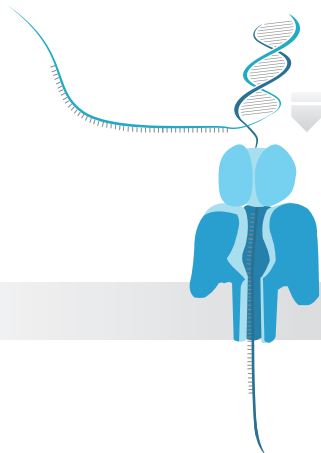


Full-length Transcriptome Sequencing–Nanopore

Product Introduction

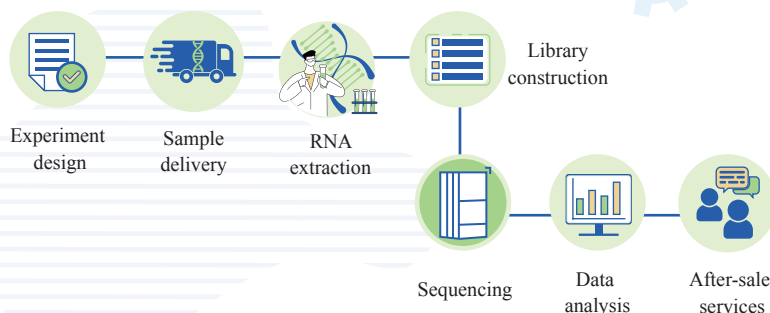
RNA sequencing has been an invaluable tool for comprehensive transcriptome analysis. Doubtlessly, traditional short-read sequencing achieved numerous important developments here. Nevertheless, it often encounters limitations in full-length isoform identifications, quantification, and PCR bias. Nanopore sequencing distinguishes itself from other sequencing platforms, in that the nucleotides are read directly and generate long reads at tens of kilobases. This empowers direct read-out crossing full-length transcripts and tackling the challenges in isoform-level studies.

Technical Features



https://nanoporetech.net/how_it_works

Service Workflow



Bioinformation List

- Full-length transcript assessment and transcript de-redundance;
- lncRNA and target gene prediction;
- SSR, CDS, TF, AS, APA analysis;
- Expression quantification and differential expression analysis;
- Functional annotation and enrichment analysis.

Service Advantages

- Nanopore technology enables scalable and high-throughput sequencing, allowing for the analysis of large and complex transcriptomes. This makes it suitable for studying diverse biological systems and samples.
- Accurately identify the alternative splicing (AS), alternative polyadenylation (APA), fusion genes, lncRNA, and their target genes that cannot be accurately identified by NGS.
- A total of 550+ Nanopore full-length transcriptome projects have been completed, and a total of 7700+ samples have been completed.
- BMKCloud facilitated data interpretation containing 20 personalized analyzing tools.
- After-sale services: After-sale services are valid for 3 months upon project completion, including project follow-up, trouble-shooting, results Q&A, etc.

Service Specifications

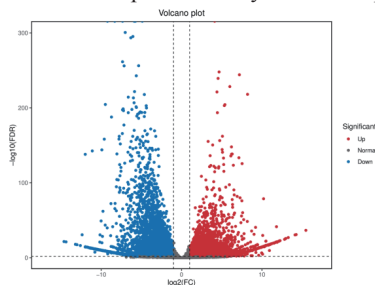
Library	Platform	Recommended data	Data QC	Time
PolyA enriched	Nanopore PromethION P48	6 / 12 Gb	Full-length ratio > 70% Average quality score: Q10	35 days

Sample Requirements

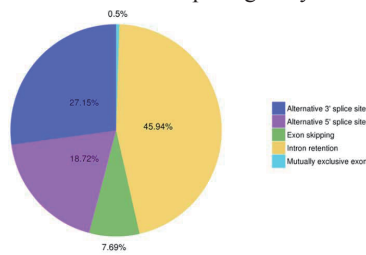
Amount (μg)	Purity	Integrity
Conc. ≥ 100 ng/μL; Volume ≥ 10 μL; Total ≥ 0.6 μg	OD260/280=1.7-2.5 OD260/230=0.5-2.5 Limited or no protein or DNA contamination shown on gel.	For plants: RIN ≥ 7.0; For animals: RIN ≥ 7.5; 5.0 ≥ 28S/18S ≥ 1.0; limited or no baseline elevation

Demo Results

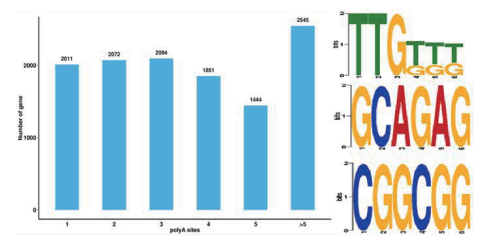
1. Differential expression analysis-Volcano plot



2. Alternative splicing analysis



3. Alternative poly-adenylation (APA)



Featured Publications

Year	Journal	Paper	Article	DOI
2023	Fish & shellfish immunology	Full-length transcriptome sequencing of lymphocytes respond to IFN-γ reveals a Th1-skewed immune response in flounder (<i>Paralichthys olivaceus</i>)	Immune response	10.1016/j.fsi.2023.108636
2023	Journal of Genetics and Genomics	Epigenetic and transcriptional activation of the secretory kinase FAM20C as an oncogene in glioma	Disease treatment	10.1016/j.jgg.2023.01.008
2023	Stem Cell Research & Therapy	Nano-seq analysis reveals different functional tendency between exosomes and microvesicles derived from hUMSC	Disease treatment	10.1186/s13287-023-03491-5



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