

Full-length Transcriptome Sequencing-PacBio

Product Introduction

De novo Iso-Seq takes advantage of PacBio sequencer in read length, which enables sequencing of full-length cDNA mol -ecules. This completely avoids any errors generated in transcript assembly steps and constructs unigene sets with isoform -level resolution. This unigene set provides powerful genetic information as the "reference genome" at the transcriptome level. In addition, combined with next-generation sequencing data, this service empowers an accurate quantification of isoform-level expression.



<u>Service,Advantages ••••</u>

- 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.
- ▶ A total of 450+ PB full-length transcriptome projects have been completed, with 700+ completed samples. We have published articles with high-impact factors in NG, NC, PNAS, etc.
- BMKCloud facilitated data interpretation containing 16 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 mRNA CCS library	Pacbio sequel II	20 /40 Gb	FLNC (%)≥75%	40 days

<u>Sample Requirements</u> ·····

Amount (µg)	Purity	Integrity
Conc. \geq 120 ng/µL; Volume \geq 10 µL; Total \geq 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



3. KEGG pathway enrichment analysis



Featured Publications

Year	Journal	Paper	Article	DOI
2023	Genomics	Comparative analysis of PacBio and ONT RNA sequencing methods for Nemopilema 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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