



Integrated Solution of Transcriptome sequencing

Transcriptome Sequencing— Comprehensive RNA investigation

Transcriptome Sequencing is defined as the high-throughput next generation sequencing technique, capable of fully and quickly acquiring the overall transcripts information including the mRNA information and non-coding RNA information in the specific tissues or organs of eukaryotic species under a certain status.

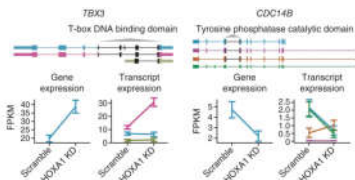
Service Type

mRNA
sequencing

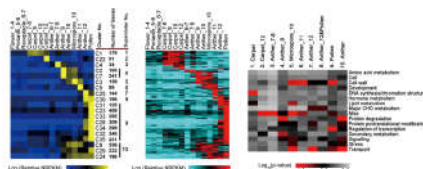
lncRNA
sequencing

CircRNA
sequencing

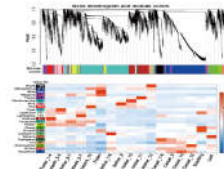
Advanced bio-information analysis



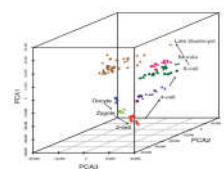
Transcript quantification analysis



Condition specific expression analysis

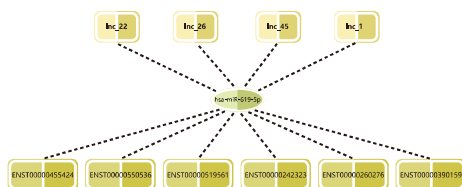


WGCNA analysis

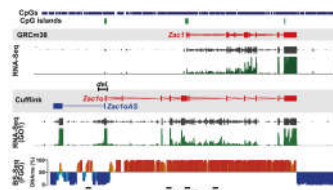


PCA analysis

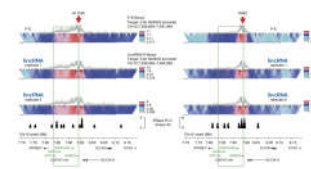
Multi-omics association analysis



LncRNA-miRNA-mRNA interaction network



Association analysis between RNA-seq and DNA methylation patterns



Association analysis between LncRNA-seq and Hi-C

Paper publications of cooperated partner

Journal	Title
<i>Journal of Cellular and Molecular Medicine</i>	Heterogeneous nuclear ribonucleoprotein K is associated with poor prognosis and regulates proliferation and apoptosis in bladder cancer
<i>Molecular Cell Research</i>	Deep sequencing reveals a global reprogramming of lncRNA transcriptome during EMT
<i>Cell Death and Disease</i>	Restricting the induction of NGF in ovarian stroma engenders selective follicular activation through the mTOR signaling pathway
<i>Nanotoxicology</i>	Cutaneous applied nano-ZnO reduce the ability of hair follicle stem cells to differentiate
<i>PLOS Pathogens</i>	Exosome-mediated miR-146a transfer suppresses type I interferon response and facilitates EV71 infection
<i>Cellular Physiology and Biochemistry</i>	Integrated High Throughput Analysis Identifies GSK3 as a Crucial Determinant of p53-Mediated Apoptosis in Lung Cancer Cells
<i>leukemia</i>	miR-34c-5p promotes eradication of acute myeloid leukemia stem cells by inducing senescence through selective RAB27B targeting to inhibit exosome shedding
<i>Cellular and Molecular Life Sciences</i>	HBeAg induces the expression of macrophage miR 155 to accelerate liver injury via promoting production of inflammatory cytokines
<i>Frontiers in Plant Science</i>	Transcriptome Profiling to Identify Genes Involved in Mesosulfuron-Methyl Resistance in <i>Alopecurus aequalis</i>
<i>Molecular Plant</i>	Circadian Evening Complex Represses Jasmonate-Induced Leaf Senescence in <i>Arabidopsis</i>

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