

# Whole Genome Re-Sequencing (WGS)

BMKGENE offers professional whole-genome sequencing services, backed by extensive species experience and a team of experts. Our mature workflows for next-generation and long-read sequencing enable compre -hensive analysis of genetic variation at different levels, including SNP, InDel, SV, CNV.

Comparison		WGS-NGS	WGS-Long Reads	
Platform		Illumina	Nanopore/PacBio	
Read	length	PE150	> 10 kb	
The dominant type of detected variation		SNP, InDel	SNP, InDel (PacBio), SV, CNV	
Base mo	Base modification		Yes	
SV detection	Accuracy	-	High	
	ction Sensitivity		High	
	Complexity	-	Yes	







- Raw data QC
- Reference genome alignment
- SNP calling and annotation
- SV calling and annotation
- CNV calling and annotation
- Small InDel calling and annotation Genome wide distribution of variations
  - Non-synonymous mutations
  - Function annotation on mutated genes

Service,Advantages ·····

- WGS enables the identification of genetic variatio -ns associated with different phenotypic traits.
- ▶ WGS provides valuable insights into the mechani -sms underlying evolution.
- Extensive experience in genome sequencing for over **1000** species.
- Over 800 published cases with an accumulative impact factor of over 4000. •
- Comprehensive bioinformatics analysis on variation calling and function analysis.

# Service Specifications ·····





Pla	atform	Library	Recommended seq depth	
Illumina		PE150	For SNP, InDel calling $\ge 10x$	
		1 LIUU	For SV, CNV calling $\ge 30x$	
Nanopore		9 lth	For SV, CNV calling $\geq 20x$	
		8 KU	For base modification $\ge 30x$	
PacBio	CCS	15 kb	For SNP, SV, CNV calling $\geq 10x$	



## Sample,Requirements ....

Platform	Conc.(ng/µL)	Amount (ng)	Pur OD260/280	rity   OD260/230	Agarose gel
Illumina	≥1	≥30	-	-	1. Clear main band with no or limited
Nanopore	≥30	Depends on	1.7-2.2	≥1.5	degradation observed on gel.
PacBio CCS	≥50	10 μg/cell	1.7-2.2	1.8-2.5	contamination.





Circos diagram on SNP and InDel

GO classification

## Featured Publications

	A FMR processing and modification
	R Checrate and dynamics
-	C Creege production and conversion
	0 Cell syste control, cell division, divornacione partitione
	E Anixo acid haneport and metabolism
	P. Nucleotide transport and metabolism
	G: Callofyphate transport and netidedism
	H. Coencyme traveport and metabolism
e-	Epid transport and metabolian
	2. Translation, ribosomal structure and biogeneois
	K Taraciptor
	L: Replication, recombination and repair
	M. Cet watiment/raneisn-whipe biogenesis
	N: Out waitly
	O Partraneatoral nodificator, provintantovic, diape
	P. Inogenic on Tanepot and metabolish
	Q. Becondary netabolities Unoperheats, hanaport and ca
	R. General function predictor-only
	3 Funder utroin
	T. Signal Versiduation methanisme
	U Interestular halfoking, secretion, and resicular hang
	V Celense montaname
	Vc Extracalizar structures
	Y. Nuclear structure

COG classification



KEGG pathway

Journal	Article	Applications
Nature Genetics	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars	Plant WGS
Nature Communications	Genome sequences reveal global dispersal routes and suggest convergent genetic adaptations in seahorse evolution	Animal WGS

### BMKGENE

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