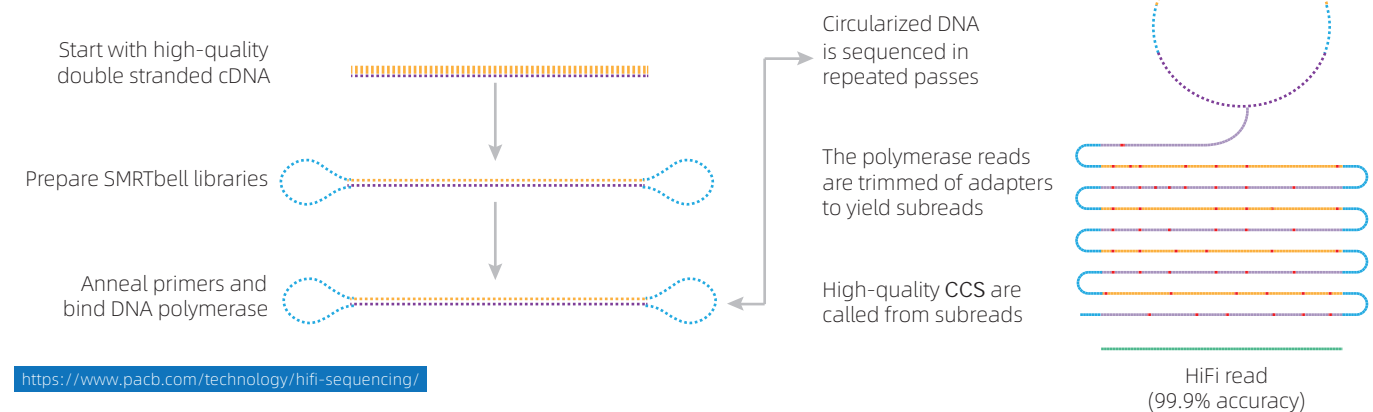


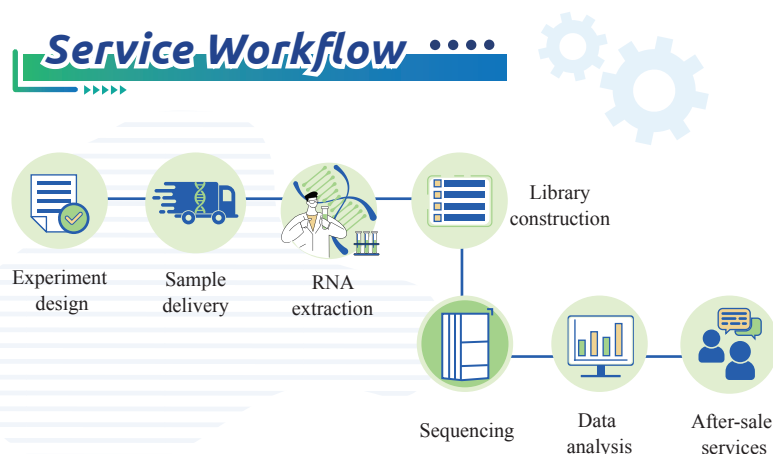
# Full-length Transcriptome Sequencing–PacBio

Harnessing the PacBio sequencer's long-read capability, BMKGENE sequences full-length cDNA molecules, eliminating errors in transcript assembly. Our service constructs unigene sets with isoform-level precision, serving as a robust "reference genome" at the isoform level. Joint with next-generation sequencing data, BMKGENE offers precise quantification of isoform-level expression.

## Technical Features



## Service Workflow



## Bioinformatics

- Assessment on full-length transcripts and isoform clustering;
- LncRNA and target gene prediction;
- SSR, CDS, SNP, TF, AS, APA analysis;
- Expression quantification analysis (NGS mRNA data required);
- Functional annotation and enrichment analysis.

## Service Advantages

- **High accuracy:** With PacBio circular consensus sequencing, the error rates have been greatly reduced, making it more reliable for accurate transcriptome analysis.
- PacBio sequencing is particularly useful for isoform identification and characterization. It can accurately resolve transcript isoforms and identify alternative splicing events.
- Extensive experience: A total of 1000+ PB full-length transcriptome projects have been completed, with 2000+ completed samples. We have published articles with high-impact factors in NG, NC, PNAS, etc.
- PacBio "2+3" strategy for accurate isoform-level quantification.
- After-sale services: After-sale services are valid for 3 months upon project completion, including project follow-up, trouble-shooting, results Q&A, etc.

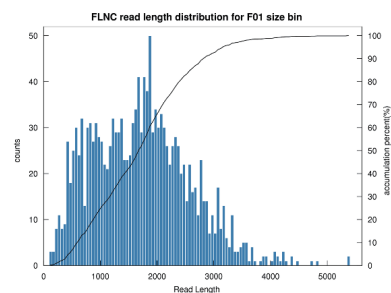
## Service Specifications

Library	Platform	Recommended Data
PolyA enriched mRNA CCS library	PacBio sequel II	20 /40 Gb

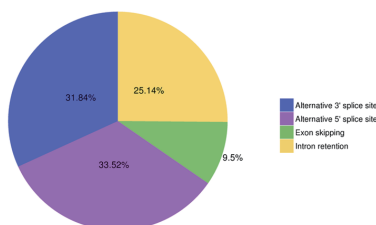
## Sample Requirements

Amount (μg)	Purity	Integrity
Conc. ≥ 120 ng/μL; Volume ≥ 10 μL; Total ≥ 0.75 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 ≥ 7.5; For animals: RIN ≥ 8.0; 5.0 ≥ 28S/18S ≥ 1.0; limited or no baseline elevation

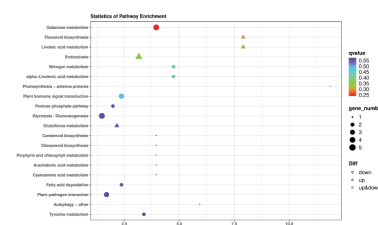
## Demo Results



1. FLNC length distribution



2. Alternative splicing analysis



3. KEGG pathway enrichment analysis

## Featured Publications

Year	Journal	Article	Applications	DOI
2023	Genomics	Comparative analysis of PacBio and ONT RNA sequencing methods for Nempilema Nomurai venom identification	Technical comparison	10.1016/j.ygeno.2023.110709
2022	International Journal of Molecular Sciences	Dynamic changes in ascorbic acid content during fruit development and ripening of actinidia latifolia (an ascorbate-rich fruit crop) and the associated molecular mechanisms	Developmental regulation	10.3390/ijms23105808
2022	Communications Biology	Effective prediction of biosynthetic pathway genes involved in bioactive polyphyllins in Paris polyphylla	Synthetic biology	10.1038/s42003-022-03000-z



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