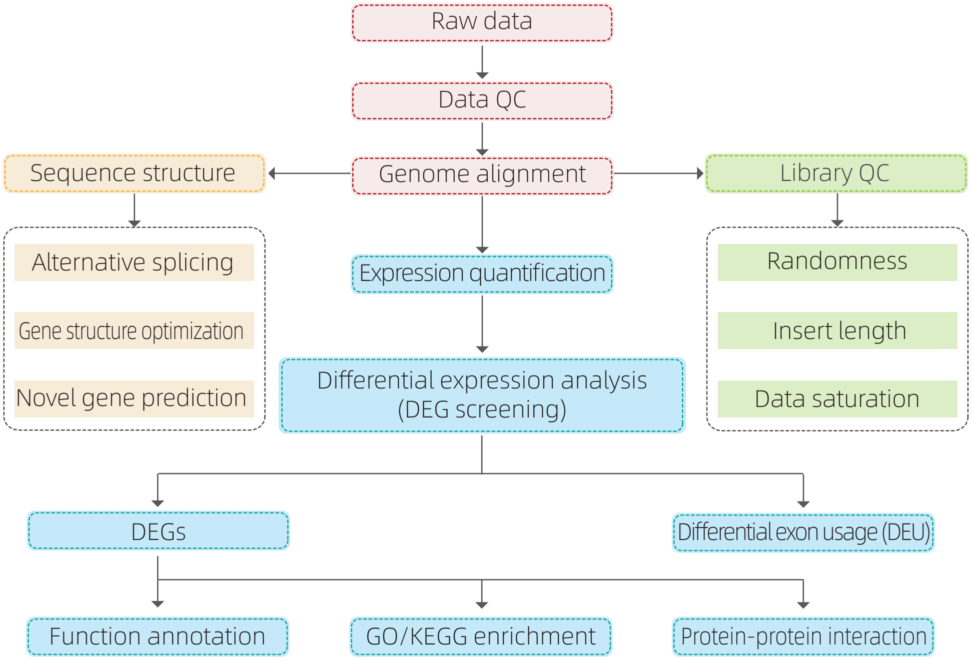
mRNA Sequencing (NGS)

BMKGENE

mRNA sequencing adopts next-generation sequencing technique (NGS) to capture the messenger RNA(mRNA) from Eukaryote at specific period that some special functions are activating.

Standard bioinformatics analyses include:

(1) Reference genome alignment
(2) Gene structure and novel gene prediction
(3) Gene expression quantification
(4) Differential expression analysis
(5) Function annotation, enrichment and interaction networks



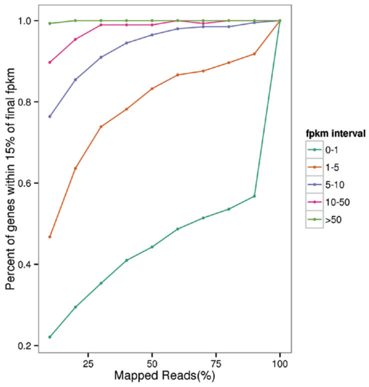
Service Advantages

1. Comprehensive bioinformatics including sequence structure, differential expression analysis and function interpretation using diverse database.
2. Experienced: processed over 200K samples, sample type include cell, tissue, body fluid and hair follicle et al.
3. Strict quality control system: strict QC standard of all steps in a project(Sample QC, library QC, data QC and NT Blast)

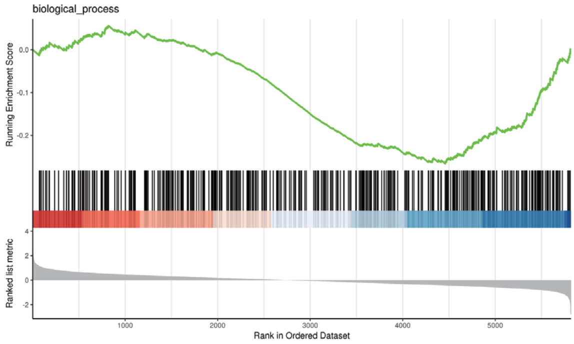
Service specifications

Purity	Integrity	Amount	Reads	Time
OD260/280: 1.7-2.5; OD260/230: 0.5-2.5;	For plants: RIN≥6.0; For animals: RIN≥6.5;	Conc. ≥20 ng/μL; Volume ≥ 10 μl; Total ≥ 0.5 μg	6 G/10 G	30 days

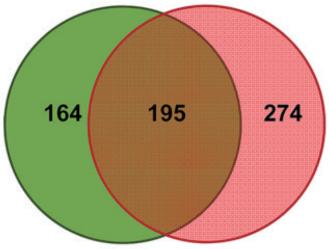
Domo Results



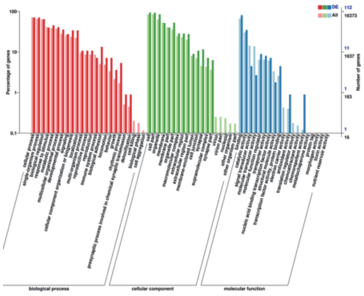
Data Saturation analysis



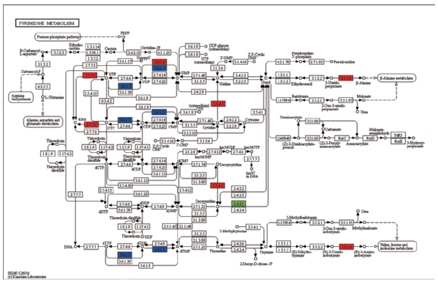
GSEA Analysis



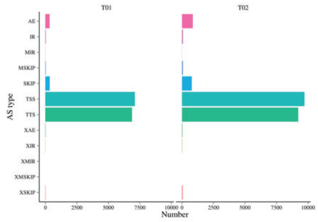
Venn diagram



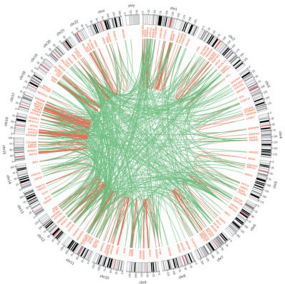
GO classifications



KEGG pathway



Alternative splicing



Fusion gene

Case Study

Title: Transcriptome analysis of bagging-treated red Chinese sand pear peels reveals light-responsive pathway functions in anthocyanin accumulation

1.In total, 8,870 differentially expressed genes were further analysed by a weighted gene coexpression network analysis and early-middle and late light responsive genes were identified.

2. The “blue” module was highly correlated with the total anthocyanin content ($r=0.93$, $p=2\times10-9$), and 11 structural genes involved in anthocyanin biosynthesis and transportation.

3.A Gene Ontology (GO) enrichment analysis of the early light-responsive genes identified 19 significantly enriched GO terms. Most of them were related to photosynthesis and light response.To obtain more detailed information, a pathway analysis was carried out using MapMan.

* Bai S , Sun Y , Qian M , et al. Transcriptome analysis of bagging-treated red Chinese sand pear peels reveals light-responsive pathway functions in anthocyanin accumulation[J]. Scientific Reports.10.1038/s41598-017-00069-z