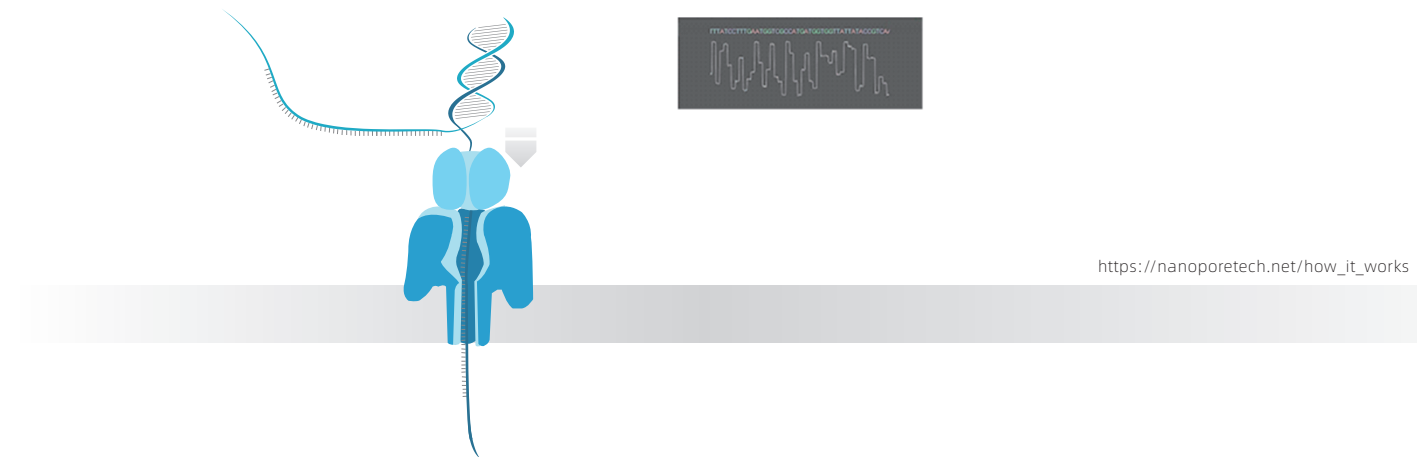


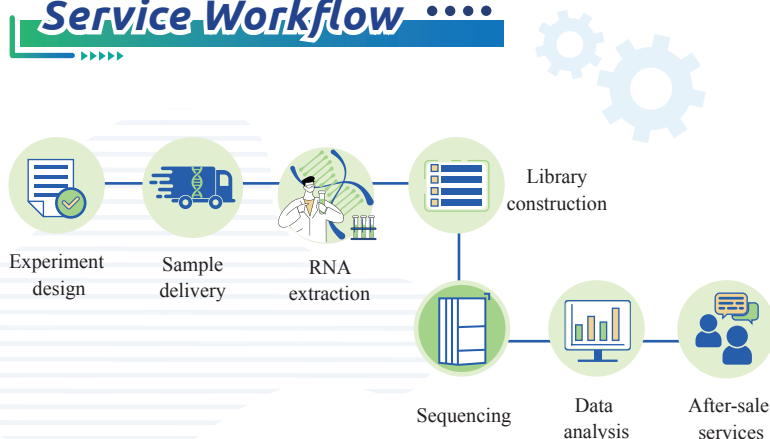
Full-length Transcriptome Sequencing–Nanopore

While traditional short-read sequencing has made significant strides, it falls short in identifying full-length isoforms, quantification, and PCR bias. Enter Nanopore sequencing—generating long reads spanning tens of kilobases. With BMKGENE, experience the power of full-length isoform sequencing, overcoming challenges in isoform-level studies and unlocking comprehensive transcriptome analysis.

Technical Features



Service Workflow



Bioinformatics

- 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.
- Accurate identification of the alternative splicing (AS), alternative polyadenylation (APA), fusion genes, and lncRNA. And realize isoform level expression quantification.
- Extensive experience: A total of 800+ Nanopore full-length transcriptome projects have been completed, and a total of 7700+ samples have been completed in BMKGENE.
- The expression quantification at the isoform level can be realized by combining NGS data.
- After-sale services: After-sale services are valid for 3 months upon project completion, including project follow-up, trouble-shooting, results Q&A, etc.

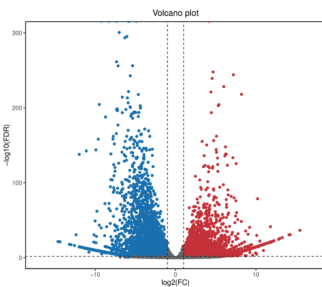
Service Specifications

Library	Platform	Recommended Data	Data Quality
PolyA enriched	Nanopore PromethION 48	6 /12 Gb	Full-length ratio > 70%

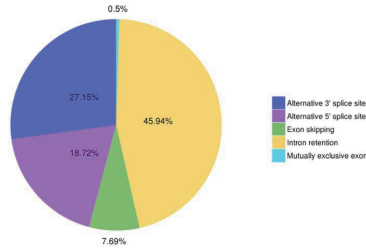
Sample Requirements

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

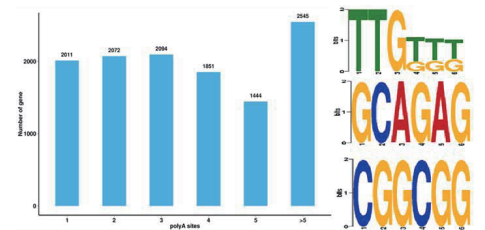
Demo Results



1. Differential expression analysis-Volcano plot



2. Alternative splicing analysis



3. Alternative poly-adenylation (APA)

Featured Publications

Year	Journal	Article	Applications	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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