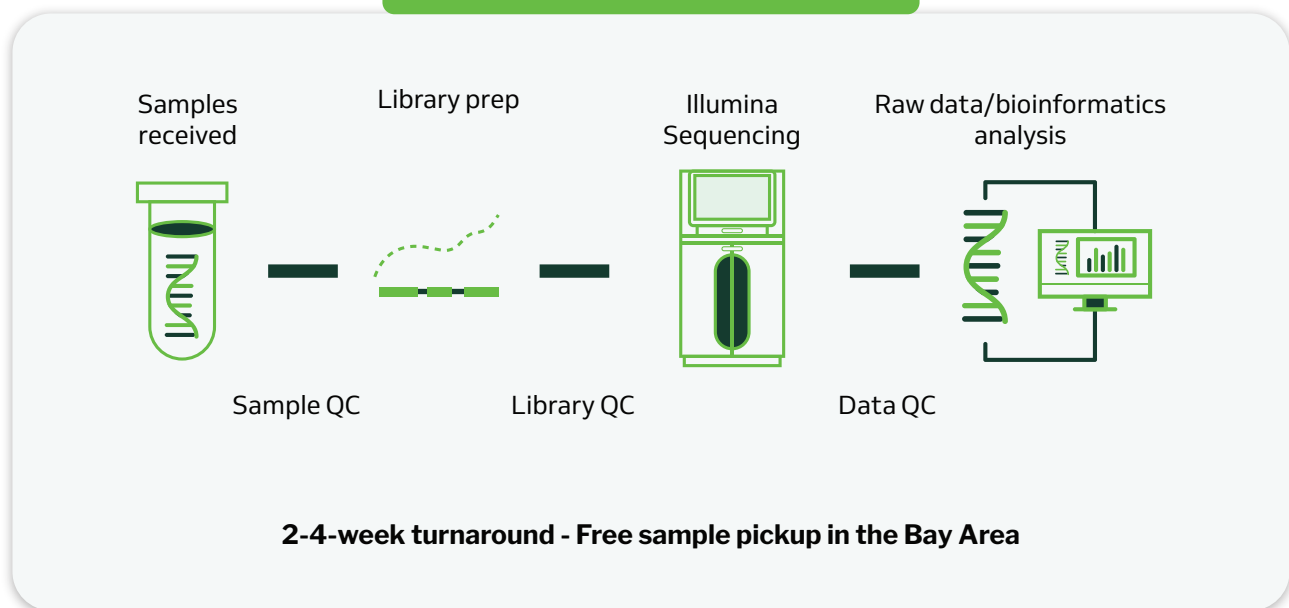


# End-to-end RNA Seq solutions from sample to insight

## RNA Service Workflow



## Advantages of Signios RNA sequencing services

Signios Bio is a scientist-led genomics services company with a dedicated lab in Foster City, CA. We offer flexible, end-to-end workflows to accommodate your research needs.

## Why choose us?

- We accept tissue, cells, FFPE, blood, degraded/low-input RNA samples, and more.
- Free sample QC consultation to optimize library preparation for your samples.
- Fast turnarounds from our California lab.
- Advanced bioinformatics support from study design to publication-ready data.
- Multi-omics integration: genomic, transcriptomic, and proteomic data.

## Library prep options

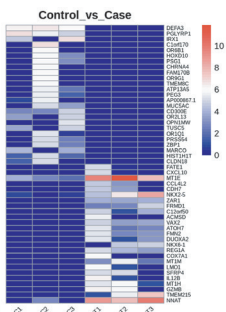
Signios Bio's team will guide you on the best library prep solutions for your research goal with sample compatibility based on quantity and quality.

| Library prep kit                                      | RNA obtained                    | RNA input required      | Quality threshold | Accepted sample types                                                                                                                                                                                                |
|-------------------------------------------------------|---------------------------------|-------------------------|-------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Illumina stranded mRNA Prep                           | mRNA, stranded                  | 0.05 µg in 25 µl        | RIN >7            | <ul style="list-style-type: none"> <li>- Cells (&gt;50,000, frozen/pelleted)</li> <li>- Tissue (60 mg fresh or frozen)</li> <li>- Blood (3 mL recommended)</li> <li>- FFPE slides &amp; blocks</li> </ul>            |
| Takara SMART -Seq mRNA                                | mRNA, non-stranded              | 10 pg – 10 ng in 15 µl  | RIN >7            | <ul style="list-style-type: none"> <li>- Cells (&gt;10,000 rec.; 1–1,000 low input)</li> <li>- Tissue (60 mg fresh or frozen)</li> <li>- Purified RNA</li> </ul>                                                     |
| Illumina Stranded Total RNA w/ RiboZero Plus (Globin) | Total RNA, stranded             | 0.2 µg in 25 µl         | DV200 >25         | <ul style="list-style-type: none"> <li>- Cells (min. 1×10<sup>6</sup>, frozen/pelleted)</li> <li>- Tissue (60 mg fresh or frozen)</li> <li>- Blood (3 mL recommended)</li> <li>- FFPE slides &amp; blocks</li> </ul> |
| Takara SMART -Seq Total RNA Pico Input (ZapR)         | Total RNA, stranded (low input) | 250 pg – 10 ng in 15 µl | DV200 >25         | <ul style="list-style-type: none"> <li>- Cells (&gt;10,000 rec.; 50–1,000 low input)</li> <li>- Tissue (60 mg fresh or frozen)</li> <li>- FFPE slides &amp; blocks</li> <li>- Purified RNA</li> </ul>                |

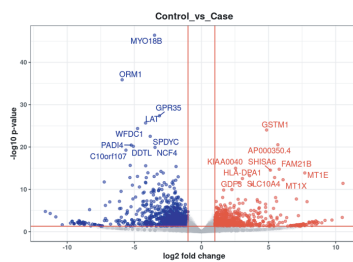
## Advanced bioinformatics analysis

Choose the analysis package that fits your project scope, from raw data delivery to full differential expression, pathway analysis, and custom pipelines.

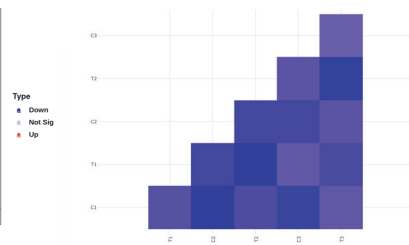
| Basic                                                                                         | Standard                                                                                                                                                                                                                       | Advanced                                                                                                                                                                                                                 | Specialized                                                                                                                                                |
|-----------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <ul style="list-style-type: none"> <li>- Data QC report</li> <li>- Raw FASTQ files</li> </ul> | <ul style="list-style-type: none"> <li>- All Basic outputs</li> <li>- Alignment (BAM) file</li> <li>- Germline VCF</li> <li>- Germline variant annotation</li> <li>- Low-frequency variant calling &amp; annotation</li> </ul> | <ul style="list-style-type: none"> <li>- All Standard outputs</li> <li>- Differential gene expression</li> <li>- Pathway analysis &amp; gene ontology</li> <li>- TME analysis</li> <li>- Fusion gene analysis</li> </ul> | <ul style="list-style-type: none"> <li>- Custom analysis package</li> <li>- Project-specific bioinformatics</li> <li>- Billed at an hourly rate</li> </ul> |



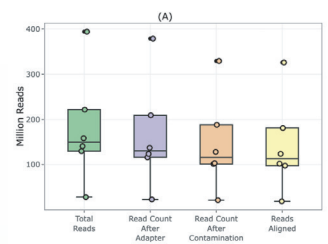
Heatmap



Volcano Plot



Correlation Plot



Read filtration stats

## Ready to get started?

Contact us today for pricing and to begin planning your customized solution.

✉ info@signiosbio.com

☎ (888) 440-0954

📍 348 Hatch Drive, Foster City, CA 94404, USA