Novogene

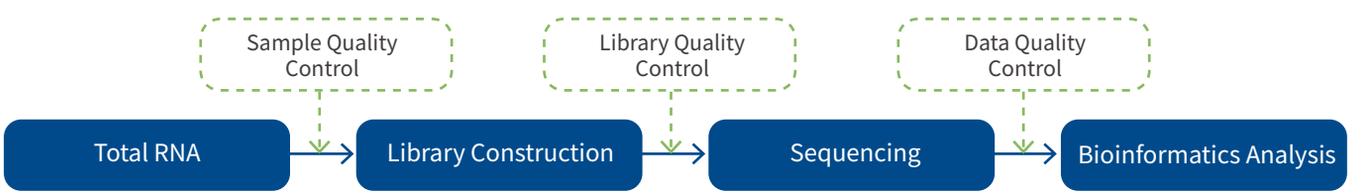
Prokaryotic RNA Sequencing Solution

Prokaryotic RNA sequencing uses next generation sequencing (NGS) to reveal the presence and quantity of RNA at a given moment, by analyzing the changing cellular transcriptome. Novogene' s prokaryotic RNA sequencing, specifically aims at prokaryotes with reference genomes, providing you with transcriptome profiling, gene structure analysis, etc. It has been widely applied to basic science research, drug research and development, and more.

The Novogene Advantage

- Extensive experience with more than 200,000 samples successfully sequenced
- Unsurpassed data quality with a guaranteed Q30 ⩾80%, exceeding Illumina's official benchmark
- Free in-house software to visualize data flexibly per project needs

Project Workflow



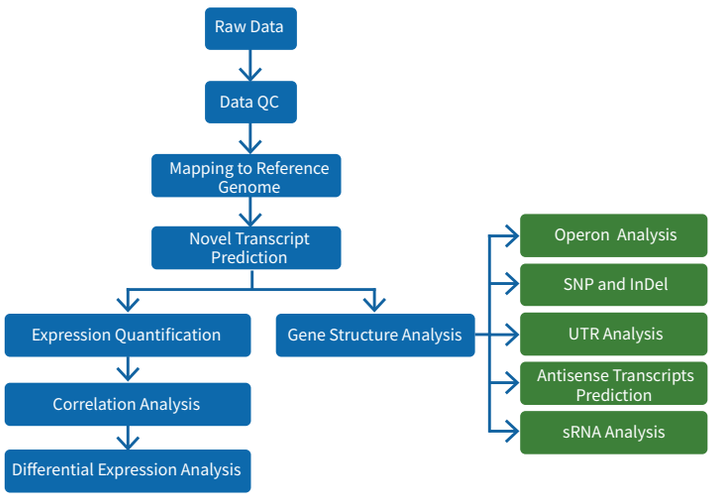
Service Highlights

Sequencing Strategy:
NovaSeq 6000 platform, paired-end 150 bp, 250-300 bp insert cDNA library, 2 Gb raw data/sample

Turnaround Time:
18 working days after verification of sample quality without data analysis (depending on sample size)

Data Analysis:
Standard analysis and customized analysis, assisting you to realize your research objectives easily and cost-effectively

Analysis Pipeline



Note: The standard analysis pipeline above is for a species with a reference genome, and if you work on a species without a reference genome, please consult us for solutions.

Novogene Powered Literature

Competitive control of endoglucanase gene *engXCA* expression in the plant pathogen *Xanthomonas campestris* by the global transcriptional regulators HpaR1 and Clp

Background: Transcriptional regulators are key players in pathways. However, how such transcriptional regulatory networks interact in bacterial plant pathogens is poorly understood.

Results and Conclusion: The impact of mutation of hpaR1 on the *Xanthomonas campestris* pv. *campestris (Xcc)* transcriptome was established by RNA sequencing. The findings suggest that HpaR1 affects the expression of a larger number of genes, and a subset of genes are controlled by both HpaR1 and Clp (Table 1). This study describes how two global transcriptional regulators, HpaR1 and Clp, co-regulate a subset of virulence genes in *Xcc.* The RNA-seq helps to revel the influence of HpaR1 on the global transcriptome of *Xcc.*

Table 1.* HpaR1 is a global regulatory protein that affects the expression of a number of genes overlapping with the Clp protein.

Functional category	ORF number in strain 8004(AT33913)	Gene name	Predicted product	Fold change *(hpaR1-/wt)*	Putative HpaR1/Clp co-binding sites
Cell envelope and cell structure	*XC_1459 (XCC2658)*	*phuR*	Outer membrane haemin receptor	2.11	
Energy and carbon metabolism	*XC_0279 (XCC0269)*		2,5-Diketo-d-gluconate reductase B	–2.63	GTGTGCGGAACGCT-GAATCCACACC
	XC_0281 (XCC0271)	*mocA*	Oxidoreductase	–2.80	
	XC_3683 (XCC0549)	*atpE*	F0F1 ATP synthase subunit C	–2.56	

* Only part of genes affected by HpaR1 are listed in this table. Please refer to the literature for more information.

Reference: GF Liu, HZ Su, HY Sun, *et al.* Competitive control of endoglucanase gene *engXCA* expression in the plant pathogen *Xanthomonas campestris* by the global transcriptional regulators HpaR1 and Clp[J]. *Molecular Plant Pathology,* 2019, 20(1): 51–68.

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