

Transcriptomics

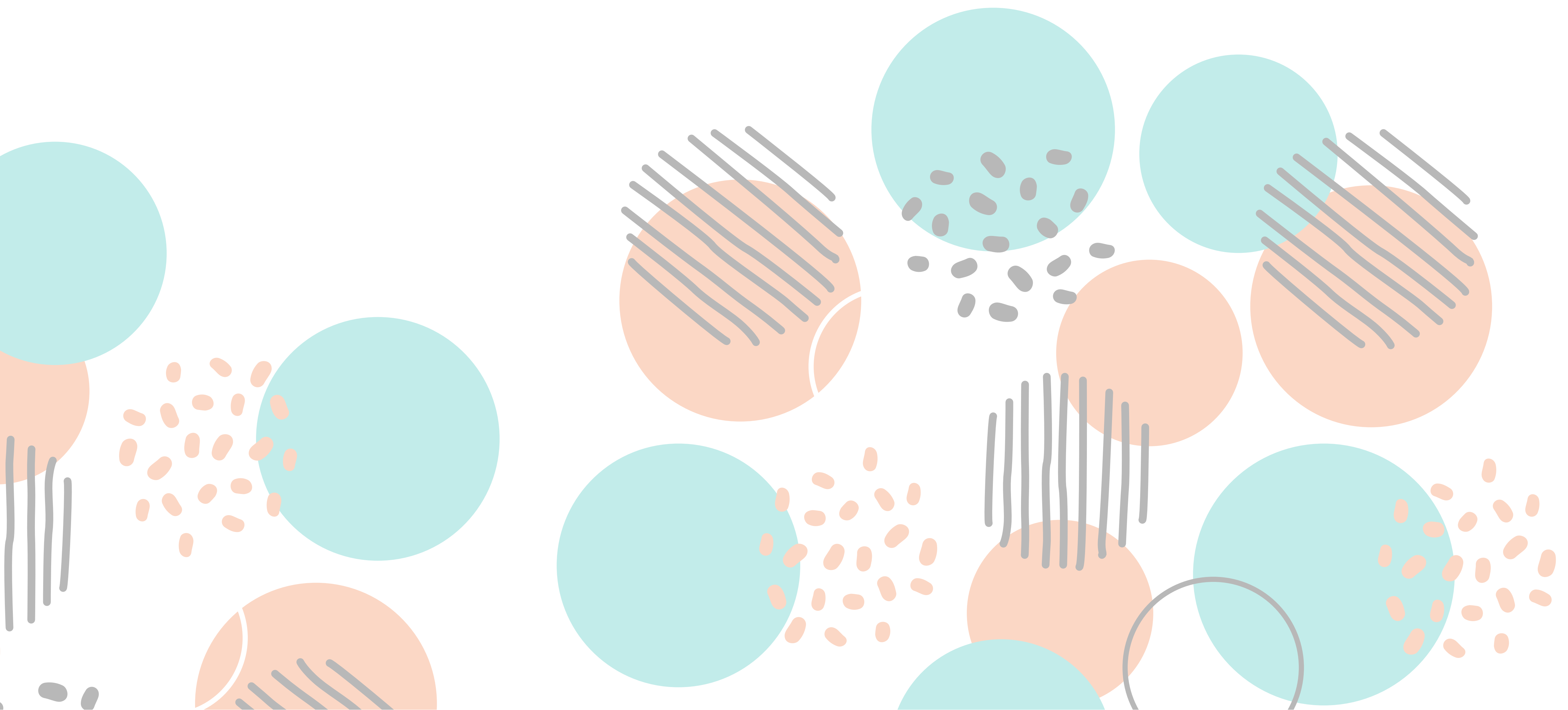
ONE MOLECULE, INFINITE TOOLS





Our continuous commitment to follow and test the latest protocols and tools, as well as to develop new ones, assures the implementation of the state-of-the-art procedures and the optimization of the experimental design.

A quality-centric RNA-Seq service.

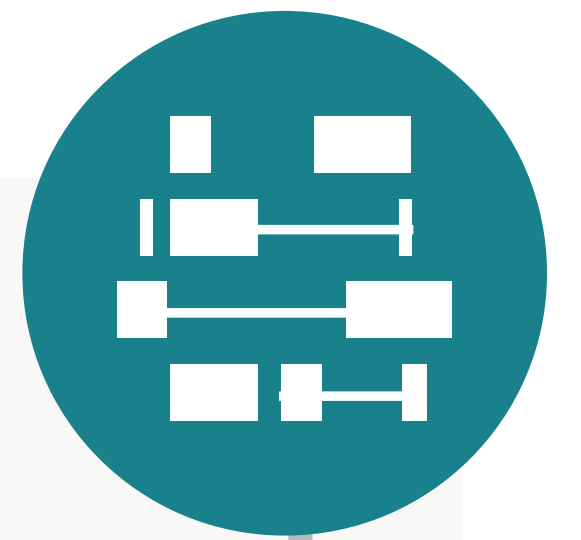


mRNA-Seq / total RNA-Seq

One size does not fit all.

- Stranded libraries
- Depletion of unwanted transcripts
- UMI-tagged libraries
- Ultra-low input
- rRNA depletion

We apply a wide portfolio of kits and procedures to meet specific needs of each project while providing pre- and post-experiment consultancy.



Single-cell RNA

We manage customized experimental designs and collaborate on dedicated sample logistics and scheduling to ensure high-quality results.

- Simultaneously processing up to 80,000 cells
- Cell hashing for sample batching and costs reduction
- Antibody tagging for cell population discriminant analysis
- Vitality assessment and count for high-quality experiments
- Fresh, frozen and methanol-fixed cells
- Free basic bioinformatics

Our laboratories can host external scientists if special preparation of samples (tissue dissociation, chemical treatment) is required.





Long-read RNA-Seq: end-to-end sequencing of entire RNA

Give more value to your experiments by adopting latest resources in RNA-Seq world.

- Full-length transcripts without assembly
- Discovery and characterization of isoforms
- Characterization of lncRNA
- Defining full exonic structure of complex genes
- Improving genome annotation
- Targeted isoform sequencing

By adopting long- and linked-reads technologies we are offering the possibility for discovery and characterization of RNA isoforms that are difficult to observe by using short read cDNA methods.

Our protocol for the direct assessment of clinical samples with low virus abundance is suitable for discovering common and new viruses, distinguishing co-infections, and dissecting virus-host interactions



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