Single Cell Transcriptomics

Product Catalog

Contents

1 Why Smart-Seq2 Single Cell Full Transcriptomics?

Single Cell Transcriptome Sequencing uses Smart-Seq2 single cell full-length transcriptome amplification and high throughput DNBSEQ sequencing for full transcriptome analysis at cellular level. This powerful approach enables increased biological insight into areas not possible with traditional bulk transcriptome sequencing, for example the analysis of scarce cells, highly heterogenous inner tissue cells in early embryo development, stem cells, immune system research and single cell profiling of tumor heterogeneity.

2 Our Service

We do not provide mouth-pipetting single cell isolation services, however we do provide you with lysis buffer formulation. Simply select the cell of your choice and put it in the lysis buffer, then ship your sample to our laboratory with dry ice. We will perform Smart-Seq2 amplification, and if the sample is amplified successfully, we then proceed to sequencing using the DNBSEQ sequencing platform with a PE100 sequencing strategy. Bioinformatics analysis services can be provided. (See Fig 1). Typical 28 working days from sample QC acceptance to filtered raw data availability. Expedited services are available. Contact our specialist for details.

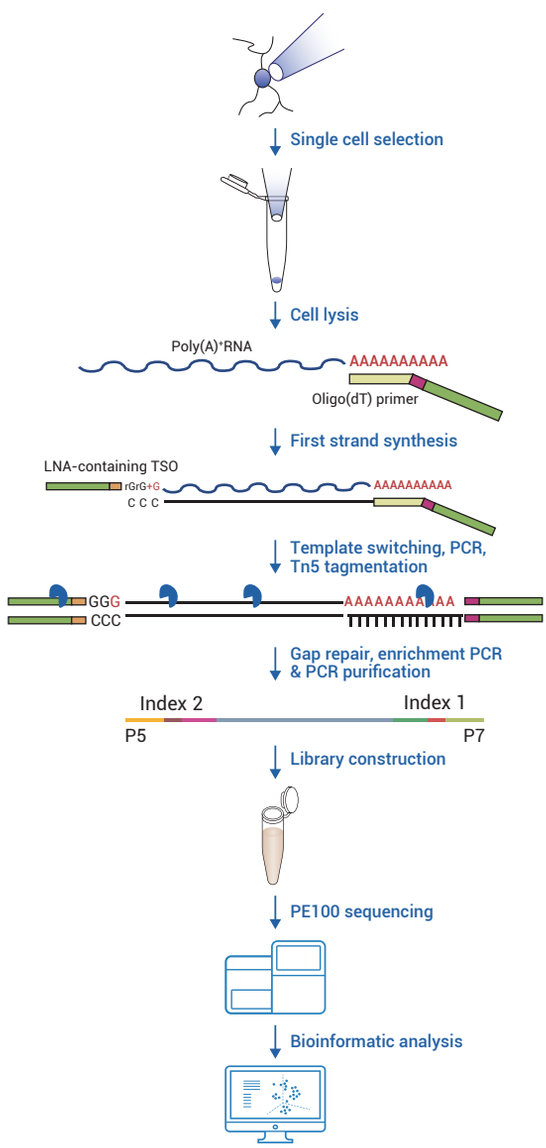

Fig 1. Service Workflow

3 Bioinformatics Workflow

Customers can choose two kinds of bioinformatics analysis service: standardized analysis delivered by Dr. Tom system or customized bioinformatics analysis performed according to customers' needs. (See Fig 2-5)

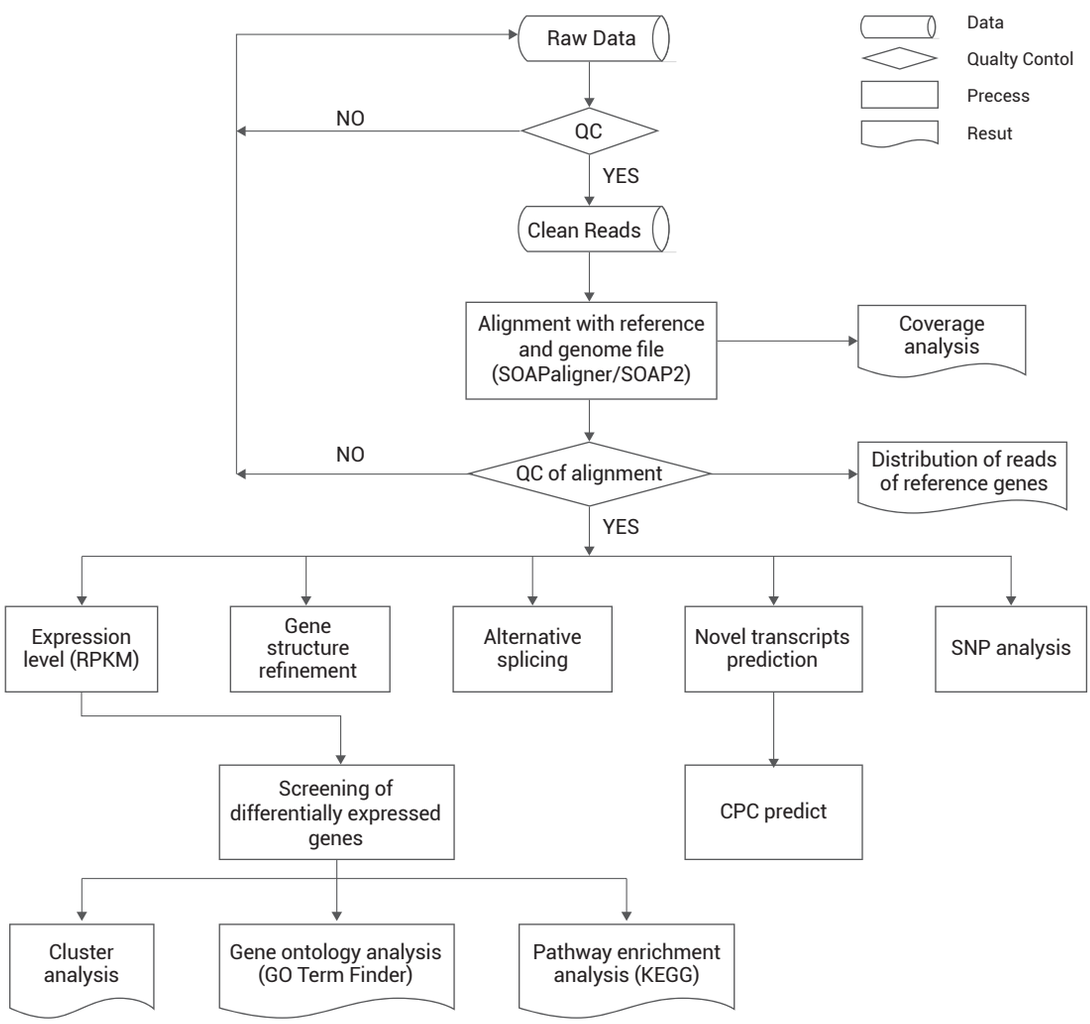

Fig 2. Bioinformatics Workflow

Bioinformatics Analysis	Bioinformatics Analysis Contents
Standard Bioinformatics Analysis	1, Data filtering includes removing adaptors contamination – low quality reads from raw reads. 2, Assessment of sequencing (Alignment statistics, Randomness assessment of sequencing, distribution of reads on the reference genome) 3, Gene expression and annotation (Gene coverage and coverage depth) 4, Gene expression difference analysis 5, Expression pattern analysis of DEGs 6, Gene ontology analysis of DEGs 7, Pathway enrichment analysis of DEGs 8, Refinement of gene structures 9, Identification of alternative spliced transcripts 10, Prediction and annotation of novel transcripts 11, SNP analysis
Advanced Bioinformatics Analysis	12, Gene fusion analysis (only for human) 13, Principal component analysis (PCA) 14, Condition - specific expressed analysis
Customized Bioinformatics Analysis	Customized according to client's needs

Fig 3. Heatmap by Dr. Tom

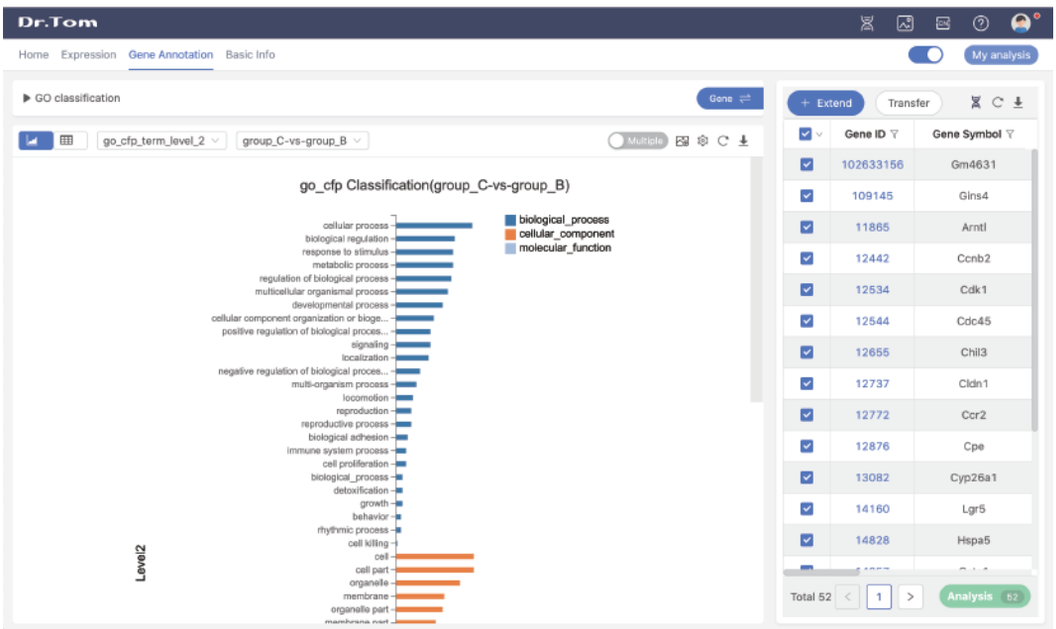

Fig 4. DEGs GO Annotation by Dr. Tom

Fig 5. KEGG Pathway Enrichment by Dr. Tom

4 Sample Requirements

You can choose from two types of service: 'Single Cell Service' or 'Few Cell Service'.

For single cell service, you can send samples in 1 or 2 cells per tube with a cell diameter greater than 10 μm, such as oocyte, single cell isolated from morula or cell lines.

For few cells service, you can send in sample with a few cells per tube, such as morula or blastocyst.

For specific requirement and guideline, please refer to our sample preparation guideline.

Sample	Transcriptome
Single cell	1-2 cells (4 μL lysis buffer)
Few cells	2≤X≤200 (4 μL lysis buffer)
Total RNA	Total RNA>2 ng; RNA 28S/18S≥1, RIN≥7; concentration>50 pg/μL

5 Case Study

SMART RNA SEQUENCING REVEALS THE TOXICOLOGICAL EFFECTS OF DIISOBUTYL PHTHALATE (DIBP) IN PORCINE OOCYTES.

SUN, X., ET AL., (2024). ***ENVIRONSCITECHNOL.***

DiBP impaires the maturation and fertilization ability of porcine oocytes, through cytoplasmic fragmentation, disordered spindle and actin cytoskeleton dynamics, dysregulated endoplasmic reticulum distribution, and partial extravasation of cortical granules and phosphatidylcholine.

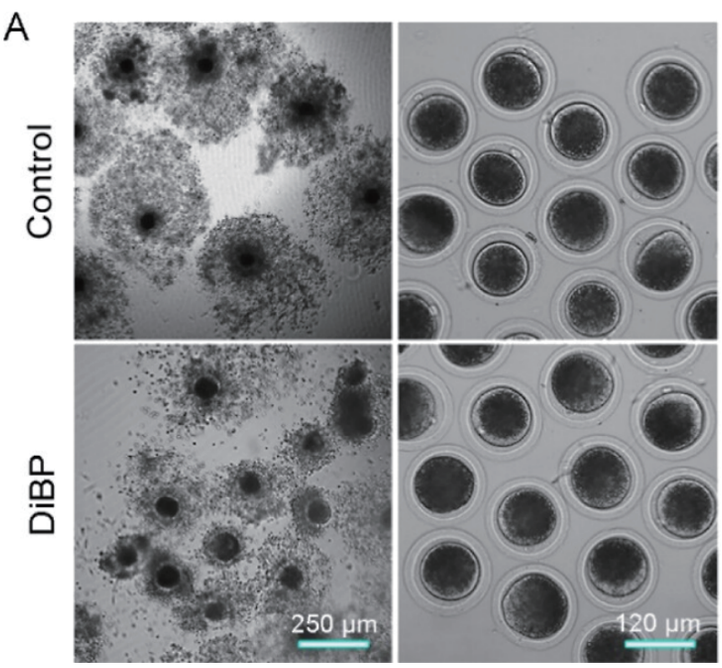

Fig 6A Diisobutyl phthalate (DiBP) causes abnormal meiotic progression in porcine oocytes.

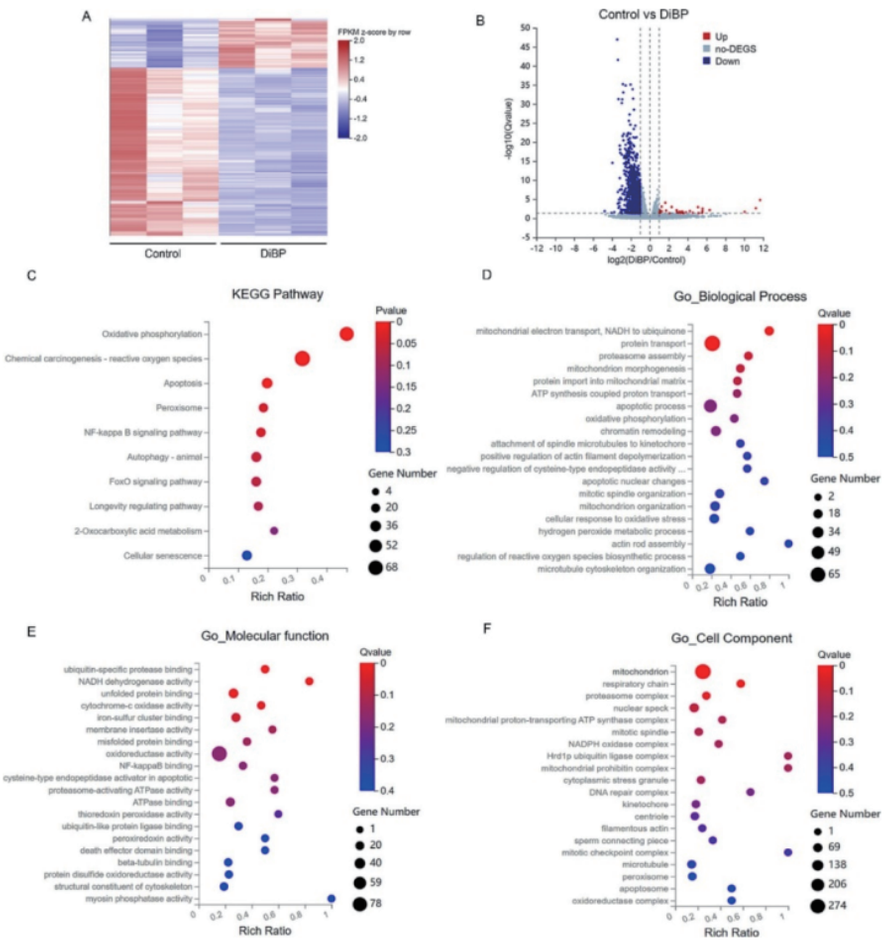

Fig 6B DiBP causes oxidative stress in oocytes by damaging mitochondrial function.

KEGG analysis of indicated that genes enriched in oxidative metabolism, apoptosis, and autophagy pathway were abnormally expressed in DiBP-exposed oocytes. GO analysis of DEGs were all focused on mitochondrial function, oxidative metabolism, and meiosis development (Fig 6B). These results suggest that DiBP is likely to cause oxidative stress in oocytes by damaging mitochondrial function and ultimately leading to the disruption of oocyte meiotic development.

Request for Information or Quotation

Contact a BGI Genomics representative to discuss how we can meet your specific needs or for expert advice on experiment design, from sample to bioinformatics.

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